FASTR Documentation

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Contents

FASTR is a framework that helps creating workflows of different tools. The workflows created in FASTR are automatically enhanced with flexible data input/output, execution options (local, cluster, etc) and solid provenance.

We chose to create tools by creating wrappers around executables and connecting everything with Python.

Fastr is open-source (licensed under the Apache 2.0 license) and hosted on bitbucket at https://bitbucket.org/bigr_erasmusmc/fastr

For support, go to https://groups.google.com/d/forum/fastr-users

To get yourself a copy:

```
hg clone https://bitbucket.org/bigr_erasmusmc/fastr
```

or if you have a ssh key pair:

```
hg clone ssh://hg@bitbucket.org/bigr_erasmusmc/fastr
```

The official documentation can be found at fastr.readthedocs.io

The Fastr workflow system is presented in the following article:

> Hakim Achterberg, Marcel Koek, and Wiro Niessen. "Fastr: a workflow engine for advanced data flows in medical image analysis." Frontiers in ICT 3 (2016): 15.

CHAPTER 1

FASTR Documentation

Introduction

Fastr is a system for creating workflows for automated processing of large scale data. A processing workflow might also be called a processing pipeline, however we feel that a pipeline suggests a linear flow of data. Fastr is designed to handle complex flows of data, so we prefer to use the term network. We see the workflow a network of processing tool, through which the data will flow.

The original authors worked in a medical image analysis group at Erasmus MC. There they often had to run analysis that used multiple programs written in different languages. Every time a experiment was set up, the programs had to be glued together by scripts (often in bash or python).

At some point the authors got fed up by doing these things again and again, and so decided to create a flexible, powerful scripting base to create these scripts easily. The idea evolved to a framework in which the building blocks could be defined in XML and the networks could be constructed in very simple scripts (similar to creating a GUI).

Philosophy

Researchers spend a lot of time processing data. In image analysis this often includes using multiple tools in succession and feeding the output of one tool to the next. A significant amount of time is spent either executing these tools by hand or writing scripts to automate this process. This process is time consuming and error-prone. Considering all these tasks are very similar, we want to write one elaborate framework that makes it easy to create pipelines, reduces the risk of errors, generates extensive logs, and guarantees reproducibility.

The Fastr framework is applicable to multiple levels of usage: from a single researcher who wants to design a processing pipeline and needs to get reproducible results for publishing; to applying a consolidated image processing pipeline to a large population imaging study. On all levels of application the pipeline provenance and managed execution of the pipeline enables you to get reliable results.

System overview

There are a few key requirements for the design of the system:

- Any tool that your computer can run using the command line (without user interaction) should be usable by the system without modifying the tool.
- The creation of a workflow should be simple, conceptual and require no real programming.

- Networks, once created, should be usable by anyone like a simple program. All processing should be done automatically.
- All processing of the network should be logged extensively, allowing for complete reproducibility of the system (guaranteeing data provenance).

Using these requirements we define a few key elements in our system:

- A `fastr.Tool` is a definition of any program that can be used as part of a pipeline (e.g. a segmentation tool)
- A *`fastr.Node`* is a single operational step in the workflow. This represents the execution of a `fastr.Tool`.
- A *`fastr.Link`* indicates how the data flows between nodes.
- A *`fastr.Network`* is an object containing a collection of *`fastr.Node`* and *`fastr.Link`* that form a workflow.

With these building blocks the creation of a pipeline will boil down to just specifying the steps in the pipeline and the flow of the data between them. For example a simple neuro-imaging pipeline could like like:

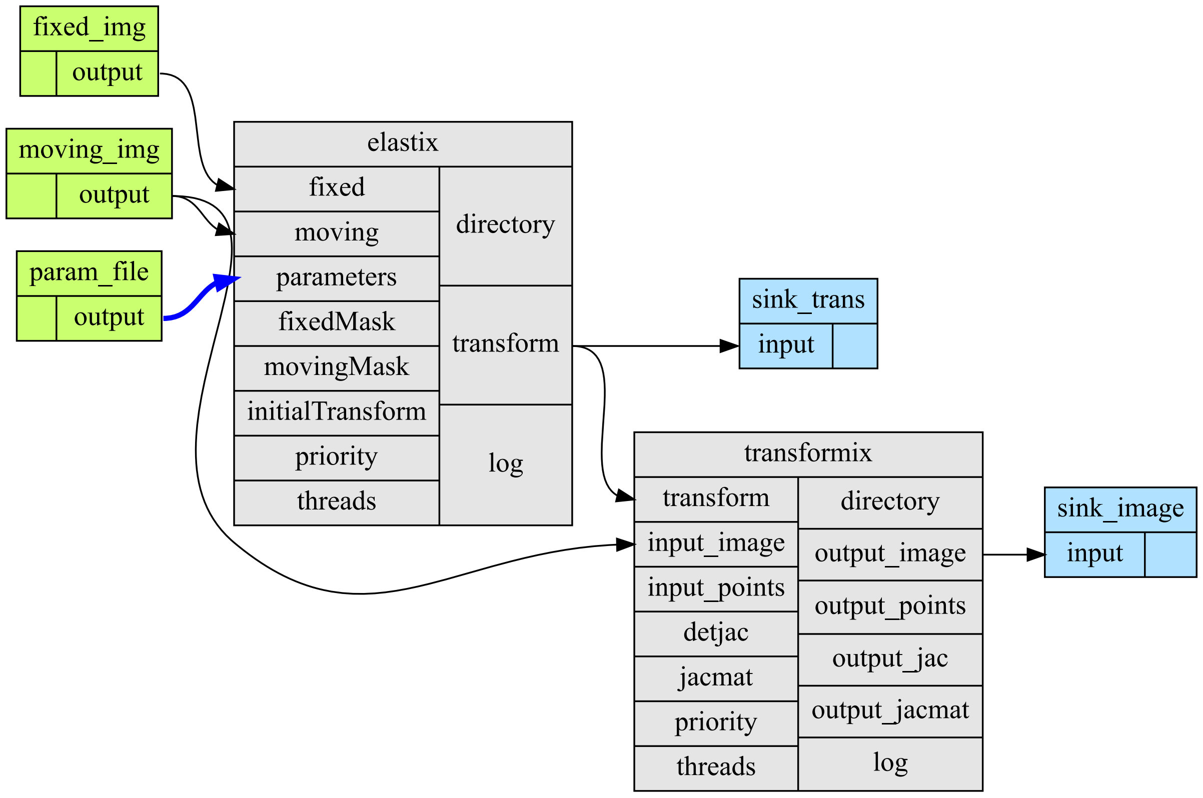


Fig. 1.1: A simple workflow that registers two images and uses the resulting transform to resample the moving image.

In Fastr this translates to:

- Create a *`fastr.Network`* for your pipeline
- Create a *`fastr.SourceNode`* for the fixed image
- Create a *`fastr.SourceNode`* for the moving image
- Create a *`fastr.SourceNode`* for the registration parameters
- Create a *`fastr.Node`* for the registration (in this case elastix)
- Create a *`fastr.Node`* for the resampling of the image (in this case transformix)

- Create a *fastr.SinkNode* for the transformations to save
- Create a *fastr.SinkNode* for the transformed images to save
- *fastr.Link* the output of fixed image source node to the fixed image input of the registration node
- *fastr.Link* the output of moving image source node to the moving image input of the registration node
- *fastr.Link* the output of registration parameters source node to the registration parameters input of the registration node
- *fastr.Link* the output transform of the registration node to the transform input of the resampling
- *fastr.Link* the output transform of the registration node to the input of transformation SinkNode
- *fastr.Link* the output image of the resampling node to the input of image SinkNode
- Run the *fastr.Network* for subjects X

This might seem like a lot of work for a registration, but the Fastr framework manages all other things, executes the pipeline and builds a complete paper trail of all executed operations. The execution can be on any of the supported execution environments (local, cluster, etc). The data can be imported from and exported to any of the supported data connections (file, XNAT, etc). It is also important to keep in mind that this is a simple example, but for more complex pipelines, managing the workflow with Fastr will be easier and less error-prone than writing your own scripts.

Quick start guide

This manual will show users how to install Fastr, configure Fastr, construct and run simple networks, and add tool definitions.

Installation

Installing via pip

You can simply install fastr using `pip`:

```
pip install fastr
```

Installing from source code

To install from source code, use Mercurial via the command-line:

```
hg clone https://<yourusername>@bitbucket.org/bigr_erasmusmc/fastr  # for http
hg clone ssh://hg@bitbucket.org/bigr_erasmusmc/fastr # for ssh
```

If you prefer a GUI you can try TortoiseHG (Windows, Linux and Mac OS X) or SourceTree (Windows and Mac OS X). The address of the repository is (given for both http and ssh):

```
https://<yourusername>@bitbucket.org/bigr_erasmusmc/fastr
ssh://hg@bitbucket.org/bigr_erasmusmc/fastr
```

To install to your site packages run:

```
cd fastr/
pip install .
```

This installs the scripts and packages in the default system folders. For windows this is the python `site-packages` directory for the fastr python library and `Scripts` directory for the executable scripts.

For Ubuntu this is in the `/usr/local/lib/python2.7/dist-packages/` and `/usr/local/bin/` respectively.

Note: If you want to develop fastr, you might want to use `pip install -e .` to get an editable install

Note: You might want to consider installing `fastr` in a virtualenv

Note:

- On windows `python` and the `Scripts` directory are not on the system PATH by default. You can add these by going to `System -> Advanced Options -> Environment variables`.
- On mac you need the Xcode Command Line Tools. These can be installed using the command `xcode-select --install`.

Configuration

Fastr has defaults for all settings so it can be run out of the box to test the examples. However, when you want to create your own Networks, use your own data or use your own Tools, it is required to edit your config file.

Fastr will search for a config file named `config.py` in the `$FASTRHOME` and `~/.fastr/` directories. If both config files contain values for a single settings, the version in `~/.fastr/` has priority.

For a sample configuration file and a complete overview of the options in `config.py` see the *Config file* section.

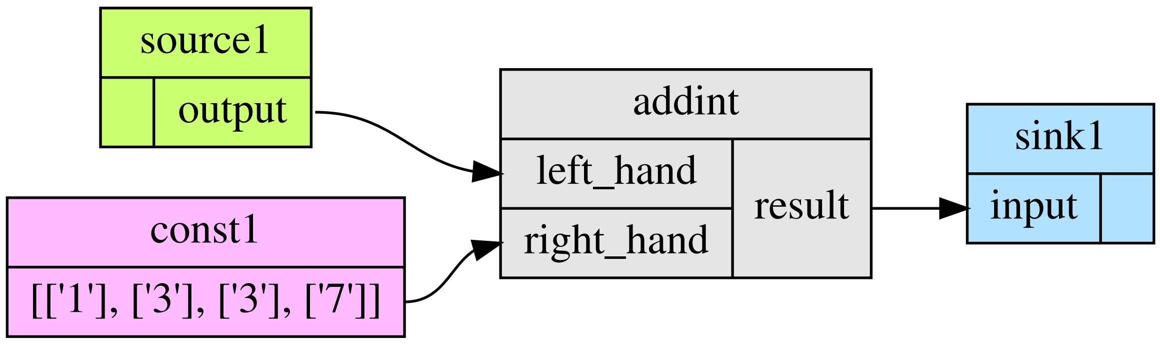
Creating a simple network

If Fastr is properly installed and configured, we can start creating networks. Creating a network is very simple:

```
>>> import fastr

>>> network = fastr.Network()
```

Now we have an empty network, the next step is to create some nodes and links. Imagine we want to create the following network:



Creating nodes

We will create the nodes and add them to the network. The easiest way to do this is via the network `create_` methods. Let's create two source nodes, one normal node and one sink:

```
>>> source1 = network.create_source('Int', id_='source1')
>>> constant1 = network.create_constant('Int', [1, 3, 3, 7], id_='const1')
>>> sink1 = network.create_sink('Int', id_='sink1')
>>> addint = network.create_node('AddInt', id_='addint')
```

The functions *Network.create_source*, *Network.create_constant*, *Network.create_source* and *Network.create_source* are shortcut functions for calling the *SourceNode*, *ConstantNode*, *SinkNode* and *Node* constructors and adding them to the network. A *SourceNode* and *SinkNode* only require the datatype to be specified. A *ConstantNode* requires both the datatype and the data to be set on creation. A *Node* requires a *Tool* template to be instantiated from. The `id_` option is optional for all three, but makes it easier to identify the nodes and read the logs.

There is an easier way to add a constant to an input, by using a shortcut method. If you assign a `list` or `tuple` to an item in the input list, it will automatically create a *ConstantNode* and a *Link* between the contant and the input:

```
>>> addint.inputs['right_hand'] = [1, 3, 3, 7]
```

The created constant would have the id `addint__right_hand__const` as it automatically names the new constant `$nodeid__$inputid__const`.

In an interactive python session we can simply look at the basic layout of the node using the `repr` function. Just type the name of the variable holding the node and it will print a human readable representation:

```
>>> source1
SourceNode source1 (tool: source v1.0)
      Inputs          |       Outputs
-------------------------------------------
                      |  output    (Int)
>>> addint
Node addint (tool: AddInt v1.0)
       Inputs           |       Outputs
---------------------------------------------
left_hand  (Int)        |  result    (Int)
right_hand (Int)        |
```

This tool has inputs of type Int, so the sources and sinks need to have a matching datatype.

The tools and datatypes available are stored in *fastr.toollist* and *fastr.typelist*. These variables are created when `fastr` is imported for the first time. They contain all the datatype and tools specified by the xml files in the search paths. To get an overview of the tools and datatypes loaded by fastr:

```
>>> fastr.toollist
ToolManager
Add                             v0.1           :  /home/hachterberg/dev/fastr-
↪develop/fastr/fastr/resources/tools/add/v1_0/add.xml
AddImages                       v0.1           :  /home/hachterberg/dev/fastr-
↪develop/fastr/fastr/resources/tools/addimages/v1_0/addimages.xml
AddInt                          v0.1           :  /home/hachterberg/dev/fastr-
↪develop/fastr/fastr/resources/tools/addint/v1_0/addint.xml

>>> fastr.typelist
DataTypeManager
AnyType                     :  <class 'fastr.datatypes.AnyType'>
Boolean                     :  <class 'fastr.datatypes.Boolean'>
Directory                   :  <class 'fastr.datatypes.Directory'>
Float                       :  <class 'fastr.datatypes.Float'>
Int                         :  <class 'fastr.datatypes.Int'>
String                      :  <class 'fastr.datatypes.String'>
```

The `fastr.toollist` variable contains all tools that Fastr could find during initalization. Tools can be chosen in two tways:

- `toollist[id]` which returns the newest version of the tool
- `toollist[id, version]` which returns the specified version of the tool

Creating links

So now we have a network with 4 nodes defined, however there is no relation between the nodes yet. For this we have to create some links.

```
>>> link1 = network.create_link(source1.output, addint.inputs['left_hand'])
>>> link2 = network.create_link(constant1.output, addint.inputs['right_hand'])
>>> link3 = network.create_link(addint.outputs['result'], sink1.inputs['input'])
```

This asks the network to create links and immediatly store them inside the network. A link always points from an Output to an Input (note that SubOutput or SubInputs are also valid). A SourceNode has only 1 output which is fixed, so it is easy to find. However, addImage has two inputs and one output, this requires us to specify which output we need. A normal node has a mapping with Inputs and one with Outputs. They can be indexed with the approriate id's. The function returns the links, but you only need that if you are planning to change a link. If not, it is possible to use a short-hand which creates a link but gives you no easy access to it for later.

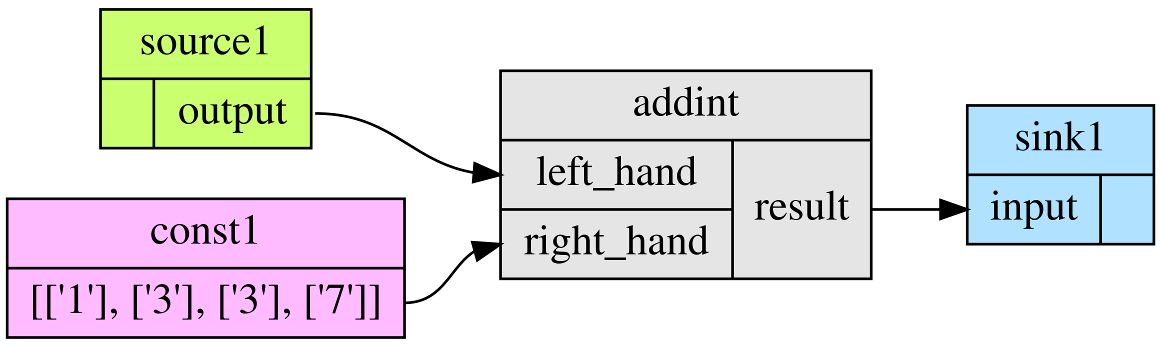
```
>>> addint.inputs['left_hand'] = source1.output
>>> addint.inputs['right_hand'] = constant1.output
>>> sink1.inputs['input'] = addint.outputs['result']
```

Create an image of the Network

For checking your Network it is very useful to have a graphical representation of the network. This can be achieved using the `Network.draw_network` method.

```
>>> network.draw_network()
'/home/username/network_layout.dot.svg'
```

This will create a figure in the path returned by the function that looks like:



Note: for this to work you need to have graphviz installed

Running a Network

Running a network locally is almost as simple as calling the `Network.execute` method:

```
>>> source_data = {'source1': {'s1': 4, 's2': 5, 's3': 6, 's4': 7}}
>>> sink_data = {'sink1': 'vfs://tmp/fastr_result_{sample_id}.txt'}
>>> network.execute(source_data, sink_data)
```

As you can see the execute method needs data for the sources and sinks. This has to be supplied in two `dict` that have keys matching every source/sink `id` in the network. Not supplying data for every source and sink will result in an error, although it is possible to pass an empty `list` to a source.

Note: The values of the source data have to be simple values or urls and values of the sink data have to be url templates. To see what url schemes are available and how they work see *IOPlugin Reference*. For the sink url templates see *`SinkNode.set_data`*

For source nodes you can supply a `list` or a `dict` with values. If you supply a `dict` the keys will be interpreted as sample ids and the values as the corresponding values. If you supply a `list`, keys will be generated in the form of `id_{N}` where N will be index of the value in the list.

Warning: As a `dict` does not have a fixed order, when a `dict` is supplied the samples are ordered by key to get a fixed order! For a `list` the original order is retained.

For the sink data, an url template has to be supplied that governs how the data is stored. The mini-lanuage (the replacement fields) are described in the *`SinkNode.set_data`* method.

To rerun a stopped/crashed pipeline check the user manual on *Continuing a Network*

User Manual

In this chapter we will discuss the parts of Fastr in more detail. We will give a more complete overview of the system and describe the more advanced features.

Tools

The *`Tools`* in Fastr are the building blocks of each workflow. A tool represents a program/script/binary that can be called by Fastr and can be seens as a template. A *`Node`* can be created based on a *`Tool`*. The Node will be one processing step in a workflow, and the tool defines what the step does.

On the import of Fastr, all available *`Tools`* will be loaded in a default *`ToolManager`* that can be accessed via `fastr.toollist`. To get an overview of the tools in the system, just print the `repr()` of the *`ToolManager`*:

```
>>> fastr.toollist
AddImages                v0.1    :  /home/hachterberg/dev/fastr/fastr/resources/
↪tools/addimages/v1_0/addimages.xml
AddInt                   v0.1    :  /home/hachterberg/dev/fastr/fastr/resources/
↪tools/addint/v1_0/addint.xml
```

As you can see it gives the tool id, version and the file from which it was loaded for each tool in the system. To view the layout of a tool, just print the `repr()` of the tool itself.

```
>>> fastr.toollist['AddInt']
Tool AddInt v0.1 (Add two integers)
       Inputs          |       Outputs
---------------------------------------------
left_hand  (Int)       |  result   (Int)
right_hand (Int)       |
```

To add a *`Tool`* to the system a file should be added to one of the path in `fastr.config.tools_path`. The structure of a tool file is described in *Tool description*

Create your own tool

There are 4 steps in creating a tool:

1. CREATE FOLDERS. We will call the tool ThrowDie. Create the folder throw_die in the folder fastr-tools. In this folder create another folder called bin.
2. PLACE EXECUTABLE IN CORRECT PLACE. In this example we will use a snippet of executable python code:

```
#!/usr/bin/env python
import sys
import random
import json

if (len(sys.argv) > 1):
    sides = int(sys.argv[1])
else:
    sides = 6
result = [int(random.randint(1, sides ))]

print('RESULT={}'.format(json.dumps(result)))
```

   Save this text in a file called `throw_die.py`

   Place the executable python script in the folder `throw_die/bin`

3. CREATE AND EDIT XML FILE FOR TOOL.

   Put the following text in file called `throw_die.xml`.

```
<tool id="ThrowDie" description="Simulates a throw of a die. Number of sides␣
↪of the die is provided by user"
      name="throw_die" version="1.0">
  <authors>
    <author name="John Doe" />
  </authors>
  <command version="1.0" >
    <authors>
      <author name="John Doe" url="http://a.b/c" />
    </authors>
    <targets>
      <target arch="*" bin="throw_die.py" interpreter="python" os="*" paths=
↪'bin/'/>
    </targets>
    <description>
       throw_die.py number_of_sides
       output = simulated die throw
    </description>
  </command>
  <interface>
    <inputs>
      <input cardinality="1" datatype="Int" description="Number of die sides"␣
↪id="die_sides" name="die sides" nospace="False" order="0" required="True"/>
     </inputs>
    <outputs>
      <output id="output" name="output value" datatype="Int" automatic="True"␣
↪cardinality="1" method="json" location="^RESULT=(.*)$" />
    </outputs>
  </interface>
</tool>
```

   Put throw_die.xml in the folder example_tool. All Attributes in the example above are required. For a complete overview of the xml Attributes that can be used to define a tool, check the *Tool description*. The most important Attributes in this xml are:

```
id      : The id is used in in FASTR to create an instance of your tool, this␣
↪name will appear in the toollist when you type fastr.toollist.
targets : This defines where the executables are located and on which platform␣
↪they are available.
inputs  : This defines the inputs that you want to be used in FASTR, how FASTR␣
↪should use them and what data is allowed to be put in there.
```

More xml examples can be found in the fastr-tools folder.

4. EDIT CONFIGURATION FILE. Append the line `[PATH TO LOCATION OF FASTR-TOOLS]/fastr-tools/throw_die/` to the `config.py` (located in ~/.fastr/ directory) to the `tools_path`. See *Config file* for more information on configuration.

   You should now have a working tool. To test that everything is ok do the following in python:

```
>>> import fastr
>>> fastr.toollist
```

Now a list of available tools should be produced, including the tool throw_die

To test the tool create the script test_throwdie.py:

```
import fastr
network = fastr.Network()
source1 = network.create_source(fastr.typelist['Int'], id_='source1')
sink1 = network.create_sink(fastr.typelist['Int'], id_='sink1')
throwdie = network.create_node(fastr.toollist['ThrowDie'], id_='throwdie')
link1 = network.create_link(source1.output, throwdie.inputs['die_sides'])
link2 = network.create_link(throwdie.outputs['output'], sink1.inputs[
↪'input'])
source_data = {'source1': {'s1': 4, 's2': 5, 's3': 6, 's4': 7}}
sink_data = {'sink1': 'vfs://tmp/fastr_result_{sample_id}.txt'}
network.draw_network()
network.execute(source_data, sink_data)
```

Call the script from commandline by

```
>>> python test_throwdie.py
```

An image of the network will be created in the current directory and result files will be put in the tmp directory. The result files are called `fastr_result_s1.txt`, `fastr_result_s2.txt`, `fastr_result_s3.txt`, and `fastr_result_s4.txt`

Note: If you have code which is operating system depend you will have to edit the xml file. The following gives and example of how the elastix tool does this:

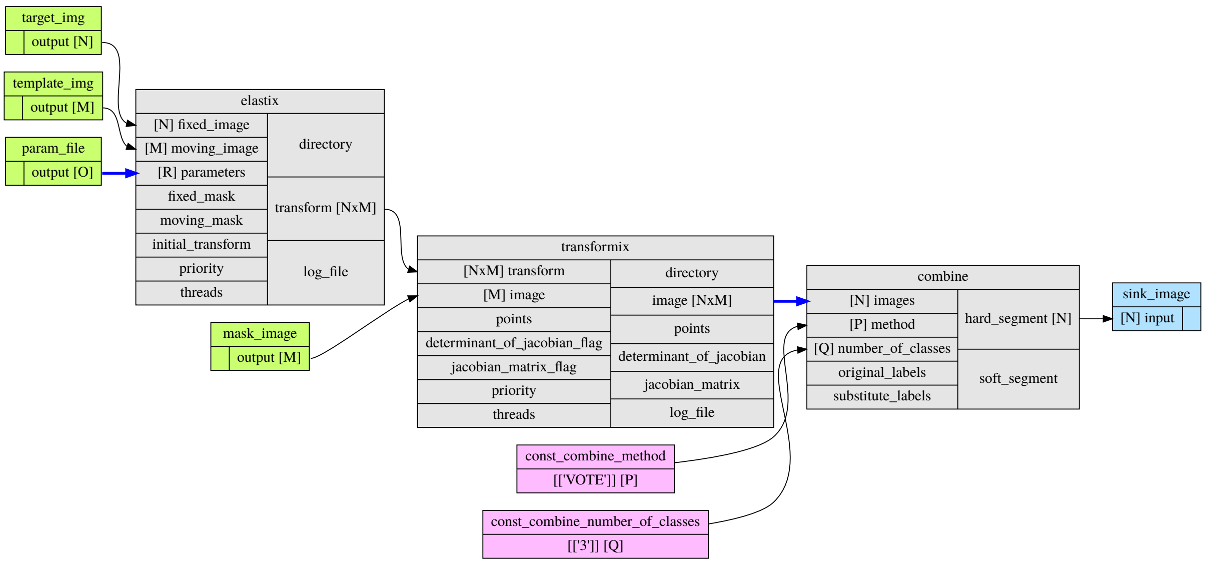
```
<targets>
      <target os="windows" arch="*" bin="elastix.exe">
        <paths>
          <path type="bin" value="vfs://apps/elastix/4.7/install/" />
          <path type="lib" value="vfs://apps/elastix/4.7/install/lib" />
        </paths>
      </target>
      <target os="linux" arch="*" modules="elastix/4.7" bin="elastix">
        <paths>
          <path type="bin" value="vfs://apps/elastix/4.7/install/" />
          <path type="lib" value="vfs://apps/elastix/4.7/install/lib" />
        </paths>
      </target>
      <target os="darwin" arch="*" modules="elastix/4.7" bin="elastix">
        <paths>
          <path type="bin" value="vfs://apps/elastix/4.7/install/" />
```

```
            <path type="lib" value="vfs://apps/elastix/4.7/install/lib" />
          </paths>
        </target>
    </targets>
```

vfs is the virtual file system path, more information can be found at VirtualFileSystem.

Network

A *Network* represented an entire workflow. It hold all *Nodes*, *Links* and other information required to execute the workflow. Networks can be visualized as a number of building blocks (the Nodes) and links between them:



An empty network is easy to create, all you need is to name it:

```
>>> network = fastr.Network(id_="network_name")
```

The *Network* is the main interface to Fastr, from it you can create all elements to create a workflow. In the following sections the different elements of a *Network* will be described in more detail.

Node

Nodes are the point in the *Network* where the processing happens. A *Node* takes the input data and executes jobs as specified by the underlying *Tool*. A *Nodes* can be created in a two different ways:

```
>>> node1 = fastr.Node(tool, id_='node1', parent=network)
>>> node2 = network.create_node(tool, id_='node2', stepid='step1')
```

In the first way, we specifically create a *Node* object. We pass it an id and the parent network. If the parent is None the fastr.curent_network will be used. The *Node* constructor will automaticaly add the new node to the parent network.

Note: For a Node, the tool can be given both as the *Tool* class or the id of the

tool.

The second way, we tell the network to create a *Node*. The network will automatically assign itself as the parent. Optionally you can add define a stepid for the node which is a logical grouping of *Nodes* that is mostly used for visualization.

A *Node* contains *Inputs* and *Outputs*. To see the layout of the *Node* one can simply look at the `repr()`.

```
>>> addint = fastr.Node(fastr.toollist['AddInt'], id_='addint')
>>> addint
Node addint (tool: AddInt v1.0)
       Inputs           |       Outputs
---------------------------------------------
left_hand  (Int)        |  result   (Int)
right_hand (Int)        |
```

The inputs and outputs are located in mappings with the same name:

```
>>> addint.inputs
InputDict([('left_hand', <Input: fastr:///networks/unnamed_network/nodelist/addint/
↪inputs/left_hand>), ('right_hand', <Input: fastr:///networks/unnamed_network/
↪nodelist/addint/inputs/right_hand>)])

>>> addint.outputs
OutputDict([('result', Output fastr:///networks/unnamed_network/nodelist/addint/
↪outputs/result)])
```

The *InputDict* and *OutputDict* are classes that behave like mappings. The *InputDict* also facilitaties the linking shorthand. By assigning an *Output* to an existing key, the *InputDict* will create a *Link* between the *InputDict* and *Output*.

SourceNode

A *SourceNode* is a special kind of node that is the start of a workflow. The *SourceNodes* are given data at run-time that fetched via *IOPlugins*. On create, only the datatype of the data that the *SourceNode* supplied needs to be known. Creating a *SourceNode* is very similar to an ordinary node:

```
>>> source1 = fastr.SourceNode('Int', id_='source1')
>>> source2 = network.create_source(fastr.typelist['Int'], id_='source2', stepid=
↪'step1')
```

In both cases, the source is automatically automaticall assigned to a network. In the first case to the `fastr.current_network` and in the second case to the `network` used to call the method. A *SourceNode* only has a single output which has a short-cut access via `source.output`.

Note: For a source or constant node, the datatype can be given both as the *BaseDataType* class or the id of the datatype.

ConstantNode

A *ConstantNode* is another special node. It is a subclass of the *SourceNode* and has a similar function. However, instead of setting the data at run-time, the data of a constant is given at creation and saved in the object. Creating a *ConstantNode* is similar as creating a source, but with supplying data:

```
>>> constant1 = fastr.ConstantNode('Int', [42], id_='constant1')
>>> constant2 = network.create_constant('Int', [42], id_='constant2', stepid='step1
↪')
```

Often, when a *ConstantNode* is created, it is created specifically for one input and will not be reused. In this case there is a shorthand to create and link a constant to an input:

```
>>> addint.inputs['value1'] = [42]
```

will create a constant node with the value 42 and create a link between the output and input `addint.value1`.

SinkNode

The *SinkNode* is the counter-part of the source node. Instead of get data into the workflow, it saves the data resulting from the workflow. For this a rule has to be given at run-time that determines where to store the data. The information about how to create such a rule is described at *SinkNode.set_data*. At creation time, only the datatype has to be specified:

```
>>> sink1 = fastr.Sink('Int', id_='sink1')
>>> sink2 = network.create_sink(fastr.typelist['Int'], id_='sink2', stepid='step1')
```

Link

Links indicate how the data flows between *Nodes*. Links can be created explicitly using on of the following:

```
>>> link = fastr.Link(node1.outputs['image'], node2.inputs['image'])
>>> link = network.create_link(node1.outputs['image'], node2.inputs['image'])
```

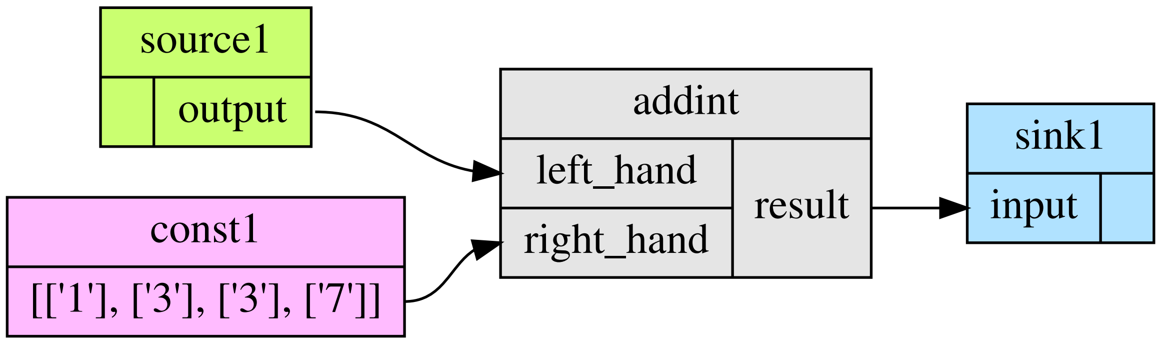
or can be create implicitly by assigning an *Output* to an *Input* in the *InputDict*.

```
# This style of assignment will create a Link similar to above
>>> node2.inputs['image'] = node1.outputs['image']
```

Note that a *Link* is also create automatically when using the short-hand for the *ConstantNode*

Data Flow

The data enters the *Network* via *SourceNodes*, flows via other *Nodes* and leaves the *Network* via *SinkNodes*. The flow between *Nodes* goes from an *Output* via a *Link* to an *Input*. In the following image it is simple to track the data from the *SourceNodes* at the left to the *SinkNodes* at right side:



Note that the data in Fastr is stored in the *Output* and the *Link* and *Input* just give access to it (possible while transforming the data).

Data flow inside a Node

In a *Node* all data from the *Inputs* will be combined and the jobs will be generated. There are strict rules to how this combination is performed. In the default case all inputs will be used pair-wise, and if there is only a single value for an input, it it will be considered as a constant.

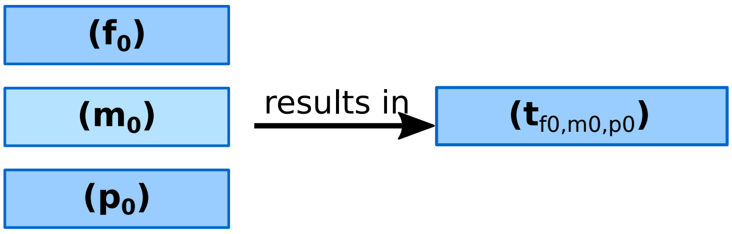
To illustrate this we will consider the following *Tool* (note this is a simplified version of the real tool):

```
>>> fastr.toollist['Elastix']
Tool Elastix v4.8 (Elastix Registration)
                          Inputs                              |              Outputs
---------------------------------------------------------------------------------------
↪-----------
```

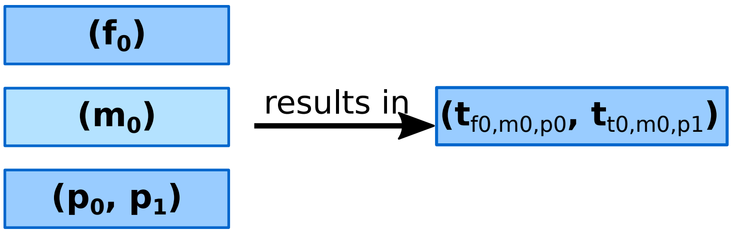
```
fixed_image        (ITKImageFile)                              |  transform␣
↪(ElastixTransformFile)
moving_image       (ITKImageFile)                              |
parameters         (ElastixParameterFile)                      |
```

Also it is important to know that for this tool (by definition) the cardinality of the `transform` *`Output`* will match the cardinality of the `parameters` *`Inputs`*

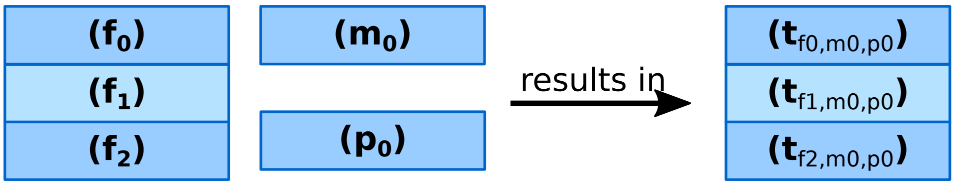
If we supply a *`Node`* based on this *`Tool`* with a single sample on each *`Input`*, there will be one single matching *`Output`* sample created:



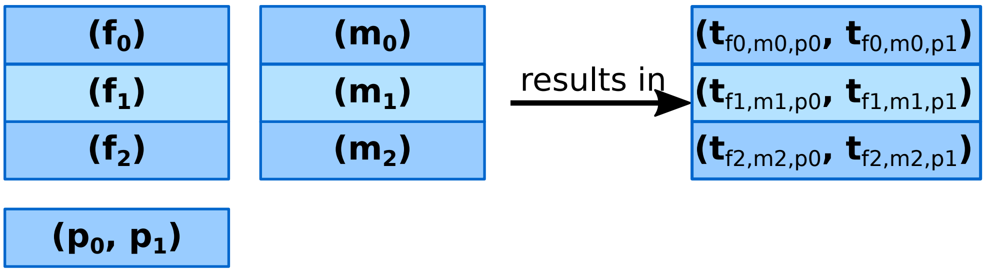
If the cardinality of the `parameters` sample would be increased to 2, the resulting `transform` sample would also become 2:



Now if the number of samples on `fixed_image` would be increased to 3, the `moving_image` and `parameters` will be considered constant and be repeated, resulting in 3 `transform` samples.



Then if the amount of samples for `moving_image` is also increased to 3, the `moving_image` and `fixed_image` will be used pairwise and the `parameters` will be constant.

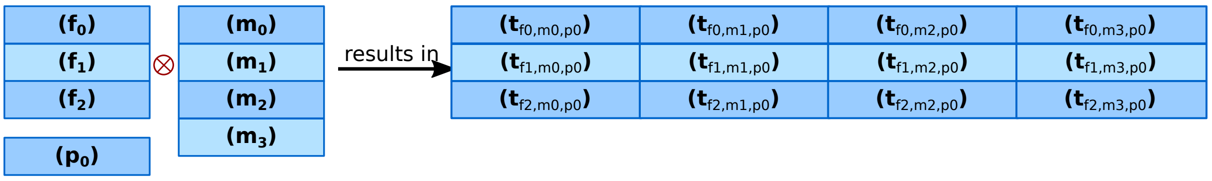

(f_0)
(f_1)
(f_2)
(m_0)
(m_1)
(m_2)
(p_0, p_1)
results in
$(t_{f0,m0,p0}, t_{f0,m0,p1})$
$(t_{f1,m1,p0}, t_{f1,m1,p1})$
$(t_{f2,m2,p0}, t_{f2,m2,p1})$

Advanced flows in a Node

Sometimes the default pairwise behaviour is not desirable. For example if you want to test all combinations of certain input samples. To achieve this we can change the *`input_group`* of *`Inputs`* to set them apart from the rest. By default all *`Inputs`* are assigned to the `default` input group. Now let us change that:

```
>>> node = network.create_node('Elastix', id_='elastix')
>>> node.inputs['moving_image'].input_group = 'moving'
```

This will result in `moving_image` to be put in a different input group. Now if we would supply `fixed_image` with 3 samples and `moving_image` with 4 samples, instead of an error we would get the following result:

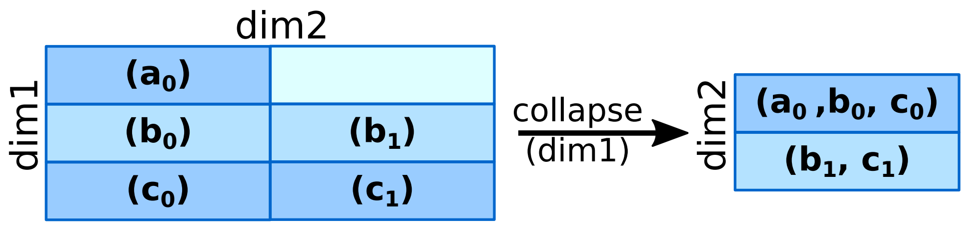

(f0)
(f1)
(f2)
(p0)
⊗
(m0)
(m1)
(m2)
(m3)
results in
(tf0,m0,p0) (tf0,m1,p0) (tf0,m2,p0) (tf0,m3,p0)
(tf1,m0,p0) (tf1,m1,p0) (tf1,m2,p0) (tf1,m3,p0)
(tf2,m0,p0) (tf2,m1,p0) (tf2,m2,p0) (tf2,m3,p0)

Warning: TODO: Expand this section with the merging dimensions

Data flows in a Link

As mentioned before the data flows from an *Output* to an *Input* throuhg a *Link*. By default the *Link* passed the data as is, however there are two special directives that change the shape of the data:

1. Collapsing flow, this collapses certain dimensions from the sample array into the cardinality. As a user you have to specify the dimension or tuple of dimensions you want to collapse.

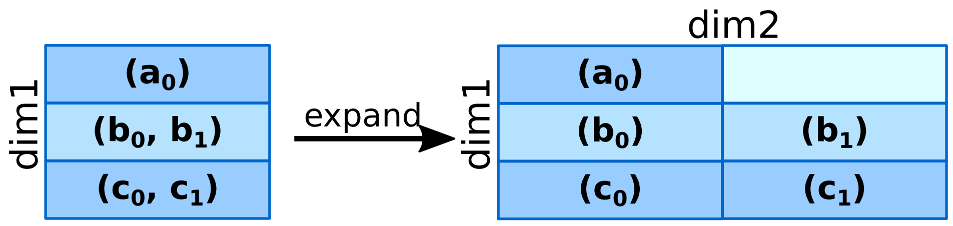


   This is useful in situation where you want to use a tool that aggregates over a number of samples (e.g. take a mean or sum).

   To achieve this you can set the *collapse* property of the *Link* as follows:

```
>>> link.collapse = 'dim1'
>>> link.collapse = ('dim1', 'dim2')  # In case you want to collapse multiple␣
↪dimensions
```

2. Expanding flow, this turns the cardinality into a new dimension. The new dimension will be named after the *Output* from which the link originates. It will be in the form of `{nodeid}__{outputid}`

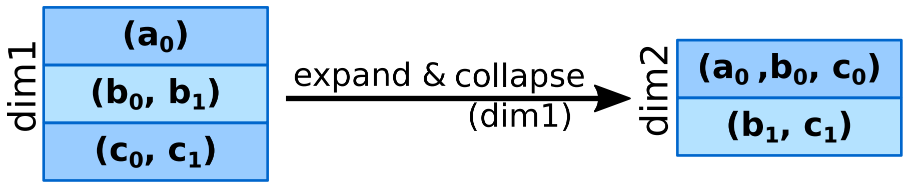


   This flow directive is useful if you want to split a large sample in multiple smaller samples. This could be because processing the whole sample is not feasible because of resource constraints. An example would be splitting a 3D image into slices to process separately to avoid high memory use or to achieve parallelism.

   To achieve this you can set the *expand* property of the *Link* to `True`:

```
>>> link.expand = True
```

Note: both collapsing and expanding can be used on the same link, it will executes similar to a expand-collapse sequence, but the newly created expand dimension is ignored in the collapse.



```
>>> link.collapse = 'dim1'
>>> link.expand = True
```

Data flows in an Input

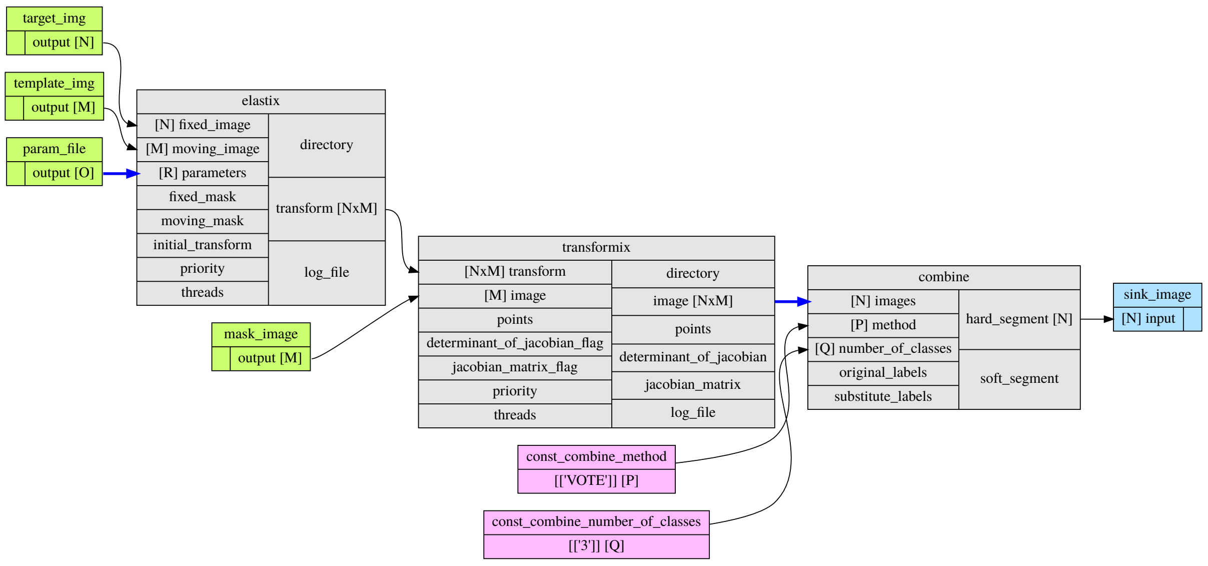
If an `Inputs` has multiple `Links` attached to it, the data will be combined by concatenating the values for each corresponding sample in the cardinality.

Broadcasting (matching data of different dimensions)

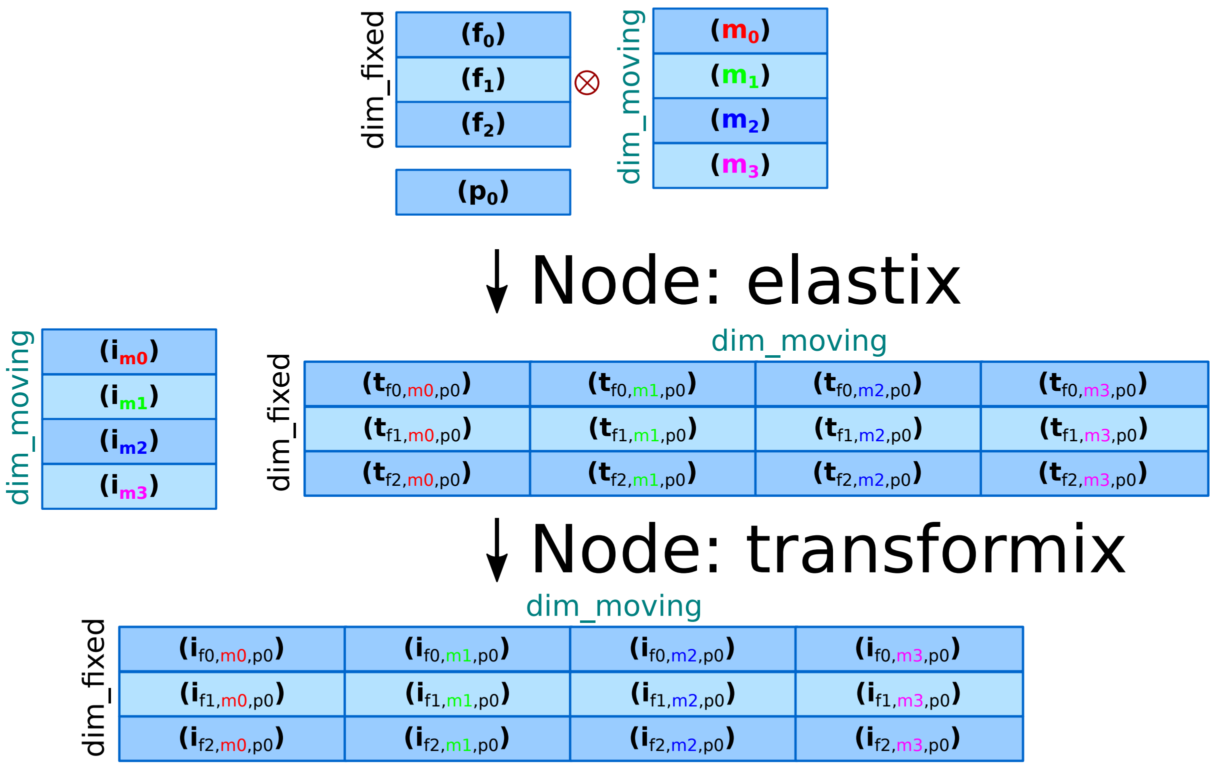
Sometimes you might want to combine data that does not have the same number of dimensions. As long as all dimensions of the lower dimensional datasets match a dimension in the higher dimensional dataset, this can be achieved using *broadcasting*. The term *broadcasting* is borrowed from NumPy and described as:

> "The term broadcasting describes how numpy treats arrays with different shapes during arithmetic operations. Subject to certain constraints, the smaller array is "broadcast" across the larger array so that they have compatible shapes."
>
> —NumPy manual on broadcasting

In fastr it works similar, but to combined different Inputs in an InputGroup. To illustrate broadcasting it is best to use an example, the following network uses broadcasting in the `transformix` Node:



As you can see this visualization prints the dimensions for each Input and Output (e.g. the `elastix.fixed_image` Input has dimensions `[N]`). To explain what happens in more detail, we present an image illustrating the details for the samples in `elastix` and `transformix`:


dim_fixed
(f_0)
(f_1)
(f_2)
$\otimes$
dim_moving
(m_0)
(m_1)
(m_2)
(m_3)
(p_0)
Node: elastix
dim_moving
(i_{m0})
(i_{m1})
(i_{m2})
(i_{m3})
dim_fixed
dim_moving
$(t_{f0,m0,p0})$ $(t_{f0,m1,p0})$ $(t_{f0,m2,p0})$ $(t_{f0,m3,p0})$
$(t_{f1,m0,p0})$ $(t_{f1,m1,p0})$ $(t_{f1,m2,p0})$ $(t_{f1,m3,p0})$
$(t_{f2,m0,p0})$ $(t_{f2,m1,p0})$ $(t_{f2,m2,p0})$ $(t_{f2,m3,p0})$
Node: transformix
dim_moving
dim_fixed
$(i_{f0,m0,p0})$ $(i_{f0,m1,p0})$ $(i_{f0,m2,p0})$ $(i_{f0,m3,p0})$
$(i_{f1,m0,p0})$ $(i_{f1,m1,p0})$ $(i_{f1,m2,p0})$ $(i_{f1,m3,p0})$
$(i_{f2,m0,p0})$ $(i_{f2,m1,p0})$ $(i_{f2,m2,p0})$ $(i_{f2,m3,p0})$

In the figure the `moving_image` (and references to it) are identified with different colors, so they are easy to track across the different steps.

At the top the Inputs for the `elastix` Node are illustrated. Because the input groups a set differently, output samples are generated for all combinations of `fixed_image` and `moving_image` (see *Advanced flows in a Node* for details).

In the `transformix` Node, we want to combine a list of samples that is related to the `moving_image` (it has the same dimension name and sizes) with the resulting `transform` samples from the `elastix` Node. As you can see the sizes of the sample collections do not match (`[N]` vs `[N x M]`). This is where *broadcasting* comes into play, it allows the system to match these related sample collections. Because all the dimensions in `[N]` are known in `[N x M]`, it is possible to match them uniquely. This is done automatically and the result is a new `[N xM]` sample collection. To create a matching sample collections, the samples in the `transformix.image` Input are reused as indicated by the colors.

Warning: Note that this might fail when there are data-blocks with non-unique dimension names, as it will be not be clear which of the dimensions with identical names should be matched!

DataTypes

In Fastr all data is contained in object of a specific type. The types in Fastr are represented by classes that subclass `BaseDataType`. There are a few different other classes under `BaseDataType` that are each a base class for a family of types:

- `DataType` – The base class for all types that hold data
  - `ValueType` – The base class for types that contain simple data (e.g. Int, String) that can be represented as a str
  - `EnumType` – The base class for all types that are a choice from a `set` of options
  - `URLType` – The base class for all types that have their data stored in files (which are referenced by URL)
- `TypeGroup` – The base class for all types that actually represent a group of types

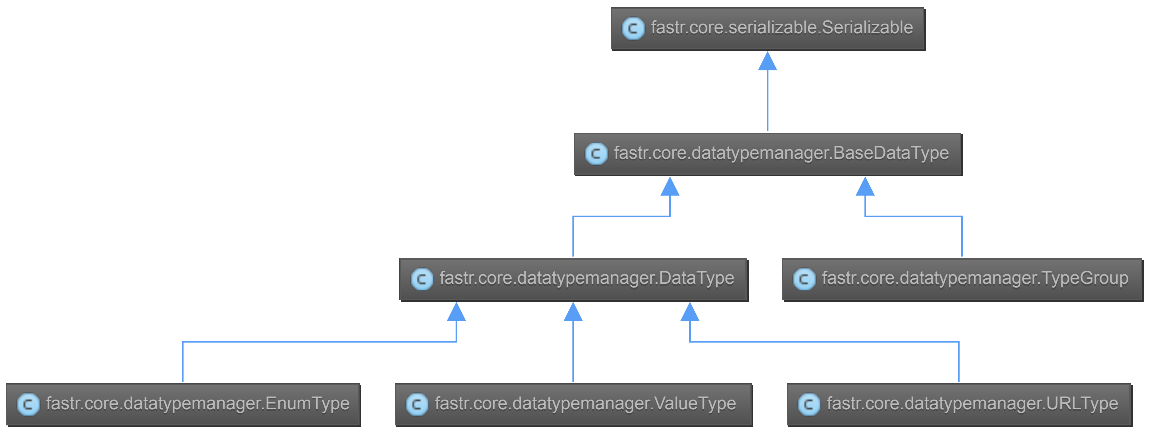

fastr.core.serializable.Serializable
fastr.core.datatypemanager.BaseDataType
fastr.core.datatypemanager.DataType
fastr.core.datatypemanager.TypeGroup
fastr.core.datatypemanager.EnumType
fastr.core.datatypemanager.ValueType
fastr.core.datatypemanager.URLType

Fig. 1.2: The relation between the different DataType classes

The types are defined in xml files and created by the `DataTypeManager`. The `DataTypeManager` acts as a container containing all Fastr types. It is automatically instantiated as `fastr.typelist`. In fastr the created DataTypes classes are also automatically place in the `fastr.datatypes` module once created.

Resolving Datatypes

`Outputs` in fastr can have a `TypeGroup` or a number of `DataTypes` associated with them. The final `DataType` used will depend on the linked `Inputs`. The `DataType` resolving works as a two-step procedure.

1. All possible `DataTypes` are determined and considered as *options*.
2. The best possible `DataType` from *options* is selected for non-automatic Outputs

The *options* are defined as the intersection of the set of possible values for the `Output` and each separate `Input` connected to the `Output`. Given the resulting *options* there are three scenarios:

- If there are no valid `DataTypes` (*options* is empty) the result will be None.
- If there is a single valid `DataType`, then this is automatically the result (even if it is not a preferred `DataType`).
- If there are multiple valid `DataTypes`, then the preferred `DataTypes` are used to resolve conflicts.

There are a number of places where the preferred `DataTypes` can be set, these are used in the order as given:

1. The *preferred* keyword argument to `match_types`
2. The preferred types specified in the *fastr.config*

Execution

Executing a Network is very simple:

```
>>> source_data = {'source_id1': ['val1', 'val2'],
                   'source_id2': {'id3': 'val3', 'id4': 'val4'}}
>>> sink_data = {'sink_id1': 'vfs://some_output_location/{sample_id}/file.txt'}
>>> network.execute(source_data, sink_data)
```

The `Network.execute` method takes a `dict` of source data and a `dict` sink data as arguments. The dictionaries should have a key for each `SourceNode` or `SinkNode`.

TODO: add `.. figure:: images/execution_layers.*`

The execution of a Network uses a layered model:

- *Network.execute* will analyze the Network and call all Nodes.
- *Node.execute* will create jobs and fill their payload
- *execute_job* will execute the job on the execute machine and resolve any deferred values (`val://` urls).
- *Tool.execute* will find the correct target and call the interface and if required resolve `vfs://` urls
- *Interface.execute* will actually run the required command(s)

The *ExecutionPlugin* will call call the *executionscript.py* for each job, passing the job as a gzipped pickle file. The *executionscript.py* will resolve deferred values and then call *Tool.execute* which analyses the required target and executes the underlying *Interface*. The Interface actually executes the job and collect the results. The result is returned (via the Tool) to the *executionscript.py*. There we save the result, provenance and profiling in a new gzipped pickle file. The execution system will use a callback to load the data back into the Network.

The selection and settings of the *ExecutionPlugin* are defined in the *fastr config*.

Continuing a Network

Normally a random temporary directory is created for each run. To continue a previously stopped/crashed network, you should call the *Network.execute* method using the same temporary directory(tmp dir). You can set the temporary directory to a fixed value using the following code:

```
>>> tmpdir = '/tmp/example_network_rerun'
>>> network.execute(source_data, sink_data, tmpdir=tmpdir)
```

Warning: Be aware that at this moment, Fastr will rerun only the jobs where not all output files are present or if the job/tool parameters have been changed. It will not rerun if the input data of the node has changed or the actual tools have been adjusted. In these cases you should remove the output files of these nodes, to force a rerun.

IOPlugins

Sources and sink are used to get data in and out of a *Network* during execution. To make the data retrieval and storage easier, a plugin system was created that selects different plugins based on the URL scheme used. So for example, a url starting with `vfs://` will be handles by the `VirtualFileSystem plugin`. A list of all the *IOPlugins* known by the system and their use can be found at *IOPlugin Reference*.

Naming Convention

For the naming convention of the tools we tried to stay close to the Python **PEP 8** coding style. In short, we defined toolnames as classes so they should be UpperCamelCased. The inputs and outputs of a tool we considered as functions or method arguments, these should we named lower_case_with_underscores.

An overview of the mapping of Fastr to **PEP 8**:

Fastr construct	Python **PEP8** equivalent	Examples
Network.id	**module**	brain_tissue_segmentation
Tool.id	**class**	BrainExtractionTool, ThresholdImage
Node.id	**variable name**	brain_extraction, threshold_mask
Input/Output.id	**method**	image, number_of_classes, probability_image

Furthermore there are some small guidelines:

- No input or output in the input or output names. This is already specified when setting or getting the data.
- Add the type of the output that is named. i.e. enum, string, flag, image,
  - No File in the input/output name (Passing files around is what Fastr was developed for).
  - No type necessary where type is implied i.e. lower_threshold, number_of_levels, max_threads.
- Where possible/useful use the fullname instead of an abbreviation.

Provenance

For every data derived data object, Fastr records the Provenance. The `SinkNode` write provenance records next to every data object it writes out. The records contain information on what operations were performed to obtain the resulting data object.

W3C Prov

The provenance is recorded using the W3C Prov Data Model (PROV-DM). Behind the scences we are using the python prov implementation.

The PROV-DM defines 3 Starting Point Classes and and their relating properties. See Fig. 1.3 for a graphic representation of the classes and the relations. *

Fig. 1.3: The three Starting Point classes and the properties that relate them. The diagrams in this document depict Entities as yellow ovals, Activities as blue rectangles, and Agents as orange pentagons. The responsibility properties are shown in pink.*[0]

Implementation

In the workflow document the provenance classes map to fastr concepts in the following way:

Agent Fastr, *Networks*, *Tools*, *Nodes*

Activity `Jobs`

Entities Data

Usage

The provenance is stored in ProvDocument objects in pickles. The convenience command line tool `fastr prov` can be used to extract the provenance in the PROV-N notation and can be serialized to PROV-JSON and PROV-XML. The provenance document can also be vizualized using the `fastr prov` command line tool.

[0] This picture and caption is taken from http://www.w3.org/TR/prov-o/ . “Copyright © 2011-2013 World Wide Web Consortium, (MIT, ERCIM, Keio, Beihang). http://www.w3.org/Consortium/Legal/2015/doc-license“

Command Line Tools

command	description
cat	Print information from a job file
execute	Execute a fastr job file
extract_argparse	Create a stub for a Tool based on a python script using argparse
prov	Get PROV information from the result pickle.
run	Run a Network from the commandline
testtool	Run the tests of a tool to verify the proper function
verify	Print information from a job file
webapp	Start the fastr webapp and open in a new browser tab

cat

```
usage: fastr cat [-h] result.pickle.gz path
```

Required Arguments

result.pickle.gz	result file to cat
path	path of the data to print

execute

Execute a job or network from commandline

```
usage: fastr execute [-h] [JOBFILE]
```

Required Arguments

JOBFILE	File of the job to execute (default ./__fastr_command__.pickle.gz)

extract_argparse

```
usage: fastr extract_argparse [-h] SCRIPT.py TOOL.xml
```

Required Arguments

SCRIPT.py	Python script to inspect
TOOL.xml	created Tool stub

prov

Get PROV information from the result pickle. When no options are given, the provenance syntax is printed to stdout in PROV-JSON format.

```
usage: fastr prov [-h] [-so SYNTAX_OUT_FILE] [-sf SYNTAX_FORMAT] [-i INDENT]
                  [-vo VISUALIZE_OUT_FILE]
                  [RESULTFILE]
```

Required Arguments

RESULTFILE	File of the job to execute (default ./__fastr_result__.pickle.gz)

Optional Arguments

-so, --syntax-out-file	Write the syntax to file.

-sf="json", --syntax-format="json" Choices are: [json], provn or xml

-i=2, --indent=2 Indent size of the serialized documents.

-vo, --visualize-out-file Visualize the provenance. The most preferred format is svg. You can specify any format pydot supports. Specify the format by postfixing the filename with an extension.

run

Execute a job or network from commandline

```
usage: fastr run [-h] NETWORKFILE
```

Required Arguments

NETWORKFILE File of the network to execute

testtool

Run the tests for a Tool to check the function

```
usage: fastr testtool [-h] TOOL
```

Required Arguments

TOOL the id of the tool to test

verify

```
usage: fastr verify [-h] TYPE path
```

Required Arguments

TYPE Type of resource to verify (e.g. tool)

Possible choices: tool

path path of the resource to verify

webapp

Fastr web client

```
usage: fastr webapp [-h] [-d] [-o]
```

Optional Arguments

-d=False, --debug=False Debug mode.

-o=False, --openpage=False Open web page after start.

Resource File Formats

This chapter describes the various files fastr uses. The function and format of the files is described allowing the user to configure fastr and add DataTypes and Tools.

Config file

Fastr reads the config files from the following locations by default (in order):

- `$FASTRHOME/config.py`
- `~/.fastr/config.py`

Reading a new config file change or override settings, making the last config file read have the highest priority. All settings have a default value, making config files and all settings within optional.

Example config file

Here is a minimal config file:

```
# Enable debugging output
debug = False

# Define the path to the tool definitions
tools_path = ['/path/to/tools',
              '/path/to/other/tools'] + tools_path
types_path = ['/path/to/datatypes',
              '/path/to/other/datatypes'] + types_path


# Specify what your preferred output types are.
preferred_types += ["NiftiImageFileCompressed",
                    "NiftiImageFile"]

# Set the tmp mount
mounts['tmp'] = '/path/to/tmpdir'
```

Format

The config file is actually a python source file. The next syntax applies to setting configuration values:

```
# Simple values
float_value = 1.0
int_value = 1
str_value = "Some value"
other_str_value = 'name'.capitalize()

# List-like values
list_value = ['over', 'ride', 'values']
other_list_value.prepend('first')
other_list_value.append('list')

# Dict-like values
dict_value = {'this': 1, 'is': 2, 'fixed': 3}
other_dict_value['added'] = 'this key'
```

Note: Dictionaries and list always have a default, so you can always append or assign elements to them and do not have to create them in a config file. Best practice is to only edit them unless you really want to block out the earliers config files.

Most operations will be assigning values, but for list and dict values a special wrapper object is used that allows manipulations from the default. This limits the operations allowed.

List values in the `config.py` have the following supported operators/methods:

- +, `__add__` and `__radd__`
- += or `__iadd__`
- `append`
- `prepend`
- `extend`

Mapping (dict-like) values in the `config.py` have the following supported operators/methods:

- `update`
- `[]` or `__getitem__`, `__setitem__` and `__delitem__`

Configuration fields

This is a table the known config fields on the system:

name	type	description	default
debug	bool	Flag to enable/disable debugging	False
examplesdir	str	Directory containing the fastr examples	$systemdir/examples
execution_plugin	str	The default execution plugin to use	'ProcessPoolExecution'
execution-script	str	Execution script location	$systemdir/execution/executionscript.py
logdir	str	Directory where the fastr logs will be placed	$userdir/logs
logtype	str	Type of logging to use	'default'
mounts	dict	A dictionary containing all mount points in the VFS system	{'tmp': '$TMPDIR', 'home': '~/', 'example_data': '$systemdir/examples/data'}
networks_path	list	Directories to scan for networks	['$userdir/networks', '$resourcedir/networks']
plugins_path	list	Directories to scan for plugins	['$userdir/plugins', '$resourcedir/plugins']
preferred_types	list	A list indicating the order of the preferred types to use. First item is most preferred.	[]
protected_modules	list	A list of modules in the environmnet modules that are protected against unloading	[]
resourcesdir	str	Directory containing the fastr system resources	$systemdir/resources
schemadir	str	Directory containing the fastr data schemas	$systemdir/schemas
systemdir	str	Fastr installation directory	'/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/l packages/fastr-1.1.2-py2.7.egg/fastr'
tools_path	list	Directories to scan for tools	['$userdir/tools', '$resourcedir/tools']
types_path	list	Directories to scan for datatypes	['$userdir/datatypes', '$resourcedir/datatypes']
userdir	str	Fastr user configuration directory	~/.fastr
warn_develop	bool	Warning users on import if this is not a production version of fastr	True
web_hostname	str	The hostname to expose the web app for	'localhost'
web_port	str	The port to expose the web app on	'5000'
web_secret_key	str	The secret key to use for the flask web app	'VERYSECRETKEY!'

`Tool` description

`Tools` are the building blocks in the fastr network. To add new *`Tools`* to fastr, XML/json files containing a *`Tool`* definition can be added. These files have the following layout:

Attribute			Description
`id`			The id of this Tool (used internally in fastr)
`name`			The name of the Tool, for human readability
`version`			The version of the Tool wrapper (not the binary)
`url`			The url of the Tool wrapper
`authors[]`			List of authors of the Tools wrapper
	`name`		Name of the author
	`email`		Email address of the author
	`url`		URL of the website of the author
`tags`	`tag[]`		List of tags describing the Tool
`command`			Description of the underlying command
	`version`		Version of the tool that is wrapped
	`url`		Website where the tools that is wrapped can be obtained
	`targets[]`		Description of the target binaries/script of this Tool
		`os`	OS targetted (windows, linux, macos or * (for any)
		`arch`	Architecture targetted 32, 64 or * (for any)
		`module`	Environment module giving access to the Tool
		`location`	If the module is not found, try using this location to find the Tool
		`interpreter`	Interpreter to use to call the `bin` with (e.g. bash, python, Rscript)
		`bin`	Name of the Tool binary (e.g. toolname, toolname.exe, toolname.py
	`description`		Description of the Tool
	`license`		License of the Tool, either full license or a clear name (e.g. LGPL, GPL v2)
	`authors[]`		List of authors of the Tool (not the wrapper!)
		`name`	Name of the authors
		`email`	Email address of the author
		`url`	URL of the website of the author
`inputs[]`			List of Inputs that can are accepted by the Tool
	`id`		ID of the Input
	`name`		Longer name of the Input (more human readable)
	`datatype`		The ID of the DataType of the Input[1]
	`enum[]`		List of possible values for an EnumType (created on the fly by fastr)[1]
	`prefix`		Commandline prefix of the Input (e.g. –in, -i)
	`cardinality`		Cardinality of the Input
	`repeat_prefix`		Flag indicating if for every value of the Input the prefix is repeated
	`required`		Flag indicating if the input is required
	`nospace`		Flag indicating if there is no space between prefix and value (e.g. –in=val)
	`format`		For DataTypes that have multiple representations, indicate which one to use
	`default`		Default value for the Input
	`description`		Long description for an input
`outputs[]`			List of Outputs that are generated by the Tool (and accessible to fastr)
	`id`		ID of the Output
	`name`		Longer name of the Output (more human readable)
	`datatype`		The ID of the DataType of the Output[1]
	`enum[]`		List of possible values for an EnumType (created on the fly by fastr)[1]
	`prefix`		Commandline prefix of the Output (e.g. –out, -o)
	`cardinality`		Cardinality of the Output
	`repeat_prefix`		Flag indicating if for every value of the Output the prefix is repeated
	`required`		Flag indicating if the input is required
	`nospace`		Flag indicating if there is no space between prefix and value (e.g. –out=val)
	`format`		For DataTypes that have multiple representations, indicate which one to use
	`description`		Long description for an input
	`action`		Special action (defined per DataType) that needs to be performed before crea

Table 1.1 – continued from previous page

Attribute		Description
	automatic	Indicate that output doesn't require commandline argument, but is created au
	method	Method to acquire output value from the Tool can be 'path' or 'stdout'[2]
	location	Definition where to an automatically, usage depends on the method[2]
help		Help text explaining the use of the Tool
cite		Bibtext of the Citation(s) to reference when using this Tool for a publication

Resource Reference

In this chapter we describe the different plugins bundled with Fastr (e.g. IOPlugins, ExecutionPlugins). The reference is build automatically from code, so after installing a new plugin the documentation has to be rebuild for it to be included in the docs.

CollectorPlugin Reference

`CollectorPlugins` are used for finding and collecting the output data of outputs part of a `FastrInterface`

scheme	`CollectorPlugin`
JsonCollector	*JsonCollector*
PathCollector	*PathCollector*
StdoutCollector	*StdoutCollector*

JsonCollector

The JsonCollector plugin allows a program to print out the result in a pre-defined JSON format. It is then used as values for fastr.

The working is as follows:

1. The location of the output is taken
2. If the location is `None`, go to step 5
3. The substitutions are performed on the location field (see below)
4. The location is used as a regular expression and matched to the stdout line by line
5. The matched string (or entire stdout if location is `None`) is `loaded as a json`
6. The data is parsed by *`set_result`*

The structure of the JSON has to follow the a predefined format. For normal *`Nodes`* the format is in the form:

```
[value1, value2, value3]
```

where the multiple values represent the cardinality.

For a *`FlowNodes`* the format is the form:

```
{
  'sample_id1': [value1, value2, value3],
  'sample_id2': [value4, value5, value6]
}
```

This allows the tool to create multiple output samples in a single run.

[1] `datatype` and `enum` are conflicting entries, if both specified `datatype` has presedence

[2] More details on defining automatica output are given in [TODO]

PathCollector

The PathCollector plugin for the FastrInterface. This plugin uses the location fields to find data on the filesystem. To use this plugin the method of the output has to be set to `path`

The general working is as follows:

1. The location field is taken from the output
2. The substitutions are performed on the location field (see below)
3. The updated location field will be used as a regular expression filter
4. The filesystem is scanned for all matching files/directory

The special substitutions performed on the location use the Format Specification Mini-Language Format Specification Mini-Language. The predefined fields that can be used are:

- `inputs`, an objet with the input values (use like `{inputs.image[0]}`)
- `outputs`, an object with the output values (use like `{outputs.result[0]}`)
- `special` which has two subfields:
  - `special.cardinality`, the index of the current cardinality
  - `special.extension`, is the extension for the output DataType

Example use:

```
<output ... method="path" location="{output.directory[0]}/TransformParameters.
↪{special.cardinality}.{special.extension}"/>
```

Given the output directory `./nodeid/sampleid/result`, the second sample in the output and filetype with a `txt` extension, this would be translated into:

```
<output ... method="path" location="./nodeid/sampleid/result/TransformParameters.1.
↪txt>
```

StdoutCollector

The StdoutCollector can collect data from the stdout stream of a program. It filters the `stdout` line by line matching a predefined regular expression.

The general working is as follows:

1. The location field is taken from the output
2. The substitutions are performed on the location field (see below)
3. The updated location field will be used as a regular expression filter
4. The `stdout` is scanned line by line and the regular expression filter is applied

The special substitutions performed on the location use the Format Specification Mini-Language Format Specification Mini-Language. The predefined fields that can be used are:

- `inputs`, an objet with the input values (use like `{inputs.image[0]}`)
- `outputs`, an object with the output values (use like `{outputs.result[0]}`)
- `special` which has two subfields:
  - `special.cardinality`, the index of the current cardinality
  - `special.extension`, is the extension for the output DataType

Note: because the plugin scans line by line, it is impossible to catch multi-line output into a single value

ExecutionPlugin Reference

This class is the base for all Plugins to execute jobs somewhere. There are many methods already in place for taking care of stuff. Most plugins should only need to redefine a few abstract methods:

- `__init__` the constructor
- `cleanup` a clean up function that frees resources, closes connections, etc
- `_queue_job` the method that queues the job for execution
- `_cancel_job` cancels a previously queued job
- `_release_job` releases a job that is currently held
- `_job_finished` extra callback for when a job finishes

Not all of the functions need to actually do anything for a plugin. There are examples of plugins that do not really need a `cleanup`, but for safety you need to implement it. Just using a `pass` for the method could be fine in such a case.

Warning: When overwriting other function, extreme care must be taken not to break the plugins working.

scheme	`ExecutionPlugin`
BlockingExecution	*BlockingExecution*
DRMAAExecution	*DRMAAExecution*
LinearExecution	*LinearExecution*
ProcessPoolExecution	*ProcessPoolExecution*
RQExecution	*RQExecution*

BlockingExecution

The blocking execution plugin is a special plugin which is meant for debug purposes. It will not queue jobs but immediately execute them inline, effectively blocking fastr until the Job is finished. It is the simplest execution plugin and can be used as a template for new plugins or for testing purposes.

DRMAAExecution

A DRMAA execution plugin to execute Jobs on a Grid Engine cluster. It uses a configuration option for selecting the queue to submit to. It uses the python `drmaa` package.

Note: To use this plugin, make sure the `drmaa` package is installed and that the execution is started on an SGE submit host with DRMAA libraries installed.

Note: This plugin is at the moment tailored to SGE, but it should be fairly easy to make different subclasses for different DRMAA supporting systems.

Configuration fields

name	type	description	default
drmaa_queue	str	The default queue to use for jobs send to the scheduler	'week'

LinearExecution

An execution engine that has a background thread that executes the jobs in order. The queue is a simple FIFO queue and there is one worker thread that operates in the background. This plugin is meant as a fallback when other plugins do not function properly. It does not multi-processing so it is safe to use in environments that do no support that.

ProcessPoolExecution

A local execution plugin that uses multiprocessing to create a pool of worker processes. This allows fastr to execute jobs in parallel with true concurrency. The number of workers can be specified in the fastr configuration, but the default amount is the `number of cores - 1` with a minimum of `1`.

Warning: The ProcessPoolExecution does not check memory requirements of jobs and running many workers might lead to memory starvation and thus an unresponsive system.

Configuration fields

name	type	description	default
process_pool_worker_number	int	Number of workers to use in a process pool	3

RQExecution

A execution plugin based on Redis Queue. Fastr will submit jobs to the redis queue and workers will peel the jobs from the queue and process them.

This system requires a running redis database and the database url has to be set in the fastr configuration.

Note: This execution plugin required the `redis` and `rq` packages to be installed before it can be loaded properly.

Configuration fields

name	type	description	default
rq_queue	str	The redis queue to use	'default'
rq_host	str	The url of the redis serving the redis queue	'redis://localhost:6379/0'

FlowPlugin Reference

Plugin that can manage an advanced data flow. The plugins override the execution of node. The execution receives all data of a node in one go, so not split per sample combination, but all data on all inputs in one large payload. The flow plugin can then re-order the data and create resulting samples as it sees fits. This can be used for all kinds of specialized data flows, e.g. cross validation.

To create a new FlowPlugin there is only one method that needs to be implemented: `execute`.

scheme	`FlowPlugin`
CrossValidation	*CrossValidation*

CrossValidation

Advanced flow plugin that generated a cross-validation data flow. The node need an input with data and an input number of folds. Based on that the outputs test and train will be supplied with a number of data sets.

IOPlugin Reference

`IOPlugins` are used for data import and export for the sources and sinks. The main use of the *`IOPlugins`* is during execution (see *Execution*). The *`IOPlugins`* can be accessed via `fastr.ioplugins`, but generally

there should be no need for direct interaction with these objects. The use of is mainly via the URL used to specify source and sink data.

scheme	`IOPlugin`
CommaSeperatedValueFile	*CommaSeperatedValueFile*
FileSystem	*FileSystem*
Null	*Null*
Reference	*Reference*
VirtualFileSystem	*VirtualFileSystem*
VirtualFileSystemRegularExpression	*VirtualFileSystemRegularExpression*
VirtualFileSystemValueList	*VirtualFileSystemValueList*
XNATStorage	*XNATStorage*

CommaSeperatedValueFile

The CommaSeperatedValueFile an expand-only type of IOPlugin. No URLs can actually be fetched, but it can expand a single URL into a larger amount of URLs.

The `csv://` URL is a `vfs://` URL with a number of query variables available. The URL mount and path should point to a valid CSV file. The query variable then specify what column(s) of the file should be used.

The following variable can be set in the query:

variable	usage
value	the column containing the value of interest, can be int for index or string for key
id	the column containing the sample id (optional)
header	indicates if the first row is considered the header, can be `true` or `false` (optional)
delimiter	the delimiter used in the csv file (optional)
quote	the quote character used in the csv file (optional)
reformat	a reformatting string so that `value = reformat.format(value)` (used before relative_path)
relative_path	indicates the entries are relative paths (for files), can be `true` or `false` (optional)

The header is by default `false` if the neither the `value` and `id` are set as a string. If either of these are a string, the header is required to define the column names and it automatically is assumed `true`

The delimiter and quota characters of the file should be detected automatically using the `Sniffer`, but can be forced by setting them in the URL.

Example of valid `csv` URLs:

```
# Use the first column in the file (no header row assumed)
csv://mount/some/dir/file.csv?value=0

# Use the images column in the file (first row is assumed header row)
csv://mount/some/dir/file.csv?value=images

# Use the segmentations column in the file (first row is assumed header row)
# and use the id column as the sample id
csv://mount/some/dir/file.csv?value=segmentations&id=id

# Use the first column as the id and the second column as the value
# and skip the first row (considered the header)
csv://mount/some/dir/file.csv?value=1&id=0&header=true

# Use the first column and force the delimiter to be a comma
csv://mount/some/dir/file.csv?value=0&delimiter=,
```

FileSystem

The FileSystem plugin is create to handle `file://` type or URLs. This is generally not a good practice, as this is not portable over between machines. However, for test purposes it might be useful.

The URL scheme is rather simple: `file://host/path` (see wikipedia for details)

We do not make use of the `host` part and at the moment only support localhost (just leave the host empty) leading to `file:///` URLs.

Warning: This plugin ignores the hostname in the URL and does only accept driver letters on Windows in the form `c:/`

Null

The Null plugin is create to handle `null://` type or URLs. These URLs are indicating the sink should not do anything. The data is not written to anywhere. Besides the scheme, the rest of the URL is ignored.

Reference

The Reference plugin is create to handle `ref://` type or URLs. These URLs are to make the sink just write a simple reference file to the data. The reference file contains the DataType and the value so the result can be reconstructed. It for files just leaves the data on disk by reference. This plugin is not useful for production, but is used for testing purposes.

VirtualFileSystem

The virtual file system class. This is an IOPlugin, but also heavily used internally in fastr for working with directories. The VirtualFileSystem uses the `vfs://` url scheme.

A typical virtual filesystem url is formatted as `vfs://mountpoint/relative/dir/from/mount.ext`

Where the `mountpoint` is defined in the *Config file*. A list of the currently known mountpoints can be found in the `fastr.config` object

```
>>> fastr.config.mounts
{'example_data': '/home/username/fastr-feature-documentation/fastr/fastr/examples/
↪data',
 'home': '/home/username/',
 'tmp': '/home/username/FastrTemp'}
```

This shows that a url with the mount `home` such as `vfs://home/tempdir/testfile.txt` would be translated into `/home/username/tempdir/testfile.txt`.

There are a few default mount points defined by Fastr (that can be changed via the config file).

mountpoint	default location
home	the users home directory (`expanduser('~/')`)
tmp	the fastr temprorary dir, defaults to `tempfile.gettempdir()`
example_data	the fastr example data directory, defaults `$FASTRDIR/example/data`

VirtualFileSystemRegularExpression

The VirtualFileSystemValueList an expand-only type of IOPlugin. No URLs can actually be fetched, but it can expand a single URL into a larger amount of URLs.

A `vfsregex://` URL is a vfs URL that can contain regular expressions on every level of the path. The regular expressions follow the `re module` definitions.

An example of a valid URLs would be:

```
vfsregex://tmp/network_dir/.*/.*/__fastr_result__.pickle.gz
vfsregex://tmp/network_dir/nodeX/(?P<id>.*)/__fastr_result__.pickle.gz
```

The first URL would result in all the `__fastr_result__.pickle.gz` in the working directory of a Network. The second URL would only result in the file for a specific node (nodeX), but by adding the named group `id` using `(?P<id>.*)` the sample id of the data is automatically set to that group (see Regular Expression Syntax under the special characters for more info on named groups in regular expression).

Concretely if we would have a directory `vfs://mount/somedir` containing:

```
image_1/Image.nii
image_2/image.nii
image_3/anotherimage.nii
image_5/inconsistentnamingftw.nii
```

we could match these files using `vfsregex://mount/somedir/(?P<id>image_\d+)/.*\.nii` which would result in the following source data after expanding the URL:

```
{'image_1': 'vfs://mount/somedir/image_1/Image.nii',
 'image_2': 'vfs://mount/somedir/image_2/image.nii',
 'image_3': 'vfs://mount/somedir/image_3/anotherimage.nii',
 'image_5': 'vfs://mount/somedir/image_5/inconsistentnamingftw.nii'}
```

Showing the power of this regular expression filtering. Also it shows how the ID group from the URL can be used to have sensible sample ids.

Warning: due to the nature of regexp on multiple levels, this method can be slow when having many matches on the lower level of the path (because the tree of potential matches grows) or when directories that are parts of the path are very large.

VirtualFileSystemValueList

The VirtualFileSystemValueList an expand-only type of IOPlugin. No URLs can actually be fetched, but it can expand a single URL into a larger amount of URLs. A `vfslist://` URL basically is a url that points to a file using vfs. This file then contains a number lines each containing another URL.

If the contents of a file `vfs://mount/some/path/contents` would be:

```
vfs://mount/some/path/file1.txt
vfs://mount/some/path/file2.txt
vfs://mount/some/path/file3.txt
vfs://mount/some/path/file4.txt
```

Then using the URL `vfslist://mount/some/path/contents` as source data would result in the four files being pulled.

Note: The URLs in a vfslist file do not have to use the `vfs` scheme, but can use any scheme known to the Fastr system.

XNATStorage

Warning: As this IOPlugin is under development, it has not been thoroughly tested.

The XNATStorage plugin is an IOPlugin that can download data from and upload data to an XNAT server. It uses its own `xnat://` URL scheme. This is a scheme specific for this plugin and though it looks somewhat like the XNAT rest interface, a different type or URL.

Data resources can be access directly by a data url:

```
xnat://xnat.example.com/data/archive/projects/sandbox/subjects/subject001/
↪experiments/experiment001/scans/T1/resources/DICOM
xnat://xnat.example.com/data/archive/projects/sandbox/subjects/subject001/
↪experiments/*_BRAIN/scans/T1/resources/DICOM
```

In the second URL you can see a wildcard being used. This is possible at long as it resolves to exactly one item.

The `id` query element will change the field from the default experiment to subject and the `label` query element sets the use of the label as the fastr id (instead of the XNAT id) to `True` (the default is `False`)

To disable `https` transport and use `http` instead the query string can be modified to add `insecure=true`. This will make the plugin send requests over `http`:

```
xnat://xnat.example.com/data/archive/projects/sandbox/subjects/subject001/
↪experiments/*_BRAIN/scans/T1/resources/DICOM?insecure=true
```

For sinks it is import to know where to save the data. Sometimes you want to save data in a new assessor/resource and it needs to be created. To allow the Fastr sink to create an object in XNAT, you have to supply the type as a query parameter:

```
xnat://xnat.bmia.nl/data/archive/projects/sandbox/subjects/S01/experiments/_BRAIN/
↪assessors/test_assessor/resources/IMAGE/files/image.nii.gz?resource_
↪type=xnat:resourceCatalog&assessor_type=xnat:qcAssessmentData
```

Valid options are: subject_type, experiment_type, assessor_type, scan_type, and resource_type.

If you want to do a search where multiple resources are returned, it is possible to use a search url:

```
xnat://xnat.example.com/search?projects=sandbox&subjects=subject[0-9][0-9][0-9]&
↪experiments=*_BRAIN&scans=T1&resources=DICOM
```

This will return all DICOMs for the T1 scans for experiments that end with _BRAIN that belong to a subjectXXX where XXX is a 3 digit number. By default the ID for the samples will be the experiment XNAT ID (e.g. XNAT_E00123). The wildcards that can be the used are the same UNIX shell-style wildcards as provided by the module `fnmatch`.

It is possible to change the id to a different fields id or label. Valid fields are project, subject, experiment, scan, and resource:

```
xnat://xnat.example.com/search?projects=sandbox&subjects=subject[0-9][0-9][0-9]&
↪experiments=*_BRAIN&scans=T1&resources=DICOM&id=subject&label=true
```

The following variables can be set in the search query:

variable	default	usage
projects	`*`	The project(s) to select, can contain wildcards (see `fnmatch`)
subjects	`*`	The subject(s) to select, can contain wildcards (see `fnmatch`)
experiments	`*`	The experiment(s) to select, can contain wildcards (see `fnmatch`)
scans	`*`	The scan(s) to select, can contain wildcards (see `fnmatch`)
resources	`*`	The resource(s) to select, can contain wildcards (see `fnmatch`)
id	`experiment`	What field to use a the id, can be: project, subject, experiment, scan, or resource
label	`false`	Indicate the XNAT label should be used as fastr id, options `true` or `false`
insecure	`false`	Change the url scheme to be used to http instead of https
regex	`false`	Change search to use regex `re.match()` instead of fnmatch for matching

For storing credentials the `.netrc` file can be used. This is a common way to store credentials on UNIX systems. It is required that the file is only accessible by the owner only or a `NetrcParseError` will be raised. A netrc file is really easy to create, as its entries look like:

```
machine xnat.example.com
        login username
        password secret123
```

See the `netrc module` or the GNU inet utils website for more information about the `.netrc` file.

Note: On windows the location of the netrc file is assumed to be `os.path.expanduser('~/_netrc')`. The leading underscore is because windows does not like filename starting with a dot.

Note: For scan the label will be the scan type (this is initially the same as the series description, but can be updated manually or the XNAT scan type cleanup).

Warning: labels in XNAT are not guaranteed to be unique, so be careful when using them as the sample ID.

For background on XNAT, see the XNAT API DIRECTORY for the REST API of XNAT.

Interface Reference

Abstract base class of all Interfaces. Defines the minimal requirements for all Interface implementations.

scheme	`Interface`
FastrInterface	*FastrInterface*
FlowInterface	*FlowInterface*
NipypeInterface	*NipypeInterface*

FastrInterface

The default Interface for fastr. For the command-line Tools as used by fastr.

FlowInterface

The Interface use for AdvancedFlowNodes to create the advanced data flows that are not implemented in the fastr. This allows nodes to implement new data flows using the plugin system.

The definition of `FlowInterfaces` are very similar to the default `FastrInterfaces`.

Note: A flow interface should be using a specific FlowPlugin

NipypeInterface

Experimental interfaces to using `nipype` interfaces directly in fastr tools, only using a simple reference.

To create a tool using a nipype interface just create an interface with the correct type and set the `nipype` argument to the correct class. For example in an xml tool this would become:

```
<interface class="NipypeInterface">
  <nipype_class>nipype.interfaces.elastix.Registration</nipype_class>
</interface>
```

Note: To use these interfaces `nipype` should be installed on the system.

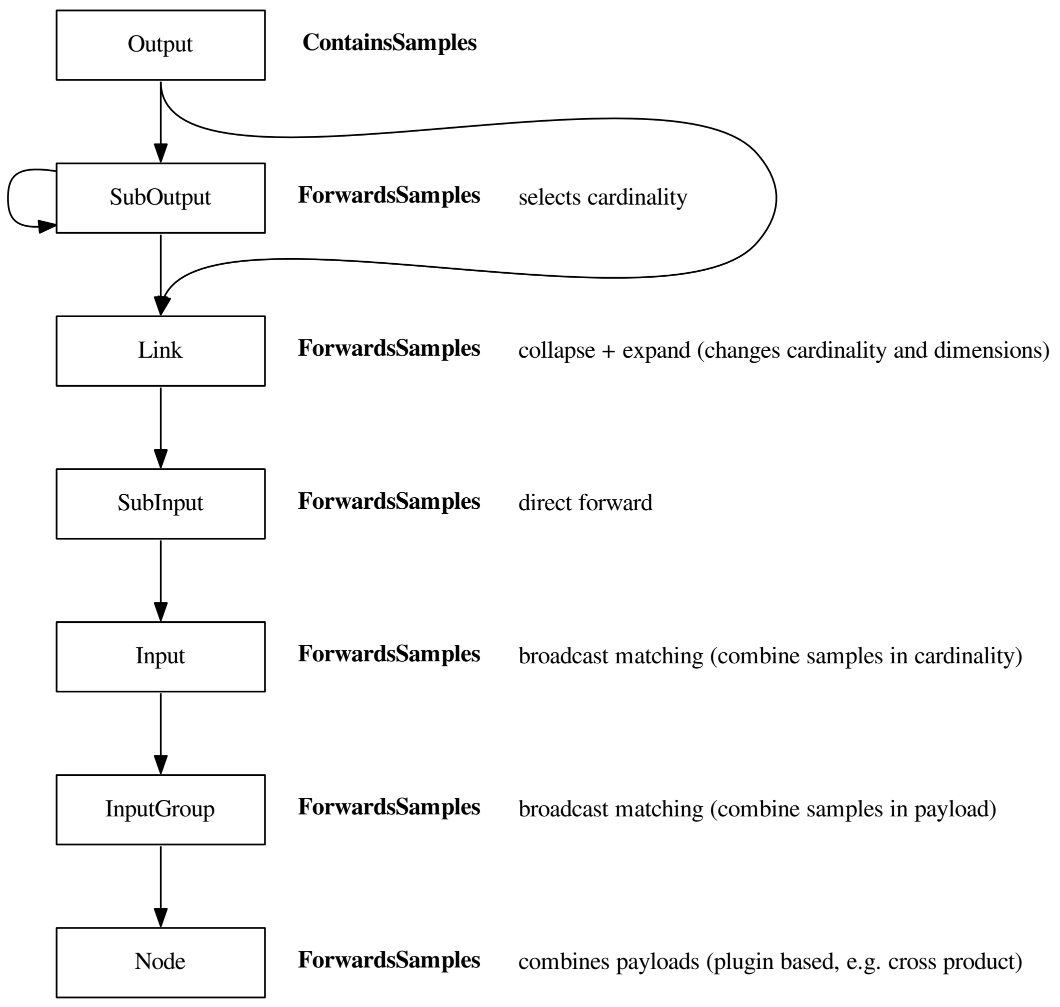
Warning: This interface plugin is basically functional, but highly experimental!

Development and Design Documentation

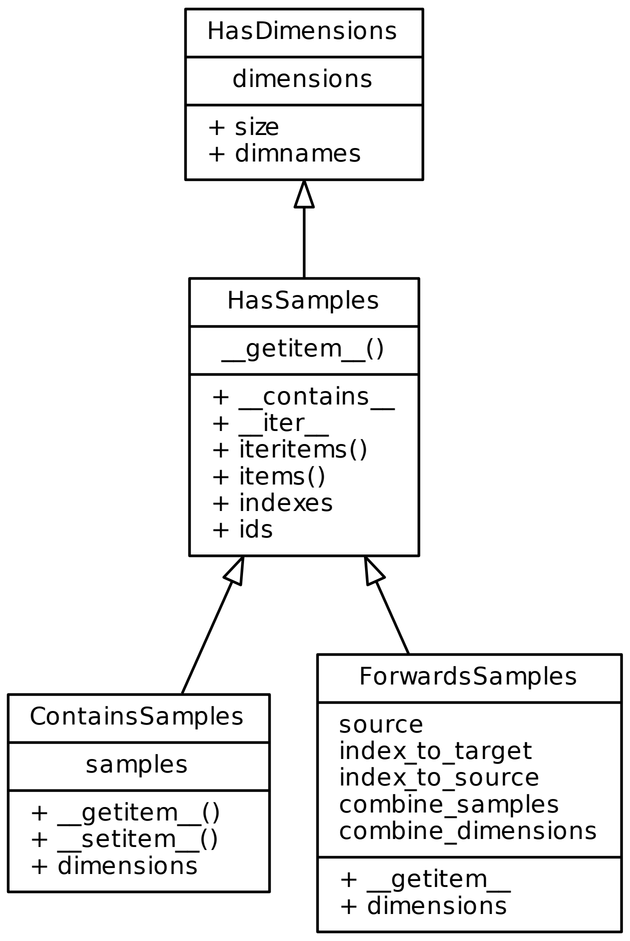
In this chapter we will discuss the design of Fastr in more detail. We give pointers for development and add the design documents as we currently envision Fastr. This is both for people who are interested in the Fastr develop and for current developers to have an archive of the design decision agreed upon.

Sample flow in Fastr

The current Sample flow is the following:


Output
ContainsSamples
SubOutput
ForwardsSamples
selects cardinality
Link
ForwardsSamples
collapse + expand (changes cardinality and dimensions)
SubInput
ForwardsSamples
direct forward
Input
ForwardsSamples
broadcast matching (combine samples in cardinality)
InputGroup
ForwardsSamples
broadcast matching (combine samples in payload)
Node
ForwardsSamples
combines payloads (plugin based, e.g. cross product)

The idea is that we make a common interface for all classes that are related to the flow of Samples. For this we propose the following mixin classes that provide the interface and allow for better code sharing. The basic structure of the classes is given in the following diagram:



The abstract and mixin methods are as follows:

ABC	Inherits from	Abstract Methods	Mixin methods
`HasDimensions`		`dimensions`	`size` `dimnames`

`HasSamples`	`HasDimensions`	`__getitem__`	`__contains__`
			`__iter__`
			`iteritems`
			`items`
			`indexes`
			`ids`

`ContainsSamples`	`HasSamples`	`samples`	`__getitem__`
			`__setitem__`
			`dimensions`

`ForwardsSamples`	`HasSamples`	`source`
		`index_to_target`
		`index_to_source`
		`combine_samples`
		`combine_dimensions`
			`__getitem__`
			`dimensions`

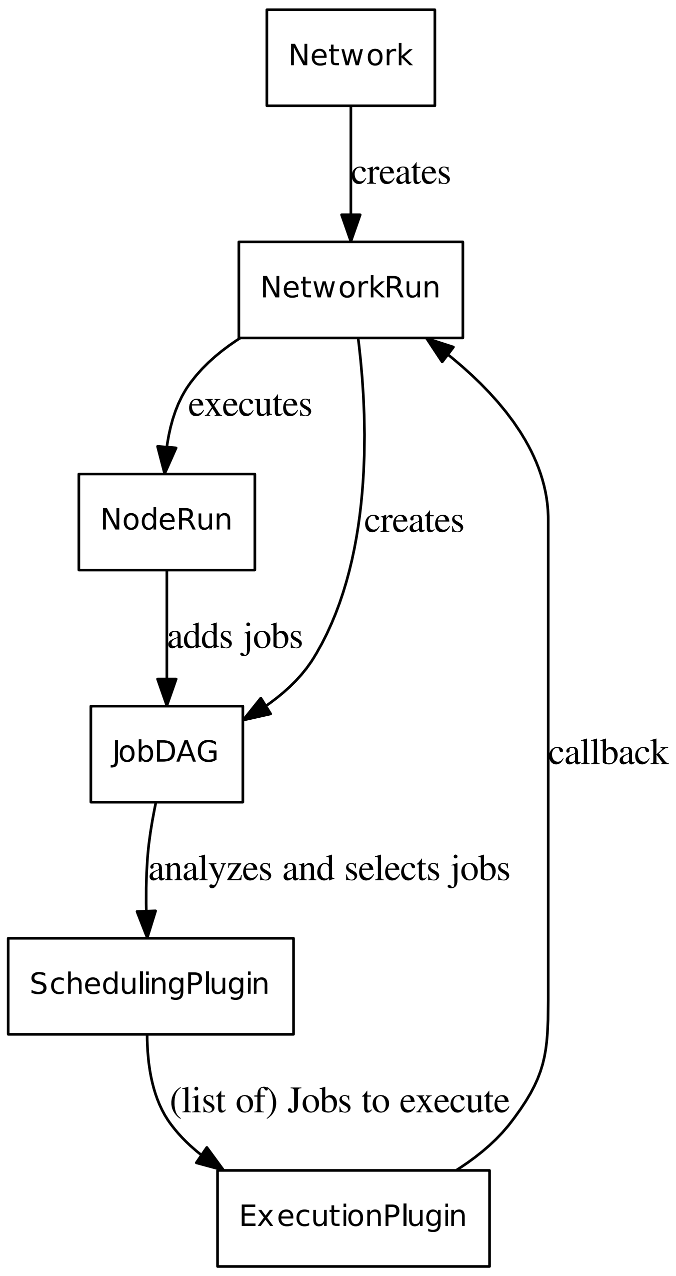
Note: Though the flow is currently working like this, the mixins are not yet created.

Network Execution

The network execution should contain a number of steps:

- `Network`
  - Creates a `NetworkRun` based on the current layout
- `NetworkRun`
  - Transform the `Network` (possibly joining Nodes of certain interface into a combined Node etc)
  - Start generation of the Job Direct Acyclic Graph (DAG)
- `SchedulingPlugin`
  - Prioritize Jobs based on some predefined rules
  - Combine certain `Jobs` to improve efficiency (e.g. minimize i/o on a grid)
- `ExecutionPlugin`
  - Run a (list of) `Jobs`. If there is more than one jobs, run them sequentially on same execution host using a local temp for intermediate files.
  - On finished callback: Updated DAG with newly ready jobs, or remove cancelled jobs

This could be visualized as the following loop:



The callback of the `ExecutionPlugin` to the `NetworkRun` would trigger the execution of the relevant `NodeRuns` and the addition of more `Jobs` to the `JobDAG`.

Note: The Job DAG should be thread-safe as it could be both read and extended at the same time.

Note: If a list of jobs is send to the `ExecutionPlugin` to be run as on Job on an external execution platform, the resources should be combined as follows: memory=max, cores=max, runtime=sum

Note: If there are execution hosts that have mutliple cores the `ExecutionPlugin` should manage this (for example by using pilot jobs). The `SchedulingPlugin` creates units that should be run sequentially on the resources noted and will not attempt parallelization

A `NetworkRun` would be contain similar information as the `Network` but not have functionality for editting/changing it. It would contain the functionality to execute the Network and track the status and samples. This would allow `Network.execute` to create multiple concurent runs that operate indepent of each other. Also editting a `Network` after the run started would have no effect on that run.

Note: This is a plan, not yet implemented

Note: For this to work, it would be important for a Jobs to have forward and backward dependency links.

SchedulingPlugins

The idea of the plugin is that it would give a priority on Jobs created by a `Network`. This could be done based on different strategies:

- Based on (sorted) sample id's, so that one sample is always prioritized over others. The idea is that samples are process as much as possible in order, finishing the first sample first. Only processing other samples if there is left-over capacity.
- Based on distance to a (particular) `Sink`. This is to generate specific results as quick as possible. It would not focus on specific samples, but give priority to whatever sample is closest to being finished.
- Based on the distance to from a `Souce`. Based on the sign of the weight it would either keep all samples on the same stage as much as possible, only progressing to a new `Node` when all samples are done with the previous `Node`, or it would push samples with accelerated rates.

Additionally it will group `Jobs` to be executed on a single host. This could reduce i/o and limited the number of jobs an external scheduler has to track.

Note: The interface for such a plugin has not yet been established.

Changelog

All notable changes to this project will be documented in this file.

The format is based on Keep a Changelog and this project adheres to Semantic Versioning

1.1.2 - 2016-12-22

Fixed

- The example network in resources/networks/add_ints.json was using an old serialization format making it non-functions. Replaced by a new network file.

1.1.1 - 2016-12-22

Fixed

- Network runs called from an interpreter (and not file) caused a crash because the network tried to report the file used. Better handling of these situations.

1.1.0 - 2016-12-08

Added

- Namespaces for resources (tools and networks)
- Network manager located at `fastr.networklist`
- RQExecution plugin. This plugin uses python-rq to manage a job queue.
- LinearExecution plugin. This plugin uses a background thread for execution.
- BlockingExecution plugin. This plugin executes jobs in a blocking fashion.
- Automatic generation of documentation for all plugins, the configuration fields and all commandline tools.

Changed

- Provenance is updated with a network dump and used tool definitions.
- New configuration system that uses python files
- New plugin system that integrates with the new configuration system and enables automatic importing of plugins
- The fastr command line tools now use an entrypoint which is located in `fastr.utils.cmd`. This code also dispatches the sub commands.

Removed

- fastr.config file. This is replaced by the config.py file. Go to the docs!

Fixed

- Adds explicit tool namespace and version to the provenance document.

CHAPTER 2

FASTR User reference

Fastr User Reference

`fastr.toollist`

A ToolManager containing all versions of all Tools loaded into the FASTR environment. The ToolManager can be indexed using the Tool id string or a tool id string and a version. For example if you have two versions (4.5 and 4.8) of a tool called *Elastix*:

```
>>> fastr.toollist['elastix.Elastix']
Tool Elastix v4.8 (Elastix Registration)
                           Inputs                                    |            ␣
↪Outputs
--------------------------------------------------------------------------------
↪-------------------
fixed_image       (ITKImageFile)                                     |  directory␣
↪(Directory)
moving_image      (ITKImageFile)                                     |  transform␣
↪(ElastixTransformFile)
parameters        (ElastixParameterFile)                             |  log_file ␣
↪(ElastixLogFile)
fixed_mask        (ITKImageFile)                                     |
moving_mask       (ITKImageFile)                                     |
initial_transform (ElastixTransformFile)                             |
priority          (__Elastix_4.8_interface__priority__Enum__)        |
threads           (Int)                                              |

>>> fastr.toollist['elastix.Elastix', '4.5']
Tool Elastix v4.5 (Elastix Registration)
                           Inputs                                    |            ␣
↪Outputs
--------------------------------------------------------------------------------
↪-------------------
fixed_image       (ITKImageFile)                                     |  directory␣
↪(Directory)
moving_image      (ITKImageFile)                                     |  transform␣
↪(ElastixTransformFile)
parameters        (ElastixParameterFile)                             |  log_file ␣
↪(ElastixLogFile)
fixed_mask        (ITKImageFile)                                     |
moving_mask        (ITKImageFile)                              |
initial_transform  (ElastixTransformFile)                      |
priority           (__Elastix_4.5_interface__priority__Enum__)  |
threads            (Int)                                        |
```

fastr.**typelist**
A dictionary containing all types loaded into the FASTR environment. The keys are the typenames and the values are the classes.

class fastr.**Network**(*id_='unnamed_network'*, *version=None*)
The Network class represents a workflow. This includes all Nodes (including ConstantNodes, SourceNodes and Sinks) and Links.

add_link(*link*)
Add a Link to the Network. Make sure the link is in the link list and the link parent is set to this Network

Parameters **link** (Link) – link to add

Raises

- ***FastrTypeError*** – if link is incorrectly typed
- ***FastrNetworkMismatchError*** – if the link already belongs to another Network

add_node(*node*)
Add a Node to the Network. Make sure the node is in the node list and the node parent is set to this Network

Parameters **node** (Node) – node to add

Raises ***FastrTypeError*** – if node is incorrectly typed

create_link(*source*, *target*, *id_=None*, *collapse=None*, *expand=None*)
Create a link between two Nodes and add it to the current Network.

Parameters

- **source** (BaseOutput) – the output that is the source of the link
- **target** (BaseInput) – the input that is the target of the link
- **id** (str) – the id of the link

Returns the created link

Type Link

create_node(*tool*, *id_=None*, *stepid=None*, *cores=None*, *memory=None*, *walltime=None*, *nodegroup=None*)
Create a Node in this Network. The Node will be automatically added to the Network.

Parameters

- **tool** (Tool) – The Tool to base the Node on
- **id** (str) – The id of the node to be created
- **stepid** (str) – The stepid to add the created node to
- **nodegroup** (str) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.

Returns the newly created node

Return type Node

create_sink(*datatype*, *id_=None*, *stepid=None*)
Create a SinkNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the sink node
- **id** (*str*) – The id of the sink node to be created
- **stepid** (*str*) – The stepid to add the created sink node to

Returns the newly created sink node

Return type *SinkNode*

create_source (*datatype*, *id_=None*, *stepid=None*, *nodegroup=None*, *sourcegroup=None*)
Create a SourceNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the source source_node
- **id** (*str*) – The id of the source source_node to be created
- **stepid** (*str*) – The stepid to add the created source source_node to
- **nodegroup** (*str*) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.
- **sourcegroup** (*str*) – *DEPRECATED!* The nodegroup this SourceNode will be added to

Returns the newly created source source_node

Return type SourceNode

draw_network (*name='network_layout'*, *img_format='svg'*, *draw_dimension=False*)
Output a dot file and try to convert it to an image file.

Parameters **img_format** (*str*) – extension of the image format to convert to

Returns path of the image created or None if failed

Return type str or None

class fastr.**Link** (*source*, *target*, *parent=None*, *id_=None*, *collapse=None*, *expand=None*)
Class for linking outputs (*BaseOutput*) to inputs (*BaseInput*)

Examples:

```
>>> import fastr
>>> network = fastr.Network()
>>> link1 = network.create_link( n1.ouputs['out1'], n2.inputs['in2'] )

link2 = Link()
link2.source = n1.ouputs['out1']
link2.target = n2.inputs['in2']
```

source
The source *BaseOutput* of the Link. Setting the source will automatically register the Link with the source BaseOutput. Updating source will also make sure the Link is unregistered with the previous source.

Raises ***FastrTypeError*** – if assigning a non *BaseOutput*

target
The target *BaseInput* of the Link. Setting the target will automatically register the Link with the target BaseInput. Updating target will also make sure the Link is unregistered with the previous target.

Raises ***FastrTypeError*** – if assigning a non *BaseInput*

class fastr.**Node** (*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)
The class encapsulating a node in the network. The node is responsible for setting and checking inputs and outputs based on the description provided by a tool instance.

`id_` = **None**
The Node id s a unique string identifying the Node

`inputgroups`

A list of inputgroups for this Node. An input group is InputGroup object filled according to the Node

`inputs` = **None**
A list of inputs of this Node

`name`
Name of the Tool the Node was based on. In case a Toolless Node was used the class name is given.

`outputs` = **None**
A list of outputs of this Node

class `fastr.`**`ConstantNode`**(*datatype*, *data*, *id_=None*)
Class encapsulating one output for which a value can be set. For example used to set a scalar value to the input of a node.

`name`
Name of the Tool the Node was based on. In case a Toolless Node was used the class name is given.

class `fastr.`**`SourceNode`**(*datatype*, *id_=None*)
Class providing a connection to data resources. This can be any kind of file, stream, database, etc from which data can be received.

`name`
Name of the Tool the Node was based on. In case a Toolless Node was used the class name is given.

class `fastr.`**`SinkNode`**(*datatype*, *id_=None*)
Class which handles where the output goes. This can be any kind of file, e.g. image files, textfiles, config files, etc.

`name`
Name of the Tool the Node was based on. In case a Toolless Node was used the class name is given.

CHAPTER 3

FASTR REST API reference

REST API

Fastr includes a webapp and a REST API. This section contains a listing of all REST paths. The full documentation is available via swagger with the paths /swagger.json for the schema or /api/doc/ for the swagger UI.

Quick reference

Resource	Operation	Description
	GET /	
	GET /api/doc/	
	GET /api/networks	
	GET /api/networks/(id)	
	POST /api/runs	
	GET /api/runs	
	DELETE /api/runs/(id)	
	GET /api/runs/(id)	
	GET /api/runs/(id)/status	
	GET /api/tools	
	GET /api/tools/(id)	
	GET /api/tools/(id)/(version)	
	GET /doc	
	GET /index	
	GET /	
	GET /network/(name)	
	GET /networks	
	GET /prov	
	GET /shutdown	
	GET /static/(path:filename)	
	GET /swagger.json	
	GET /swaggerui/(path:filename)	
	GET /tool/(toolname)/(version)	
	GET /tool/(toolname)	
	GET /tool	
	GET /websocketclient	

GET /api/networks
Get a list of the networks

GET /api/tools
Get a list of all Tools known to the server

POST /api/runs
Create a new Network run and start execution

GET /api/runs
Get a list of all Network runs on the server

GET /api/doc/
Override this method to customize the documentation page

GET /swagger.json
Render the Swagger specifications as JSON

GET /api/tools/(*id*)**/**
version Get a Tool json description from the server

GET /api/runs/(*id*)**/status**
Get the status of a Network Run on the server

GET /api/networks/(*id*)
Get a Network json description from the server

GET /api/tools/(*id*)
Get a Tool json description from the server

DELETE /api/runs/(*id*)
Abort a Network run and stop all associated execution

GET /api/runs/(*id*)
Get information about a Network run

GET /swaggerui/(**path:** *filename*)
Function used internally to send static files from the static folder to the browser.

New in version 0.5.

GET /static/(**path:** *filename*)
Function used internally to send static files from the static folder to the browser.

New in version 0.5.

CHAPTER 4

FASTR Developer Module reference

fastr Package

`fastr` Package

FASTR is a top level package which includes all parts required to create networks and edit networks.

class `fastr.__init__.`**`Network`**
The class representing a Network, this is in fact a reference to *`fastr.core.network.Network`*.

class `fastr.__init__.`**`Node`**
The class representing a Node, this is in fact a reference to *`fastr.core.node.Node`*.

class `fastr.__init__.`**`Link`**
The class representing a Link, this is in fact a reference to *`fastr.core.link.Link`*.

class `fastr.__init__.`**`SourceNode`**
The class representing a data source, this is in fact a reference to *`fastr.core.node.SourceNode`*.

class `fastr.__init__.`**`SinkNode`**
The class representing a data sink, this is in fact a reference to *`fastr.core.node.SinkNode`*.

class `fastr.__init__.`**`ConstantNode`**
The class representing a constant data source, this is in fact a reference to *`fastr.core.node.ConstantNode`*.

`fastr.__init__.`**`toollist`**
A *`fastr.core.toolmanager.ToolManager`* containing all Tools known to the FASTR environment. The toollist can be accessed in a similar way to a dict. Indexing with a tool id will return the newest version of the Tool. If a specific version of the tool is required a tuple can be used as the index:

```
>>> import fastr
>>> fastr.toollist['testtool']
<Tool: testtool version: 4.2>
>>> fastr.toollist['testtool', '2.0']
<Tool: testtool version: 2.0>
```

`fastr.__init__.`**`typelist`**
A *`fastr.core.datatypemanager.DataTypeManager`* containing all Types known to the

FASTR environment. This is usuable as a dict where the key is the datatype id and the value is the datatype itself.

class `fastr.__init__.`**`Network`**(*id_='unnamed_network'*, *version=None*)
Bases: *`fastr.core.serializable.Serializable`*

The Network class represents a workflow. This includes all Nodes (including ConstantNodes, SourceNodes and Sinks) and Links.

`NETWORK_DUMP_FILE_NAME` **= '__fastr_network__.json'**

`SOURCE_DUMP_FILE_NAME` **= '__source_data__.pickle.gz'**

`__dataschemafile__` **= 'Network.schema.json'**

`__eq__`(*other*)
Compare two Networks and see if they are equal.

Parameters **`other`** (*`Network`*) –

Returns flag indicating that the Networks are the same

Return type bool

`__getitem__`(*item*)
Get an item by its fullid. The fullid can point to a link, node, input, output or even subinput/suboutput.

Parameters **`item`** (*`str`*, *`unicode`*) – fullid of the item to retrieve

Returns the requested item

`__getstate__`()
Retrieve the state of the Network

Returns the state of the object

Rtype dict

`__init__`(*id_='unnamed_network'*, *version=None*)
Create a new, empty Network

Parameters **`name`** (*`str`*) – name of the Network

Returns newly created Network

Raises **`OSError`** – if the tmp mount in the config is not a writable directory

`__module__` **= 'fastr.core.network'**

`__ne__`(*other*)
Tests for non-equality, this is the negated version __eq__

`__repr__`()

`__setstate__`(*state*)
Set the state of the Network by the given state. This completely overwrites the old state!

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`abort`()

`add_link`(*link*)
Add a Link to the Network. Make sure the link is in the link list and the link parent is set to this Network

Parameters **`link`** (*`Link`*) – link to add

Raises

- ***`FastrTypeError`*** – if link is incorrectly typed
- ***`FastrNetworkMismatchError`*** – if the link already belongs to another Network

add_node (*node*)
Add a Node to the Network. Make sure the node is in the node list and the node parent is set to this Network

Parameters **node** (*Node*) – node to add

Raises ***FastrTypeError*** – if node is incorrectly typed

add_stepid (*stepid*, *node*)
Add a Node to a specific step id

Parameters

- **stepid** (*str*) – the stepid that the node will be added to
- **node** (*Node*) – the node to add to the stepid

check_id (*id_*)
Check if an id for an object is valid and unused in the Network. The method will always returns True if it does not raise an exception.

Parameters **id** (*str*) – the id to check

Returns True

Raises

- ***FastrValueError*** – if the id is not correctly formatted
- ***FastrValueError*** – if the id is already in use

create_constant (*datatype*, *data*, *id_=None*, *stepid=None*, *nodegroup=None*, *sourcegroup=None*)
Create a ConstantNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the constant node
- **data** (*datatype or list of datatype*) – The data to hold in the constant node
- **id** (*str*) – The id of the constant node to be created
- **stepid** (*str*) – The stepid to add the created constant node to
- **nodegroup** (*str*) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.

Returns the newly created constant node

Return type *ConstantNode*

create_link (*source*, *target*, *id_=None*, *collapse=None*, *expand=None*)
Create a link between two Nodes and add it to the current Network.

Parameters

- **source** (*BaseOutput*) – the output that is the source of the link
- **target** (*BaseInput*) – the input that is the target of the link
- **id** (*str*) – the id of the link

Returns the created link

Type *Link*

create_macro (*network*, *id_=None*)

create_node (*tool*, *id_=None*, *stepid=None*, *cores=None*, *memory=None*, *walltime=None*, *nodegroup=None*)
Create a Node in this Network. The Node will be automatically added to the Network.

Parameters

- **tool** (*Tool*) – The Tool to base the Node on
- **id** (*str*) – The id of the node to be created
- **stepid** (*str*) – The stepid to add the created node to
- **nodegroup** (*str*) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.

Returns the newly created node

Return type *Node*

create_reference (*source_data*, *output_directory*)

create_sink (*datatype*, *id_=None*, *stepid=None*)
Create a SinkNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the sink node
- **id** (*str*) – The id of the sink node to be created
- **stepid** (*str*) – The stepid to add the created sink node to

Returns the newly created sink node

Return type *SinkNode*

create_source (*datatype*, *id_=None*, *stepid=None*, *nodegroup=None*, *sourcegroup=None*)
Create a SourceNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the source source_node
- **id** (*str*) – The id of the source source_node to be created
- **stepid** (*str*) – The stepid to add the created source source_node to
- **nodegroup** (*str*) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.
- **sourcegroup** (*str*) – *DEPRECATED!* The nodegroup this SourceNode will be added to

Returns the newly created source source_node

Return type SourceNode

draw_network (*name='network_layout'*, *img_format='svg'*, *draw_dimension=False*)
Output a dot file and try to convert it to an image file.

Parameters **img_format** (*str*) – extension of the image format to convert to

Returns path of the image created or None if failed

Return type str or None

execute (*sourcedata*, *sinkdata*, *execution_plugin=None*, *tmpdir=None*, *cluster_queue=None*)
Execute the Network with the given data. This will analyze the Network, create jobs and send them to the execution backend of the system.

Parameters

- **sourcedata** (*dict*) – dictionary containing all data for the sources
- **sinkdata** (*dict*) – dictionary containing directives for the sinks
- **execution_plugin** (*str*) – the execution plugin to use (None will use the config value)

Raises

- ***FastrKeyError*** – if a source has not corresponding key in sourcedata
- ***FastrKeyError*** – if a sink has not corresponding key in sinkdata

fullid
The fullid of the Network

id
The id of the Network. This is a read only property.

is_valid()

job_finished(*job*, *execution_interface*)
Call-back handler for when a job is finished. Will collect the results and handle blocking jobs. This function is automatically called when the execution plugin finished a job.

Parameters **job** (*Job*) – the job that finished

remove(*value*)
Remove an item from the Network.

Parameters **value** (*Node* or *Link*) – the item to remove

test(*reference_data_dir*, *source_data=None*)
Execute the network with the source data specified and test the results against the refence data. This effectively tests the network execution.

Parameters

- **reference_data_dir** (*str*) – The path or vfs url of reference data to compare with
- **source_data** (*dict*) – The source data to use

class fastr.__init__.**Link**(*source*, *target*, *parent=None*, *id_=None*, *collapse=None*, *expand=None*)
Bases: *fastr.core.updateable.Updateable*, *fastr.core.serializable.Serializable*

Class for linking outputs (*BaseOutput*) to inputs (*BaseInput*)

Examples:

```
>>> import fastr
>>> network = fastr.Network()
>>> link1 = network.create_link( n1.ouputs['out1'], n2.inputs['in2'] )

link2 = Link()
link2.source = n1.ouputs['out1']
link2.target = n2.inputs['in2']
```

__abstractmethods__ = frozenset([])

__dataschemafile__ = 'Link.schema.json'

__eq__(*other*)
Test for equality between two Links

Parameters **other** (*Link*) – object to test against

Returns True for equality, False otherwise

Return type bool

__getitem__(*index*)
Get a an item for this Link. The item will be retrieved from the connected output, but a diverging or converging flow can change the number of samples/cardinality.

Parameters **index** (*SampleIndex*) – index of the item to retrieve

Returns the requested item

Return type `SampleItem`

Raises ***FastrIndexError*** – if the index length does not match the number dimensions in the source data (after collapsing/expanding)

`__getstate__`()
Retrieve the state of the Link

Returns the state of the object

Rtype dict

`__init__`(*source*, *target*, *parent=None*, *id_=None*, *collapse=None*, *expand=None*)
Create a new Link in a Network.

Parameters

- **source** (*BaseOutput*) – the source output
- **target** (*BaseInput*) – the target input
- **parent** (*Network* or None) – the parent network, if None is given the fastr.current_network is assumed to be the parent
- **id** (*str or None*) – the id of the link, if no **id_** is given, the id will be in the form of "link_{:d}"
- **collapse** (*int, str, or tuple of int/str*) – the dimensions that the link has to collapse on
- **expand** (*bool*) – Does this link need to expand the cardinality into a new sample dimension

Returns newly created Link

Raises

- ***FastrValueError*** – if parent is not given and *fastr.current_network* is not set
- ***FastrValueError*** – if the source output is not in the same network as the Link
- ***FastrValueError*** – if the target input is not in the same network as the Link

`__module__` = **'fastr.core.link'**

`__repr__`()
Get a string representation for the Link

Returns the string representation

Return type str

`__setstate__`(*state*)
Set the state of the Link by the given state.

Parameters **state** (*dict*) – The state to populate the object with

Returns None

Raises ***FastrValueError*** – if the parent network and *fastr.current_network* are not set

`cardinality`(*index=None*)
Cardinality for a Link is given by source Output and the collapse/expand settings

Parameters **key** (`SampleIndex`) – key for a specific sample (can be only a sample index!)

Returns the cardinality

Return type int, sympy.Symbol

Raises ***FastrIndexError*** – if the index length does not match the number of dimension in the data

collapse
The converging dimensions of this link. Collapsing changes some dimensions of sample lists into cardinality, reshaping the data.

Collapse can be set to a tuple or an int/str, in which case it will be automatically wrapped in a tuple. The int will be seen as indices of the dimensions to collapse. The str will be seen as the name of the dimensions over which to collapse.

Raises ***FastrTypeError*** – if assigning a collapse value of a wrong type

collapse_indexes
The converging dimensions of this link as integers. Dimension names are replaces with the corresponding int.

Collapsing changes some dimensions of sample lists into cardinality, reshaping the data

classmethod createobj(*state*, *network=None*)
Create object function for Link

Parameters

- **cls** – The class to create
- **state** – The state to use to create the Link
- **network** – the parent Network

Returns newly created Link

destroy()
The destroy function of a link removes all default references to a link. This means the references in the network, input and output connected to this link. If there is no references in other places in the code, it will destroy the link (reference count dropping to zero).

This function is called when a source for an input is set to another value and the links becomes disconnected. This makes sure there is no dangling links.

dimnames
The dimension names for this Link. The dimension names depend on the connected source output and the collapse/expand.

expand
Flag indicating that the link will expand the cardininality into a new sample dimension to be created.

fullid
The full defining ID for the Input

iteritems()
Iterate over all `SampleItems` available in this Link. This function queries the connected source output and processes the collapsing and expanding.

Returns generator function yielding `SampleItems`

parent
The Network to which this Link belongs.

size
The size of the data delivered by the link. This can be different from the source size because the link can make data collapse or expand.

source
The source `BaseOutput` of the Link. Setting the source will automatically register the Link with the source BaseOutput. Updating source will also make sure the Link is unregistered with the previous source.

Raises ***FastrTypeError*** – if assigning a non `BaseOutput`

status

target
The target *BaseInput* of the Link. Setting the target will automatically register the Link with the target BaseInput. Updating target will also make sure the Link is unregistered with the previous target.

Raises ***FastrTypeError*** – if assigning a non *BaseInput*

class fastr.__init__.**Node**(*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)
Bases: *fastr.core.updateable.Updateable*, *fastr.core.serializable.Serializable*

The class encapsulating a node in the network. The node is responsible for setting and checking inputs and outputs based on the description provided by a tool instance.

__abstractmethods__ = frozenset([])

__dataschemafile__ = 'Node.schema.json'

__eq__(*other*)
Compare two Node instances with each other. This function ignores the parent and update status, but tests rest of the dict for equality. equality

Parameters **other** (Node) – the other instances to compare to

Returns True if equal, False otherwise

__getstate__()
Retrieve the state of the Node

Returns the state of the object

Rtype dict

__init__(*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)
Instantiate a node.

Parameters

- **tool** (*Tool*) – The tool to base the node on
- **id** (*str*) – the id of the node
- **parent** (*Network*) – the parent network of the node
- **cores** (*int*) – number of cores required for executing this Node
- **memory** (*str*) – amount of memory required in the form d+[mMgG] where M is for megabyte and G for gigabyte
- **walltime** (*str*) – amount of time required in second or in the form HOURS:MINUTES:SECOND

Returns the newly created Node

__metaclass__
alias of ABCMeta

__module__ = 'fastr.core.node'

__repr__()
Get a string representation for the Node

Returns the string representation

Return type str

__setstate__(*state*)
Set the state of the Node by the given state.

Parameters **state** (*dict*) – The state to populate the object with

Returns None

`__str__`()
Get a string version for the Node

Returns the string version

Return type str

`blocking`
Indicate that the results of this Node cannot be determined without first executing the Node, causing a blockage in the creation of jobs. A blocking Nodes causes the Chunk borders.

`create_job`(*sample_id*, *sample_index*, *job_data*, *job_dependencies*, *jobid=None*, *outputurl=None*, ***kwargs*)
Create a job based on the sample id, job data and job dependencies.

Parameters

- **`sample_id`** (`SampleId`) – the id of the corresponding sample
- **`job_data`** (*`dict`*) – dictionary containing all input data for the job
- **`job_dependencies`** – other jobs that need to finish before this job can run

Returns the created job

Return type *`Job`*

classmethod `createobj`(*state*, *network=None*)

`dimnames`
Names of the dimensions in the Node output. These will be reflected in the SampleIdList of this Node.

`execute`()
Execute the node and create the jobs that need to run

Returns list of jobs to run

Return type list of *`Jobs`*

`find_source_index`(*target_index*, *target*, *source*)

`fullid`
The full defining ID for the Node

`get_sourced_nodes`()
A list of all Nodes connected as sources to this Node

Returns list of all nodes that are connected to an input of this node

`id`
The id of the Node

`inputgroups`

A list of inputgroups for this Node. An input group is InputGroup object filled according to the Node

`listeners`
All the listeners requesting output of this node, this means the listeners of all Outputs and SubOutputs

`merge_dimensions`

`name`
Name of the Tool the Node was based on. In case a Toolless Node was used the class name is given.

`nodegroup`

`outputsize`
Size of the outputs in this Node

parent
The parent network of this node.

prepare()
Prepare the node for execution. It will create a SampleIdList of the correct size and prepare the outputs.

required_cores
Number of cores required for the execution of this Node

required_memory
Amount of memory required for the execution of this Node. Follows the format d+[mMgG] so 500M or 4g would be valid ways to specify 500 megabytes or 4 gigabyte of memory.

required_time
Amount of time required for the execution of this Node. Follows the format of a number of second or H:M:S, with H the number of hours, M the number of minutes and S the number of seconds.

set_result(*job*)
Incorporate result of a job into the Node.

Parameters **job** (*Type*) – job of which the result to store

status

tool

update_inputgroups()
Update all input groups in this node

class fastr.__init__.**ConstantNode**(*datatype*, *data*, *id_=None*)
Bases: *fastr.core.node.SourceNode*

Class encapsulating one output for which a value can be set. For example used to set a scalar value to the input of a node.

__abstractmethods__ = frozenset([])

__dataschemafile__ = 'ConstantNode.schema.json'

__getstate__()
Retrieve the state of the ConstantNode

Returns the state of the object

Rtype dict

__init__(*datatype*, *data*, *id_=None*)
Instantiation of the ConstantNode.

Parameters

- **datatype** – The datatype of the output.
- **data** – the prefilled data to use.
- **id** – The url pattern.

This class should never be instantiated directly (unless you know what you are doing). Instead create a constant using the network class like shown in the usage example below.

usage example:

```
>>> import fastr
>>> network = fastr.Network()
>>> source = network.create_source(datatype=fastr.typelist['ITKImageFile'],
↪ id_='sourceN')
```

or alternatively create a constant node by assigning data to an item in an InputDict:

```
>>> node_a.inputs['in'] = ['some', 'data']
```

which automatically creates and links a ConstantNode to the specified Input

`__module__` = **'fastr.core.node'**

`__setstate__`(*state*)
Set the state of the ConstantNode by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`data`
The data stored in this constant node

`execute`()
Execute the constant node and create the jobs that need to run

Returns list of jobs to run

Return type list of *`Jobs`*

`set_data`(*data=None*, *ids=None*)
Set the data of this constant node in the correct way. This is mainly for compatibility with the parent class SourceNode

Parameters

- **`data`** (*`dict or list of urls`*) – the data to use
- **`ids`** – if data is a list, a list of accompanying ids

class `fastr.__init__.`**`SourceNode`**(*datatype*, *id_=None*)
Bases: *`fastr.core.node.FlowNode`*

Class providing a connection to data resources. This can be any kind of file, stream, database, etc from which data can be received.

`__abstractmethods__` = **frozenset([])**

`__dataschemafile__` = **'SourceNode.schema.json'**

`__eq__`(*other*)
Compare two Node instances with each other. This function ignores the parent and update status, but tests rest of the dict for equality. equality

Parameters **`other`** (`Node`) – the other instances to compare to

Returns True if equal, False otherwise

`__getstate__`()
Retrieve the state of the SourceNode

Returns the state of the object

Rtype dict

`__init__`(*datatype*, *id_=None*)
Instantiation of the SourceNode.

Parameters

- **`datatype`** – The (id of) the datatype of the output.
- **`id`** – The url pattern.

This class should never be instantiated directly (unless you know what you are doing). Instead create a source using the network class like shown in the usage example below.

usage example:

```
>>> import fastr
>>> network = fastr.Network()
>>> source = network.create_source(datatype=fastr.typelist['ITKImageFile'],
↪ id_='sourceN')
```

`__module__` = **'fastr.core.node'**

`__setstate__`(*state*)
Set the state of the SourceNode by the given state.

Parameters **state** (*dict*) – The state to populate the object with

Returns None

`create_job`(*sample_id*, *sample_index*, *job_data*, *job_dependencies*)

`datatype`
The datatype of the data this source supplies.

`dimnames`
Names of the dimensions in the SourceNode output. These will be reflected in the SampleIdLists.

`execute`()
Execute the source node and create the jobs that need to run

Returns list of jobs to run

Return type list of *Jobs*

`output`
Shorthand for `self.outputs['output']`

`outputsize`
The size of output of this SourceNode

`set_data`(*data*, *ids=None*)
Set the data of this source node.

Parameters

- **data** (*dict, OrderedDict or list of urls*) – the data to use
- **ids** – if data is a list, a list of accompanying ids

`sourcegroup`

`valid`
This does nothing. It only overloads the valid method of Node(). The original is intended to check if the inputs are connected to some output. Since this class does not implement inputs, it is skipped.

`configmanager` Module

This module defines the Fastr Config class for managing the configuration of Fastr. The config object is stored directly in the fastr top-level module.

class `fastr.configmanager.`**`Config`**(**configfiles*)
Bases: `object`

Class contain the fastr configuration

`DEFAULT_FIELDS` = **{'resourcesdir': (<type 'str'>, '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1**

`__dict__` = **dict_proxy({'_update_logging': <function _update_logging>, '__module__': 'fastr.configmanager', 'regi**

`__getattr__`(*item*)

`__init__`(**configfiles*)

`__module__` = **'fastr.configmanager'**

`__repr__`()

`__weakref__`
list of weak references to the object (if defined)

`read_config`(*filename*)
Read a configuration and update the configuration object accordingly

Parameters **`filename`** – the configuration file to read

`read_config_files` **= None**
Trace of the config files read by this object

`register_fields`(*fields_spec*)
Register extra fields to the configuration manager.

`web_url`()
Construct a fqdn from the web['hostname'] and web['port'] settings. :return: FQDN :rtype: str

`x` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fastr-1.1.2-py**

class `fastr.configmanager.`**`EmptyDefault`**(*data=None*)
Bases: `object`

`__add__`(*right*)

`__delitem__`(*key*)

`__dict__` **= dict_proxy({'extend': <function extend>, '__delitem__': <function __delitem__>, '__module__': 'fastr.c**

`__getitem__`(*item*)

`__iadd__`(*right*)

`__init__`(*data=None*)

`__module__` **= 'fastr.configmanager'**

`__radd__`(*other*)

`__setitem__`(*key, value*)

`__weakref__`
list of weak references to the object (if defined)

`append`(*value*)

`asdict`()

`aslist`()

`extend`(*other*)

`prepend`(*value*)

`update`(*other*)

`datatypes` Module

The datatypes module holds all DataTypes generated by fastr and all the base classes for these datatypes.

class `fastr.datatypes.`**`AnalyzeImageFile`**(*value=None, format_=None*)
Bases: *`fastr.datatypes.URLType`*

`__abstractmethods__` **= frozenset([])**

`__module__` **= 'fastr.datatypes'**

classmethod **`content`**(*invalue, outvalue=None*)

`description` **= 'Analyze Image file formate'**

extension = **'hdr'**

filename = **'/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

module = **<module 'AnalyzeImageFile' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/loca**

class `fastr.datatypes.`**`AnyFile`**(*value=None*)

Bases: *`fastr.datatypes.TypeGroup`*

Special Datatype in fastr that is a TypeGroup with all known DataTypes as its members.

`__abstractmethods__` = **frozenset([])**

`__module__` = **'fastr.datatypes'**

description = **'TypeGroup AnyFile\nAnyFile (AnyFile) is a group of consisting of all URLTypes known by fastr, cu**

class `fastr.datatypes.`**`AnyType`**(*value=None*)

Bases: *`fastr.datatypes.TypeGroup`*

Special Datatype in fastr that is a TypeGroup with all known DataTypes as its members.

`__abstractmethods__` = **frozenset([])**

`__module__` = **'fastr.datatypes'**

description = **'TypeGroup AnyType\nAnyType (AnyType) is a group of consisting of all DataTypes known by fast**

class `fastr.datatypes.`**`BaseDataType`**(*value=None, format_=None*)

Bases: *`fastr.core.baseplugin.BasePlugin`*

The base class for all datatypes in the fastr type system.

`__abstractmethods__` = **frozenset(['__init__'])**

`__eq__`(*other*)

Test the equality of two DataType objects

Parameters **other** (`DataType`) – the object to compare against

Returns flag indicating equality

Return type bool

`__getstate__`()

`__init__`(*value=None, format_=None*)

The BaseDataType constructor.

Parameters

- **value** – value to assign to the new BaseDataType object
- **format** – the format used for the ValueType

Returns new BaseDataType object

Raises

- ***`FastrDataTypeNotInstantiableError`*** – if not subclassed
- ***`FastrNotImplementedError`*** – if *id*, *name*, *version* or *description* is None

`__module__` = **'fastr.datatypes'**

`__ne__`(*other*)

Test if two objects are not equal. This is by default done by negating the __eq__ operator

Parameters **other** (`DataType`) – the object to compare against

Returns flag indicating equality

Return type bool

`__repr__`()
Returns string representation of the BaseDataType

Returns string represenation

Return type str

`__setstate__`(*state*)

`__str__`()
Returns the string version of the BaseDataType

Returns string version

Return type str

`checksum`()
Generate a checksum for the value of this DataType

Returns the checksum of the value

Return type str

`data_uri`

`description` = **''**

`extension` = **None**

`filename` = **'/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`fullid` = **'fastr://typelist/BaseDataType'**

`id` = **'BaseDataType'**

classmethod `isinstance`(*value*)
Indicate whether value is an instance for this DataType.

Returns the flag indicating the value is of this DataType

Return type bool

`name` = **'BaseDataType'**

`parent` = **DataTypeManager AnalyzeImageFile : <URLType: AnalyzeImageFile> AnyFile : <TypeGroup: AnyFile>**

`parsed_value`
The parsed value of object instantiation of this DataType.

`raw_value`
The raw value of object instantiation of this DataType. For datatypes that override value (like Deferred) this is the way to access the _value field.

classmethod `test`()
Define the test for the BasePluginManager. Make sure we are not one of the base classes

`valid`
A boolean flag that indicates weather or not the value assigned to this DataType is valid. This property is generally overwritten by implementation of specific DataTypes.

`value`
The value of object instantiation of this DataType.

`version` = **<Version: 1.0>**

class `fastr.datatypes.`**`Boolean`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.ValueType`*

Datatype representing a boolean

`__abstractmethods__` = **frozenset([])**

`__module__` = **'fastr.datatypes'**

`__str__()`

`description` = 'A boolean value (True of False)'

`filename` = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

`module` = <module 'Boolean' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/pytho

`value`
The value of object instantiation of this DataType.

class `fastr.datatypes.`**`DataType`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.BaseDataType`*

This class is the base class for all DataTypes that can hold a value.

`__abstractmethods__` = frozenset(['__init__'])

`__init__`(*value=None*, *format_=None*)
The DataType constructor.

Parameters

- **`value`** – value to assign to the new DataType object
- **`format`** – the format used for the ValueType

Returns new DataType object

`__module__` = 'fastr.datatypes'

`action`(*name*)
This function can be overwritten by subclasses to implement certain action that should be performed. For example, the *Directory* DataType has an action *ensure*. This method makes sure the Directory exists. A Tool can indicate an action that should be called for an Output which will be called before execution.

Parameters **`name`** (*`str`*) – name of the action to execute

Returns None

class `fastr.datatypes.`**`Deferred`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.DataType`*

`__abstractmethods__` = frozenset([])

`__getstate__`()

`__init__`(*value=None*, *format_=None*)
The Deferred constructor.

Parameters

- **`value`** – value to assign to the new DataType object
- **`format`** – This is ignore but here for compatibility

Returns new Deferred object

`__module__` = 'fastr.datatypes'

`__repr__`()
Returns string representation of the BaseDataType

Returns string represenation

Return type str

`__setstate__`(*state*)

`checksum`()
Generate a checksum for the value of this DataType

Returns the checksum of the value

Return type str

`data_uri`

`job`

classmethod `lookup`(*value*)
Look up the deferred target and return that object

Param value

Returns The value the deferred points to

Return type *DataType*

Raises

- ***`FastrKeyError`*** – if the deferred is not available (yet)
- ***`FastrValueError`*** – if the value is not a valid deferrred url

`provenance`

`target`
Target object for this deferred.

Raises

- ***`FastrKeyError`*** – if the deferred is not available (yet)
- ***`FastrValueError`*** – if the value is not a valid deferrred url

`value`
The value of object instantiation of this DataType.

class `fastr.datatypes.`**`Directory`**(*value=None, format_=None*)
Bases: *`fastr.datatypes.URLType`*

DataType representing a directory.

`__abstractmethods__` **= frozenset([])**

`__eq__`(*other*)
Directories are equal by default as long as the validatity matches.

Parameters **`other`** (`Directory`) – other to compare against

Returns equality flag

`__module__` **= 'fastr.datatypes'**

`action`(*name*)
This method makes sure the Directory exists. A Tool can indicate an action that should be called for an Output which will be called before execution.

Parameters **`name`** (*`str`*) – name of the action to execute

Returns None

`description` **= 'A directory on the disk'**

`extension` **= None**

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'Directory' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/pytl**

class `fastr.datatypes.`**`EnumType`**(*value=None, format_=None*)
Bases: *`fastr.datatypes.DataType`*

The EnumType is the base for DataTypes that can have a value which is an option from a predefined set of possibilities (similar to an enum type in many programming languages).

`__abstractmethods__` **= frozenset([])**

`__init__`(*value=None*, *format_=None*)
The EnumType constructor.

Parameters

- **`value`** – value to assign to the new EnumType object
- **`format`** – the format used for the ValueType

Returns new EnumType object

Raises *`FastrDataTypeNotInstantiableError`* – if not subclassed

`__module__` = **'fastr.datatypes'**

`description` = **'EnumType (EnumType) is a enumerate type with options:\n\n\nEnumType can take the value of ar**

`options` = **frozenset([])**

`version` = **<Version: 1.0>**

class `fastr.datatypes.`**`Float`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.ValueType`*

`__abstractmethods__` = **frozenset([])**

`__module__` = **'fastr.datatypes'**

`description` = **'A floating point value'**

`filename` = **'/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` = **<module 'Float' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2**

`value`
The value of object instantiation of this DataType.

class `fastr.datatypes.`**`ITKImageFile`**(*value=None*)
Bases: *`fastr.datatypes.TypeGroup`*

`__abstractmethods__` = **frozenset([])**

`__module__` = **'fastr.datatypes'**

`description` = **'Text file to store point coordinates'**

`filename` = **'/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` = **<module 'ITKImageFile' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lil**

class `fastr.datatypes.`**`Int`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.ValueType`*

`__abstractmethods__` = **frozenset([])**

`__module__` = **'fastr.datatypes'**

`description` = **'an integer value'**

`filename` = **'/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` = **<module 'Int' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7**

`value`
The value of object instantiation of this DataType.

class `fastr.datatypes.`**`MetaImageFile`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.URLType`*

`__abstractmethods__` = **frozenset([])**

`__eq__`(*other*)

`__module__` = **'fastr.datatypes'**

checksum()
Return the checksum of this MetaImageFile

Returns checksum string

Return type str

classmethod content(*invalue*, *outvalue=None*)

description = 'Meta Image file format'

extension = 'mhd'

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'MetaImageFile' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/li

class fastr.datatypes.**NiftiImageFile**(*value=None*)
Bases: *fastr.datatypes.TypeGroup*

__abstractmethods__ = frozenset([])

__module__ = 'fastr.datatypes'

description = 'NiftiTypeGroup'

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'NiftiImageFile' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lil

class fastr.datatypes.**NiftiImageFileCompressed**(*value=None*, *format_=None*)
Bases: *fastr.datatypes.URLType*

__abstractmethods__ = frozenset([])

__module__ = 'fastr.datatypes'

description = 'Compressed Nifti Image File format'

extension = 'nii.gz'

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'NiftiImageFileCompressed' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/

class fastr.datatypes.**NiftiImageFileUncompressed**(*value=None*, *format_=None*)
Bases: *fastr.datatypes.URLType*

__abstractmethods__ = frozenset([])

__module__ = 'fastr.datatypes'

description = 'Nifti Image File format'

extension = 'nii'

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'NiftiImageFileUncompressed' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/env

class fastr.datatypes.**Number**(*value=None*)
Bases: *fastr.datatypes.TypeGroup*

__abstractmethods__ = frozenset([])

__module__ = 'fastr.datatypes'

description = 'an numeric value'

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'Number' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/pyth

class fastr.datatypes.**String**(*value=None*, *format_=None*)
Bases: *fastr.datatypes.ValueType*

`__abstractmethods__` **= frozenset([])**

`__module__` **= 'fastr.datatypes'**

`description` **= 'A simple string value'**

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'String' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python**

class `fastr.datatypes.`**`TifImageFile`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.URLType`*

`__abstractmethods__` **= frozenset([])**

`__module__` **= 'fastr.datatypes'**

`description` **= 'Tif Image File format'**

`extension` **= 'tif'**

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'TifImageFile' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/**

class `fastr.datatypes.`**`TypeGroup`**(*value=None*)
Bases: *`fastr.datatypes.BaseDataType`*

The TypeGroup is a special DataType that does not hold a value of its own but is used to group a number of DataTypes. For example ITK has a list of supported file formats that all tools build on ITK support. A group can be used to conveniently specify this in multiple Tools that use the same set DataTypes.

`__abstractmethods__` **= frozenset(['_members'])**

`__init__`(*value=None*)
Dummy constructor. TypeGroups are not instantiable and cannot hold a value of its own.

Raises ***`FastrDataTypeNotInstantiableError`*** – if called

`__module__` **= 'fastr.datatypes'**

static **`__new__`**(*value=None*, *format_=None*)
Instantiate a TypeGroup. This will for match the value to the best matching type and instantiate that. Not that the returned object will not be of type TypeGroup but one of the TypeGroup members.

classmethod **`isinstance`**(*value*)

`members`
A descriptor that can act like a property for a class.

class `fastr.datatypes.`**`URLType`**(*value=None*, *format_=None*)
Bases: *`fastr.datatypes.DataType`*

The URLType is the base for DataTypes that point to a resource somewhere else (typically a filesystem). The true value is actually the resource referenced by the value in this object.

`__abstractmethods__` **= frozenset([])**

`__eq__`(*other*)
Test the equality of two DataType objects

Parameters **`other`** (`URLType`) – the object to compare against

Returns flag indicating equality

Return type bool

`__init__`(*value=None*, *format_=None*)
The URLType constructor

Parameters

- **`value`** – value to assign to the new URLType

- **format** – the format used for the ValueType

Returns new URLType object

__module__ = 'fastr.datatypes'

checksum()
Return the checksum of this URL type

Returns checksum string

Return type str

classmethod content(*inval*, *outval=None*)
Give the contents of a URLType, this is generally useful for filetypes that consists of multiple files (e.g. AnalyzeImageFile, DICOM). The value will indicate the main file, and the contents function can determine all files that form a single data value.

Parameters

- **inval** – a value to figure out contents for this type
- **outval** – the place where the copy should point to

Returns a list of all files part of the value (e.g. header and data file)

Return type list

parsed_value
The parsed value of object instantiation of this DataType.

valid
A boolean flag that indicates weather or not the value assigned to this DataType is valid. This property is generally overwritten by implementation of specific DataTypes.

class fastr.datatypes.**UnsignedInt**(*value=None*, *format_=None*)
Bases: *fastr.datatypes.ValueType*

__abstractmethods__ = frozenset([])

__module__ = 'fastr.datatypes'

description = 'an unsigned integer value'

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'UnsignedInt' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/p

value
The value of object instantiation of this DataType.

class fastr.datatypes.**ValueType**(*value=None*, *format_=None*)
Bases: *fastr.datatypes.DataType*

The ValueType is the base for DataTypes that hold simple values (not an EnumType and not a file/URL). The values is generally represented by a string.

__abstractmethods__ = frozenset([])

__init__(*value=None*, *format_=None*)
The ValueType constructor

Parameters

- **value** – value to assign to the new ValueType
- **format** – the format used for the ValueType

Returns new ValueType object

__module__ = 'fastr.datatypes'

class `fastr.datatypes.`**`__ioplugin__behaviour__Enum__`**(*value=None*, *format_=None*)

Bases: *`fastr.datatypes.EnumType`*

`__abstractmethods__` **= frozenset([])**

`__module__` **= 'fastr.datatypes'**

`parent` **= DataTypeManager AnalyzeImageFile : <URLType: AnalyzeImageFile> AnyFile : <TypeGroup: AnyFile>**

`fastr.datatypes.`**`fastr_isinstance`**(*obj*, *datatype*)

Check if an object is of a specific datatype.

Parameters

- **`obj`** – Object to inspect
- **`datatype`** (*`tuple`*, `BaseDataType`) – The datatype(s) to check

Returns flag indicating object is of datatype

Return type bool

`exceptions` Module

This module contains all Fastr-related Exceptions

exception `fastr.exceptions.`**`FastrAttributeError`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrError`*, `exceptions.AttributeError`

AttributeError in the fastr system

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrCannotChangeAttributeError`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrError`*

Attempting to change an attribute of an object that can be set only once.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrCardinalityError`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrError`*

The description of the cardinality is not valid.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrDataTypeFileNotReadable`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrError`*

Could not read the datatype file.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrDataTypeMismatchError`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrError`*

When using a DataType as the key for the DataTypeManager, the DataTypeManager found another DataType with the same name already in the DataTypeManager. The means fastr has two version of the same DataType in the system, which should never happen!

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrDataTypeNotAvailableError`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrError`*

The DataType requested is not found by the fastr system. Typically this means that no matching DataType is found in the DataTypeManager.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrDataTypeNotInstantiableError`**(**args*, ***kwargs*)
Bases: `fastr.exceptions.FastrError`

The base classes for DataTypes cannot be instantiated and should always be sub-classed.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrDataTypeValueError`**(**args*, ***kwargs*)
Bases: `fastr.exceptions.FastrError`

This value in fastr did not pass the validation specificied for its DataType, typically means that the data is missing or corrupt.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrError`**(**args*, ***kwargs*)
Bases: `exceptions.Exception`

This is the base class for all fastr related exceptions. Catching this class of exceptions should ensure a proper execution of fastr.

`__init__`(**args*, ***kwargs*)
Constructor for all exceptions. Saves the caller object fullid (if found) and the file, function and line number where the object was created.

`__module__` **= 'fastr.exceptions'**

`__str__`()
String representation of the error

Returns error string

Return type str

`__weakref__`
list of weak references to the object (if defined)

`excerpt`()
Return a excerpt of the Error as a tuple.

exception `fastr.exceptions.`**`FastrErrorInSubprocess`**(**args*, ***kwargs*)
Bases: `fastr.exceptions.FastrExecutionError`

Encountered an error in the subprocess started by the execution script

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrExecutableNotFoundError`**(*executable=None*, **args*, ***kwargs*)
Bases: `fastr.exceptions.FastrExecutionError`

The executable could not be found!

`__init__`(*executable=None*, **args*, ***kwargs*)

`__module__` **= 'fastr.exceptions'**

`__str__`()
String representation of the error

exception `fastr.exceptions.`**`FastrExecutionError`**(**args*, ***kwargs*)
Bases: `fastr.exceptions.FastrError`

Base class for all fastr execution related errors

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrIOError`**(**args*, ***kwargs*)
Bases: `fastr.exceptions.FastrError`, `exceptions.IOError`

IOError in the fastr system

`__module__` = 'fastr.exceptions'

`__weakref__`
list of weak references to the object (if defined)

exception `fastr.exceptions.`**`FastrImportError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*, `exceptions.ImportError`

ImportError in the fastr system

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrIndexError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*, `exceptions.IndexError`

IndexError in the fastr system

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrIndexNonexistent`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrIndexError`*

This is an IndexError for samples requested from a sparse data array. The sample is not there but is probably not there because of sparseness rather than being a missing sample (e.g. out of bounds).

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrKeyError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*, `exceptions.KeyError`

KeyError in the fastr system

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrLookupError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

Could not find specified object in the fastr environment.

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrMountUnknownError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrKeyError`*

Trying to access an undefined mount

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrNetworkMismatchError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

Two interacting objects belong to different fastr network.

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrNetworkUnknownError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrKeyError`*

Reference to a Tool that is not recognised by the fastr system. This typically means the specific id/version combination of the requested tool has not been loaded by the ToolManager.

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrNoValidTargetError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrKeyError`*

Cannot find a valid target for the tool

`__module__` = 'fastr.exceptions'

exception `fastr.exceptions.`**`FastrNodeAreadyPreparedError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrStateError`*

A attempt is made at preparing a Node for the second time. This is not allowed as it would wipe the current execution data and cause data-loss.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrNodeNotPreparedError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrStateError`*

When trying to access executation data of a Node, the Node must be prepare. The Node has not been prepared by the execution, so the data is not available!

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrNodeNotValidError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrStateError`*

A Node is not in a valid state where it should be, typically an invalid Node is passed to the executor causing trouble.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrNotExecutableError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrExecutionError`*

The command invoked by subprocess is not executable on the system

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrNotImplementedError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*, `exceptions.NotImplementedError`

This function/method has not been implemented on purpose (e.g. should be overwritten in a sub-class)

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrOSError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*, `exceptions.OSError`

OSError in the fastr system

`__module__` **= 'fastr.exceptions'**

`__weakref__`
list of weak references to the object (if defined)

exception `fastr.exceptions.`**`FastrObjectUnknownError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrKeyError`*

Reference to a Tool that is not recognised by the fastr system. This typically means the specific id/version combination of the requested tool has not been loaded by the ToolManager.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrOptionalModuleNotAvailableError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrNotImplementedError`*

A optional modules for Fastr is needed for this function, but is not available on the current python installation.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrOutputValidationError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrExecutionError`*

An output of a Job does not pass validation

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrParentMismatchError`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrError`*

Two interactive objects have different parent where they should be the same

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrPluginNotAvailable`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrKeyError`*

Indicates that a requested Plugin was not found on the system.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrPluginNotLoaded`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrStateError`*

The plugin was not successfully loaded. This means the plugin class cannot be instantiated.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrResultFileNotFound`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrExecutionError`*

Could not found the result file of job that finished. This means the executionscript process was killed during interruption. Generally this means a scheduler killed it because of resource shortage.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSerializationError`**(*message*, *serializer*, *original_exception=None*)

Bases: *`fastr.exceptions.FastrError`*

The serialization encountered a serious problem

`__init__`(*message*, *serializer*, *original_exception=None*)

`__module__` **= 'fastr.exceptions'**

`__repr__`()

Simple string representation of the exception

`__str__`()

Advanced string representation of the exception including the data about where in the schema things went wrong.

exception `fastr.exceptions.`**`FastrSerializationIgnoreDefaultError`**(*message*, *serializer*, *original_exception=None*)

Bases: *`fastr.exceptions.FastrSerializationError`*

The value and default are both None, so the value should not be serialized.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSerializationInvalidDataError`**(*message*, *serializer*, *original_exception=None*)

Bases: *`fastr.exceptions.FastrSerializationError`*

Encountered data to serialize that is invalid given the serialization schema.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSerializationMethodError`**(**args*, ***kwargs*)

Bases: *`fastr.exceptions.FastrKeyError`*

The desired serialization method does not exist.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSinkDataUnavailableError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrKeyError`*

Could not find the Sink data for the desire sink.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSizeInvalidError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

The given size cannot be valid.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSizeMismatchError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

The size of two object in fastr is not matching where it should.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSizeUnknownError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

The size of object is not (yet) known and only a theoretical estimate is available at the moment.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSourceDataUnavailableError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrKeyError`*

Could not find the Source data for the desire source.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrStateError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

An object is in an invalid/unexpected state.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrSubprocessNotFinished`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrExecutionError`*

Encountered an error before the subprocess call by the execution script was properly finished.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrToolNotAvailableError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

The tool used is not available on the current platform (OS and architecture combination) and cannot be used.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrToolTargetNotFound`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrError`*

Could not determine the location of the tools target binary/script. The tool cannot be used.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrToolUnknownError`**(**args*, ***kwargs*)
Bases: *`fastr.exceptions.FastrKeyError`*

Reference to a Tool that is not recognised by the fastr system. This typically means the specific id/version combination of the requested tool has not been loaded by the ToolManager.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrTypeError`**`(`**args*, ***kwargs*`)`
Bases: *`fastr.exceptions.FastrError`*, `exceptions.TypeError`

TypeError in the fastr system

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrUnknownURLSchemeError`**`(`**args*, ***kwargs*`)`
Bases: *`fastr.exceptions.FastrKeyError`*

Fastr encountered a data URL with a scheme that was not recognised by the IOPlugin manager.

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrValueError`**`(`**args*, ***kwargs*`)`
Bases: *`fastr.exceptions.FastrError`*, `exceptions.ValueError`

ValueError in the fastr system

`__module__` **= 'fastr.exceptions'**

exception `fastr.exceptions.`**`FastrVersionInvalidError`**`(`**args*, ***kwargs*`)`
Bases: *`fastr.exceptions.FastrValueError`*

The string representation of the version is malformatted.

`__module__` **= 'fastr.exceptions'**

`plugins` Module

The plugins module holds all plugins loaded by Fastr. It is empty on start and gets filled by the BasePluginManager

class `fastr.plugins.`**`BlockingExecution`**`(`*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*`)`
Bases: *`fastr.execution.executionpluginmanager.ExecutionPlugin`*

The blocking execution plugin is a special plugin which is meant for debug purposes. It will not queue jobs but immediately execute them inline, effectively blocking fastr until the Job is finished. It is the simplest execution plugin and can be used as a template for new plugins or for testing purposes.

`__abstractmethods__` **= frozenset([])**

`__init__``(`*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*`)`

`__module__` **= 'fastr.plugins'**

`cleanup``()`

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'blockingexecution' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/loca**

class `fastr.plugins.`**`CommaSeperatedValueFile`**
Bases: *`fastr.core.ioplugin.IOPlugin`*

The CommaSeperatedValueFile an expand-only type of IOPlugin. No URLs can actually be fetched, but it can expand a single URL into a larger amount of URLs.

The `csv://` URL is a `vfs://` URL with a number of query variables available. The URL mount and path should point to a valid CSV file. The query variable then specify what column(s) of the file should be used.

The following variable can be set in the query:

variable	usage
value	the column containing the value of interest, can be int for index or string for key
id	the column containing the sample id (optional)
header	indicates if the first row is considered the header, can be `true` or `false` (optional)
delimiter	the delimiter used in the csv file (optional)
quote	the quote character used in the csv file (optional)
reformat	a reformatting string so that `value = reformat.format(value)` (used before relative_path)
rela-tive_path	indicates the entries are relative paths (for files), can be `true` or `false` (optional)

The header is by default `false` if the neither the `value` and `id` are set as a string. If either of these are a string, the header is required to define the column names and it automatically is assumed `true`

The delimiter and quota characters of the file should be detected automatically using the `Sniffer`, but can be forced by setting them in the URL.

Example of valid `csv` URLs:

```
# Use the first column in the file (no header row assumed)
csv://mount/some/dir/file.csv?value=0

# Use the images column in the file (first row is assumed header row)
csv://mount/some/dir/file.csv?value=images

# Use the segmentations column in the file (first row is assumed header row)
# and use the id column as the sample id
csv://mount/some/dir/file.csv?value=segmentations&id=id

# Use the first column as the id and the second column as the value
# and skip the first row (considered the header)
csv://mount/some/dir/file.csv?value=1&id=0&header=true

# Use the first column and force the delimiter to be a comma
csv://mount/some/dir/file.csv?value=0&delimiter=,
```

`__abstractmethods__` = frozenset([])

`__init__`()

`__module__` = 'fastr.plugins'

`expand_url`(*url*)

`filename` = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

`module` = <module 'commaseperatedvaluefile' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.

`scheme` = 'csv'

class `fastr.plugins.`**`CrossValidation`**

Bases: `flowinterface.FlowPlugin`

Advanced flow plugin that generated a cross-validation data flow. The node need an input with data and an input number of folds. Based on that the outputs test and train will be supplied with a number of data sets.

`__abstractmethods__` = frozenset([])

`__module__` = 'fastr.plugins'

static `execute`(*payload*)

`filename` = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

`module` = <module 'crossvalidation' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/li

class `fastr.plugins.`**`DRMAAExecution`**(*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)

Bases: *`fastr.execution.executionpluginmanager.ExecutionPlugin`*

A DRMAA execution plugin to execute Jobs on a Grid Engine cluster. It uses a configuration option for selecting the queue to submit to. It uses the python `drmaa` package.

Note: To use this plugin, make sure the `drmaa` package is installed and that the execution is started on an SGE submit host with DRMAA libraries installed.

Note: This plugin is at the moment tailored to SGE, but it should be fairly easy to make different subclasses for different DRMAA supporting systems.

`__abstractmethods__` **= frozenset([])**

`__init__`(*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)

`__module__` **= 'fastr.plugins'**

`cleanup`()

`collect_jobs`()

`configuration_fields` **= {'drmaa_queue': (<type 'str'>, 'week', 'The default queue to use for jobs send to the sc**

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'drmaaexecution' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/**

`send_job`(*command*, *arguments*, *queue=None*, *walltime=None*, *job_name=None*, *memory=None*, *ncores=None*, *joinLogFiles=False*, *outputLog=None*, *errorLog=None*, *hold_job=None*)

`submit_jobs`()

class `fastr.plugins.`**`FastrInterface`**(*id_*, *document*)

Bases: *`fastr.core.interface.Interface`*

The default Interface for fastr. For the command-line Tools as used by fastr.

`__abstractmethods__` **= frozenset([])**

`__dataschemafile__` **= 'FastrInterface.schema.json'**

`__eq__`(*other*)

`__getstate__`()

Get the state of the FastrInterface object.

Returns state of interface

Return type dict

`__init__`(*id_*, *document*)

`__module__` **= 'fastr.plugins'**

`__setstate__`(*state*)

Set the state of the Interface

`check_input_id`(*id_*)

Check if an id for an object is valid and unused in the Tool. The method will always returns True if it does not raise an exception.

Parameters **`id`** (*`str`*) – the id to check

Returns True

Raises

- *FastrValueError* – if the id is not correctly formatted
- *FastrValueError* – if the id is already in use

check_output_id(*id_*)

Check if an id for an object is valid and unused in the Tool. The method will always returns True if it does not raise an exception.

Parameters **id** (*str*) – the id to check

Returns True

Raises

- *FastrValueError* – if the id is not correctly formatted
- *FastrValueError* – if the id is already in use

collect_results(*result*)

Collect all results of the interface

collector_plugin_type

alias of `CollectorPlugin`

collectors = CollectorPluginManager [37m[42m[1mLoaded[0m json : <CollectorPlugin: JsonCollector> [37m[42r

execute(*target*, *payload*)

Execute the interface using a specific target and payload (containing a set of values for the arguments)

Parameters

- **target** (*SampleId*) – the target to use
- **payload** (*dict*) – the values for the arguments

Returns result of the execution

Return type *InterfaceResult*

expanding()

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

get_arguments(*values*)

Get the argument list for this interface

Returns return list of arguments

get_specials(*payload*, *output*, *cardinality_nr*)

Get special attributes. Returns tuples for specials, inputs and outputs that are used for formatting substitutions.

Parameters

- **output** – Output for which to get the specials
- **cardinality_nr** (*int*) – the cardinality number

inputs

module = <module 'fastrinterface' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/

outputs

class fastr.plugins.**FileSystem**

Bases: *fastr.core.ioplugin.IOPlugin*

The FileSystem plugin is create to handle `file://` type or URLs. This is generally not a good practice, as this is not portable over between machines. However, for test purposes it might be useful.

The URL scheme is rather simple: `file://host/path` (see wikipedia for details)

We do not make use of the `host` part and at the moment only support localhost (just leave the host empty) leading to `file:///` URLs.

Warning: This plugin ignores the hostname in the URL and does only accept driver letters on Windows in the form `c:/`

`__abstractmethods__` **= frozenset([])**

`__init__`()

`__module__` **= 'fastr.plugins'**

`fetch_url`(*inurl*, *outpath*)
Fetch the files from the file.

Parameters

- **`inurl`** – url to the item in the data store, starts with `file://`
- **`outpath`** – path where to store the fetch data locally

`fetch_value`(*inurl*)
Fetch a value from an external file file.

Parameters **`inurl`** – url of the value to read

Returns the fetched value

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'filesystem' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/pyt**

`path_to_url`(*path*, *mountpoint=None*)
Construct an url from a given mount point and a relative path to the mount point.

`put_url`(*inpath*, *outurl*)
Put the files to the external data store.

Parameters

- **`inpath`** – path of the local data
- **`outurl`** – url to where to store the data, starts with `file://`

`put_value`(*value*, *outurl*)
Put the value in the external data store.

Parameters

- **`value`** – value to store
- **`outurl`** – url to where to store the data, starts with `file://`

`scheme` **= 'file'**

`url_to_path`(*url*)
Get the path to a file from a url. Currently supports the file:// scheme

Examples:

```
>>> 'file:///d:/data/project/file.ext'
'd:\data\project\file.ext'
```

Warning: file:// will not function cross platform and is mainly for testing

class `fastr.plugins.`**`FlowInterface`**(*id_*, *document*)

Bases: *`fastr.core.interface.Interface`*

The Interface use for AdvancedFlowNodes to create the advanced data flows that are not implemented in the fastr. This allows nodes to implement new data flows using the plugin system.

The definition of `FlowInterfaces` are very similar to the default `FastrInterfaces`.

Note: A flow interface should be using a specific FlowPlugin

`__abstractmethods__` **= frozenset([])**

`__dataschemafile__` **= 'FastrInterface.schema.json'**

`__eq__`(*other*)

`__getstate__`()

Get the state of the FastrInterface object.

Returns state of interface

Return type dict

`__init__`(*id_*, *document*)

`__module__` **= 'fastr.plugins'**

`__setstate__`(*state*)

Set the state of the Interface

`execute`(*target*, *payload*)

`expanding`()

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`flow_plugin_type`

alias of `FlowPlugin`

`flow_plugins` **= FlowPluginManager [37m[42m[1mLoaded[0m CrossValidation : <FlowPlugin: CrossValidation>**

`inputs`

`module` **= <module 'flowinterface' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/**

`outputs`

class `fastr.plugins.`**`LinearExecution`**(*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)

Bases: *`fastr.execution.executionpluginmanager.ExecutionPlugin`*

An execution engine that has a background thread that executes the jobs in order. The queue is a simple FIFO queue and there is one worker thread that operates in the background. This plugin is meant as a fallback when other plugins do not function properly. It does not multi-processing so it is safe to use in environments that do no support that.

`__abstractmethods__` **= frozenset([])**

`__init__`(*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)

`__module__` **= 'fastr.plugins'**

`cleanup`()

`exec_worker`()

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'linearexecution' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/li**

class `fastr.plugins.`**`NipypeInterface`**(*id_*, *nipype_cls=None*, *document=None*)

Bases: *`fastr.core.interface.Interface`*

Experimental interfaces to using `nipype` interfaces directly in fastr tools, only using a simple reference.

To create a tool using a nipype interface just create an interface with the correct type and set the `nipype` argument to the correct class. For example in an xml tool this would become:

```
<interface class="NipypeInterface">
  <nipype_class>nipype.interfaces.elastix.Registration</nipype_class>
</interface>
```

Note: To use these interfaces `nipype` should be installed on the system.

Warning: This interface plugin is basically functional, but highly experimental!

`__abstractmethods__` **= frozenset([])**

`__eq__`(*other*)

`__getstate__`()

`__init__`(*id_*, *nipype_cls=None*, *document=None*)

`__module__` **= 'fastr.plugins'**

`__setstate__`(*state*)

`execute`(*target*, *payload*)

Execute the interface using a specific target and payload (containing a set of values for the arguments)

Parameters

- **`target`** (*`SampleId`*) – the target to use
- **`payload`** (*`dict`*) – the values for the arguments

Returns result of the execution

Return type *InterfaceResult*

`expanding`()

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`get_type`(*trait*)

`inputs`

`module` **= <module 'nipypeinterface' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/l**

`outputs`

classmethod **`test`**()

class `fastr.plugins.`**`Null`**

Bases: *`fastr.core.ioplugin.IOPlugin`*

The Null plugin is create to handle `null://` type or URLs. These URLs are indicating the sink should not do anything. The data is not written to anywhere. Besides the scheme, the rest of the URL is ignored.

`__abstractmethods__` **= frozenset([])**

`__init__`()

`__module__` **= 'fastr.plugins'**

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'null' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.**

`put_url` (*inpath*, *outurl*)
Put the files to the external data store.

Parameters

- **`inpath`** – path of the local data
- **`outurl`** – url to where to store the data, starts with `file://`

`put_value` (*value*, *outurl*)
Put the value in the external data store.

Parameters

- **`value`** – value to store
- **`outurl`** – url to where to store the data, starts with `file://`

`scheme` **= 'null'**

class `fastr.plugins.`**`ProcessPoolExecution`** (*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*, *nr_of_workers=None*)
Bases: *`fastr.execution.executionpluginmanager.ExecutionPlugin`*

A local execution plugin that uses multiprocessing to create a pool of worker processes. This allows fastr to execute jobs in parallel with true concurrency. The number of workers can be specified in the fastr configuration, but the default amount is the `number of cores - 1` with a minimum of `1`.

> **Warning:** The ProcessPoolExecution does not check memory requirements of jobs and running many workers might lead to memory starvation and thus an unresponsive system.

`__abstractmethods__` **= frozenset([])**

`__init__` (*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*, *nr_of_workers=None*)

`__module__` **= 'fastr.plugins'**

`cleanup` ()

`configuration_fields` **= {'process_pool_worker_number': (<type 'int'>, 3, 'Number of workers to use in a proc**

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'processpoolexecution' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/l**

classmethod **`test`** ()

class `fastr.plugins.`**`RQExecution`** (*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)
Bases: *`fastr.execution.executionpluginmanager.ExecutionPlugin`*

A execution plugin based on Redis Queue. Fastr will submit jobs to the redis queue and workers will peel the jobs from the queue and process them.

This system requires a running redis database and the database url has to be set in the fastr configuration.

> **Note:** This execution plugin required the `redis` and `rq` packages to be installed before it can be loaded properly.

`__abstractmethods__` **= frozenset([])**

`__init__` (*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)

`__module__` **= 'fastr.plugins'**

check_finished()

cleanup()

configuration_fields = {'rq_queue': (<type 'str'>, 'default', 'The redis queue to use'), 'rq_host': (<type 'str'>,

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'rqexecution' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/p

classmethod run_job(*job_id*, *job_command*, *job_stdout*, *job_stderr*)

class fastr.plugins.**Reference**

Bases: *fastr.core.ioplugin.IOPlugin*

The Reference plugin is create to handle `ref://` type or URLs. These URLs are to make the sink just write a simple reference file to the data. The reference file contains the DataType and the value so the result can be reconstructed. It for files just leaves the data on disk by reference. This plugin is not useful for production, but is used for testing purposes.

__abstractmethods__ = frozenset([])

__init__()

__module__ = 'fastr.plugins'

filename = '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas

module = <module 'reference' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/pytl

push_sink_data(*value*, *outurl*, *datatype=None*)

Write out the sink data from the inpath to the outurl.

Parameters

- **value** (*str*) – the path of the data to be pushed
- **outurl** (*str*) – the url to write the data to
- **datatype** (DataType) – the datatype of the data, used for determining the total contents of the transfer

Returns None

scheme = 'ref'

class fastr.plugins.**VirtualFileSystem**

Bases: *fastr.core.ioplugin.IOPlugin*

The virtual file system class. This is an IOPlugin, but also heavily used internally in fastr for working with directories. The VirtualFileSystem uses the `vfs://` url scheme.

A typical virtual filesystem url is formatted as `vfs://mountpoint/relative/dir/from/mount.ext`

Where the `mountpoint` is defined in the *Config file*. A list of the currently known mountpoints can be found in the `fastr.config` object

```
>>> fastr.config.mounts
{'example_data': '/home/username/fastr-feature-documentation/fastr/fastr/
↪examples/data',
 'home': '/home/username/',
 'tmp': '/home/username/FastrTemp'}
```

This shows that a url with the mount `home` such as `vfs://home/tempdir/testfile.txt` would be translated into `/home/username/tempdir/testfile.txt`.

There are a few default mount points defined by Fastr (that can be changed via the config file).

mountpoint	default location
home	the users home directory (`expanduser('~/')`)
tmp	the fastr temprorary dir, defaults to `tempfile.gettempdir()`
example_data	the fastr example data directory, defaults `$FASTRDIR/example/data`

`__abstractmethods__` = frozenset([])

`__init__`()
Instantiate the VFS plugin

Returns the VirtualFileSysten plugin

`__module__` = 'fastr.plugins'

static **`copy_file_dir`**(*inpath*, *outpath*)
Helper function, copies a file or directory not caring what the inpath actually is

Parameters

- **`inpath`** – path of the things to be copied
- **`outpath`** – path of the destination

Returns the result of shutil.copy2 or shutil.copytree (depending on inpath pointing to a file or directory)

`expand_url`(*url*)
Try to expand the url. For vfs with will return the original url.

Parameters **`url`** – url to expand

Returns the expanded url (same as url)

`fetch_url`(*inurl*, *outpath*)
Fetch the files from the vfs.

Parameters

- **`inurl`** – url to the item in the data store, starts with `vfs://`
- **`outpath`** – path where to store the fetch data locally

`fetch_value`(*inurl*)
Fetch a value from an external vfs file.

Parameters **`inurl`** – url of the value to read

Returns the fetched value

`path_to_url`(*path*, *mountpoint=None*, *scheme=None*)
Construct an url from a given mount point and a relative path to the mount point.

Parameters **`path`** (`str`) – the path to find the url for

Mountpoint str mountpoint the url should be under

Returns url of the

`put_url`(*inpath*, *outurl*)
Put the files to the external data store.

Parameters

- **`inpath`** – path of the local data
- **`outurl`** – url to where to store the data, starts with `vfs://`

`put_value`(*value*, *outurl*)
Put the value in the external data store.

Parameters

- **`value`** – value to store

- **outurl** – url to where to store the data, starts with `vfs://`

scheme

setup()
The plugin setup, does nothing but needs to be implemented

url_to_path(*url*, *scheme=None*)
Get the path to a file from a vfs url

Parameters **url** (*str*) – url to get the path for

Returns the matching path

Return type str

Raises

- ***FastrMountUnknownError*** – if the mount in url is unknown
- ***FastrUnknownURLSchemeError*** – if the url scheme is not correct

Example (the mountpoint tmp points to /tmp):

```
>>> fastr.vfs.url_to_path('vfs://tmp/file.ext')
'/tmp/file.ext'
```

class fastr.plugins.**VirtualFileSystemRegularExpression**
Bases: *fastr.core.ioplugin.IOPlugin*

The VirtualFileSystemValueList an expand-only type of IOPlugin. No URLs can actually be fetched, but it can expand a single URL into a larger amount of URLs.

A `vfsregex://` URL is a vfs URL that can contain regular expressions on every level of the path. The regular expressions follow the `re module` definitions.

An example of a valid URLs would be:

```
vfsregex://tmp/network_dir/.*/.*/__fastr_result__.pickle.gz
vfsregex://tmp/network_dir/nodeX/(?P<id>.*)/__fastr_result__.pickle.gz
```

The first URL would result in all the `__fastr_result__.pickle.gz` in the working directory of a Network. The second URL would only result in the file for a specific node (nodeX), but by adding the named group `id` using `(?P<id>.*)` the sample id of the data is automatically set to that group (see Regular Expression Syntax under the special characters for more info on named groups in regular expression).

Concretely if we would have a directory `vfs://mount/somedir` containing:

```
image_1/Image.nii
image_2/image.nii
image_3/anotherimage.nii
image_5/inconsistentnamingftw.nii
```

we could match these files using `vfsregex://mount/somedir/(?P<id>image_\d+)/.*\.nii` which would result in the following source data after expanding the URL:

```
{'image_1': 'vfs://mount/somedir/image_1/Image.nii',
 'image_2': 'vfs://mount/somedir/image_2/image.nii',
 'image_3': 'vfs://mount/somedir/image_3/anotherimage.nii',
 'image_5': 'vfs://mount/somedir/image_5/inconsistentnamingftw.nii'}
```

Showing the power of this regular expression filtering. Also it shows how the ID group from the URL can be used to have sensible sample ids.

Warning: due to the nature of regexp on multiple levels, this method can be slow when having many matches on the lower level of the path (because the tree of potential matches grows) or when directories that are parts of the path are very large.

`__abstractmethods__` **= frozenset([])**

`__init__``()`

`__module__` **= 'fastr.plugins'**

`expand_url``(`*url*`)`

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'virtualfilesystemregularexpression' from '/home/docs/checkouts/readthedocs.org/user_builds/fas**

`scheme` **= 'vfsregex'**

class `fastr.plugins.`**`VirtualFileSystemValueList`**

Bases: *`fastr.core.ioplugin.IOPlugin`*

The VirtualFileSystemValueList an expand-only type of IOPlugin. No URLs can actually be fetched, but it can expand a single URL into a larger amount of URLs. A `vfslist://` URL basically is a url that points to a file using vfs. This file then contains a number lines each containing another URL.

If the contents of a file `vfs://mount/some/path/contents` would be:

```
vfs://mount/some/path/file1.txt
vfs://mount/some/path/file2.txt
vfs://mount/some/path/file3.txt
vfs://mount/some/path/file4.txt
```

Then using the URL `vfslist://mount/some/path/contents` as source data would result in the four files being pulled.

Note: The URLs in a vfslist file do not have to use the `vfs` scheme, but can use any scheme known to the Fastr system.

`__abstractmethods__` **= frozenset([])**

`__init__``()`

`__module__` **= 'fastr.plugins'**

`expand_url``(`*url*`)`

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'virtualfilesystemvaluelist' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.**

`scheme` **= 'vfslist'**

class `fastr.plugins.`**`XNATStorage`**

Bases: *`fastr.core.ioplugin.IOPlugin`*

Warning: As this IOPlugin is under development, it has not been thoroughly tested.

The XNATStorage plugin is an IOPlugin that can download data from and upload data to an XNAT server. It uses its own `xnat://` URL scheme. This is a scheme specific for this plugin and though it looks somewhat like the XNAT rest interface, a different type or URL.

Data resources can be access directly by a data url:

```
xnat://xnat.example.com/data/archive/projects/sandbox/subjects/subject001/
↪experiments/experiment001/scans/T1/resources/DICOM
xnat://xnat.example.com/data/archive/projects/sandbox/subjects/subject001/
↪experiments/*_BRAIN/scans/T1/resources/DICOM
```

In the second URL you can see a wildcard being used. This is possible at long as it resolves to exactly one item.

The `id` query element will change the field from the default experiment to subject and the `label` query element sets the use of the label as the fastr id (instead of the XNAT id) to `True` (the default is `False`)

To disable `https` transport and use `http` instead the query string can be modified to add `insecure=true`. This will make the plugin send requests over `http`:

```
xnat://xnat.example.com/data/archive/projects/sandbox/subjects/subject001/
↪experiments/*_BRAIN/scans/T1/resources/DICOM?insecure=true
```

For sinks it is import to know where to save the data. Sometimes you want to save data in a new assessor/resource and it needs to be created. To allow the Fastr sink to create an object in XNAT, you have to supply the type as a query parameter:

```
xnat://xnat.bmia.nl/data/archive/projects/sandbox/subjects/S01/experiments/_
↪BRAIN/assessors/test_assessor/resources/IMAGE/files/image.nii.gz?resource_
↪type=xnat:resourceCatalog&assessor_type=xnat:qcAssessmentData
```

Valid options are: subject_type, experiment_type, assessor_type, scan_type, and resource_type.

If you want to do a search where multiple resources are returned, it is possible to use a search url:

```
xnat://xnat.example.com/search?projects=sandbox&subjects=subject[0-9][0-9][0-
↪9]&experiments=*_BRAIN&scans=T1&resources=DICOM
```

This will return all DICOMs for the T1 scans for experiments that end with _BRAIN that belong to a subjectXXX where XXX is a 3 digit number. By default the ID for the samples will be the experiment XNAT ID (e.g. XNAT_E00123). The wildcards that can be the used are the same UNIX shell-style wildcards as provided by the module `fnmatch`.

It is possible to change the id to a different fields id or label. Valid fields are project, subject, experiment, scan, and resource:

```
xnat://xnat.example.com/search?projects=sandbox&subjects=subject[0-9][0-9][0-
↪9]&experiments=*_BRAIN&scans=T1&resources=DICOM&id=subject&label=true
```

The following variables can be set in the search query:

variable	default	usage
projects	`*`	The project(s) to select, can contain wildcards (see `fnmatch`)
subjects	`*`	The subject(s) to select, can contain wildcards (see `fnmatch`)
experiments	`*`	The experiment(s) to select, can contain wildcards (see `fnmatch`)
scans	`*`	The scan(s) to select, can contain wildcards (see `fnmatch`)
resources	`*`	The resource(s) to select, can contain wildcards (see `fnmatch`)
id	`experiment`	What field to use a the id, can be: project, subject, experiment, scan, or resource
label	`false`	Indicate the XNAT label should be used as fastr id, options `true` or `false`
insecure	`false`	Change the url scheme to be used to http instead of https
regex	`false`	Change search to use regex `re.match()` instead of fnmatch for matching

For storing credentials the `.netrc` file can be used. This is a common way to store credentials on UNIX systems. It is required that the file is only accessible by the owner only or a `NetrcParseError` will be raised. A netrc file is really easy to create, as its entries look like:

```
machine xnat.example.com
        login username
        password secret123
```

See the `netrc module` or the GNU inet utils website for more information about the `.netrc` file.

Note: On windows the location of the netrc file is assumed to be `os.path.expanduser('~/_netrc')`. The leading underscore is because windows does not like filename starting with a dot.

Note: For scan the label will be the scan type (this is initially the same as the series description, but can be updated manually or the XNAT scan type cleanup).

Warning: labels in XNAT are not guaranteed to be unique, so be careful when using them as the sample ID.

For background on XNAT, see the XNAT API DIRECTORY for the REST API of XNAT.

`__abstractmethods__` **= frozenset([])**

`__init__`()

`__module__` **= 'fastr.plugins'**

`cleanup`()

`connect`(*server*, *path=''*, *insecure=False*)

`expand_url`(*url*)

`fetch_url`(*inurl*, *outpath*)
Get the file(s) or values from XNAT.

Parameters

- **`inurl`** – url to the item in the data store
- **`outpath`** – path where to store the fetch data locally
- **`datatype`** – the DataType of the retrieved URL

`filename` **= '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packages/fas**

`module` **= <module 'xnatstorage' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/p**

`put_url`(*inpath*, *outurl*)
Upload the files to the XNAT storage

Parameters

- **`inpath`** – path to the local data
- **`outurl`** – url to where to store the data in the external data store.

`scheme` **= 'xnat'**

`server`

`xnat`

`fastr.plugins.`**`json`**
alias of `JsonCollector`

`fastr.plugins.`**`path`**
alias of `PathCollector`

`fastr.plugins.`**`stdout`**
alias of `StdoutCollector`

`version` Module

This module keeps track of the version of the currently used Fastr framework. It can check its version from mercurial or a saved file

`fastr.version.`**`clear_version`**`()`
Remove the cached version info

`fastr.version.`**`get_base_version`**`()`
Get the version from the top-level version file

Returns the version

Rtype str

`fastr.version.`**`get_hg_info`**`()`
Read information about the current mercurial branch and revision

Returns tuple containing head revision and branch

`fastr.version.`**`get_saved_version`**`()`
Get cached version from file

Returns tuple with version, head revision and branch

`fastr.version.`**`save_version`**`(`*current_version*, *current_hg_head*, *current_hg_branch*`)`
Cache the version information (useful for when installing)

Parameters

- **`current_version`** (`str`) – version
- **`current_hg_head`** (`str`) – mercurial head revision
- **`current_hg_branch`** (`str`) – mercurial branch

Returns

Subpackages

core Package

`core` Package

This module contains all of the core components of fastr. It has the classes to create networks and work with them.

`basemanager` Module

This module contains the core class for all managers

class `fastr.core.basemanager.`**`BaseManager`**`(`*path=None*, *recursive=False*`)`
Bases: `_abcoll.MutableMapping`

Baseclass for a Manager, subclasses needs to override the following methods:
BaseManager._item_extension, BaseManager._load_item()

_item_extension()

Abstract property that sets the extension of the files to be loaded by the BaseManager. When scanning for items, only files with this extension will be loaded.

Returns desired extension

Return type str

Raises ***FastrNotImplementedError*** – if property not reimplemented in subclass

_load_item(*filepath*, *namespace*)

Abstract method to load an item of the BaseManager. This function is not implemented and needs to be reimplemented by a subclass.

Parameters

- **filepath** (*str*) – path of the item to load
- **namespace** (*str*) – the namespace of the item to be loaded

Returns the loaded item

Raises ***FastrNotImplementedError*** – if called without being reimplemented by a subclass

__abstractmethods__ = frozenset(['_load_item', '_item_extension'])

__delitem__(*key*)

Remove item from the BaseManager

Parameters key – key of the item to remove

Returns None

Raises ***FastrKeyError*** – if the key is not found in the BaseManager

__getitem__(*key*)

Retrieve item from BaseManager

Parameters key – the key of the item to retrieve

Returns the value indicated by the key

Raises ***FastrKeyError*** – if the key is not found in the BaseManager

__init__(*path=None*, *recursive=False*)

The BaseManager constructor

Parameters

- **path** (*str or None*) – path to scan for items, or None for no path
- **recursive** (*bool*) – Flag to indicate a recursive search is desired

Returns the newly created BaseManager

Return type *BaseManager*

__iter__()

Get an iterator from the BaseManager. The iterator will iterate over the keys of the BaseManager.

Returns the iterator

Return type dictionary-keyiterator

__keytransform__(*key*)

Identity transform for the keys. This function can be reimplemented by a subclass to implement a different key transform.

Parameters key – key to transform

Returns the transformed key (in this case the same key as inputted)

`__len__`()
Return the number of items in the BaseManager

Returns number of items in the BaseManager

Return type int

`__metaclass__`
alias of `ABCMeta`

`__module__` = 'fastr.core.basemanager'

`__repr__`()
Convert the BaseManager to a representation string.

Returns Representation string

Return type str

`__setitem__`(*key*, *value*)
Set item in the BaseManager

Parameters

- **`key`** – the key of the item to store
- **`value`** – the value of the item to store

Returns None

`data`
The actual data dict underlying this Manager

`match_filename`(*filename*)
Check if the filename matches the pattern the manager expects.

Parameters **`filename`** – filename to match

Returns flag indicating that the filename matches

`populate`()
Populate the manager with the data. This is a method that will be called when the Managers data is first accessed. This way we avoid doing expensive directory scans when the data is never requested.

`reload`()
Reload entire contents of this manager.

`baseplugin` Module

The base class for all Plugins in the fastr system

class `fastr.core.baseplugin.`**`BasePlugin`**
Bases: `object`

Base class for Plugins in the fastr system.

`__abstractmethods__` = frozenset([])

`__dict__` = dict_proxy({'status': <fastr.utils.classproperty.ClassPropertyDescriptor object>, '__module__': 'fastr.cc

`__init__`()
The BasePlugin constructor.

Returns the created plugin

Return type *BasePlugin*

Raises ***`FastrPluginNotLoaded`*** – if the plugin did not load correctly

`__metaclass__`
alias of *`PluginMeta`*

`__module__` = **'fastr.core.baseplugin'**

`__repr__`()

`__str__`()
Creare string representation of the plugin.

Returns string represenation

Return type str

`__weakref__`
list of weak references to the object (if defined)

`cleanup`()
Perform any cleanup action needed when the plugin use ended. This can be closing files/streams etc.

`configuration_fields` = **{}**

`fullid` = **'fastr://plugins/BasePlugin'**

`id` = **'BasePlugin'**

`instantiate` = **False**

`module` = **None**

classmethod `register_configuration`()
Register and test the configuation fields of the plugin

classmethod `set_code`(*source_code*)
Set the filename and source code of the plugin

Parameters **`source_code`** (`str`) – the source code of the plugin

classmethod `set_status`(*status*, *message*, *exception=None*)
Update the status of the plugin

Parameters

- **`status`** (`str`) – the new status
- **`message`** (`str`) – message explaining the status change
- **`exception`** (`str`) – stacktrace of the exception causing the failed load

`source_code`
A descriptor that can act like a property for a class.

`status` = **'\x1b[46mUnInitialized\x1b[0m'**

`status_message` = **'Plugin object created'**

classmethod `test`()
Test the plugin, default behaviour is just to instantiate the plugin

class `fastr.core.baseplugin.`**`Plugin`**
Bases: *`fastr.core.baseplugin.BasePlugin`*

`__abstractmethods__` = **frozenset([])**

`__module__` = **'fastr.core.baseplugin'**

class `fastr.core.baseplugin.`**`PluginMeta`**
Bases: `abc.ABCMeta`

`__module__` = **'fastr.core.baseplugin'**

`__repr__`()

class `fastr.core.baseplugin.`**`PluginState`**
Bases: `enum.Enum`

`__format__`(*format_spec*)

`__module__` = **'fastr.core.baseplugin'**

static `__new__`(*value*)

`__reduce_ex__`(*proto*)

`__repr__`()

`__str__`()

`failed` = **'\x1b[37m\x1b[41m\x1b[1mFailed\x1b[0m'**

`loaded` = **'\x1b[37m\x1b[42m\x1b[1mLoaded\x1b[0m'**

`preload` = **'\x1b[102mPreLoad\x1b[0m'**

`uninitialized` = **'\x1b[46mUnInitialized\x1b[0m'**

`unloaded` = **'\x1b[46mUnLoaded\x1b[0m'**

`datatypemanager` Module

This module manages datatypes. These datatypes are python classes generated from the XML/JSON datatype files.

class `fastr.core.datatypemanager.`**`DataTypeManager`**

Bases: *`fastr.core.pluginmanager.BasePluginManager`*

The DataTypeManager hold a mapping of all DataTypes in the fast system and can create new DataTypes from files/data structures.

`__abstractmethods__` = **frozenset([])**

`__init__`()

The DataTypeManager constructor will create a new DataTypeManager and populate it with all DataTypes it can find in the paths set in `fastr.config.types_path`.

Returns the created DataTypeManager

`__keytransform__`(*key*)

Key transformation for this mapping. The key transformation allows indexing by both the DataType name as well as the DataType it self.

Parameters **`key`** (`fastr.datatypes.BaseDataType` *or* `str`) – The name of the requested datatype or the datatype itself

Returns The requested datatype

`__module__` = **'fastr.core.datatypemanager'**

`create_enumtype`(*type_id*, *options*, *name=None*)

Create a python class based on an XML file. This function return a completely functional python class based on the contents of a DataType XML file.

Such a class will be of type EnumType.

Parameters

- **`type_id`** (*`str`*) – the id of the new class
- **`options`** (*`iterable`*) – an iterable of options, each option should be str

Returns the newly created subclass of EnumType

Raises ***`FastrTypeError`*** – if the options is not an iterable of str

`fullid`

The fullid of the datatype manager

get_type (*name*)

Read a type given a typename. This will scan all directories in types_path and attempt to load the newest version of the DataType.

Parameters **name** (*str*) – Name of the datatype that should be imported in the system

Returns the datatype with the requested name, or None if datatype is not found

Note: If type is already in TypeManager it will not load anything and return the already loaded version.

guess_type (*value*, *exists=True*, *options=None*, *preferred=None*)

Guess the DataType based on a value str.

Parameters

- **value** (*str*) – the value to guess the type for
- **options** (*TypeGroup, DataType or tuple of DataTypes*) – The options that are allowed to be guessed from
- **exists** (*bool*) – Indicate the value exists (if file) and can be checked for validity, if false skip validity check
- **preferred** (*iterable*) – An iterable of preferred types in case multiple types match.

Returns The resulting DataType or None if no match was found

Raises ***FastrTypeError*** – if the options argument is of the wrong type

The function will first create a list of all candidate DataTypes. Subsequently, it will check for each candidate if the value would valid. If there are multiple matches, the config value for preferred types is consulted to break the ties. If non of the DataTypes are in the preferred types list, a somewhat random DataType will be picked as the most optimal result.

has_type (*name*)

Check if the datatype with requested name exists

Parameters **name** (*str*) – the name of the requested datatype

Returns flag indicating if the datatype exists

Return type bool

static **isdatatype** (*item*)

Check if item is a valid datatype for the fastr system.

Parameters **item** – item to check

Returns flag indicating if the item is a fastr datatype

Return type bool

match_types (**args*, ***kwargs*)

Find the match between a list of DataTypes/TypeGroups, see resolve-datatype for details

Parameters

- **args** – A list of DataType/TypeGroup objects to match
- **kwargs** – A 'preferred' keyword argument can be used to indicate a list of DataTypes to prefer in case of ties (first has precedence over later in list)

Returns The best DataType match, or None if no match is possible.

Raises ***FastrTypeError*** – if not all args are subclasses of BaseDataType

match_types_any (**args*)

Find the match between a list of DataTypes/TypeGroups, see resolve-datatype for details

Parameters **`args`** – A list of DataType/TypeGroup objects to match

Returns A tuple with all DataTypes that match.

Return type set

Raises ***`FastrTypeError`*** – if not all args are subclasses of BaseDataType

`plugin_class`
The PluginClass of the items of the BasePluginManager

`poll_datatype`(*filename*)
Poll an xml file to see if there is a definition of a datatype in it.

Parameters **`filename`** (*`str`*) – path of the file to poll

Returns tuple with (id, version, basetype) if a datatype is found or (None, None, None) if no datatype is found

`populate`()
Populate Manager. After scanning for DataTypes, create the AnyType and set the preferred types

`dimension` Module

class `fastr.core.dimension.`**`Dimension`**(*name*, *size*)
Bases: `object`

A class representing a dimension. It contains the name and size of the dimension.

`__dict__` **= dict_proxy({'__dict__': <attribute '__dict__' of 'Dimension' objects>, '__module__': 'fastr.core.dimensi**

`__init__`(*name*, *size*)
The constructor for the dimension.

Parameters

- **`name`** (*`str`*) – Name of the dimension
- **`size`** (*`int or sympy.Symbol`*) – Size fo the dimension

`__module__` **= 'fastr.core.dimension'**

`__weakref__`
list of weak references to the object (if defined)

class `fastr.core.dimension.`**`HasDimensions`**
Bases: `object`

A Mixin class for any object that has a notion of dimensions and size. It uses the dimension property to expose the dimension name and size.

`__abstractmethods__` **= frozenset(['dimensions'])**

`__dict__` **= dict_proxy({'__module__': 'fastr.core.dimension', '__metaclass__': <class 'abc.ABCMeta'>, '_abc_nega**

`__metaclass__`
alias of `ABCMeta`

`__module__` **= 'fastr.core.dimension'**

`__weakref__`
list of weak references to the object (if defined)

`dimensions`
The dimensions has to be implemented by any subclass. It has to provide a tuple of Dimensions.

Returns dimensions

Return type tuple

dimnames
A tuple containing the dimension names of this object. All items of the tuple are of type str.

size
A tuple containing the size of this object. All items of the tuple are of type int or sympy.Symbol.

`inputoutput` Module

Classes for arranging the input and output for nodes.

Exported classes:

Input – An input for a node (holding datatype). Output – The output of a node (holding datatype and value). ConstantOutput – The output of a node (holding datatype and value).

> **Warning:** Don't mess with the Link, Input and Output internals from other places. There will be a huge chances of breaking the network functionality!

class `fastr.core.inputoutput.`**`AdvancedFlowOutput`**(*node*, *description*)
Bases: *`fastr.core.inputoutput.Output`*

`__abstractmethods__` **= frozenset([])**

`__module__` **= 'fastr.core.inputoutput'**

dimnames
The dimnames of AdvancedFlowNodes have the output id appended, as the sizes per output can be different.

class `fastr.core.inputoutput.`**`BaseInput`**(*node*, *description*)
Bases: *`fastr.core.inputoutput.BaseInputOutput`*

Base class for all inputs.

`__abstractmethods__` **= frozenset(['_update', 'fullid', '__getitem__', 'num_subinput', 'itersubinputs', 'size'])**

`__init__`(*node*, *description*)
Instantiate a BaseInput

Parameters

- **node** – the parent node the input/output belongs to.
- **description** – the `ParameterDescription` describing the input/output.

Returns the created BaseInput

Raises

- ***FastrTypeError*** – if description is not of class `ParameterDescription`
- ***FastrDataTypeNotAvailableError*** – if the DataType requested cannot be found in the `fastr.typelist`

`__module__` **= 'fastr.core.inputoutput'**

itersubinputs()
Iterator over the SubInputs

Returns iterator

example:

```
>>> for subinput in input_a.itersubinputs():
        print subinput
```

num_subinput
The number of SubInputs in this Input

class fastr.core.inputoutput.**BaseInputOutput**(*node*, *description*)
Bases: *fastr.core.samples.HasSamples*, *fastr.core.updateable.Updateable*, *fastr.core.serializable.Serializable*

Base class for Input and Output classes. It mainly implements the properties to access the data from the underlying ParameterDescription.

__abstractmethods__ = frozenset(['_update', 'fullid', '__getitem__', 'size'])

__getstate__()
Retrieve the state of the BaseInputOutput

Returns the state of the object

Rtype dict

__init__(*node*, *description*)
Instantiate a BaseInputOutput

Parameters

- **node** – the parent node the input/output belongs to.
- **description** – the ParameterDescription describing the input/output.

Returns created BaseInputOutput

Raises

- ***FastrTypeError*** – if description is not of class ParameterDescription
- ***FastrDataTypeNotAvailableError*** – if the DataType requested cannot be found in the fastr.typelist

__iter__()
This function is blocked to avoid support for iteration using a lecacy __getitem__ method.

Returns None

Raises ***FastrNotImplementedError*** – always

__module__ = 'fastr.core.inputoutput'

__repr__()
Get a string representation for the Input/Output

Returns the string representation

Return type str

__setstate__(*state*)
Set the state of the BaseInputOutput by the given state.

Parameters **state** (*dict*) – The state to populate the object with

Returns None

cardinality(*key=None*, *job_data=None*)
Determine the cardinality of this Input/Output. Optionally a key can be given to determine for a sample.

Parameters **key** – key for a specific sample

Returns the cardinality

Return type int, sympy.Symbol, or None

check_cardinality(*key=None*)
Check if the actual cardinality matches the cardinality specified in the ParameterDescription. Optionally you can use a key to test for a specific sample.

Parameters **`key`** – sample_index (tuple of int) or `SampleId` for desired sample

Returns flag indicating that the cardinality is correct

Return type bool

Raises ***`FastrCardinalityError`*** – if the Input/Output has an incorrect cardinality description.

`datatype`
The datatype of this Input/Output

`description`
The description object of this input/output

`fullid`
The fullid of the Input/Output, the fullid should be unnique and makes the object retrievable by the network.

`id`
Id of the Input/Output

`node`
The Node to which this Input/Output belongs

`numel`
The number of elements in this Input/Output

`required`
Flag indicating that the Input/Output is required

`size`
The size of the Input/Output

class `fastr.core.inputoutput.`**`BaseOutput`**(*node*, *description*)
Bases: *`fastr.core.inputoutput.BaseInputOutput`*

Base class for all outputs.

`__abstractmethods__` **= frozenset(['_update', 'fullid', '__getitem__', 'size'])**

`__init__`(*node*, *description*)
Instantiate a BaseOutput

Parameters

- **`node`** – the parent node the output belongs to.
- **`description`** – the `ParameterDescription` describing the output.

Returns created BaseOutput

Raises

- ***`FastrTypeError`*** – if description is not of class `ParameterDescription`
- ***`FastrDataTypeNotAvailableError`*** – if the DataType requested cannot be found in the `fastr.typelist`

`__module__` **= 'fastr.core.inputoutput'**

`automatic`
Flag indicating that the Output is generated automatically without being specified on the command line

class `fastr.core.inputoutput.`**`Input`**(*node*, *description*)
Bases: *`fastr.core.inputoutput.BaseInput`*

Class representing an input of a node. Such an input will be connected to the output of another node or the output of an constant node to provide the input value.

`__abstractmethods__` **= frozenset([])**

`__eq__`(*other*)
Compare two Input instances with each other. This function ignores the parent node and update status, but tests rest of the dict for equality.

Parameters **`other`** (*`Input`*) – the other instances to compare to

Returns True if equal, False otherwise

Return type bool

`__getitem__`(*key*)
Retrieve an item from this Input.

Parameters **`key`** (str, `SampleId` or tuple) – the key of the requested item, can be a key str, sample index tuple or a `SampleId`

Returns the return value depends on the requested key. If the key was an int the corresponding *`SubInput`* will be returned. If the key was a `SampleId` or sample index tuple, the corresponding `SampleItem` will be returned.

Return type `SampleItem` or *`SubInput`*

Raises

- ***`FastrTypeError`*** – if key is not of a valid type
- ***`FastrKeyError`*** – if the key is not found

`__getstate__`()
Retrieve the state of the Input

Returns the state of the object

Rtype dict

`__init__`(*node, description*)
Instantiate an input.

Parameters

- **`node`** (*`Node`*) – the parent node of this input.
- **`description`** (*`ParameterDescription`*) – the ParameterDescription of the input.

Returns the created Input

`__module__` **= 'fastr.core.inputoutput'**

`__setitem__`(*key, value*)
Create a link between a SubInput of this Inputs and an Output/Constant

Parameters

- **`key`** (*`int`*, *`str`*) – the key of the SubInput
- **`value`** (`BaseOutput`, *`list`*, *`tuple`*, *`dict`*, *`OrderedDict`*) – the target to link, can be an output or a value to create a constant for

Raises ***`FastrTypeError`*** – if key is not of a valid type

`__setstate__`(*state*)
Set the state of the Input by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`__str__`()
Get a string version for the Input

Returns the string version

Return type str

append(*value*)
When you want to append a link to an Input, you can use the append property. This will automatically create a new SubInput to link to.

example:

```
>>> link = node2['input'].append(node1['output'])
```

will create a new SubInput in node2['input'] and link to that.

cardinality(*key=None, job_data=None*)
Cardinality for an Input is the sum the cardinalities of the SubInputs, unless defined otherwise.

Parameters **key** (tuple of int or `SampleId`) – key for a specific sample, can be sample index or id

Returns the cardinality

Return type int, sympy.Symbol, or None

datatype
The datatype of this Input

dimnames
The list names of the dimensions in this Input. This will be a list of str.

fullid
The full defining ID for the Input

get_sourced_nodes()
Get a list of all *Nodes* connected as sources to this Input

Returns list of all connected *Nodes*

Return type list

get_sourced_outputs()
Get a list of all *Outputs* connected as sources to this Input

Returns tuple of all connected *Outputs*

Return type tuple

get_subinput(*key*)
Get a requested *SubInput*

Parameters **key** (*int*) – the index of the *SubInput* to retrieve

Returns requested *SubInput*

index(*value*)
Find index of a SubInput

Parameters **value** (*SubInput*) – the *SubInput* to find the index of

Returns key

Return type int, str

input_group
The id of the *InputGroup* this Input belongs to.

insert(*index*)
Insert a new SubInput at index in the sources list

Parameters **key** (*int*) – positive integer for position in _source list to insert to

Returns newly inserted *SubInput*

Return type *SubInput*

itersubinputs()
Iterate over the *SubInputs* in this Input.

Returns iterator yielding *SubInput*

example:

```
>>> for subinput in input_a.itersubinputs():
        print subinput
```

num_subinput
The number of SubInputs in this Input

prepare(*sample_size=None*)
This function makes sure the `SampleIdList` has the correct size.

Parameters **sample_size** (*tuple of int*) – the required size of the `SampleIdList`. If no size is given, `self.size` will be used by default.

remove(*value*)
Remove a SubInput from the SubInputs list based on the connected Link.

Parameters **value** (*SubInput*, <fastr.core.inputoutput.SubInput>') – the *SubInput* to removed from this Input

set_subinput(*key*, *value*)
Set a specified SubInput.

Parameters

- **key** (*int*) – positive integer for position in _source list
- **value** – new *SubInput* to assign to the selected location

size
The size of the sample collections that can accessed via this Input.

source
The mapping of *SubInputs* that are connected and have more than 0 elements.

class `fastr.core.inputoutput.`**Output**(*node*, *description*)
Bases: *fastr.core.inputoutput.BaseOutput*

Class representing an output of a node. It holds the output values of the tool ran. Output fields can be connected to inputs of other nodes.

__abstractmethods__ = frozenset([])

__eq__(*other*)
Compare two Output instances with each other. This function ignores the parent node, listeners and update status, but tests rest of the dict for equality.

Parameters **other** (Output) – the other instances to compare to

Returns True if equal, False otherwise

Return type bool

__getitem__(*key*)
Retrieve an item from this Output. The returned value depends on what type of key used:

•Retrieving data using index tuple: [index_tuple]

•Retrieving data sample_id str: [SampleId]

•Retrieving a list of data using SampleId list: [sample_id1, ..., sample_idN]

•Retrieving a *SubOutput* using an int or slice: [n] or [n:m]

Parameters **key** (int, slice, `SampleId` or tuple) – the key of the requested item, can be a number, slice, sample index tuple or a `SampleId`

Returns the return value depends on the requested key. If the key was an int or slice the corresponding *`SubOutput`* will be returned (and created if needed). If the key was a `SampleId` or sample index tuple, the corresponding `SampleItem` will be returned. If the key was a list of `SampleId` a tuple of `SampleItem` will be returned.

Return type *`SubInput`* or `SampleItem` or list of `SampleItem`

Raises

- ***`FastrTypeError`*** – if key is not of a valid type
- ***`FastrKeyError`*** – if the parent Node has not been executed

`__getstate__`()

Retrieve the state of the Output

Returns the state of the object

Rtype dict

`__init__`(*node*, *description*)

Instantiate an Output

Parameters

- **`node`** – the parent node the output belongs to.
- **`description`** – the `ParameterDescription` describing the output.

Returns created Output

Raises

- ***`FastrTypeError`*** – if description is not of class `ParameterDescription`
- ***`FastrDataTypeNotAvailableError`*** – if the DataType requested cannot be found in the `fastr.typelist`

`__module__` = **'fastr.core.inputoutput'**

`__setitem__`(*key*, *value*)

Store an item in the Output

Parameters

- **`key`** (tuple of int or `SampleId`) – key of the value to store
- **`value`** – the value to store

Returns None

Raises ***`FastrTypeError`*** – if key is not of correct type

`__setstate__`(*state*)

Set the state of the Output by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`__str__`()

Get a string version for the Output

Returns the string version

Return type str

`blocking`

Flag indicating that this Output will cause blocking in the execution

cardinality(*key=None*, *job_data=None*)
Cardinality of this Output, may depend on the inputs of the parent Node.

Parameters **key** (tuple of int or `SampleId`) – key for a specific sample, can be sample index or id

Returns the cardinality

Return type int, sympy.Symbol, or None

Raises

- ***FastrCardinalityError*** – if cardinality references an invalid *Input*
- ***FastrTypeError*** – if the referenced cardinality values type cannot be case to int
- ***FastrValueError*** – if the referenced cardinality value cannot be case to int

datatype
The datatype of this Output

dimnames
The list names of the dimensions in this Output. This will be a list of str.

fullid
The full defining ID for the Output

iterconvergingindices(*collapse_dims*)
Iterate over all data, but collapse certain dimension to create lists of data.

Parameters **collapse_dims** (*iterable of int*) – dimension to collapse

Returns iterator SampleIndex (possibly containing slices)

listeners
The list of *Links* connected to this Output.

ndims
The number of dimensions in this Output

preferred_types
The list of preferred `DataTypes` for this Output.

prepare()
This function makes sure that a value storage will be created

resulting_datatype
The `DataType` that will the results of this Output will have.

samples
The SampleCollection of the samples in this Output. None if the Node has not yet been executed. Otherwise a SampleCollection.

size
The sample size of the Output

valid
Check if the output is valid, i.e. has a valid cardinality

class `fastr.core.inputoutput.`**SourceOutput**(*node*, *description*)
Bases: *fastr.core.inputoutput.Output*

Output for a SourceNode, this type of Output determines the cardinality in a different way than a normal Node.

__abstractmethods__ = frozenset([])

__getitem__(*item*)
Retrieve an item from this Output. The returned value depends on what type of key used:

•Retrieving data using index tuple: [index_tuple]

•Retrieving data sample_id str: [SampleId]

•Retrieving a list of data using SampleId list: [sample_id1, ..., sample_idN]

•Retrieving a *SubOutput* using an int or slice: [n] or [n:m]

Parameters **key** (int, slice, `SampleId` or tuple) – the key of the requested item, can be a number, slice, sample index tuple or a `SampleId`

Returns the return value depends on the requested key. If the key was an int or slice the corresponding *SubOutput* will be returned (and created if needed). If the key was a `SampleId` or sample index tuple, the corresponding `SampleItem` will be returned. If the key was a list of `SampleId` a tuple of `SampleItem` will be returned.

Return type *SubInput* or `SampleItem` or list of `SampleItem`

Raises

- ***FastrTypeError*** – if key is not of a valid type
- ***FastrKeyError*** – if the parent Node has not been executed

__init__(*node*, *description*)
Instantiate a FlowOutput

Parameters

- **node** – the parent node the output belongs to.
- **description** – the `ParameterDescription` describing the output.

Returns created FlowOutput

Raises

- ***FastrTypeError*** – if description is not of class `ParameterDescription`
- ***FastrDataTypeNotAvailableError*** – if the DataType requested cannot be found in the `fastr.typelist`

__module__ = 'fastr.core.inputoutput'

__setitem__(*key*, *value*)
Store an item in the Output

Parameters

- **key** (tuple of int or `SampleId`) – key of the value to store
- **value** – the value to store

Returns None

Raises ***FastrTypeError*** – if key is not of correct type

cardinality(*key=None*, *job_data=None*)
Cardinality of this SourceOutput, may depend on the inputs of the parent Node.

Parameters **key** (tuple of int or `SampleId`) – key for a specific sample, can be sample index or id

Returns the cardinality

Return type int, sympy.Symbol, or None

linearized
A linearized version of the sample data, this is lazily cached linearized version of the underlying SampleCollection.

ndims
The number of dimensions in this SourceOutput

size
The sample size of the SourceOutput

class `fastr.core.inputoutput.`**`SubInput`**(*input_*)
Bases: *`fastr.core.inputoutput.BaseInput`*

This class is used by *`Input`* to allow for multiple links to an *`Input`*. The SubInput class can hold only a single Link to a (Sub)Output, but behaves very similar to an *`Input`* otherwise.

`__abstractmethods__` **= frozenset([])**

`__eq__`(*other*)
Compare two SubInput instances with each other. This function ignores the parent, node, source and update status, but tests rest of the dict for equality.

Parameters **`other`** (`SubInput`) – the other instances to compare to

Returns True if equal, False otherwise

`__getitem__`(*key*)
Retrieve an item from this SubInput.

Parameters **`key`** (int, `SampleId` or `SampleIndex`) – the key of the requested item, can be a number, sample index tuple or a `SampleId`

Returns the return value depends on the requested key. If the key was an int the corresponding *`SubInput`* will be returned. If the key was a `SampleId` or sample index tuple, the corresponding `SampleItem` will be returned.

Return type `SampleItem` or *`SubInput`*

Raises ***`FastrTypeError`*** – if key is not of a valid type

Note: As a SubInput has only one SubInput, only requesting int key 0 or -1 is allowed, and it will return self

`__getstate__`()
Retrieve the state of the SubInput

Returns the state of the object

Rtype dict

`__init__`(*input_*)
Instantiate an SubInput.

Parameters **`input`** (*`Input`*) – the parent of this SubInput.

Returns the created SubInput

`__module__` **= 'fastr.core.inputoutput'**

`__setstate__`(*state*)
Set the state of the SubInput by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`__str__`()
Get a string version for the SubInput

Returns the string version

Return type str

`cardinality`(*key=None, job_data=None*)
Get the cardinality for this SubInput. The cardinality for a SubInputs is defined by the incoming link.

Parameters **key** (SampleIndex or SampleId) – key for a specific sample, can be sample index or id

Returns the cardinality

Return type int, sympy.Symbol, or None

description

dimnames
List of dimension names for this SubInput

fullid
The full defining ID for the SubInput

get_sourced_nodes()
Get a list of all *Nodes* connected as sources to this SubInput

Returns list of all connected *Nodes*

Return type list

get_sourced_outputs()
Get a list of all *Outputs* connected as sources to this SubInput

Returns list of all connected *Outputs*

Return type list

input_group
The id of the *InputGroup* this SubInputs parent belongs to.

iteritems()
Iterate over the SampleItems that are in the SubInput.

Returns iterator yielding SampleItem objects

itersubinputs()
Iterate over SubInputs (for a SubInput it will yield self and stop iterating after that)

Returns iterator yielding *SubInput*

example:

```
>>> for subinput in input_a.itersubinputs():
        print subinput
```

node
The Node to which this SubInputs parent belongs

num_subinput
The number of SubInputs in this SubInput, this is always 1.

remove(*value*)
Remove a SubInput from parent Input.

Parameters **value** (*SubInput*) – the *SubInput* to removed from this Input

size
The sample size of the SubInput

source
A list with the source *Link*. The list is to be compatible with *Input*

source_output
The *Output* linked to this SubInput

class fastr.core.inputoutput.**SubOutput**(*output*, *index*)
Bases: *fastr.core.inputoutput.Output*

The SubOutput is an Output that represents a slice of another Output.

`__abstractmethods__` = frozenset([])

`__eq__`(*other*)

Compare two SubOutput instances with each other. This function ignores the parent, node and update status, but tests rest of the dict for equality. equality

Parameters **`other`** (`SubOutput`) – the other instances to compare to

Returns True if equal, False otherwise

Return type bool

`__getitem__`(*key*)

Retrieve an item from this SubOutput. The returned value depends on what type of key used:

- Retrieving data using index tuple: [index_tuple]
- Retrieving data sample_id str: [SampleId]
- Retrieving a list of data using SampleId list: [sample_id1, ..., sample_idN]
- Retrieving a *`SubOutput`* using an int or slice: [n] or [n:m]

Parameters **`key`** (int, slice, `SampleId` or tuple) – the key of the requested item, can be a number, slice, sample index tuple or a `SampleId`

Returns the return value depends on the requested key. If the key was an int or slice the corresponding *`SubOutput`* will be returned (and created if needed). If the key was a `SampleId` or sample index tuple, the corresponding `SampleItem` will be returned. If the key was a list of `SampleId` a tuple of `SampleItem` will be returned.

Return type *`SubInput`* or `SampleItem` or list of `SampleItem`

Raises ***`FastrTypeError`*** – if key is not of a valid type

`__getstate__`()

Retrieve the state of the SubOutput

Returns the state of the object

Rtype dict

`__init__`(*output*, *index*)

Instantiate a SubOutput

Parameters

- **`output`** – the parent output the suboutput slices.
- **`index`** (*`int or slice`*) – the way to slice the parent output

Returns created SubOutput

Raises

- ***`FastrTypeError`*** – if the output argument is not an instance of *`Output`*
- ***`FastrTypeError`*** – if the index argument is not an `int` or `slice`

`__len__`()

Return the length of the Output.

Note: In a SubOutput this is always 1.

`__module__` = 'fastr.core.inputoutput'

`__setitem__`(*key*, *value*)

A function blocking the assignment operator. Values cannot be assigned to a SubOutput.

Raises ***`FastrNotImplementedError`*** – if called

`__setstate__`(*state*)
Set the state of the SubOutput by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`__str__`()
Get a string version for the SubOutput

Returns the string version

Return type str

`cardinality`(*key=None*, *job_data=None*)
Cardinality of this SubOutput depends on the parent Output and `self.index`

Parameters **`key`** (tuple of int or `SampleId`) – key for a specific sample, can be sample index or id

Returns the cardinality

Return type int, sympy.Symbol, or None

Raises

- ***`FastrCardinalityError`*** – if cardinality references an invalid *`Input`*
- ***`FastrTypeError`*** – if the referenced cardinality values type cannot be case to int
- ***`FastrValueError`*** – if the referenced cardinality value cannot be case to int

`datatype`
The datatype of this SubOutput

`fullid`
The full defining ID for the SubOutput

`indexrep`
Simple representation of the index.

`listeners`
The list of *`Links`* connected to this Output.

`node`
The Node to which this SubOutput belongs

`preferred_types`
The list of preferred `DataTypes` for this SubOutput.

`resulting_datatype`
The `DataType` that will the results of this SubOutput will have.

`samples`
The `SampleCollection` for this SubOutput

`interface` Module

A module that describes the interface of a Tool. It specifies how a set of input values will be translated to commands to be executed. This creates a generic interface to different ways of executing underlying software.

class `fastr.core.interface.`**`InputSpec`**
Bases: *`fastr.core.interface.InputSpec`*

`__dict__` **= dict_proxy({'__dict__': <attribute '__dict__' of 'InputSpec' objects>, '__module__': 'fastr.core.interfac**

`__module__` **= 'fastr.core.interface'**

static **__new__**(*id_*, *cardinality*, *datatype*, *required=False*, *description=''*, *default=None*, *hidden=False*)

`fastr.core.interface.`**`InputSpecBase`**
alias of *`InputSpec`*

class `fastr.core.interface.`**`Interface`**
Bases: *`fastr.core.baseplugin.Plugin`*, *`fastr.core.serializable.Serializable`*

Abstract base class of all Interfaces. Defines the minimal requirements for all Interface implementations.

`__abstractmethods__` **= frozenset(['inputs', 'execute', '__setstate__', 'expanding', '__getstate__', 'outputs'])**

`__getstate__`()
Retrieve the state of the Interface

Returns the state of the object

Rtype dict

`__metaclass__`
alias of `ABCMeta`

`__module__` **= 'fastr.core.interface'**

`__setstate__`(*state*)
Set the state of the Interface

`execute`(*target*, *payload*)
Execute the interface given the a target and payload. The payload should have the form {'input': {'input_id_a': (value, value), 'input_id_b': (value, value)}, 'output': {'output_id_a': (value, value), 'output_id_b': (value, value)}}

Parameters

- **`target`** – the target to call
- **`payload`** – the payload to use

Returns the result of the execution

Return type (tuple of) *InterfaceResult*

`expanding`
Indicates whether or not this Interface will result in multiple samples per run. If the flow is unaffected, this will be zero, if it is nonzero it means that number of dimension will be added to the sample array.

`inputs`
OrderedDict of Inputs connected to the Interface. The format should be {input_id: InputSpec}.

`outputs`
OrderedDict of Output connected to the Interface. The format should be {output_id: OutputSpec}.

classmethod **`test`**()
Test the plugin, interfaces do not need to be tested on import

class `fastr.core.interface.`**`InterfacePluginManager`**
Bases: *`fastr.core.pluginmanager.PluginSubManager`*

Container holding all the CollectorPlugins

`__abstractmethods__` **= frozenset([])**

`__init__`()
Create the Coll :param path: :param recursive: :return:

`__module__` **= 'fastr.core.interface'**

`plugin_class`
The class of the Plugins in the collection

class `fastr.core.interface.`**`InterfaceResult`**(*result_data*, *log_data*, *payload*, *sample_index=None*, *sample_id=None*)

Bases: `object`

The class in which Interfaces should wrap their results to be picked up by fastr

`__dict__` **= dict_proxy({'__dict__': <attribute '__dict__' of 'InterfaceResult' objects>, '__module__': 'fastr.core.int**

`__init__`(*result_data*, *log_data*, *payload*, *sample_index=None*, *sample_id=None*)

`__module__` **= 'fastr.core.interface'**

`__weakref__`

list of weak references to the object (if defined)

class `fastr.core.interface.`**`OutputSpec`**

Bases: *`fastr.core.interface.OutputSpec`*

`__dict__` **= dict_proxy({'__dict__': <attribute '__dict__' of 'OutputSpec' objects>, '__module__': 'fastr.core.interfa**

`__module__` **= 'fastr.core.interface'**

static **`__new__`**(*id_*, *cardinality*, *datatype*, *automatic=True*, *required=False*, *description=''*, *hidden=False*)

`fastr.core.interface.`**`OutputSpecBase`**

alias of *`OutputSpec`*

`ioplugin` Module

This module contains the manager class for IOPlugins and the base class for all IOPlugins

class `fastr.core.ioplugin.`**`IOPlugin`**

Bases: *`fastr.core.baseplugin.Plugin`*

`IOPlugins` are used for data import and export for the sources and sinks. The main use of the *`IOPlugins`* is during execution (see *Execution*). The *`IOPlugins`* can be accessed via `fastr.ioplugins`, but generally there should be no need for direct interaction with these objects. The use of is mainly via the URL used to specify source and sink data.

`__abstractmethods__` **= frozenset(['scheme'])**

`__init__`()

Initialization for the IOPlugin

Returns newly created IOPlugin

`__metaclass__`

alias of `ABCMeta`

`__module__` **= 'fastr.core.ioplugin'**

`cleanup`()

`(abstract)` Clean up the IOPlugin. This is to do things like closing files or connections. Will be called when the plugin is no longer required.

`expand_url`(*url*)

`(abstract)` Expand an URL. This allows a source to collect multiple samples from a single url. The URL will have a wildcard or point to something with info and multiple urls will be returned.

Parameters **`url`** (*`str`*) – url to expand

Returns the resulting url(s), a tuple if multiple, otherwise a str

Return type str or tuple of str

`fetch_url`(*inurl*, *outfile*)

`(abstract)` Fetch a file from an external data source.

Parameters

- **inurl** – url to the item in the data store
- **outpath** – path where to store the fetch data locally

fetch_value(*inurl*)

(abstract) Fetch a value from an external data source.

Parameters **inurl** – the url of the value to retrieve

Returns the fetched value

static **isurl**(*string*)

Test if given string is an url.

Parameters **string** (*str*) – string to test

Returns True if the string is an url, False otherwise

Return type bool

path_to_url(*path*, *mountpoint=None*)

(abstract) Construct an url from a given mount point and a relative path to the mount point.

Parameters

- **path** (*str*) – the path to determine the url for
- **mountpoint** (*str or None*) – the mount point to use, will be automatically detected if None is given

Returns url matching the path

Return type str

static **print_result**(*result*)

Print the result of the IOPlugin to stdout to be picked up by the tool

Parameters **result** – value to print as a result

Returns None

pull_source_data(*inurl*, *outdir*, *sample_id*, *datatype=None*)

Transfer the source data from inurl to be available in outdir.

Parameters

- **inurl** (*str*) – the input url to fetch data from
- **outdir** (*str*) – the directory to write the data to
- **datatype** (DataType) – the datatype of the data, used for determining the total contents of the transfer

Returns None

push_sink_data(*inpath*, *outurl*, *datatype=None*)

Write out the sink data from the inpath to the outurl.

Parameters

- **inpath** (*str*) – the path of the data to be pushed
- **outurl** (*str*) – the url to write the data to
- **datatype** (DataType) – the datatype of the data, used for determining the total contents of the transfer

Returns None

put_url(*inpath*, *outurl*)

(abstract) Put the files to the external data store.

Parameters

- **inpath** – path to the local data
- **outurl** – url to where to store the data in the external data store.

put_value(*value*, *outurl*)
(abstract) Put the files to the external data store.

Parameters

- **value** – the value to store
- **outurl** – url to where to store the data in the external data store.

scheme
(abstract) This abstract property is to be overwritten by a subclass to indicate the url scheme associated with the IOPlugin.

setup(**args*, ***kwargs*)
(abstract) Setup before data transfer. This can be any function that needs to be used to prepare the plugin for data transfer.

url_to_path(*url*)
(abstract) Get the path to a file from a url.

Parameters **url** (*str*) – the url to retrieve the path for

Returns the corresponding path

Return type str

class fastr.core.ioplugin.**IOPluginManager**
Bases: *fastr.core.pluginmanager.PluginSubManager*

A mapping containing the IOPlugins known to this system

__abstractmethods__ = frozenset([])

__init__()
Create the IOPluginManager and populate it.

Returns newly created IOPluginManager

__iter__()

__keytransform__(*key*)

__module__ = 'fastr.core.ioplugin'

cleanup()
Cleanup all plugins, this closes files, connections and other things that could be left dangling otherwise.

static create_ioplugin_tool()
Create the tools which handles sinks and sources. The command of this tool is the main of core.ioplugin.

expand_url(*url*)
Expand the url by filling the wildcards. This function checks the url scheme and uses the expand function of the correct IOPlugin.

Parameters **url** (*str*) – url to expand

Returns list of urls

Return type list of str

plugin_class
The PluginClass of the items of the BasePluginManager

populate()
Populate the IOPlugins manager. After the default directory scan, add the vfs IOPlugin and create the Tools for the IOPlugins

pull_source_data (*url*, *outdir*, *sample_id*, *datatype=None*)
Retrieve data from an external source. This function checks the url scheme and selects the correct IOPlugin to retrieve the data.

Parameters

- **url** – url to pull
- **outdir** (*str*) – the directory to write the data to
- **datatype** (*DataType*) – the datatype of the data, used for determining the total contents of the transfer

Returns None

put_url (*inpath*, *outurl*)
Put the files to the external data store.

Parameters

- **inpath** – path to the local data
- **outurl** – url to where to store the data in the external data store.

static **register_url_scheme** (*scheme*)
Register a custom scheme to behave http like. This is needed to parse all things properly with urlparse.

Parameters **scheme** – the scheme to register

url_to_path (*url*)
Retrieve the path for a given url

Parameters **url** (*str*) – the url to parse

Returns the path corresponding to the input url

Return type str

fastr.core.ioplugin.**main** ()
The main entry point for command line access to the IOPlugin

link Module

The link module contain the Link class. This class represents the links in a network. These links lead from an output (BaseOutput) to an input (BaseInput) and indicate the desired data flow. Links are smart objects, in the sense that when you set their start or end point, they register themselves with the Input and Output. They do all the book keeping, so as long as you only set the source and target of the Link, the link should be valid.

Warning: Don't mess with the Link, Input and Output internals from other places. There will be a huge chances of breaking the network functionality!

class fastr.core.link.**Link** (*source*, *target*, *parent=None*, *id_=None*, *collapse=None*, *expand=None*)
Bases: *fastr.core.updateable.Updateable*, *fastr.core.serializable.Serializable*

Class for linking outputs (*BaseOutput*) to inputs (*BaseInput*)

Examples:

```
>>> import fastr
>>> network = fastr.Network()
>>> link1 = network.create_link( n1.ouputs['out1'], n2.inputs['in2'] )

link2 = Link()
```

```
link2.source = n1.ouputs['out1']
link2.target = n2.inputs['in2']
```

`__abstractmethods__` **= frozenset([])**

`__dataschemafile__` **= 'Link.schema.json'**

`__eq__`(*other*)
Test for equality between two Links

Parameters **`other`** (`Link`) – object to test against

Returns True for equality, False otherwise

Return type bool

`__getitem__`(*index*)
Get a an item for this Link. The item will be retrieved from the connected output, but a diverging or converging flow can change the number of samples/cardinality.

Parameters **`index`** (`SampleIndex`) – index of the item to retrieve

Returns the requested item

Return type `SampleItem`

Raises ***`FastrIndexError`*** – if the index length does not match the number dimensions in the source data (after collapsing/expanding)

`__getstate__`()
Retrieve the state of the Link

Returns the state of the object

Rtype dict

`__init__`(*source*, *target*, *parent=None*, *id_=None*, *collapse=None*, *expand=None*)
Create a new Link in a Network.

Parameters

- **`source`** (*`BaseOutput`*) – the source output
- **`target`** (*`BaseInput`*) – the target input
- **`parent`** (*`Network`* or None) – the parent network, if None is given the fastr.current_network is assumed to be the parent
- **`id`** (*`str or None`*) – the id of the link, if no **id_** is given, the id will be in the form of "link_{:d}"
- **`collapse`** (*`int, str, or tuple of int/str`*) – the dimensions that the link has to collapse on
- **`expand`** (*`bool`*) – Does this link need to expand the cardinality into a new sample dimension

Returns newly created Link

Raises

- ***`FastrValueError`*** – if parent is not given and *fastr.current_network* is not set
- ***`FastrValueError`*** – if the source output is not in the same network as the Link
- ***`FastrValueError`*** – if the target input is not in the same network as the Link

`__module__` **= 'fastr.core.link'**

`__repr__`()
Get a string representation for the Link

Returns the string representation

Return type str

`__setstate__`(*state*)

Set the state of the Link by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

Raises ***`FastrValueError`*** – if the parent network and *fastr.current_network* are not set

`cardinality`(*index=None*)

Cardinality for a Link is given by source Output and the collapse/expand settings

Parameters **`key`** (`SampleIndex`) – key for a specific sample (can be only a sample index!)

Returns the cardinality

Return type int, sympy.Symbol

Raises ***`FastrIndexError`*** – if the index length does not match the number of dimension in the data

`collapse`

The converging dimensions of this link. Collapsing changes some dimensions of sample lists into cardinality, reshaping the data.

Collapse can be set to a tuple or an int/str, in which case it will be automatically wrapped in a tuple. The int will be seen as indices of the dimensions to collapse. The str will be seen as the name of the dimensions over which to collapse.

Raises ***`FastrTypeError`*** – if assigning a collapse value of a wrong type

`collapse_indexes`

The converging dimensions of this link as integers. Dimension names are replaces with the corresponding int.

Collapsing changes some dimensions of sample lists into cardinality, reshaping the data

classmethod `createobj`(*state*, *network=None*)

Create object function for Link

Parameters

- **`cls`** – The class to create
- **`state`** – The state to use to create the Link
- **`network`** – the parent Network

Returns newly created Link

`destroy`()

The destroy function of a link removes all default references to a link. This means the references in the network, input and output connected to this link. If there is no references in other places in the code, it will destroy the link (reference count dropping to zero).

This function is called when a source for an input is set to another value and the links becomes disconnected. This makes sure there is no dangling links.

`dimnames`

The dimension names for this Link. The dimension names depend on the connected source output and the collapse/expand.

`expand`

Flag indicating that the link will expand the cardininality into a new sample dimension to be created.

fullid
The full defining ID for the Input

iteritems()
Iterate over all `SampleItems` available in this Link. This function queries the connected source output and processes the collapsing and expanding.

Returns generator function yielding `SampleItems`

parent
The Network to which this Link belongs.

size
The size of the data delivered by the link. This can be different from the source size because the link can make data collapse or expand.

source
The source `BaseOutput` of the Link. Setting the source will automatically register the Link with the source BaseOutput. Updating source will also make sure the Link is unregistered with the previous source.

Raises ***FastrTypeError*** – if assigning a non `BaseOutput`

status

target
The target `BaseInput` of the Link. Setting the target will automatically register the Link with the target BaseInput. Updating target will also make sure the Link is unregistered with the previous target.

Raises ***FastrTypeError*** – if assigning a non `BaseInput`

`network` Module

Network module containing Network facilitators and analysers.

class `fastr.core.network.`**Network**(*id_='unnamed_network'*, *version=None*)
Bases: `fastr.core.serializable.Serializable`

The Network class represents a workflow. This includes all Nodes (including ConstantNodes, SourceNodes and Sinks) and Links.

NETWORK_DUMP_FILE_NAME = '__fastr_network__.json'

SOURCE_DUMP_FILE_NAME = '__source_data__.pickle.gz'

__dataschemafile__ = 'Network.schema.json'

__eq__(*other*)
Compare two Networks and see if they are equal.

Parameters **other** (`Network`) –

Returns flag indicating that the Networks are the same

Return type bool

__getitem__(*item*)
Get an item by its fullid. The fullid can point to a link, node, input, output or even subinput/suboutput.

Parameters **item** (`str`, `unicode`) – fullid of the item to retrieve

Returns the requested item

__getstate__()
Retrieve the state of the Network

Returns the state of the object

Rtype dict

`__init__`(*id_='unnamed_network'*, *version=None*)
Create a new, empty Network

Parameters **`name`** (*`str`*) – name of the Network

Returns newly created Network

Raises **`OSError`** – if the tmp mount in the config is not a writable directory

`__module__` **= 'fastr.core.network'**

`__ne__`(*other*)
Tests for non-equality, this is the negated version __eq__

`__repr__`()

`__setstate__`(*state*)
Set the state of the Network by the given state. This completely overwrites the old state!

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`abort`()

`add_link`(*link*)
Add a Link to the Network. Make sure the link is in the link list and the link parent is set to this Network

Parameters **`link`** (*`Link`*) – link to add

Raises

- ***`FastrTypeError`*** – if link is incorrectly typed
- ***`FastrNetworkMismatchError`*** – if the link already belongs to another Network

`add_node`(*node*)
Add a Node to the Network. Make sure the node is in the node list and the node parent is set to this Network

Parameters **`node`** (*`Node`*) – node to add

Raises ***`FastrTypeError`*** – if node is incorrectly typed

`add_stepid`(*stepid*, *node*)
Add a Node to a specific step id

Parameters

- **`stepid`** (*`str`*) – the stepid that the node will be added to
- **`node`** (*`Node`*) – the node to add to the stepid

`check_id`(*id_*)
Check if an id for an object is valid and unused in the Network. The method will always returns True if it does not raise an exception.

Parameters **`id`** (*`str`*) – the id to check

Returns True

Raises

- ***`FastrValueError`*** – if the id is not correctly formatted
- ***`FastrValueError`*** – if the id is already in use

`create_constant`(*datatype*, *data*, *id_=None*, *stepid=None*, *nodegroup=None*, *sourcegroup=None*)
Create a ConstantNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the constant node
- **data** (datatype *or* list *of* datatype) – The data to hold in the constant node
- **id** (*str*) – The id of the constant node to be created
- **stepid** (*str*) – The stepid to add the created constant node to
- **nodegroup** (*str*) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.

Returns the newly created constant node

Return type *ConstantNode*

create_link (*source*, *target*, *id_=None*, *collapse=None*, *expand=None*)
Create a link between two Nodes and add it to the current Network.

Parameters

- **source** (*BaseOutput*) – the output that is the source of the link
- **target** (*BaseInput*) – the input that is the target of the link
- **id** (*str*) – the id of the link

Returns the created link

Type *Link*

create_macro (*network*, *id_=None*)

create_node (*tool*, *id_=None*, *stepid=None*, *cores=None*, *memory=None*, *walltime=None*, *nodegroup=None*)
Create a Node in this Network. The Node will be automatically added to the Network.

Parameters

- **tool** (*Tool*) – The Tool to base the Node on
- **id** (*str*) – The id of the node to be created
- **stepid** (*str*) – The stepid to add the created node to
- **nodegroup** (*str*) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.

Returns the newly created node

Return type *Node*

create_reference (*source_data*, *output_directory*)

create_sink (*datatype*, *id_=None*, *stepid=None*)
Create a SinkNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the sink node
- **id** (*str*) – The id of the sink node to be created
- **stepid** (*str*) – The stepid to add the created sink node to

Returns the newly created sink node

Return type *SinkNode*

create_source (*datatype*, *id_=None*, *stepid=None*, *nodegroup=None*, *sourcegroup=None*)
Create a SourceNode in this Network. The Node will be automatically added to the Network.

Parameters

- **datatype** (BaseDataType) – The DataType of the source source_node

- **id** (*str*) – The id of the source source_node to be created
- **stepid** (*str*) – The stepid to add the created source source_node to
- **nodegroup** (*str*) – The group the node belongs to, this can be important for FlowNodes and such, as they will have matching dimension names.
- **sourcegroup** (*str*) – *DEPRECATED!* The nodegroup this SourceNode will be added to

Returns the newly created source source_node

Return type SourceNode

draw_network (*name='network_layout'*, *img_format='svg'*, *draw_dimension=False*)
Output a dot file and try to convert it to an image file.

Parameters **img_format** (*str*) – extension of the image format to convert to

Returns path of the image created or None if failed

Return type str or None

execute (*sourcedata*, *sinkdata*, *execution_plugin=None*, *tmpdir=None*, *cluster_queue=None*)
Execute the Network with the given data. This will analyze the Network, create jobs and send them to the execution backend of the system.

Parameters

- **sourcedata** (*dict*) – dictionary containing all data for the sources
- **sinkdata** (*dict*) – dictionary containing directives for the sinks
- **execution_plugin** (*str*) – the execution plugin to use (None will use the config value)

Raises

- ***FastrKeyError*** – if a source has not corresponding key in sourcedata
- ***FastrKeyError*** – if a sink has not corresponding key in sinkdata

fullid
The fullid of the Network

id
The id of the Network. This is a read only property.

is_valid ()

job_finished (*job*, *execution_interface*)
Call-back handler for when a job is finished. Will collect the results and handle blocking jobs. This function is automatically called when the execution plugin finished a job.

Parameters **job** (*Job*) – the job that finished

remove (*value*)
Remove an item from the Network.

Parameters **value** (*Node* or *Link*) – the item to remove

test (*reference_data_dir*, *source_data=None*)
Execute the network with the source data specified and test the results against the refence data. This effectively tests the network execution.

Parameters

- **reference_data_dir** (*str*) – The path or vfs url of reference data to compare with
- **source_data** (*dict*) – The source data to use

`networkmanager` Module

This module contains the tool manager class

class `fastr.core.networkmanager.`**`NetworkManager`**(*path*)

Bases: *`fastr.core.objectmanager.ObjectManager`*

`__abstractmethods__` **= frozenset([])**

`__module__` **= 'fastr.core.networkmanager'**

`get_object_version`(*obj*)

`object_class`

`fastr.core.networkmanager.`**`networklist`** **= NetworkManager add_ints v0.0 : /home/docs/checkouts/readthedocs.**

The fastr networklist

`node` Module

A module to maintain a network node.

Exported classes:

Node – A class encapsulating a tool. ConstantNode – A node encapsulating an Output to set scalar values. SourceNode – A class providing a handle to a file.

class `fastr.core.node.`**`AdvancedFlowNode`**(*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)

Bases: *`fastr.core.node.FlowNode`*

`__abstractmethods__` **= frozenset([])**

`__module__` **= 'fastr.core.node'**

`execute`()

Execute the node and create the jobs that need to run

Returns list of jobs to run

Return type list of *`Jobs`*

`set_result`(*job*)

class `fastr.core.node.`**`ConstantNode`**(*datatype*, *data*, *id_=None*)

Bases: *`fastr.core.node.SourceNode`*

Class encapsulating one output for which a value can be set. For example used to set a scalar value to the input of a node.

`__abstractmethods__` **= frozenset([])**

`__dataschemafile__` **= 'ConstantNode.schema.json'**

`__getstate__`()

Retrieve the state of the ConstantNode

Returns the state of the object

Rtype dict

`__init__`(*datatype*, *data*, *id_=None*)

Instantiation of the ConstantNode.

Parameters

- **`datatype`** – The datatype of the output.
- **`data`** – the prefilled data to use.

- **id** – The url pattern.

This class should never be instantiated directly (unless you know what you are doing). Instead create a constant using the network class like shown in the usage example below.

usage example:

```
>>> import fastr
>>> network = fastr.Network()
>>> source = network.create_source(datatype=fastr.typelist['ITKImageFile'],
↪ id_='sourceN')
```

or alternatively create a constant node by assigning data to an item in an InputDict:

```
>>> node_a.inputs['in'] = ['some', 'data']
```

which automatically creates and links a ConstantNode to the specified Input

__module__ = 'fastr.core.node'

__setstate__(*state*)
Set the state of the ConstantNode by the given state.

Parameters **state** (*dict*) – The state to populate the object with

Returns None

data
The data stored in this constant node

execute()
Execute the constant node and create the jobs that need to run

Returns list of jobs to run

Return type list of *Jobs*

set_data(*data=None*, *ids=None*)
Set the data of this constant node in the correct way. This is mainly for compatibility with the parent class SourceNode

Parameters

- **data** (*dict or list of urls*) – the data to use
- **ids** – if data is a list, a list of accompanying ids

class fastr.core.node.**DefaultInputGroupCombiner**(*input_groups*)
Bases: object

__dict__ = dict_proxy({'__module__': 'fastr.core.node', 'merge_sample_jobs': <function merge_sample_jobs>, '__

__init__(*input_groups*)

__iter__()

__module__ = 'fastr.core.node'

__weakref__
list of weak references to the object (if defined)

dimnames

iter_input_groups()

merge(*list_of_items*)
Given a list of items for each input group, it returns the combined list of items.

Parameters **list_of_items** (*list*) – items to combine

Returns combined list

merge_payloads(*sample_payloads*)

merge_sample_data(*list_of_sample_data*)

merge_sample_id(*list_of_sample_ids*)

merge_sample_index(*list_of_sample_indexes*)

merge_sample_jobs(*list_of_sample_jobs*)

outputsize

unmerge(*item*)

Given a item it will recreate the seperate items, basically this is the inverse operation of merge. However, this create an OrderedDict so that specific input groups can be easily retrieved. To get a round trip, the values of the OrderedDict should be taken:

```
>>> list_of_items = combiner.unmerge(item)
>>> item = combiner.merge(list_of_items.values())
```

Parameters **item** (*list*) – the item to unmerge

Returns items

Return type OrderedDict

update()

class fastr.core.node.**FlowNode**(*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)

Bases: *fastr.core.node.Node*

A Flow Node is a special subclass of Nodes in which the amount of samples can vary per Output. This allows non-default data flows.

__abstractmethods__ = frozenset([])

__init__(*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)

Instantiate a flow node.

Parameters

- **tool** (*Tool*) – The tool to base the node on
- **id** (*str*) – the id of the node
- **parent** (*Network*) – the parent network of the node

Returns the newly created FlowNode

__module__ = 'fastr.core.node'

blocking

A FlowNode is (for the moment) always considered blocking.

Returns True

dimnames

Names of the dimensions in the Node output. These will be reflected in the SampleIdList of this Node.

outputsize

Size of the outputs in this Node

set_result(*job*)

Incorporate result of a job into the FlowNode.

Parameters **job** (*Type*) – job of which the result to store

class `fastr.core.node.`**`InputDict`**(**args*, ***kwds*)

Bases: `collections.OrderedDict`

The container containing the Inputs of Node. Implements helper functions for the easy linking syntax.

`__module__` **= 'fastr.core.node'**

`__setitem__`(*key*, *value*, *dict_setitem=<slot wrapper '__setitem__' of 'dict' objects>*)

Set an item in the input dictionary. The behaviour depends on the type of the value. For a `BaseInput`, the input will simply be added to the list of inputs. For a `BaseOutput`, a link between the output and input will be created.

Parameters

- **`key`** (`str`) – id of the input to assign/link
- **`value`** (`BaseInput` or `BaseOutput`) – either the input to add or the output to link
- **`dict_setitem`** – the setitem function to use for the underlying OrderedDict insert

class `fastr.core.node.`**`InputGroup`**(**args*, ***kwargs*)

Bases: `collections.OrderedDict`

A class representing a group of inputs. Input groups allow the

`__abstractmethods__` **= frozenset([])**

`__delitem__`(**args*, ***kwargs*)

od.__delitem__(y) <==> del od[y]

Note: This is a wrapped version of `collections.__delitem__` which triggers an update of the object after being called

`__getitem__`(*key*)

`__init__`(**args*, ***kwargs*)

Create a new InputGroup representation

Parameters

- **`parent`** (`Node`) – the parent node
- **`id`** (`str`) – the id of the input group

Raises ***`FastrTypeError`*** – if parent is not a Node

Note: This is a wrapped version of `fastr.core.node.__init__` which triggers an update of the object after being called

`__metaclass__`

alias of `UpdateableMeta`

`__module__` **= 'fastr.core.node'**

`__setitem__`(**args*, ***kwargs*)

Assign an input to this input group.

Parameters

- **`key`** (`str`) – id of the input
- **`value`** (`Input`) – the input to assign

Raises ***`FastrTypeError`*** – if value of valid type

> **Note:** This is a wrapped version of `fastr.core.node.__setitem__` which triggers an update of the object after being called

`__updatefunc__`()
Update the InputGroup. Triggers when a change is made to the content of the InputGroup. Automatically recalculates the size, primary Input etc.

`__updatetriggers__` **= ['__init__', '__setitem__', '__delitem__', 'clear', 'pop', 'popitem', 'setdefault', 'update']**

`clear`() → None. Remove all items from od.

> **Note:** This is a wrapped version of `collections.clear` which triggers an update of the object after being called

`dimnames`
The names of the dimensions in this InputGroup

`empty`
Bool indicating that this InputGroup is empty (has no data connected)

classmethod `find_source_index`(*target_size*, *target_dimnames*, *source_size*, *source_dimnames*, *target_index*)

`iterinputvalues`
Iterate over the item in this InputGroup

Returns iterator yielding `SampleItems`

`parent`
The parent node of this InputGroup

`pop`(*k*[, *d*]) → v, remove specified key and return the corresponding

value. If key is not found, d is returned if given, otherwise KeyError is raised.

> **Note:** This is a wrapped version of `collections.pop` which triggers an update of the object after being called

`popitem`() → (k, v), return and remove a (key, value) pair.
Pairs are returned in LIFO order if last is true or FIFO order if false.

> **Note:** This is a wrapped version of `collections.popitem` which triggers an update of the object after being called

`primary`
The primary Input in this InputGroup. The primary Input is the Input that defines the size of this InputGroup. In case of ties it will be the first in the tool definition.

`setdefault`(*k*[, *d*]) → od.get(k,d), also set od[k]=d if k not in od

> **Note:** This is a wrapped version of `collections.setdefault` which triggers an update of the object after being called

`size`
The sample size of this InputGroup

classmethod **solve_broadcast**(*target_size*, *target_dimnames*, *source_size*, *source_dimnames*, *target_index*, *nodegroups=None*)

update([*E*], ***F*) → None. Update D from mapping/iterable E and F.

If E present and has a .keys() method, does: for k in E: D[k] = E[k] If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v In either case, this is followed by: for k, v in F.items(): D[k] = v

Note: This is a wrapped version of `_abcoll.update` which triggers an update of the object after being called

class fastr.core.node.**MacroNode**(*network*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)

Bases: *fastr.core.node.Node*

MacroNode encapsulates an entire network in a single node.

__abstractmethods__ = frozenset([])

__getstate__()

Retrieve the state of the MacroNode

Returns the state of the object

Rtype dict

__init__(*network*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)

Parameters **network** (Network) – network to create macronode for

__module__ = 'fastr.core.node'

__setstate__(*state*)

execute()

class fastr.core.node.**MergingInputGroupCombiner**(*input_groups*, *merge_dimension*)

Bases: *fastr.core.node.DefaultInputGroupCombiner*

__init__(*input_groups*, *merge_dimension*)

__module__ = 'fastr.core.node'

iter_input_groups()

merge(*list_of_items*)

unmerge(*item*)

update()

class fastr.core.node.**Node**(*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)

Bases: *fastr.core.updateable.Updateable*, *fastr.core.serializable.Serializable*

The class encapsulating a node in the network. The node is responsible for setting and checking inputs and outputs based on the description provided by a tool instance.

__abstractmethods__ = frozenset([])

__dataschemafile__ = 'Node.schema.json'

__eq__(*other*)

Compare two Node instances with each other. This function ignores the parent and update status, but tests rest of the dict for equality. equality

Parameters **other** (Node) – the other instances to compare to

Returns True if equal, False otherwise

`__getstate__`()
Retrieve the state of the Node

Returns the state of the object

Rtype dict

`__init__`(*tool*, *id_=None*, *parent=None*, *cores=None*, *memory=None*, *walltime=None*)
Instantiate a node.

Parameters

- **`tool`** (*`Tool`*) – The tool to base the node on
- **`id`** (*`str`*) – the id of the node
- **`parent`** (*`Network`*) – the parent network of the node
- **`cores`** (*`int`*) – number of cores required for executing this Node
- **`memory`** (*`str`*) – amount of memory required in the form d+[mMgG] where M is for megabyte and G for gigabyte
- **`walltime`** (*`str`*) – amount of time required in second or in the form HOURS:MINUTES:SECOND

Returns the newly created Node

`__metaclass__`
alias of `ABCMeta`

`__module__` = 'fastr.core.node'

`__repr__`()
Get a string representation for the Node

Returns the string representation

Return type str

`__setstate__`(*state*)
Set the state of the Node by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

Returns None

`__str__`()
Get a string version for the Node

Returns the string version

Return type str

`blocking`
Indicate that the results of this Node cannot be determined without first executing the Node, causing a blockage in the creation of jobs. A blocking Nodes causes the Chunk borders.

`create_job`(*sample_id*, *sample_index*, *job_data*, *job_dependencies*, *jobid=None*, *outputurl=None*, ***kwargs*)
Create a job based on the sample id, job data and job dependencies.

Parameters

- **`sample_id`** (`SampleId`) – the id of the corresponding sample
- **`job_data`** (*`dict`*) – dictionary containing all input data for the job
- **`job_dependencies`** – other jobs that need to finish before this job can run

Returns the created job

Return type *Job*

classmethod **`createobj`**(*state*, *network=None*)

`dimnames`
Names of the dimensions in the Node output. These will be reflected in the SampleIdList of this Node.

`execute`()
Execute the node and create the jobs that need to run

Returns list of jobs to run

Return type list of *Jobs*

`find_source_index`(*target_index*, *target*, *source*)

`fullid`
The full defining ID for the Node

`get_sourced_nodes`()
A list of all Nodes connected as sources to this Node

Returns list of all nodes that are connected to an input of this node

`id`
The id of the Node

`id_` **= None**
The Node id s a unique string identifying the Node

`inputgroups`

A list of inputgroups for this Node. An input group is InputGroup object filled according to the Node

`inputs` **= None**
A list of inputs of this Node

`listeners`
All the listeners requesting output of this node, this means the listeners of all Outputs and SubOutputs

`merge_dimensions`

`name`
Name of the Tool the Node was based on. In case a Toolless Node was used the class name is given.

`nodegroup`

`outputs` **= None**
A list of outputs of this Node

`outputsize`
Size of the outputs in this Node

`parent`
The parent is the Network this Node is part of

`prepare`()
Prepare the node for execution. It will create a SampleIdList of the correct size and prepare the outputs.

`required_cores`
Number of cores required for the execution of this Node

`required_memory`
Amount of memory required for the execution of this Node. Follows the format d+[mMgG] so 500M or 4g would be valid ways to specify 500 megabytes or 4 gigabyte of memory.

`required_time`
Amount of time required for the execution of this Node. Follows the format of a number of second or H:M:S, with H the number of hours, M the number of minutes and S the number of seconds.

set_result (*job*)
Incorporate result of a job into the Node.

Parameters **job** (*Type*) – job of which the result to store

status

tool

update_inputgroups ()
Update all input groups in this node

class fastr.core.node.**OutputDict** (**args*, ***kwds*)
Bases: `collections.OrderedDict`

The container containing the Inputs of Node. Only checks if the inserted values are actually outputs.

__module__ = 'fastr.core.node'

__setitem__ (*key*, *value*, *dict_setitem=<slot wrapper '__setitem__' of 'dict' objects>*)
Set an output.

Parameters

- **key** (*str*) – the of the item to set
- **value** (*BaseOutput*) – the output to set
- **dict_setitem** – the setitem function to use for the underlying OrderedDict insert

class fastr.core.node.**SinkNode** (*datatype*, *id_=None*)
Bases: *fastr.core.node.Node*

Class which handles where the output goes. This can be any kind of file, e.g. image files, textfiles, config files, etc.

__abstractmethods__ = frozenset([])

__dataschemafile__ = 'SinkNode.schema.json'

__getstate__ ()

__init__ (*datatype*, *id_=None*)
Instantiation of the SourceNode.

Parameters

- **datatype** – The datatype of the output.
- **id** – the id of the node to create

Returns newly created sink node

usage example:

```
>>> import fastr
>>> network = fastr.Network()
>>> sink = network.create_sink(datatype=fastr.typelist['ITKImageFile'], id_
↪='SinkN')
```

__module__ = 'fastr.core.node'

__setstate__ (*state*)

create_job (*sample_id*, *sample_index*, *job_data*, *job_dependencies*)
Create a job for a sink based on the sample id, job data and job dependencies.

Parameters

- **sample_id** (SampleId) – the id of the corresponding sample
- **job_data** (*dict*) – dictionary containing all input data for the job

- **job_dependencies** – other jobs that need to finish before this job can run

Returns the created job

Return type *Job*

datatype
The datatype of the data this sink can store.

execute()
Execute the sink node and create the jobs that need to run

Returns list of jobs to run

Return type list of *Jobs*

input
The default input of the sink Node

set_data(*data*)
Set the targets of this sink node.

Parameters **data** (*dict or list of urls*) – the targets rules for where to write the data

The target rules can include a few fields that can be filled out:

field	description
sample_id	the sample id of the sample written in string form
cardinality	the cardinality of the sample written
ext	the extension of the datatype of the written data, including the .
network	the id of the network the sink is part of
node	the id of the node of the sink
timestamp	the iso formatted datetime the network execution started
uuid	the uuid of the network run (generated using uuid.uuid1)

An example of a valid target could be:

```
>>> target = 'vfs://output_mnt/some/path/image_{sample_id}_{cardinality}
↪{ext}'
```

class fastr.core.node.**SourceNode**(*datatype*, *id_=None*)
Bases: *fastr.core.node.FlowNode*

Class providing a connection to data resources. This can be any kind of file, stream, database, etc from which data can be received.

__abstractmethods__ = frozenset([])

__dataschemafile__ = 'SourceNode.schema.json'

__eq__(*other*)
Compare two Node instances with each other. This function ignores the parent and update status, but tests rest of the dict for equality. equality

Parameters **other** (Node) – the other instances to compare to

Returns True if equal, False otherwise

__getstate__()
Retrieve the state of the SourceNode

Returns the state of the object

Rtype dict

__init__(*datatype*, *id_=None*)
Instantiation of the SourceNode.

Parameters

- **datatype** – The (id of) the datatype of the output.
- **id** – The url pattern.

This class should never be instantiated directly (unless you know what you are doing). Instead create a source using the network class like shown in the usage example below.

usage example:

```
>>> import fastr
>>> network = fastr.Network()
>>> source = network.create_source(datatype=fastr.typelist['ITKImageFile'],
↪ id_='sourceN')
```

__module__ = 'fastr.core.node'

__setstate__(*state*)
Set the state of the SourceNode by the given state.

Parameters **state** (*dict*) – The state to populate the object with

Returns None

create_job(*sample_id*, *sample_index*, *job_data*, *job_dependencies*)

datatype
The datatype of the data this source supplies.

dimnames
Names of the dimensions in the SourceNode output. These will be reflected in the SampleIdLists.

execute()
Execute the source node and create the jobs that need to run

Returns list of jobs to run

Return type list of *Jobs*

output
Shorthand for `self.outputs['output']`

outputsize
The size of output of this SourceNode

set_data(*data*, *ids=None*)
Set the data of this source node.

Parameters

- **data** (*dict, OrderedDict or list of urls*) – the data to use
- **ids** – if data is a list, a list of accompanying ids

sourcegroup

valid
This does nothing. It only overloads the valid method of Node(). The original is intended to check if the inputs are connected to some output. Since this class does not implement inputs, it is skipped.

objectmanager Module

This module contains the object manager class

class fastr.core.objectmanager.**ObjectManager**(*path*)
Bases: *fastr.core.basemanager.BaseManager*

Class for managing all the objects loaded in the fastr system

__abstractmethods__ = frozenset(['object_class', 'get_object_version'])

`__contains__`(*key*)
Check if an item is in the ObjectManager

Parameters **`key`** (`str or tuple`) – object id or tuple (Objectid, version)

Returns flag indicating the item is in the manager

`__getitem__`(*key*)
Retrieve a Object from the ObjectManager. You can request by only an id, which results in the newest version of the Object being returned, or request using both an id and a version.

Parameters **`key`** (`str or tuple`) – object id or tuple (Objectid, version)

Returns the requested Object

Raises **`FastrObjectUnknownError`** – if a non-existing Object was requested

`__init__`(*path*)
Create a ObjectManager and scan path to search for Objects

Parameters **`path`** (`str or iterable of str`) – the path(s) to scan for Objects

Returns newly created ObjectManager

`__keytransform__`(*key*)
Key transform, used for allowing indexing both by id-only and by `(id, version)`

Parameters **`key`** – key to transform

Returns key in form `(id, version)`

`__module__` **= 'fastr.core.objectmanager'**

`get_object_version`(*obj*)
Get the version of a given object

Parameters **`object`** – the object to use

Returns the version of the object

`object_class`
The class of the objects to populate the manager with

`objectversions`(*obj*)
Return a list of available versions for the object

Parameters **`object`** – The object to check the versions for. Can be either a *Object* or a *str*.

Returns List of version objects. Returns *None* when the given object is not known.

`todict`()
Return a dictionary version of the Manager

Returns manager as a dict

`pluginmanager` Module

This module contains the Manager class for Plugins in the fastr system

class `fastr.core.pluginmanager.`**`BasePluginManager`**(*path=None*, *recursive=False*)
Bases: *`fastr.core.basemanager.BaseManager`*

Baseclass for PluginManagers, need to override the self._plugin_class

`__abstractmethods__` **= frozenset(['plugin_class'])**

`__getitem__`(*key*)
Retrieve item from BaseManager

Parameters **`key`** – the key of the item to retrieve

Returns the value indicated by the key

Raises ***FastrKeyError*** – if the key is not found in the BaseManager

`__init__`(*path=None*, *recursive=False*)

Create a BasePluginManager and scan the give path for matching plugins

Parameters

- **`path`** (*`str`*) – path to scan
- **`recursive`** (*`bool`*) – flag to indicate a recursive search

Returns newly created plugin manager

Raises ***FastrTypeError*** – if self._plugin_class is set to a class not subclassing BasePlugin

`__module__` **= 'fastr.core.pluginmanager'**

`load_plugin`(*plugin_key*)

`plugin_class`

The class from which the plugins must be subclassed

`populate`()

Populate the manager with the data. This is a method that will be called when the Managers data is first accessed. This way we avoid doing expensive directory scans when the data is never requested.

class `fastr.core.pluginmanager.`**`LazyModule`**(*name*, *parent*, *plugin_manager*)

Bases: `module`

A module that allows content to be loaded lazily from plugins. It generally is (almost) empty and gets (partially) populated when an attribute cannot be found. This allows lazy loading and plugins depending on other plugins.

`__getattr__`(*item*)

The getattr is called when getattribute does not return a value and is used as a fallback. In this case we try to find the value normally and will trigger the plugin manager if it cannot be found.

Parameters **`item`** (*`str`*) – attribute to retrieve

Returns the requested attribute

`__init__`(*name*, *parent*, *plugin_manager*)

`__module__` **= 'fastr.core.pluginmanager'**

`__repr__`()

`__weakref__`

list of weak references to the object (if defined)

class `fastr.core.pluginmanager.`**`PluginManager`**(*path=None*)

Bases: *`fastr.core.pluginmanager.BasePluginManager`*

`__abstractmethods__` **= frozenset([])**

`__init__`(*path=None*)

`__module__` **= 'fastr.core.pluginmanager'**

`__setitem__`(*key*, *value*)

Store an item in the BaseManager, will ignore the item if the key is already present in the BaseManager.

Parameters

- **`name`** – the key of the item to save
- **`value`** – the value of the item to save

Returns None

plugin_class
The plugin manager contains any Plugin subclass

class fastr.core.pluginmanager.**PluginSubManager**(*parent*, *plugin_class*)
Bases: *fastr.core.pluginmanager.BasePluginManager*

A PluginManager that is a selection of a parent plugin manger. It uses the PluginsView to only expose part of the parent PluginManager. This is used to create plugin managers for only certain types of plugins (e.g. IOPlugins) without loading them multiple times.

__abstractmethods__ = frozenset([])

__init__(*parent*, *plugin_class*)

__module__ = 'fastr.core.pluginmanager'

data

plugin_class
PluginSubManagers only expose the plugins of a certain class

class fastr.core.pluginmanager.**PluginsView**(*parent*, *plugin_class*)
Bases: _abcoll.MutableMapping

A collection that acts like view of the plugins of another plugin manager. This is a proxy object that only gives access the plugins of a certain plugin class. It behaves like a mapping and is used as the data object for a PluginSubManager.

__abstractmethods__ = frozenset([])

__delitem__(*key*)

__getitem__(*item*)

__init__(*parent*, *plugin_class*)
Constructor for the plugins view

Parameters

- **parent** (BasePluginManager) – the parent plugin manager
- **plugin_class** (*class*) – the class of the plugins to expose

__iter__()

__len__()

__module__ = 'fastr.core.pluginmanager'

__setitem__(*key*, *value*)

filter_plugin(*plugin*)

class fastr.core.pluginmanager.**plugin_option_type**(*filename*, *name*, *namespace*, *id*)
Bases: tuple

__dict__ = dict_proxy({'__module__': 'fastr.core.pluginmanager', '_make': <classmethod object>, '_replace': <fu

__getnewargs__()
Return self as a plain tuple. Used by copy and pickle.

__getstate__()
Exclude the OrderedDict from pickling

__module__ = 'fastr.core.pluginmanager'

static __new__(*_cls*, *filename*, *name*, *namespace*, *id*)
Create new instance of plugin_option_type(filename, name, namespace, id)

__repr__()
Return a nicely formatted representation string

__slots__ = ()

filename
Alias for field number 0

id
Alias for field number 3

name
Alias for field number 1

namespace
Alias for field number 2

provenance Module

class fastr.core.provenance.**Provenance**(*parent*, *host=None*)
Bases: object

The Provenance object keeps track of everything that happens to a data object.

__dict__ = dict_proxy({'__module__': 'fastr.core.provenance', '__init__': <function __init__>, 'activity': <function

__init__(*parent*, *host=None*)

__module__ = 'fastr.core.provenance'

__weakref__
list of weak references to the object (if defined)

activity(*identifier*, *start_time=None*, *end_time=None*, *other_attributes=None*)

agent(*identifier*, *other_attributes=None*)

entity(*identifier*, *other_attributes=None*)

samples Module

This package holds the classes for working with samples.

class fastr.core.samples.**HasSamples**
Bases: object

Base class for all classes that supply samples. This base class allows to only define __getitem__ and size and get all other basic functions mixed in so that the object behaves similar to a Mapping.

__abstractmethods__ = frozenset(['__getitem__', 'size'])

__contains__(*item*)

__dict__ = dict_proxy({'_abc_cache': <_weakrefset.WeakSet object>, '__module__': 'fastr.core.samples', '__metac

__getitem__(*item*)

__iter__()

__metaclass__
alias of ABCMeta

__module__ = 'fastr.core.samples'

__weakref__
list of weak references to the object (if defined)

ids()

indexes()

items()

iteritems()

size

class fastr.core.samples.**SampleBaseId**

Bases: `tuple`

This class represents a sample id. A sample id is a multi-dimensional id that has a simple, consistent string representation.

__add__(*other*)

Add another SampleId, this allows to add parts to the SampleId in a convenient way.

__dict__ = dict_proxy({'__module__': 'fastr.core.samples', '__new__': <staticmethod object>, '__str__': <function

__module__ = 'fastr.core.samples'

static **__new__**(**args*)

Create a new SampleId

Parameters args (*iterator/iterable of element type or element type*) – the strings to make sample id for

__radd__(*other*)

Add another SampleId, this allows to add parts to the SampleId in a convenient way. This is the right-hand version of the operator.

__repr__()

Get a string representation for the SampleBaseId

Returns the string representation

Return type str

__str__()

Get a string version for the SampleId, joins the SampleId with __ to create a single string version.

Returns the string version

Return type str

class fastr.core.samples.**SampleCollection**(*dimnames*, *parent*)

Bases: `_abcoll.MutableMapping`

The SampleCollections is a class that contains the data including a form of ordering. Each sample is reachable both by its SampleId and a SampleIndex. The object is sparse, so not all SampleId have to be defined allowing for non-rectangular data shapes.

Note: This object is meant to replace both the SampleIdList and the ValueStorage.

__abstractmethods__ = frozenset([])

__contains__(*item*)

Check if an item is in the SampleCollection. The item can be a SampleId or SampleIndex. If the item is a slicing SampleIndex, then check if it would return any data (True) or no data (False)

Parameters item (`SampleId`, `SampleIndex`) – the item to check for

Returns flag indicating item is in the collections

Return type bool

__delitem__(*key*)

Remove an item from the SampleCollection

Parameters key (`SampleId`, `SampleIndex`, *tuple of both, or* `SampleItem`) – the key of the item to remove

__getitem__(*item*)

Retrieve (a) SampleItem(s) from the SampleCollection using the SampleId or SampleIndex. If the item is a tuple, it should be valid tuple for constructing either a SampleId or SampleIndex.

Parameters **item** (SampleId, SampleIndex, *or tuple*) – the identifier of the item to retrieve

Returns the requested item

Return type *SampleItem*

Raises

- ***FastrTypeError*** – if the item parameter is of incorrect type
- **KeyError** – if the item is not found

__init__(*dimnames*, *parent*)
Createa a new SampleCollection

__iter__()
Iterate over the indices

__len__()
Get the number of samples in the SampleCollections.

__module__ = 'fastr.core.samples'

__repr__()

__setitem__(*key*, *value*)
Set an item to the SampleCollection. The key can be a SampleId, SampleIndex or a tuple containing a SampleId and SampleIndex. The value can be a SampleItem (with the SampleId and SampleIndex matching), a tuple with values (assuming no depending jobs), or a with a list of values and a set of depending jobs.

Parameters

- **key** (SampleId, SampleIndex, *tuple of both, or* SampleItem) – the key of the item to store
- **value** (SampleItem, *tuple of values, or tuple of tuple of values and set of depending jobs*) – the value of the SampleItem to store

Raises

- ***FastrTypeError*** – if the key or value types are incorrect
- ***FastrValueError*** – if the id or values are incorrectly formed

dimnames
The dimnames of the SampleCollection

fullid
The full defining ID for the SampleIdList

ndims
The number of dimensions in this SampleCollection

parent
The parent object holding the SampleCollection

size
The size of the SampleCollection. The size is the largest index in every dimension. For a 2D SampleCollection with 2 entries (10, 2) and (6, 6) the size would be (10, 6). As that is the rectangular grid that contains all data points.

class fastr.core.samples.**SampleId**
Bases: *fastr.core.samples.SampleBaseId*

SampleId is an identifier for data using human readable strings

__module__ = 'fastr.core.samples'

class `fastr.core.samples.`**`SampleIndex`**

Bases: *`fastr.core.samples.SampleBaseId`*

SampleId is an identifier for data using the location in the N-d data structure.

`__module__` **= 'fastr.core.samples'**

`__repr__``()`

Get a string representation for the SampleIndex

Returns the string representation

Return type str

`__str__``()`

Get a string version for the SampleId, joins the SampleId with __ to create a single string version.

Returns the string version

Return type str

`expand``(`*size*`)`

Function expanding a slice SampleIndex into a list of non-slice SampleIndex objects

Parameters **`size`** – the size of the collection to slice

`isslice`

Flag indicating that the SampleIndex is a slice (as opposed to a simple single index).

class `fastr.core.samples.`**`SampleItem`**

Bases: *`fastr.core.samples.SampleItemBase`*

`__module__` **= 'fastr.core.samples'**

static **`__new__`**`(`*index*, *id_*, *data*, *jobs=None*`)`

Create a SampleItem. Data should be an OrderedDict of tuples.

Parameters

- **`index`** (*`tuple`*, *`slice`*) – the sample index
- **`id`** (`SampleId`) – the sample id
- **`data`** (`SampleValue`, *`Mapping`*) – the data values
- **`jobs`** (*`set`*) – set of jobs on which this SampleItems data depends.

class `fastr.core.samples.`**`SampleItemBase`**

Bases: `tuple`

This class represents a sample item, a combination of a SampleIndex, SampleID, value and required jobs. The SampleItem based on a named tuple and has some extra methods to combine SampleItems easily.

`__add__``(`*other*`)`

The addition operator combines two SampleItems into a single SampleItems. It merges the data and jobs and takes the index and id of the left-hand item.

Parameters **`other`** (`SampleItem`) – The other item to add to this one

Returns the combined SampleItem

Return type *SampleItem*

`__dict__` **= dict_proxy({'index': <property object>, '__module__': 'fastr.core.samples', 'dimensionality': <property**

`__getnewargs__``()`

Get new args gives the arguments to use to re-create this object, This is used for serialization.

`__module__` **= 'fastr.core.samples'**

static **`__new__`**`(`*index*, *id_*, *data*, *jobs=None*`)`

Create a SampleItem. Data should be an OrderedDict of tuples.

Parameters

- **index** (*tuple, slice*) – the sample index
- **id** (SampleId) – the sample id
- **data** (SampleValue, *Mapping*) – the data values
- **jobs** (*set*) – set, tuple or list of jobs on which this SampleItems data depends.

__repr__()

Get a string representation for the SampleItem

Returns the string representation

Return type str

cardinality

The cardinality of this Sample

static combine(**args*)

Combine a number of SampleItems into a new one.

Parameters ***args** – the SampleItems to combine

Returns the combined SampleItem

Return type *SampleItem*

It is possible to both give multiple arguments, where each argument is a SampleItem, or a single argument which is an iterable yielding SampleItems.

```
# variables a, b, c, d are SampleItems to combine
# These are all valid ways of combining the SampleItems
comb1 = SampleItem.combine(a, b, c, d)  # Using multiple arguments
l = [a, b, c, d]
comb2 = SampleItem.combine(l)  # Using a list of arguments
comb3 = SampleItem.combine(l.__iter__())  # Using an iterator
```

data

The data SampleValue of the SampleItem

Returns The value of this SampleItem

Return type *SampleValue*

dimensionality

The dimensionality of this Sample

id

The sample id of the SampleItem

Returns The id of this SampleItem

Return type *SampleId*

index

The index of the SampleItem

Returns The index of this SampleItem

Return type *SampleIndex*

jobs

The set of the jobs on which this SampleItem depends

Returns The jobs that generated the data for this SampleItem

Return type set

class fastr.core.samples.**SamplePayload**

Bases: *fastr.core.samples.SampleItemBase*

`__add__`(*other*)

The addition operator combines two SampleItems into a single SampleItems. It merges the data and jobs and takes the index and id of the left-hand item.

Parameters **`other`** (`SampleItem`) – The other item to add to this one

Returns the combined SamplePayload

Return type *SamplePayload*

`__module__` **= 'fastr.core.samples'**

static `__new__`(*index*, *id_*, *data*, *jobs=None*)

Create a SampleItem. Data should be an OrderedDict of tuples.

Parameters

- **`index`** (*`tuple`*, *`slice`*) – the sample index
- **`id`** (`SampleId`) – the sample id
- **`data`** (`SampleValue`, *`Mapping`*) – the data values
- **`jobs`** (*`set`*) – set of jobs on which this SampleItems data depends.

class `fastr.core.samples.`**`SampleValue`**(**args*, ***kwargs*)

Bases: `_abcoll.MutableMapping`

A collection containing the content of a sample

`__abstractmethods__` **= frozenset([])**

`__add__`(*other*)

`__delitem__`(*key*)

`__getitem__`(*item*)

`__getstate__`()

`__init__`(**args*, ***kwargs*)

`__iter__`()

`__len__`()

`__module__` **= 'fastr.core.samples'**

`__radd__`(*other*)

`__repr__`()

`__setitem__`(*key*, *value*)

`__setstate__`(*state*)

`cast`(*datatype*)

`is_mapping`

`is_sequence`

`iterelements`()

`mapping_part`()

`sequence_part`()

`serializable` Module

This package contains the base class and meta class for all serializable objects in the Fastr system.

class `fastr.core.serializable.`**`PassThroughSerializer`**

Bases: `object`

`__dict__` **= dict_proxy({'__module__': 'fastr.core.serializable', 'dumps': <staticmethod object>, '__dict__': <attrib**

`__module__` **= 'fastr.core.serializable'**

`__weakref__`

list of weak references to the object (if defined)

static `dumps` (*data*)

static `loads` (*data*)

class `fastr.core.serializable.`**`Serializable`**

Bases: `object`

Superclass for all classes that can be serialized.

`SERIALIZERS` **= {'/home/docs/checkouts/readthedocs.org/user_builds/fastr/envs/1.1.2/local/lib/python2.7/site-packag**

`__dict__` **= dict_proxy({'load': <classmethod object>, '__module__': 'fastr.core.serializable', 'SERIALIZERS': {'/h**

`__getstate__` ()

`__module__` **= 'fastr.core.serializable'**

`__weakref__`

list of weak references to the object (if defined)

classmethod `createobj` (*state*, *_=None*)

Create object function for generic objects

Parameters

- **`cls`** – The class to create
- **`state`** – The state to use to create the Link
- **`network`** – the parent Network

Returns newly created Link

`dump` (*file_handle*, *method='json'*, ***kwargs*)

Dump the object to a file like object.

Parameters

- **`file_handle`** – file descriptor to write the data to
- **`method`** (`str`) – method of final serialization to use (e.g. json, xml, pickle)
- **`kwargs`** – extra arguments passed to the final serializer

`dumpf` (*path*, *method=None*, ***kwargs*)

Dump the object to a file

Parameters

- **`path`** – path where to write the file
- **`method`** (`str`) – method of final serialization to use (e.g. json, xml, pickle)
- **`kwargs`** – extra arguments passed to the final serializer

Note: The dumpf function can determine the method based on the desired output filename. Also, if the filename ends with .gz it will continue search for another extension (so .json.gz could be found) and will then compress the result with gzip.

dumpfuncs = {'xml': <module 'fastr.utils.xmltodict' from '/home/docs/checkouts/readthedocs.org/user_builds/fastr/e

dumps (*method='json'*, ***kwargs*)
Dump the object to a string

Parameters

- **method** (*str*) – method of final serialization to use (e.g. json, xml, pickle)
- **kwargs** – extra arguments passed to the final serializer

Returns serialization string

Return type str

classmethod get_serializer (*filename=None*)

classmethod load (*file_handle*, *method=None*, *network=None*, ***kwargs*)
Load the object from a file-like object

Parameters

- **cls** – class of the object
- **file_handle** – file descriptor to write the data to
- **method** (*str*) – method of final serialization to use (e.g. json, xml, pickle)
- **network** – network in which to place the loaded object
- **kwargs** – extra arguments passed to the final serializer

Returns newly created object

Warning: Unlike the loadf functions, this function does not automatically detect gzip compression. You read a gzip using the gzip.open method, but not but simply opening a stream and hopeing this function will function.

classmethod loadf (*path*, *method=None*, *network=None*, ***kwargs*)
Load the object from a file

Parameters

- **cls** – class of the object
- **path** – path where to write the file
- **method** (*str*) – method of final serialization to use (e.g. json, xml, pickle)
- **network** – network in which to place the loaded object
- **kwargs** – extra arguments passed to the final serializer

Returns newly created object

Note: The loadf function can determine the method of loading based on the filename. Also it can automatically determine whether a file is gzipped.

classmethod loads (*string*, *method=None*, *network=None*, ***kwargs*)
Load the object from a string

Parameters

- **cls** – class of the object
- **string** (*str*) – the string containing the serialized data
- **method** (*str*) – method of final serialization to use (e.g. json, xml, pickle)
- **network** – network in which to place the loaded object
- **kwargs** – extra arguments passed to the final serializer

Returns newly created object

`target` Module

The module containing the classes describing the targets.

class `fastr.core.target.`**`DockerTarget`** (*binary*, *docker_image*, ***kwargs*)

Bases: *fastr.core.target.Target*

A tool target that is located in a Docker images. Can be run using docker-py.

`__abstractmethods__` = **frozenset([])**

`__enter__` ()

`__exit__` (*exc_type*, *exc_value*, *traceback*)

`__init__` (*binary*, *docker_image*, ***kwargs*)

Define a new docker target.

Parameters **docker_image** (*str*) – Docker image to use

`__module__` = **'fastr.core.target'**

`container`

`docker_api` = **None**

Docker api to use for docker target

`monitor_docker` (*container*, *resources*)

Monitor a process and profile the cpu, memory and io use. Register the resource use every _MONITOR_INTERVAL seconds.

Parameters

- **process** (*subproces.Popen*) – process to monitor
- **resources** – list to append measurements to

`run_command` (*command*)

class `fastr.core.target.`**`LocalBinaryTarget`** (*binary*, *paths=None*, *environment_variables=None*, *initscripts=None*, *modules=None*, *interpreter=None*, ***kwargs*)

Bases: *fastr.core.target.Target*

A tool target that is a local binary on the system. Can be found using environmentmodules or vfs-path on the executing machine

`DYNAMIC_LIBRARY_PATH_DICT` = **{'windows': 'PATH', 'darwin': 'DYLD_LIBRARY_PATH', 'linux': 'LD_LIBR**

`__abstractmethods__` = **frozenset([])**

`__enter__` ()

Set the environment in such a way that the target will be on the path.

`__exit__` (*exc_type*, *exc_value*, *traceback*)

Cleanup the environment

`__init__`(*binary*, *paths=None*, *environment_variables=None*, *initscripts=None*, *modules=None*, *interpreter=None*, ***kwargs*)
Define a new local binary target. Must be defined either using paths and optionally environment_variables and initscripts, or enviroment modules.

`__module__` **= 'fastr.core.target'**

`call_subprocess`(*command*)
Call a subprocess with logging/timing/profiling

Parameters **`command`** (`list`) – the command to execute

Returns execution info

Return type dict

`monitor_process`(*process*, *resources*)
Monitor a process and profile the cpu, memory and io use. Register the resource use every _MONITOR_INTERVAL seconds.

Parameters

- **`process`** (`subproces.Popen`) – process to monitor
- **`resources`** – list to append measurements to

`run_command`(*command*)

class `fastr.core.target.`**`ProcessUsageCollection`**
Bases: `_abcoll.Sequence`

`__abstractmethods__` **= frozenset([])**

`__getitem__`(*item*)

`__init__`()

`__len__`()

`__module__` **= 'fastr.core.target'**

`aggregate`(*number_of_points*)

`append`(*value*)

`usage_type`
alias of `SystemUsageInfo`

class `fastr.core.target.`**`SystemUsageInfo`**(*timestamp*, *cpu_percent*, *vmem*, *rmem*, *read_bytes*, *write_bytes*)
Bases: `tuple`

`__dict__` **= dict_proxy({'__module__': 'fastr.core.target', '_make': <classmethod object>, 'timestamp': <property**

`__getnewargs__`()
Return self as a plain tuple. Used by copy and pickle.

`__getstate__`()
Exclude the OrderedDict from pickling

`__module__` **= 'fastr.core.target'**

static **`__new__`**(*_cls*, *timestamp*, *cpu_percent*, *vmem*, *rmem*, *read_bytes*, *write_bytes*)
Create new instance of SystemUsageInfo(timestamp, cpu_percent, vmem, rmem, read_bytes, write_bytes)

`__repr__`()
Return a nicely formatted representation string

`__slots__` **= ()**

cpu_percent
Alias for field number 1

read_bytes
Alias for field number 4

rmem
Alias for field number 3

timestamp
Alias for field number 0

vmem
Alias for field number 2

write_bytes
Alias for field number 5

class fastr.core.target.**Target**(***kwargs*)
Bases: object

The abstract base class for all targets. Execution with a target should follow the following pattern:

```
>>> with Target() as target:
...     target.run_commmand(['sleep', '10'])
...     target.run_commmand(['sleep', '10'])
...     target.run_commmand(['sleep', '10'])
```

The Target context operator will set the correct paths/initialization. Within the context command can be ran and when leaving the context the target reverts the state before.

__abstractmethods__ = frozenset(['run_command'])

__dict__ = dict_proxy({'_abc_cache': <_weakrefset.WeakSet object>, '__module__': 'fastr.core.target', '__enter__

__enter__()
Set the environment in such a way that the target will be on the path.

__exit__(*exc_type*, *exc_value*, *traceback*)
Cleanup the environment where needed

__init__(***kwargs*)

__metaclass__
alias of ABCMeta

__module__ = 'fastr.core.target'

__weakref__
list of weak references to the object (if defined)

run_command(*command*)

tool Module

A module to maintain a tool.

Exported classes:

- Tool – A class encapsulating a tool.
- ParameterDescription – The base class containing the shared description of a parameter (both input and ouput).
- InputParameterDescription – A class containing the description of an input parameter.
- Output ParameterDescription – A class containing the description of an output parameter.

class `fastr.core.tool.`**`Tool`**(*doc=None*)

Bases: *`fastr.core.serializable.Serializable`*

The class encapsulating a tool.

`__dataschemafile__` = **'Tool.schema.json'**

`__eq__`(*other*)

Compare two Tool instances with each other.

Parameters **`other`** (`Tool`) – the other instances to compare to

Returns True if equal, False otherwise

`__getstate__`()

Retrieve the state of the Tool

Returns the state of the object

Rtype dict

`__init__`(*doc=None*)

Create a new Tool :param doc: path of toolfile or a dict containing the tool data :type doc: str or dict

`__module__` = **'fastr.core.tool'**

`__repr__`()

Get a string representation for the Tool. This will show the inputs and output defined in a table-like structure.

Returns the string representation

Return type str

`__setstate__`(*state*)

Set the state of the Tool by the given state.

Parameters **`state`** (*`dict`*) – The state to populate the object with

`__str__`()

Get a string version for the Tool

Returns the string version

Return type str

`authors` = **None**

List of authors of the tool. These people wrapped the executable but are not responsible for executable itself.

`cite` = **None**

This holds the citation you should use when publishing something based on this Tool

`command` = **None**

Command is a dictionary contain information about the command which is called by this Tool: command['interpreter'] holds the (possible) interpreter to use command['targets'] holds a per os/arch dictionary of files that should be executed command['url'] is the webpage of the command to be called command['version'] is the version of the command used command['description'] can help a description of the command command['authors'] lists the original authors of the command

`command_version`

`description` = **None**

Description of the tool and it's functionality

`execute`(*payload=None*, ***kwargs*)

Execute a Tool given the payload for a single run

Parameters **`payload`** – the data to execute the Tool with

Returns The result of the execution

Return type InterFaceResult

`fullid`
The full id of this tool

`hash`

`help` = **None**
Man page for the Tool. Here usage and examples can be described in detail

`inputs`

`interface_class` = **None**
Create the Interface based on the class specified in the tool file

`name` = **None**
Name of the tool, this should be a descriptive, human readable name.

`namespace` = **None**
The namespace this tools lives in, this will be set by the ToolManager on load

`node_class` = **None**
Class for of the Node to use

`ns_id`
The namespace and id of the Tool

`outputs`

`path`
The path of the directory in which the tool definition file was located.

`references` = **None**
A list of documents and in depth reading about the methods used in this tool

`regex` = **None**
Identifier for the tool

`requirements` = **None**
Requirements for this Tool

Warning: Not yet implemented

`tags` = **None**
List of tags for this tool

`target`
The OS and arch matched target definition.

`test`()
Run the tests for this tool

`test_spec`
alias of `TestSpecification`

`tests` = **None**
Test for this tool. A test should be a collection of inputs, parameters and outputs to verify the proper functioning of the Tool.

The format of the tests is a list of namedtuples, that have 3 fields: - input: a dict of the input data - command: a list given the expected command-line arguments - output: a dict of the output data to validate

Warning: Not yet implemented

url = None
URL to website where this tool can be downloaded from

version = None
Version of the tool, not of the underlying software

toolmanager Module

This module contains the tool manager class

class fastr.core.toolmanager.**ToolManager**(*path*)
Bases: *fastr.core.objectmanager.ObjectManager*

__abstractmethods__ = frozenset([])

__module__ = 'fastr.core.toolmanager'

get_object_version(*obj*)

object_class

populate()

toolversions(*tool*)
Return a list of available versions for the tool

Parameters **tool** – The tool to check the versions for. Can be either a *Tool* or a *str*.

Returns List of version objects. Returns *None* when the given tool is not known.

fastr.core.toolmanager.**toollist = ToolManager fastr.Sink v1.0 : /home/docs/checkouts/readthedocs.org/user_bu**
The fastr toollist

updateable Module

This module contains both the Updateable class and UpdateableMeta meta-class for objects which support updates within the fastr system

class fastr.core.updateable.**Updateable**
Bases: object

Super class for all classes that can be updated and have a status. These objects can be valid/invalid and ready/not-ready depending on their state. These states are set by the function update. This allows for interactively checking the network.

__abstractmethods__ = frozenset(['_update'])

__dict__ = dict_proxy({'__module__': 'fastr.core.updateable', '_update': <function _update>, '__metaclass__': <cl

__getstate__()
Retrieve the state of the object, make sure the status is not part of the description as it will not be valid after re-creating the object.

Returns the state of the object

Rtype dict

__init__()
Constructor, creates the status field

Returns newly created object

__metaclass__
alias of *UpdateableMeta*

__module__ = 'fastr.core.updateable'

`__setstate__`(*state*)
Set the state of the object by the given state. This adds a clean status field, making sure it is not unintended, outdated information from before serialization.

Parameters **`state`** (`dict`) – The state to populate the object with

`__updatefunc__`(*key=None*, *forward=True*, *backward=False*)
Default function for updating, it can be called without key to have a new update started with a new key.

Parameters

- **`key`** (`int`) – a key for this update, should be different than the last update key
- **`forward`** (`bool`) – flag indicating to update forward in the network
- **`backward`** (`bool`) – flag indicating to update backward in the network

`__updateinprogress__` = <thread.lock object>
Lock to avoid multiple updates happening at the same time

`__updatetriggers__` = []
Which methods need to be wrapped to trigger an update. Override this value to have the functions automatically wrapped. E.g. `__update_triggers__ = ['append', 'insert', '__setitem__']` to have these functions wrapped.

`__updating__` = True
Flag to indicate that this object is allowed to update

`__weakref__`
list of weak references to the object (if defined)

`messages`
The messages of the last update

`ready`
Flag indicating that the object is ready

`update`(*key=None*, *forward=True*, *backward=False*)
Default function for updating, it can be called without key to have a new update started with a new key.

Parameters

- **`key`** (`int`) – a key for this update, should be different than the last update key
- **`forward`** (`bool`) – flag indicating to update forward in the network
- **`backward`** (`bool`) – flag indicating to update backward in the network

`valid`
Flag indicating that the object is valid

class `fastr.core.updateable.`**`UpdateableMeta`**
Bases: `abc.ABCMeta`

A metaclass for objects which are updateable and need some methods/properties to trigger an update.

`__module__` = 'fastr.core.updateable'

static `__new__`(*mcs*, *name*, *parents*, *dct*)

classmethod `calcmro`(*mcs*, *bases*)
Calculate the Method Resolution Order of bases using the C3 algorithm.

Suppose you intended creating a class K with the given base classes. This function returns the MRO which K would have, *excluding* K itself (since it doesn't yet exist), as if you had actually created the class.

Another way of looking at this, if you pass a single class K, this will return the linearization of K (the MRO of K, *including* itself).

Parameters **bases** – the list of bases for which create the MRO

Returns the list representing the entire MRO, except the (non-existing) class itself

Note: Taken from http://code.activestate.com/recipes/577748-calculate-the-mro-of-a-class/
Created by Steven D'Aprano and licensed under the MIT license

classmethod **find_member** (*mcs*, *name*, *parents*, *dct*)
Find a member of the class in the same way as Python would if it had a given dict and set of bases

Parameters

- **mcs** – metaclass at work
- **name** – name of the class to be created
- **parents** – list of the bases for the new class
- **dct** – the dict of the class being created

Returns the firstly resolved member or None if nothing found

static **updatetrigger** (*fnc*)
Function decorator to make a function trigger an update after being called. This is a way to easily have function trigger an update after setting a value without writing tons of wrapper functions. The function keeps the original docstring and appends a note to it.

`version` Module

Module containing the class that represent versions

class `fastr.core.version.`**Version**
Bases: `tuple`

Class representing a software version definition. Allows for sorting and extraction of parts.

__dict__ = dict_proxy({'status': <property object>, '__module__': 'fastr.core.version', '__new__': <staticmethod o

__module__ = 'fastr.core.version'

static **__new__** (**version*)
Class containing a version

Can be constructed by:

```
Version( 'major.$minor.$extra[0].$extra[1]$seperator$status$build$suffix' )
Version( major, minor, extra, status, build, suffix, seperator )
Version( (major, minor, extra, status, build, suffix, seperator) )
Version( [major, minor, extra, status, build, suffix, seperator] )
```

Parameters

- **major** (*int*) – interger giving major version
- **minor** (*int*) – is an integer (required)
- **extra** (*list of int*) – is a list of integers
- **status** (*str*) – can be "a", "alpha", "b", "beta", "rc", or "r"
- **build** (*int*) – is an integer
- **suffix** (*str*) – can contain any combination of alpha-numeric character and "._-"
- **seperator** (*str*) – is any of ".", "-", or "_", which is located between $extra and $build

Note: The method based on strings is the recommended method. For strings the major and minor version are required, where for tuple and list constructors all seven elements are optional.

Examples:

```
>>> a = Version('0.1')
>>> print(tuple(a))
(0, 1, None, None, None, '', None)
>>> b = Version('2.5.3-rc2')
>>> print(tuple(b))
(2, 5, [3], 'rc', 2, '', '-')
>>> c = Version('1.2.3.4.5.6.7-beta8_with_suffix')
>>> print(tuple(c))
(1, 2, [3, 4, 5, 6, 7], 'beta', 8, '_with_suffix', '-')
```

`__repr__`()
Return a in-editor representation of the version

`__str__`()
Return a string representation of the version

`build`
the build number, this is following the status (e.g. for 3.2-beta4, this would be 4)

`extra`
extra version extension as a list

`extra_string`
extra version extension as a string

`major`
major version

`minor`
minor version

`status`
the status of the version (a, alpha, b, beta, rc or r)

`suffix`
the remainder of the version which was not formatted in a known way

`version_matcher` = <_sre.SRE_Pattern object at 0x13d61d0>

`vfs` Module

This module contains the virtual file system code. This is both an internally used object as well as an IOPlugin.

Subpackages

test Package

`test` Package

`testdatatypemanager` Module

`testdimension` Module

`testnetwork` Module

`testnode` Module

`testsamples` Module

`testtool` Module

`testversion` Module

`testvfs` Module

data Package

`data` Package

Package containig data related modules

`url` Module

Module providing tools to parse and create valid urls and paths.

usage example:

When in fastr.config under the mounts section the data mount is set to /media/data, you will get the following. .. code-block:: python

```
>>> import fastrdata.url import get_path_from_url
>>> get_path_from_url('vfs://data/temp/blaat1.png')
'/media/data/temp/blaat1.png'
```

`fastr.data.url.`**`basename`**(*url*)
Get basename of url

Parameters **`url`** (*`str`*) – the url

Returns the basename of the path in the url

`fastr.data.url.`**`create_vfs_url`**(*mountpoint*, *path*)
Construct an url from a given mount point and a relative path to the mount point.

Parameters

- **`mountpoint`** (*`str`*) – the name of the mountpoint
- **`path`** (*`str`*) – relative path from the mountpoint

Returns the created vfs url

`fastr.data.url.`**`dirname`**(*url*)
Get the dirname of the url

Parameters **`url`** (*`str`*) – the url

Returns the dirname of the path in the url

`fastr.data.url.`**`dirurl`**(*url*)
Get the a new url only having the dirname as the path

Parameters **`url`** (*`str`*) – the url

Returns the modified url with only dirname as path

`fastr.data.url.`**`full_split`**`(`*urlpath*`)`
Split the path in the url in a list of parts

Parameters **`urlpath`** – the url path

Returns a list of parts

`fastr.data.url.`**`get_path_from_url`**`(`*url*`)`
Get the path to a file from a url. Currently supports the file:// and vfs:// scheme's

Examples:

```
>>> url.get_path_from_url('vfs://neurodata/user/project/file.ext')
'Y:\neuro3\user\project\file.ext'


>>> 'file:///d:/data/project/file.ext'
'd:\data\project\file.ext'
```

Warning: file:// will not function cross platform and is mainly for testing

`fastr.data.url.`**`get_url_scheme`**`(`*url*`)`
Get the schem of the url

Parameters **`url`** (`str`) – url to extract scheme from

Returns the url scheme

Return type str

`fastr.data.url.`**`isurl`**`(`*string*`)`
Check if string is a valid url

Parameters **`string`** (`str`) – potential url

Returns flag indicating if string is a valid url

`fastr.data.url.`**`join`**`(`*url*, **p*`)`
Join the path in the url with p

Parameters

- **`url`** (`str`) – the base url to join with
- **`p`** – additional parts of the path

Returns the url with the parts added to the path

`fastr.data.url.`**`normurl`**`(`*url*`)`
Normalized the path of the url

Parameters **`url`** (`str`) – the url

Returns the normalized url

`fastr.data.url.`**`register_url_scheme`**`(`*scheme*`)`
Register a custom scheme to behave http like. This is needed to parse all things properly.

`fastr.data.url.`**`split`**`(`*url*`)`
Split a url in a url with the dirname and the basename part of the path of the url

Parameters **`url`** (`str`) – the url

Returns a tuple with (dirname_url, basename)

examples Package

`examples` Package

`add_ints` Module

`fastr.examples.add_ints.`**`create_network`**`()`

`fastr.examples.add_ints.`**`main`**`()`

`fastr.examples.add_ints.`**`sink_data`**`(`*network*`)`

`fastr.examples.add_ints.`**`source_data`**`(`*network*`)`

`collapse` Module

`fastr.examples.collapse.`**`create_network`**`()`

`fastr.examples.collapse.`**`main`**`()`

`fastr.examples.collapse.`**`sink_data`**`(`*network*`)`

`fastr.examples.collapse.`**`source_data`**`(`*network*`)`

`collapse_expand` Module

`fastr.examples.collapse_expand.`**`create_network`**`()`

`fastr.examples.collapse_expand.`**`main`**`()`

`fastr.examples.collapse_expand.`**`sink_data`**`(`*network*`)`

`fastr.examples.collapse_expand.`**`source_data`**`(`*network*`)`

`cross_validation` Module

`fastr.examples.cross_validation.`**`create_network`**`()`

`fastr.examples.cross_validation.`**`main`**`()`

`fastr.examples.cross_validation.`**`sink_data`**`(`*network*`)`

`fastr.examples.cross_validation.`**`source_data`**`(`*network*`)`

`expand` Module

`fastr.examples.expand.`**`create_network`**`()`

`fastr.examples.expand.`**`main`**`()`

`fastr.examples.expand.`**`sink_data`**`(`*network*`)`

`fastr.examples.expand.`**`source_data`**`(`*network*`)`

`macro_node` Module

`fastr.examples.macro_node.`**`create_macro_network`**`()`

`fastr.examples.macro_node.`**`create_network`**`()`

`fastr.examples.macro_node.`**`create_super_macro_node`**`()`

fastr.examples.macro_node.**main**()

fastr.examples.macro_node.**sink_data**(*network*)

fastr.examples.macro_node.**source_data**(*network*)

source_sink Module

fastr.examples.source_sink.**create_network**()

fastr.examples.source_sink.**main**()

fastr.examples.source_sink.**sink_data**(*network*)

fastr.examples.source_sink.**source_data**(*network*)

Subpackages

test Package

test_examples Module

execution Package

execution Package

This package contains all modules related directly to the execution

environmentmodules Module

This module contains a class to interact with EnvironmentModules

class fastr.execution.environmentmodules.**EnvironmentModules**(*protected=None*)
    Bases: object

    This class can control the module environments in python. It can list, load and unload environmentmodules. These modules are then used if subprocess is

        called from python.

    __dict__ = dict_proxy({'load': <function load>, '__module__': 'fastr.execution.environmentmodules', 'sync': <func

    __init__(*protected=None*)
        Create the environmentmodules control object

        Parameters protected (*list*) – list of modules that should never be unloaded

        Returns newly created EnvironmentModules

    __module__ = 'fastr.execution.environmentmodules'

    __weakref__
        list of weak references to the object (if defined)

    avail(*namestart=None*)
        Print available modules in same way as commandline version

        Parameters namestart – filter on modules that start with namestart

    avail_modules
        List of avaible modules

clear()
Unload all modules (except the protected modules as they cannot be unloaded). This should result in a clean environment.

isloaded(*module*)
Check if a specific module is loaded

Parameters **module** – module to check

Returns flag indicating the module is loaded

load(*module*)
Load specified module

Parameters **module** – module to load

loaded_modules
List of currently loaded modules

reload(*module*)
Reload specified module

Parameters **module** – module to reload

swap(*module1*, *module2*)
Swap one module for another one

Parameters

- **module1** – module to unload
- **module2** – module to load

sync()
Sync the object with the underlying enviroment. Re-checks the available and loaded modules

static **tostring_modvalue**(*value*)
Turn a representation of a module into a string representation

Parameters **value** – module representation (either str or tuple)

Returns string representation

static **totuple_modvalue**(*value*)
Turn a representation of a module into a tuple representation

Parameters **value** – module representation (either str or tuple)

Returns tuple representation (name, version, default)

unload(*module*)
Unload specified module

Parameters **module** – module to unload

executionpluginmanager Module

This module holds the ExecutionPluginManager as well as the base-class for all ExecutionPlugins.

class fastr.execution.executionpluginmanager.**ExecutionPlugin**(*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)
Bases: *fastr.core.baseplugin.Plugin*

This class is the base for all Plugins to execute jobs somewhere. There are many methods already in place for taking care of stuff. Most plugins should only need to redefine a few abstract methods:

- `__init__` the constructor
- `cleanup` a clean up function that frees resources, closes connections, etc
- `_queue_job` the method that queues the job for execution
- `_cancel_job` cancels a previously queued job
- `_release_job` releases a job that is currently held
- `_job_finished` extra callback for when a job finishes

Not all of the functions need to actually do anything for a plugin. There are examples of plugins that do not really need a `cleanup`, but for safety you need to implement it. Just using a `pass` for the method could be fine in such a case.

Warning: When overwriting other function, extreme care must be taken not to break the plugins working.

`__abstractmethods__` **= frozenset(['cleanup', '_queue_job', '_cancel_job', '_job_finished', '_release_job', '__init**

`__del__`()
Cleanup if the variable was deleted on purpose

`__enter__`()

`__exit__`(*type_*, *value*, *tb*)

`__init__`(*finished_callback=None*, *cancelled_callback=None*, *status_callback=None*)
Setup the ExecutionPlugin

Parameters

- **`finished_callback`** – the callback to call after a job finished
- **`cancelled_callback`** – the callback to call after a job cancelled

Returns newly created ExecutionPlugin

`__module__` **= 'fastr.execution.executionpluginmanager'**

`cancel_job`(*job*)
Cancel a job previously queued

Parameters **`job`** – job to cancel

`check_job_requirements`(*jobid*)
Check if the requirements for a job are fulfilled.

Parameters **`jobid`** – job to check

Returns directive what should happen with the job

Return type *JobAction*

`check_job_status`(*jobid*)
Get the status of a specified job

Parameters **`jobid`** – the target job

Returns the status of the job (or None if job not found)

`cleanup`()
Method to call to clean up the ExecutionPlugin. This can be to clear temporary data, close connections, etc.

Parameters **`force`** – force cleanup (e.g. kill instead of join a process)

`get_job`(*jobid*)

`get_status`(*job*)

job_finished(*job*, *blocking=False*)
The default callback that is called when a Job finishes. This will create a new thread that handles the actual callback.

Parameters **job** (Job) – the job that finished

Returns

queue_job(*job*)
Add a job to the execution queue

Parameters **job** (Job) – job to add

release_job(*job*)
Release a job that has been put on hold

Parameters **jobid** – job to release

show_jobs(*req_status=None*)
List the queued jobs, possible filtered by status

Parameters **req_status** – requested status to filter on

Returns list of jobs

class fastr.execution.executionpluginmanager.**ExecutionPluginManager**
Bases: *fastr.core.pluginmanager.PluginSubManager*

Container holding all the ExecutionPlugins known to the Fastr system

__abstractmethods__ = frozenset([])

__init__()
Initialize a ExecutionPluginManager and load plugins.

Parameters

- **path** – path to search for plugins
- **recursive** – flag for searching recursively

Returns newly created ExecutionPluginManager

__module__ = 'fastr.execution.executionpluginmanager'

plugin_class
The class of the Plugins expected in this BasePluginManager

class fastr.execution.executionpluginmanager.**JobAction**
Bases: enum.Enum

Job actions that can be performed. This is used for checking if held jobs should be queued, held longer or be cancelled.

__format__(*format_spec*)

__module__ = 'fastr.execution.executionpluginmanager'

static __new__(*value*)

__reduce_ex__(*proto*)

__repr__()

__str__()

cancel = 'cancel'

hold = 'hold'

queue = 'queue'

`executionscript` Module

The executionscript is the script that wraps around a tool executable. It takes a job, builds the command, executes the command (while profiling it) and collects the results.

`fastr.execution.executionscript.`**`execute_job`**(*job*)

Execute a Job and save the result to disk

Parameters **`job`** – the job to execute

`fastr.execution.executionscript.`**`main`**(*joblist=None*)

This is the main code. Wrapped inside a function to avoid the variables being seen as globals and to shut up pylint. Also if the joblist argument is given it can run any given job, otherwise it takes the first command line argument.

`job` Module

This module contains the Job class and some related classes.

class `fastr.execution.job.`**`InlineJob`**(**args*, ***kwargs*)

Bases: *`fastr.execution.job.Job`*

`__init__`(**args*, ***kwargs*)

`__module__` **= 'fastr.execution.job'**

`get_result`()

class `fastr.execution.job.`**`Job`**(*jobid*, *tool_name*, *tool_version*, *nodeid*, *sample_id*, *sample_index*, *input_arguments*, *output_arguments*, *tmpdir*, *hold_jobs=None*, *timestamp=None*, *cores=None*, *memory=None*, *walltime=None*, *status_callback=None*, *preferred_types=None*)

Bases: *`fastr.core.serializable.Serializable`*

Class describing a job.

Arguments: tool_name - the name of the tool (str) tool_version - the version of the tool (Version) argument - the arguments used when calling the tool (list) tmpdir - temporary directory to use to store output data hold_jobs - list of jobs that need to finished before this job can run (list)

`COMMAND_DUMP` **= '__fastr_command__.pickle.gz'**

`RESULT_DUMP` **= '__fastr_result__.pickle.gz'**

`STDERR_DUMP` **= '__fastr_stderr__.txt'**

`STDOUT_DUMP` **= '__fastr_stdout__.txt'**

`__getstate__`()

Get the state of the job

Returns job state

Return type dict

`__init__`(*jobid*, *tool_name*, *tool_version*, *nodeid*, *sample_id*, *sample_index*, *input_arguments*, *output_arguments*, *tmpdir*, *hold_jobs=None*, *timestamp=None*, *cores=None*, *memory=None*, *walltime=None*, *status_callback=None*, *preferred_types=None*)

Create a job

Parameters

- **`jobid`** (*`str`*) – the job id
- **`tool_name`** (*`str`*) – the id of the tool
- **`tool_version`** (`fastr.core.version.Version`) – the version of the tool
- **`nodeid`** (*`str`*) – the id of the creating node

- **sample_id** (`fastr.core.samples.SampleId`) – the id of the sample
- **input_arguments** (*list[dict]*) – the argument list
- **output_arguments** (*list[dict]*) – the argument list
- **tmpdir** (*str*) – the workdir for this job
- **hold_jobs** (*list[str]*) – the jobs on which this jobs depend
- **timestamp** (*datetime.datetime*) – the time this job was spawned
- **cores** (*int*) – number of cores this jobs is allowed consume
- **memory** (*str*) – max amount of memory that this job is allowed to consume
- **walltime** (*str*) – max amount of time this job is allowed to run

Returns

__module__ = **'fastr.execution.job'**

__repr__()
String representation of the Job

__setstate__(*state*)
Set the state of the job

Parameters **state** (*dict*) –

static calc_cardinality(*desc*, *payload*)

commandfile
The path of the command pickle

commandurl
The url of the command pickle

create_payload()
Create the payload for this object based on all the input/output arguments

Returns the payload

Return type dict

execute()
Execute this job

Returns The result of the execution

Return type InterFaceResult

fill_output_argument(*output_spec*, *cardinality*, *desired_type*)
This is an abstract class method. The method should take the argument_dict generated from calling self.get_argument_dict() and turn it into a list of commandline arguments that represent this Input/Output.

Parameters

- **cardinality** (*int*) – the cardinality for this output (can be non for automatic outputs)
- **desired_type** (`DataType`) – the desired datatype for this output

Returns the values for this output

Return type list

fullid
The full id of the job

get_output_datatype(*output_id*)
Get the datatype for a specific output

Parameters **`output_id`** (*str*) – the id of the output to get the datatype for

Returns the requested datatype

Return type *BaseDataType*

`get_result`()
Get the result of the job if it is available. Load the output file if found and check if the job matches the current object. If so, load and return the result.

Returns Job after execution or None if not available

Return type Job | None

classmethod `get_value`(*value*)
Get a value

Parameters

- **`value`** – the url of the value
- **`datatype`** – datatype of the value

Returns the retrieved value

`hash_results`()
Create hashes of all output values and store them in the info store

`id`
The id of this job

`logfile`
The path of the result pickle

`logurl`
The url of the result pickle

`required_cores`
Number of required cores

`required_memory`
Number of required memory

`required_time`
Number of required runtime

`status`
The status of the job

`stderrfile`
The path where the stderr text is saved

`stderrurl`
The url where the stderr text is saved

`stdoutfile`
The path where the stdout text is saved

`stdouturl`
The url where the stdout text is saved

`tool`

`translate_argument`(*value*)
Translate an argument from a URL to an actual path.

Parameters

- **`value`** – value to translate
- **`datatype`** – the datatype of the value

Returns the translated value

`translate_results`(*result*)

Translate the results of an interface (using paths etc) to the proper form using URI's instead.

Parameters **`result`** (`dict`) – the result data of an interface

Returns the translated result

Return type dict

`validate_results`(*payload*)

Validate the results of the Job

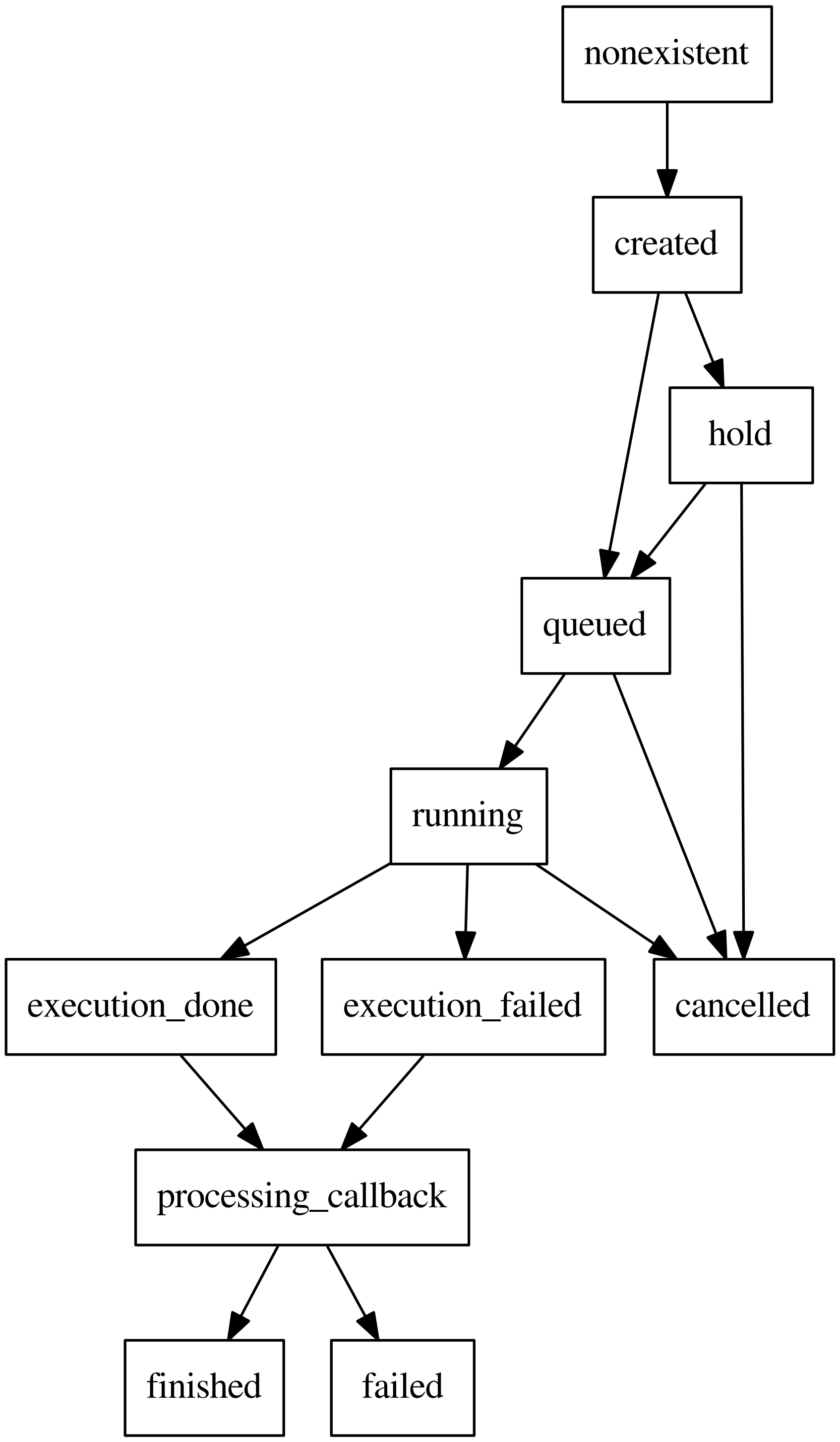
Returns flag indicating the results are complete and valid

`write`()

class `fastr.execution.job.`**`JobState`**(_, *stage*, *error*)

Bases: `enum.Enum`

The possible states a Job can be in. An overview of the states and the adviced transitions are depicted in the following figure:



`__format__`(*format_spec*)

`__init__`(*_*, *stage*, *error*)

`__module__` = **'fastr.execution.job'**

static `__new__`(*value*)

`__reduce_ex__`(*proto*)

`__repr__`()

`__str__`()

`cancelled` = ('cancelled', 'done', True)

`created` = ('created', 'idle', False)

`done`

`execution_done` = ('execution_done', 'in_progress', False)

`execution_failed` = ('execution_failed', 'in_progress', True)

`failed` = ('failed', 'done', True)

`finished` = ('finished', 'done', False)

`hold` = ('hold', 'idle', False)

`in_progress`

`nonexistent` = ('nonexistent', 'idle', False)

`processing_callback` = ('processing_callback', 'in_progress', False)

`queued` = ('queued', 'idle', False)

`running` = ('running', 'in_progress', False)

class `fastr.execution.job.`**`SinkJob`**(*jobid*, *tool_name*, *tool_version*, *nodeid*, *sample_id*, *sample_index*, *input_arguments*, *output_arguments*, *tmpdir*, *hold_jobs=None*, *timestamp=None*, *cores=None*, *memory=None*, *walltime=None*, *substitutions=None*, *status_callback=None*, *preferred_types=None*)

Bases: `fastr.execution.job.Job`

Special SinkJob for the Sink

`__init__`(*jobid*, *tool_name*, *tool_version*, *nodeid*, *sample_id*, *sample_index*, *input_arguments*, *output_arguments*, *tmpdir*, *hold_jobs=None*, *timestamp=None*, *cores=None*, *memory=None*, *walltime=None*, *substitutions=None*, *status_callback=None*, *preferred_types=None*)

`__module__` = 'fastr.execution.job'

`__repr__`()

String representation for the SinkJob

`create_payload`()

Create the payload for this object based on all the input/output arguments

Returns the payload

Return type dict

`get_result`()

Get the result of the job if it is available. Load the output file if found and check if the job matches the current object. If so, load and return the result.

Returns Job after execution

`substitute`(*value*, *datatype=None*)

Substitute the special fields that can be used in a SinkJob.

Parameters

- **`value`** (`str`) – the value to substitute fields in
- **`datatype`** (`BaseDataType`) – the datatype for the value

Returns string with substitutions performed

Return type str

validate_results(*payload*)
Validate the results of the SinkJob

Returns flag indicating the results are complete and valid

class fastr.execution.job.**SourceJob**(*jobid*, *tool_name*, *tool_version*, *nodeid*, *sample_id*, *sample_index*, *input_arguments*, *output_arguments*, *tmpdir*, *hold_jobs=None*, *timestamp=None*, *cores=None*, *memory=None*, *walltime=None*, *status_callback=None*, *preferred_types=None*)
Bases: *fastr.execution.job.Job*

Special SourceJob for the Source

__module__ = 'fastr.execution.job'

__repr__()
String representation for the SourceJob

get_output_datatype(*output_id*)
Get the datatype for a specific output

Parameters **output_id** (*str*) – the id of the output to get the datatype for

Returns the requested datatype

Return type *BaseDataType*

validate_results(*payload*)
Validate the results of the Job

Returns flag indicating the results are complete and valid

networkanalyzer Module

Module that defines the NetworkAnalyzer and holds the reference implementation.

class fastr.execution.networkanalyzer.**DefaultNetworkAnalyzer**
Bases: *fastr.execution.networkanalyzer.NetworkAnalyzer*

Default implementation of the NetworkAnalyzer.

__module__ = 'fastr.execution.networkanalyzer'

analyze_network(*network*, *chunk*)
Analyze a chunk of a Network. Simply process the Nodes in the chunk sequentially.

Parameters

- **network** – Network corresponding with the chunk
- **chunk** – The chunk of the network to analyze

class fastr.execution.networkanalyzer.**NetworkAnalyzer**
Bases: object

Base class for NetworkAnalyzers

__dict__ = dict_proxy({'__dict__': <attribute '__dict__' of 'NetworkAnalyzer' objects>, '__weakref__': <attribute

__module__ = 'fastr.execution.networkanalyzer'

__weakref__
list of weak references to the object (if defined)

analyze_network (*network*, *chunk*)
Analyze a chunk of a Network.

Parameters

- **network** – Network corresponding with the chunk
- **chunk** – The chunk of the network to analyze

networkchunker Module

This module contains the NetworkChunker class and its default implementation the DefaultNetworkChunker

class fastr.execution.networkchunker.**DefaultNetworkChunker**
Bases: *fastr.execution.networkchunker.NetworkChunker*

The default implementation of the NetworkChunker. It tries to create as large as possible chunks so the execution blocks as little as possible.

__init__ ()

__module__ = 'fastr.execution.networkchunker'

chunck_network (*network*)
Create a list of Network chunks that can be pre-analyzed completely. Each chunk needs to be executed before the next can be analyzed and executed.

The returned chunks are (at the moment) in the format of a tuple (start, nodes) which are both tuples. The tuple contain the nodes where to start execution (should ready if previous chunks are done) and all nodes of the chunk respectively.

Parameters **network** – Network to split into chunks

Returns tuple containing chunks

class fastr.execution.networkchunker.**NetworkChunker**
Bases: object

The base class for NetworkChunkers. A Network chunker is a class that takes a Network and produces a list of chunks that can each be analyzed and executed in one go.

__dict__ = dict_proxy({'__dict__': <attribute '__dict__' of 'NetworkChunker' objects>, '__module__': 'fastr.execu

__module__ = 'fastr.execution.networkchunker'

__weakref__
list of weak references to the object (if defined)

chunck_network (*network*)
Create a list of Network chunks that can be pre-analyzed completely. Each chunk needs to be executed before the next can be analyzed and executed.

Parameters **network** – Network to split into chunks

Returns list containing chunks

resources Package

resources Package

Subpackages

datatypes Package

`datatypes` Package

`AnalyzeImageFile` Module

`Boolean` Module

`Directory` Module

`Float` Module

`ITKImageFile` Module

`Int` Module

`MetaImageFile` Module

`NiftiImageFile` Module

`NiftiImageFileCompressed` Module

`NiftiImageFileUncompressed` Module

`Number` Module

`String` Module

`TifImageFile` Module

`UnsignedInt` Module

tools Package

`tools` Package

utils Package

`utils` Package

A collections of utils for fastr (command line tools or non-core functionality)

`checksum` Module

This module contains a number of functions for checksumming files and objects

`fastr.utils.checksum.`**`checksum`**(*filepath*, *algorithm='md5'*, *hasher=None*)

Generate the checksum of a file

Parameters

- **`filepath`** (`str`, `list`) – path of the file(s) to checksum
- **`algorithm`** (`str`) – the algorithm to use

- **hasher** (*_hashlib.HASH*) – a hasher to continue updating (rather then creating a new one)

Returns the checksum

Return type str

`fastr.utils.checksum.`**`checksum_directory`**(*directory*, *algorithm='md5'*, *hasher=None*)
Generate the checksum of an entire directory

Parameters

- **directory** (*str*) – path of the file(s) to checksum
- **algorithm** (*str*) – the algorithm to use
- **hasher** (*_hashlib.HASH*) – a hasher to continue updating (rather then creating a new one)

Returns the checksum

Return type str

`fastr.utils.checksum.`**`hashsum`**(*objects*, *hasher=None*)
Generate the md5 checksum of (a) python object(s)

Parameters

- **objects** – the objects to hash
- **hasher** – the hasher to use as a base

Returns the hash generated

Return type str

`fastr.utils.checksum.`**`md5_checksum`**(*filepath*)
Generate the md5 checksum of a file

Parameters **filepath** (*str, list*) – path of the file(s) to checksum

Returns the checksum

Return type str

`fastr.utils.checksum.`**`sha1_checksum`**(*filepath*)
Generate the sha1 checksum of a file

Parameters **filepath** (*str, list*) – path of the file(s) to checksum

Returns the checksum

Return type str

`classproperty` Module

Module containing the code to create class properties.

class `fastr.utils.classproperty.`**`ClassPropertyDescriptor`**(*fget*)
Bases: `object`

A descriptor that can act like a property for a class.

`__dict__` = **dict_proxy({'__module__': 'fastr.utils.classproperty', '__dict__': <attribute '__dict__' of 'ClassProperty**

`__get__`(*obj*, *cls=None*)

`__init__`(*fget*)

`__module__` = **'fastr.utils.classproperty'**

`__weakref__`
list of weak references to the object (if defined)

`fastr.utils.classproperty.`**`classproperty`**`(`*func*`)`
Decorator to create a "class property"

Parameters **`func`** – the function to wrap

Returns a class property

Return type *ClassPropertyDescriptor*

`clear_pycs` Module

A small tool to wipe all .pyc files from fastr

`fastr.utils.clear_pycs.`**`dir_list`**`(`*directory*`)`
Find all .pyc files

Parameters **`directory`** (*`str`*) – directory to search

Returns all .pyc files

Return type list

`fastr.utils.clear_pycs.`**`main`**`()`
Main entry poitn

`compare` Module

Module to compare various fastr specific things such as a execution directory or a reference directory.

`fastr.utils.compare.`**`compare_execution_dir`**`(`*path1*, *path2*`)`

`dicteq` Module

Some helper function to compare dictionaries and find the parts of the dict that are different. This is mostly to help in debugging.

`fastr.utils.dicteq.`**`dicteq`**`(`*self*, *other*`)`
Compare two dicts for equality

Parameters

- **`self`** – the first object to compare
- **`other`** – the oth

Returns

`fastr.utils.dicteq.`**`diffdict`**`(`*self*, *other*, *path=None*, *visited=None*`)`
Find the differences in two dictionaries.

Parameters

- **`self`** – the first object to compare
- **`other`** (*`dict`*) – other dictionary
- **`path`** (*`list`*) – the path for nested dicts (too keep track of recursion)

Returns list of messages indicating the differences

Return type list

`fastr.utils.dicteq.`**`diffobj`**`(`*self*, *other*, *path=None*, *visited=None*`)`
Compare two objects by comparing their __dict__ entries

Parameters

- **self** – the first object to compare
- **other** – other objects to compare
- **path** (*list*) – the path for nested dicts (too keep track of recursion)

Returns list of messages

Return type list

fastr.utils.dicteq.**diffobj_str**(*self*, *other*)

Compare two objects by comparing their __dict__ entries, but returns the differences in a single string ready for logging.

Parameters

- **self** – the first object to compare
- **other** – other object to compare to

Returns the description of the differences

Return type str

gettools Module

fastr.utils.gettools.**main**()

iohelpers Module

fastr.utils.iohelpers.**load_gpickle**(*path*, *retry_scheme=None*)

fastr.utils.iohelpers.**save_gpickle**(*path*, *data*)

jsonschemaparser Module

The JSON schema parser validates a json data structure and if possible casts data to the correct type and fills out default values. The result in a valid document that can be used to construct objects.

class fastr.utils.jsonschemaparser.**FastrRefResolver**(*base_uri*, *referrer*, *store=()*, *cache_remote=True*, *handlers=()*)

Bases: jsonschema.validators.RefResolver

Adapted version of the RefResolver for handling inter-file references more to our liking

__init__(*base_uri*, *referrer*, *store=()*, *cache_remote=True*, *handlers=()*)

Create a new FastrRefResolver

Parameters

- **base_uri** (*str*) – URI of the referring document
- **referrer** – the actual referring document
- **store** (*dict*) – a mapping from URIs to documents to cache
- **cache_remote** (*bool*) – whether remote refs should be cached after first resolution
- **handlers** (*dict*) – a mapping from URI schemes to functions that should be used to retrieve them

__module__ = 'fastr.utils.jsonschemaparser'

classmethod **`from_schema`**(*schema*, **args*, ***kwargs*)
Instantiate a RefResolver based on a schema

static **`readfastrschema`**(*name*)
Open a json file based on a fastr:// url that points to a file in the fastr.schemadir

Parameters **`name`** (`str`) – the url of the file to open

Returns the resulting json schema data

static **`readfile`**(*filename*)
Open a json file based on a simple filename

Parameters **`filename`** (`str`) – the path of the file to read

Returns the resulting json schema data

`fastr.utils.jsonschemaparser.`**`any_of_draft4`**(*validator*, *any_of*, *instance*, *schema*)
The oneOf directory needs to be done stepwise, because a validation even if it fails will try to change types / set defaults etc. Therefore we first create a copy of the data per subschema and test if they match. Then for all the schemas that are valid, we perform the validation on the actual data so that only the valid subschemas will effect the data.

Parameters

- **`validator`** – the json schema validator
- **`any_of`** (`dict`) – the current oneOf
- **`instance`** – the current object instance
- **`schema`** (`dict`) – the current json schema

`fastr.utils.jsonschemaparser.`**`extend`**(*validator_cls*)
Extend the given `jsonschema.IValidator` with the Seep layer.

`fastr.utils.jsonschemaparser.`**`getblueprinter`**(*uri*, *blueprint=None*)
Instantiate the given data using the blueprinter.

Parameters **`blueprint`** – a blueprint (JSON Schema with Seep properties)

`fastr.utils.jsonschemaparser.`**`items_prevalidate`**(*validator*, *items*, *instance*, *schema*)
The pre-validation function for items

Parameters

- **`validator`** – the json schema validator
- **`items`** (`dict`) – the current items
- **`instance`** – the current object instance
- **`schema`** (`dict`) – the current json schema

`fastr.utils.jsonschemaparser.`**`not_draft4`**(*validator*, *not_schema*, *instance*, *schema*)
The not needs to use a temporary copy of the instance, not to change the instance with the invalid schema

Parameters

- **`validator`** – the json schema validator
- **`not_schema`** (`dict`) – the current oneOf
- **`instance`** – the current object instance
- **`schema`** (`dict`) – the current json schema

`fastr.utils.jsonschemaparser.`**`one_of_draft4`**(*validator*, *one_of*, *instance*, *schema*)
The one_of directory needs to be done stepwise, because a validation even if it fails will try to change types / set defaults etc. Therefore we first create a copy of the data per subschema and test if they match. Once we found a proper match, we only validate that branch on the real data so that only the valid piece of schema will effect the data.

Parameters

- **validator** – the json schema validator
- **one_of** (*dict*) – the current one_of
- **instance** – the current object instance
- **schema** (*dict*) – the current json schema

`fastr.utils.jsonschemaparser.`**`pattern_properties_prevalid`**(*validator*, *pattern_properties*, *instance*, *schema*)

The pre-validation function for patternProperties

Parameters

- **validator** – the json schema validator
- **pattern_properties** (*dict*) – the current patternProperties
- **instance** (*dict*) – the current object instance
- **schema** (*dict*) – the current json schema

`fastr.utils.jsonschemaparser.`**`properties_postvalidate`**(*validator*, *properties*, *instance*, *schema*)

# All arguments must be used because this function is called like this # pylint: disable=unused-argument The post-validation function for properties

Parameters

- **validator** – the json schema validator
- **properties** (*dict*) – the current properties
- **instance** – the current object instance
- **schema** (*dict*) – the current json schema

`fastr.utils.jsonschemaparser.`**`properties_prevalidate`**(*validator*, *properties*, *instance*, *schema*)

The pre-validation function for properties

Parameters

- **validator** – the json schema validator
- **properties** (*dict*) – the current properties
- **instance** – the current object instance
- **schema** (*dict*) – the current json schema

`multiprocesswrapper` Module

`fastr.utils.multiprocesswrapper.`**`function_wrapper`**(*filepath*, *fnc_name*, **args*, ***kwargs*)

`procutils` Module

`fastr.utils.procutils.`**`which`**(*name*)

Find executable by name on the PATH, returns the executable that will be found in case it is used for a Popen call

`rest_generation` Module

`fastr.utils.rest_generation.`**`create_rest_table`**`(`*data*, *headers*`)`

Create a ReST table from data. The data should be a list of columns and the headers should be a list of column names.

Parameters

- **`data`** (*`list`*) – List of lists/tuples representing the columns
- **`headers`** (*`list`*) – List of strings for the column names

Returns a string representing the table in ReST

Return type str

`schematotable` Module

A module to generate reStructuredText tables from json schema files

class `fastr.utils.schematotable.`**`SchemaPrinter`**`(`*schema*, *skipfirst=False*`)`

Bases: `object`

Object that create a table in reStructuedText from a json schema

`__dict__` = dict_proxy({'parse': <function parse>, '__module__': 'fastr.utils.schematotable', 'descend': <function d

`__init__``(`*schema*, *skipfirst=False*`)`

Create the printer object

Parameters

- **`schema`** (*`dict`*) – the json schema to print
- **`skipfirst`** (*`bool`*) – flag to indicate that the first line should not be printed

`__module__` = 'fastr.utils.schematotable'

`__str__``()`

String representation of json schema (that is the printed table)

`__weakref__`

list of weak references to the object (if defined)

`descend``(`*properties*`)`

Descend into a subschema

Parameters **`properties`** (*`dict`*) – the properties in the subschema

`parse``(`*schema=None*`)`

Parse a schema

Parameters **`schema`** (*`dict`*) – the schema to parse

`printlines``()`

Given a parsed schema (parsing happens when the object is constructed), print all the lines

Returns the printed table

Return type str

`sysinfo` Module

This module contains function to help gather system information use for the provenance of the Job execution.

`fastr.utils.sysinfo.`**`get_cpu_usage`**`()`

Get the current CPU usage

Returns CPU usage info

Return type dict

`fastr.utils.sysinfo.`**`get_drmaa_info`**`()`
Get information about the SGE cluster (if applicable)

Returns cluster info

Return type dict

`fastr.utils.sysinfo.`**`get_hostinfo`**`()`
Get all information about the current host machine

Returns host info

Return type dict

`fastr.utils.sysinfo.`**`get_memory_usage`**`()`
Get the current memory usage

Returns memory usage info

Return type dict

`fastr.utils.sysinfo.`**`get_mounts`**`()`
Get the current mounts known on the system

Returns mount info

Return type dict

`fastr.utils.sysinfo.`**`get_os`**`()`
Get information about the OS

Returns OS information

Return type dict

`fastr.utils.sysinfo.`**`get_processes`**`()`
Get a list of all currently running processes

Returns process information

Return type list

`fastr.utils.sysinfo.`**`get_python`**`()`
Get information about the currently used Python implementation

Returns python info

Return type dict

`fastr.utils.sysinfo.`**`get_sysinfo`**`()`
Get system information (cpu, memory, mounts and users)

Returns system information

Return type dict

`fastr.utils.sysinfo.`**`get_users`**`()`
Get current users on the system

Returns user info

Return type dict

`fastr.utils.sysinfo.`**`namedtuple_to_dict`**`(`*ntuple*`)`
Helper function to convert a named tuple into a dict

Parameters **`ntuple`** (*`namedtuple`*) – the namedtuple to convert

Returns named tuple as a dict

Return type dict

`verify` Module

`fastr.utils.verify.`**`verify_resource_loading`**(*filename*)

`fastr.utils.verify.`**`verify_tool`**(*filename*)

Verify that a file

`xmltodict` Module

This module contains tool for converting python dictionaries into XML object and vice-versa.

`fastr.utils.xmltodict.`**`dump`**(*data*, *filehandle*)

Write a dict to an XML file

Parameters

- **`data`** – data to write
- **`filehandle`** – file handle to write to

`fastr.utils.xmltodict.`**`dumps`**(*data*)

Write a dict to an XML string

Parameters **`data`** – data to write

Returns the XML data

Return type str

`fastr.utils.xmltodict.`**`load`**(*filehandle*)

Load an xml file and parse it to a dict

Parameters **`filehandle`** – file handle to load

Returns the parsed data

`fastr.utils.xmltodict.`**`loads`**(*data*)

Load an xml string and parse it to a dict

Parameters **`data`** (*`str`*) – the xml data to load

Returns the parsed data

Subpackages

cmd Package

`cmd` Package

`fastr.utils.cmd.`**`find_commands`**()

`fastr.utils.cmd.`**`get_command_module`**(*command*)

`fastr.utils.cmd.`**`main`**()

`fastr.utils.cmd.`**`print_help`**(*commands=None*)

`cat` Module

`fastr.utils.cmd.cat.`**`get_parser`**`()`

`fastr.utils.cmd.cat.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Print information from a job file

`execute` Module

`fastr.utils.cmd.execute.`**`get_parser`**`()`

`fastr.utils.cmd.execute.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Execute a fastr job file

`extract_argparse` Module

`fastr.utils.cmd.extract_argparse.`**`cardinality_from_nargs`**`(`*value*`)`

`fastr.utils.cmd.extract_argparse.`**`datatype_from_type`**`(`*type_*, *metavar*`)`

`fastr.utils.cmd.extract_argparse.`**`extract_argparser`**`(`*filepath*`)`

`fastr.utils.cmd.extract_argparse.`**`find_argparser`**`(`*entry*,
basename='/home/docs/checkouts/readthedocs.org/user_bu
build'`)`

`fastr.utils.cmd.extract_argparse.`**`get_parser`**`()`

`fastr.utils.cmd.extract_argparse.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Create a stub for a Tool based on a python script using argparse

`prov` Module

`fastr.utils.cmd.prov.`**`get_parser`**`()`

`fastr.utils.cmd.prov.`**`get_prov_document`**`(`*result*`)`

`fastr.utils.cmd.prov.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Get PROV information from the result pickle.

`run` Module

`fastr.utils.cmd.run.`**`create_network_parser`**`(`*network*`)`

`fastr.utils.cmd.run.`**`get_parser`**`()`

`fastr.utils.cmd.run.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Run a Network from the commandline

`testtool` Module

`fastr.utils.cmd.testtool.`**`get_parser`**`()`

`fastr.utils.cmd.testtool.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Run the tests of a tool to verify the proper function

`verify` Module

`fastr.utils.cmd.verify.`**`get_parser`**`()`

`fastr.utils.cmd.verify.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Print information from a job file

`webapp` Module

`fastr.utils.cmd.webapp.`**`get_parser`**`()`

`fastr.utils.cmd.webapp.`**`main`**`(`*args=None*, *unknown_args=None*`)`
Start the fastr webapp and open in a new browser tab

`fastr.utils.cmd.webapp.`**`open_url`**`(`*url*`)`

web Package

`web` Package

`api` Module

class `fastr.web.api.`**`NetworkApi`**`(`*api=None*, **args*, ***kwargs*`)`
Bases: `flask_restplus.resource.Resource`

`__module__` **= 'fastr.web.api'**

`endpoint` **= 'api_network'**

`get``(`*id_*`)`
Get a Network json description from the server

`mediatypes``(`*resource_cls*`)`

`methods` **= ['GET']**

class `fastr.web.api.`**`NetworkListApi`**`(`*api=None*, **args*, ***kwargs*`)`
Bases: `flask_restplus.resource.Resource`

`__module__` **= 'fastr.web.api'**

`endpoint` **= 'api_networks'**

`get``(`**args*, ***kwargs*`)`
Get a list of the networks

`mediatypes``(`*resource_cls*`)`

`methods` **= ['GET']**

class `fastr.web.api.`**`ObjectUrl`**`(`*object_classs*, ***kwargs*`)`
Bases: `flask_restplus.fields.Raw`

`__init__``(`*object_classs*, ***kwargs*`)`

`__module__` **= 'fastr.web.api'**

`__schema_type__` **= 'string'**

`__slotnames__` **= []**

`format``(`*value*`)`

class `fastr.web.api.`**`Run`**`(`*id_*, *network*, *source_data*, *sink_data*`)`
Bases: `object`

__dict__ = dict_proxy({'status': <function status>, '__module__': 'fastr.web.api', 'abort': <function abort>, '__dic

__init__(*id_*, *network*, *source_data*, *sink_data*)

__module__ = 'fastr.web.api'

__weakref__
list of weak references to the object (if defined)

abort()

run_network(*network*, *source_data*, *sink_data*, *abort_lock*)

status()

class `fastr.web.api.`**RunApi**(*api=None*, **args*, ***kwargs*)
Bases: `flask_restplus.resource.Resource`

Run API documentation

__module__ = 'fastr.web.api'

delete(*id_*)
Abort a Network run and stop all associated execution

endpoint = 'api_run'

get(**args*, ***kwargs*)
Get information about a Network run

mediatypes(*resource_cls*)

methods = ['DELETE', 'GET']

class `fastr.web.api.`**RunListApi**(*api=None*, **args*, ***kwargs*)
Bases: `flask_restplus.resource.Resource`

__module__ = 'fastr.web.api'

endpoint = 'api_runs'

get(**args*, ***kwargs*)
Get a list of all Network runs on the server

mediatypes(*resource_cls*)

methods = ['GET', 'POST']

post()
Create a new Network run and start execution

request_parser = <flask_restplus.reqparse.RequestParser object>

class `fastr.web.api.`**StatusApi**(*api=None*, **args*, ***kwargs*)
Bases: `flask_restplus.resource.Resource`

__module__ = 'fastr.web.api'

endpoint = 'api_status'

get(*id_*)
Get the status of a Network Run on the server

mediatypes(*resource_cls*)

methods = ['GET']

class `fastr.web.api.`**SubUrl**(*object_classs*, *subfield*, ***kwargs*)
Bases: `flask_restplus.fields.Raw`

__init__(*object_classs*, *subfield*, ***kwargs*)

__module__ = 'fastr.web.api'

`__schema_type__` = 'string'

`format` (*value*)

class `fastr.web.api.`**`ToolApi`** (*api=None*, **args*, ***kwargs*)
Bases: `flask_restplus.resource.Resource`

`__module__` = 'fastr.web.api'

`endpoint` = 'api_version_tool'

`get` (*id_*, *version=None*)
Get a Tool json description from the server

`mediatypes` (*resource_cls*)

`methods` = ['GET']

class `fastr.web.api.`**`ToolListApi`** (*api=None*, **args*, ***kwargs*)
Bases: `flask_restplus.resource.Resource`

`__module__` = 'fastr.web.api'

`endpoint` = 'api_tools'

`get` (**args*, ***kwargs*)
Get a list of all Tools known to the server

`mediatypes` (*resource_cls*)

`methods` = ['GET']

`fastr.web.api.`**`network_lock_thread`** (*lock*, *network*)

`fastr.web.api.`**`network_runner`** (*network*, *source_data*, *sink_data*, *chuck_status*, *job_status*, *job_results*, *abort_lock*)

`fastr.web.api.`**`update_job_result`** (*job*, *job_status*, *job_results*)

`fastr.web.api.`**`update_status`** (*job*, *job_status*)

`run` Module

`fastr.web.run.`**`main`** ()

`fastr.web.run.`**`runapp`** (*debug=False*)

`views` Module

`fastr.web.views.`**`doc`** ()

`fastr.web.views.`**`index`** ()

`fastr.web.views.`**`network`** (*name=None*)

`fastr.web.views.`**`networks`** ()

`fastr.web.views.`**`prov`** ()

`fastr.web.views.`**`shutdown`** ()

`fastr.web.views.`**`shutdown_server`** ()

`fastr.web.views.`**`tool`** (*toolname=None*, *version=None*)

`fastr.web.views.`**`websocket_client`** ()

CHAPTER 5

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