



Tool service

Aleksandra Pawlik myGrid Team University of Manchester

VLIZ, 2014-10-06 / 2014-10-08 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

9	Workflow1:Tool	×
Command String replacen	nents File inputs File outputs Advanced Location	
to replace parts of	s that you want to run. You can use data arriving at an input the command or to write to a file. You can also take data we it to an output port.	-
java -version		
Line: 1 Column: 13		
	Valid return codes: 0	
	Show STDIN 🗸 Show STDOUT 🗸 Show STDERR	
	Load description Export description Clear script	
	Help Apply	Close











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 <u>Christian</u> <u>Zmasek</u>
- Download
 - forester_1037.jar as by following the links on <u>https://sites.google.com/site/cmzmasek/home/software/forest</u> <u>er/phyloxml-converter</u>
 - If you get a Google Drives doc rightclick and Save link as..
 - .. or download it from the myExperiment group
 - See http://www.myexperiment.org/files/1316.html
- Remember which folder you downloaded it to
 - Your will have to change
 "C:\Users\stain\Downloads" to this folder











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_1037.jar

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











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

java -cp C:\Users\stain\Downloads\forester_1037.jar
org.forester.application.phyloxml_converter -f=nn
infile outfile

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











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

8		Workflow	w3:Tool		x
Command String	replacements File	inputs File outputs A	Advanced Location		
	file input to tten to the sp		the service via an in	put port and have	
Taverna port na	me: infile				
Use port name f	or file: 🔽				
To file:					
File type:	Text				~
				Remove	
				Add file in	put
			Н	elp Apply Clo	se







• Add a file output called outfile

0	Workflow3:Tool	x			
Command String replace	ments File inputs File outputs Advanced Location				
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	~			
	Remove				
L	Add file out	put			
	Help Apply Close	se			











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













- Run the workflow
- As input, you can use the contents of <u>http://www.myexperiment.org/files/1055/versions/1/d</u> <u>ownload/example.nh.txt</u>
- (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_1037.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

<u></u>	Archaeopteryx 0.9813 A1ST (130528)	- 🗆 🗙
File Inference Analysis	Tools View Font Size Options Type Help	
Phylogram	infle	
✓ Dyna Hide		
Rollover		
Show Internal Data	raccoon	
✓ Taxonomy Colorize		
Colorize Branches		
Use Branch-Widths		
Display Data:	bear bear	
V Node Name		
V Taxonomy Code		
Maxonomy Scientific		
Taxonomy Common	sea_lion	
Taxonomy Images		
✓ Seq Symbol		
V Seq Name		
Seq Acc	seal seal	
Confidence Values		
Node Events		
Click on Node to:		- monkey
Display Node Data		monikey
Zoom:		
Y+	cat	
Х- F Х+		
Y-		
Back to Super Tree	weasel	
Order Subtrees		
Uncollapse All		
Search:	dog	











Using string replacement - 1

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

8	Workflow3:converter	x
Command String repla	acements File inputs File outputs Advanced Location	
	ring replacement to feed data into the service via an input port as aplace part of the command.	nd
Taverna port name:	options	ור
Replace port name:	\checkmark	
String to replace:		
	Remove	
	Add string replaceme	ent
	Help Apply Clos	e











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 secondlevel 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.





