Introduction to the Taverna Tool service

Stian Soiland-Reyes and Christian Brenninkmeijer
University of Manchester
material by Mr Alan Williams

http://orcid.org/0000-0001-9842-9718
http://orcid.org/0000-0002-2937-7819
http://orcid.org/0000-0003-3156-2105

Bonn University, 2014-09-01 / 2014-09-03
http://www.taverna.org.uk/

What is a tool service?

- Allows you to call a command line script as part of a workflow
    - Simplest case is calling a single tool
- Can be run on your local machine or a machine that you can ssh to
- Data is passed by reference
    - No big transfers to/from Taverna
- Data kept where the script is run until/unless needed

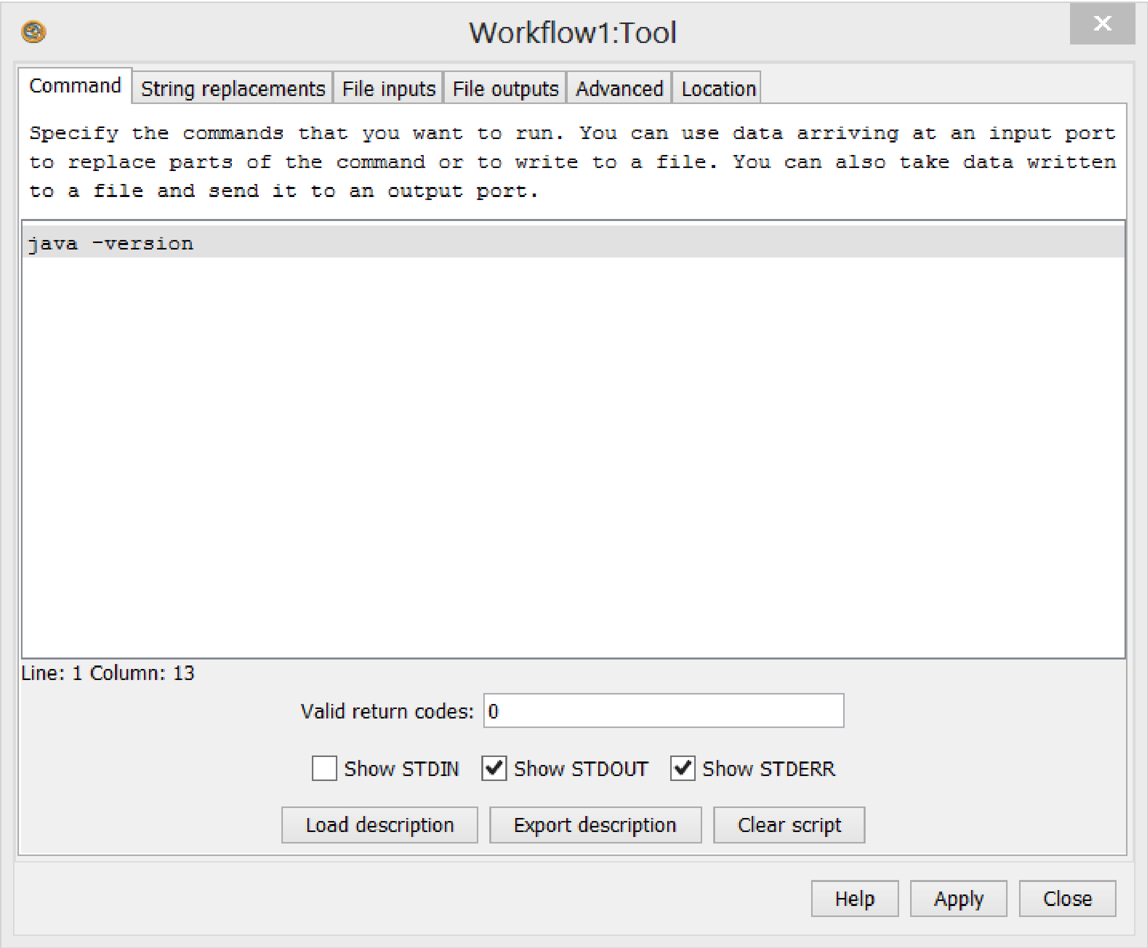
Using a simple tool service

- Choose “Tool” from the “Insert” menu
- In the tool service popup type

```
java -version
```

- Close the configuration
- Connect the STDERR and STDOUT ports of the tool service to workflow output ports

Simple tool service configuration



Specify the commands that you want to run. You can use data arriving at an input port to replace parts of the command or to write to a file. You can also take data written to a file and send it to an output port.

```
java -version
```

Line: 1 Column: 13

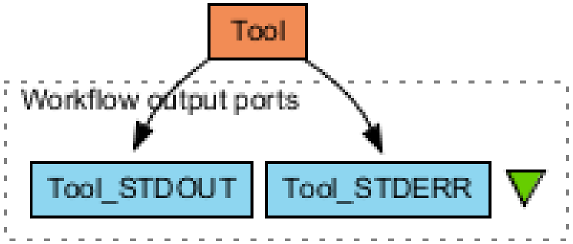
Valid return codes: 0

☐ Show STDIN ☑ Show STDOUT ☑ Show STDERR

MANCHESTER
1824
The University of Manchester

Simple tool workflow

- Run the workflow



- STDERR should look similar to:

```
java version "1.8.0"
Java(TM) SE Runtime Environment (build 1.8.0-b132)
Java HotSpot(TM) 64-Bit Server VM (build 25.0-b70,
mixed mode)
```

Downloading an example tool

- We are going to use the *forester* utilities by Christian Zmasek
- Download
  - forester_1028.jar by following the links on https://sites.google.com/site/cmzmasek/home/software/forester/phyloxml-converter
  - ..or download it from the myExperiment group
  - Remember which folder you downloaded it to

Calling the example tool - 1

- Create a new workflow with a tool service that calls the jar (modify the path)

```
java -cp C:\Users\stain\Downloads\forester_1035.jar
```

- Connect STDERR and STDOUT
- Run the workflow
- It fails. We cannot just call the jar

Calling the converter - 1

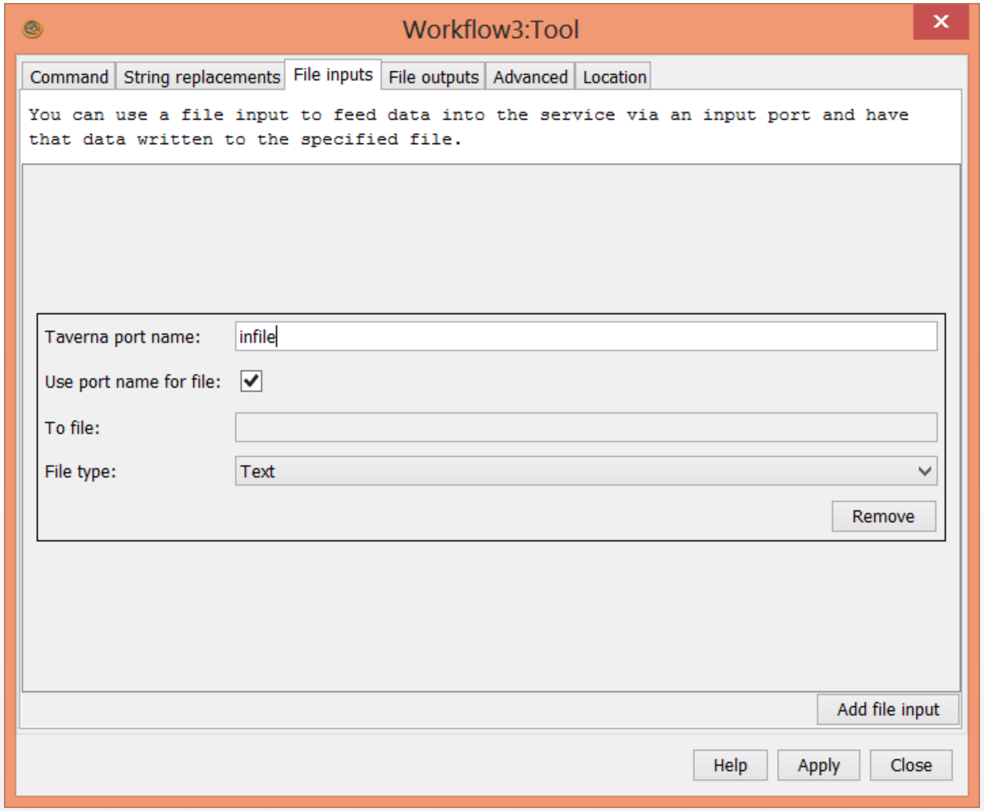
- We cannot just call the jar
- Look for the parameters of this tool at https://sites.google.com/site/cmzmasek/home/software/forester/phyloxml-converter
- Change the tool service so the script says on one line:

```
java -cp C:\Users\stain\Downloads\forester_1035.jar
org.forester.application.phyloxml_converter -f=nn
infile outfile
```

- This converts the **infile** to PhyloXML and writes it to **outfile**
- Run the workflow

Calling the converter - 2

- We need to pass an input file
- Configure the tool service and add a file input called infile



You can use a file input to feed data into the service via an input port and have that data written to the specified file.

Taverna port name: infile

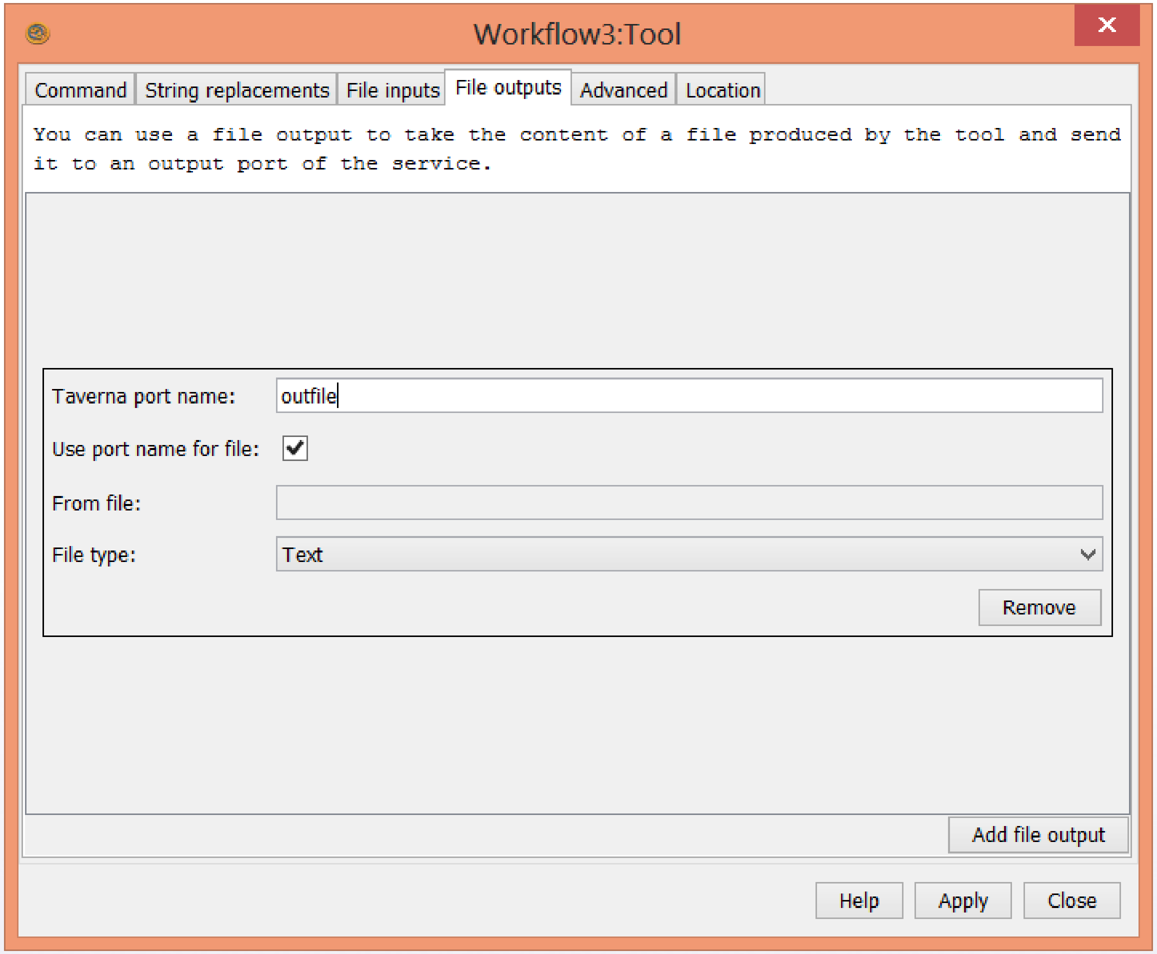
Use port name for file: ☑

To file:

File type: Text

Calling the converter - 3

- Add a file output called outfile



You can use a file output to take the content of a file produced by the tool and send it to an output port of the service.

Taverna port name: outfile

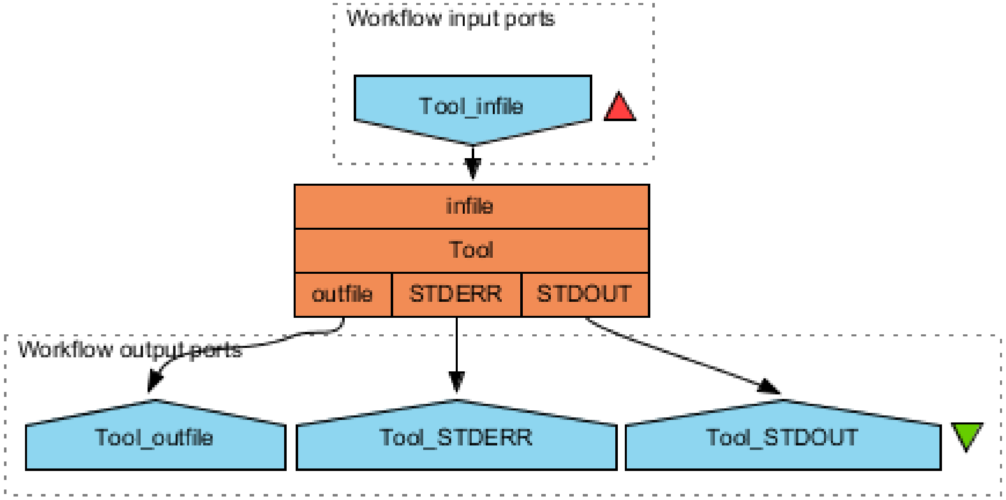
Use port name for file: ☑

From file:

File type: Text

Calling the converter - 4

- The tool service now has two extra ports
- Connect infile to a workflow input port and outfile to a workflow output port



Calling the converter - 6

- Run the workflow
- As input, you can use the contents of http://www.myexperiment.org/files/1055/versions/1/download/example.nh.txt

(or use **Set URL**)

- The *outfile* is in PhyloXML format
  - Click **Value type:** *XML tree*

Showing the PhyloXML - 1

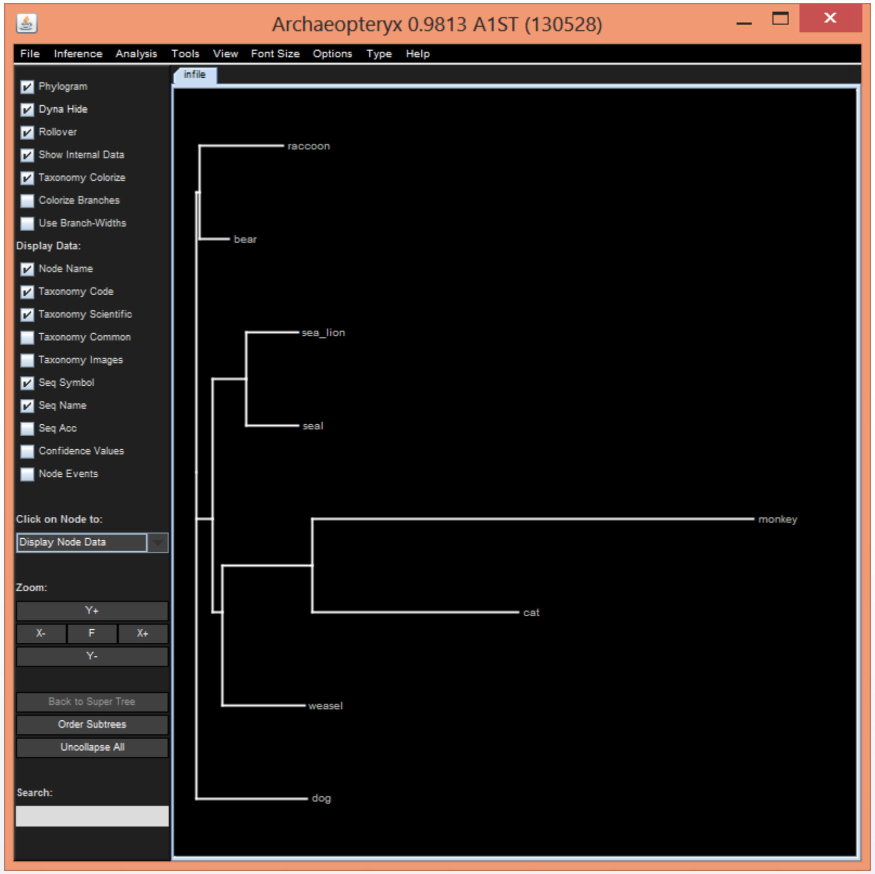
- Rename the first tool to **converter**
- Add a new tool service that calls

```
java -cp C:\Users\stain\Downloads\forester_1035.jar
org.forester.archaeopteryx.Archaeopteryx infile
```

- Add a file input called **infile**
- Rename the tool service to **display**
- Connect the **outfile** of converter to the **infile** of **display**
- Run the workflow

Showing the PhyloXML - 2

- The archaeopteryx display tool will show – exit it to finish the run



☑ Phylogram
☑ Dyna Hide
☑ Rollover
☑ Show Internal Data
☑ Taxonomy Colorize
☐ Colorize Branches
☐ Use Branch-Widths

Display Data:
☑ Node Name
☑ Taxonomy Code
☑ Taxonomy Scientific
☐ Taxonomy Common
☐ Taxonomy Images
☑ Seq Symbol
☑ Seq Name
☐ Seq Acc
☐ Confidence Values
☐ Node Events

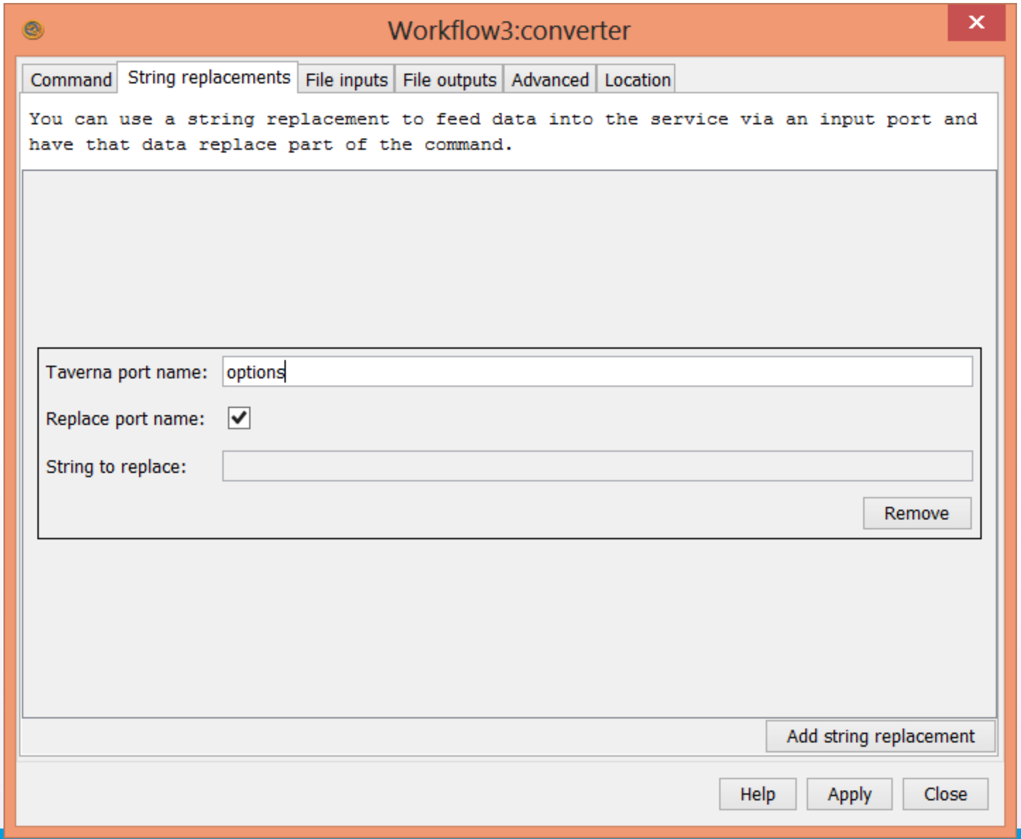
Click on Node to: Display Node Data

Zoom:

Search:

Using string replacement - 1

- PhyloXML **converter** can take options
- Add a new String replacement port to the converter service called **options**



You can use a string replacement to feed data into the service via an input port and have that data replace part of the command.

Taverna port name: options

Replace port name: ☑

String to replace:

Using string replacement - 2

- Change the converter script to include the options

```
java -cp C:\Users\stain\Downloads\forester_1035.jar
org.forester.application.phyloxml_converter -f=nn
%%options%% infile outfile
```

- **`%%options%%`** will be replaced by the string passed to the service
- Connect the options port to a workflow input port
- Run the workflow with options as the empty string
- Run the workflow with options as **`–o`**
- Compare the *outfile* with that from the previous run

Further exercises

- Add the **Xpath service** to pick up the species name of the second-level clade branch (bear, raccoon)
- Create a **component** family in your local registry called *forester*
- Create a components in the forester family for the *converter* and *display* services
- Build a workflow using the two components from *Available Services*
- What possible problems can you imagine if you want to share a workflow using the External Tool service?
- Expert: Are you able to modify your workflow to be sharable? Hint: Look at **Advanced** tab of Tool service.