Shim (Helper) Services and Beanshell Services

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

Taverna Tutorial
Building a simple workflow

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Taverna / Web Services

- Taverna is good way to access lots of globally distributed services out there on the Web
- This saves you the considerable trouble of installing stuff (e.g. databases, tools etc) on your personal machine or laboratory server

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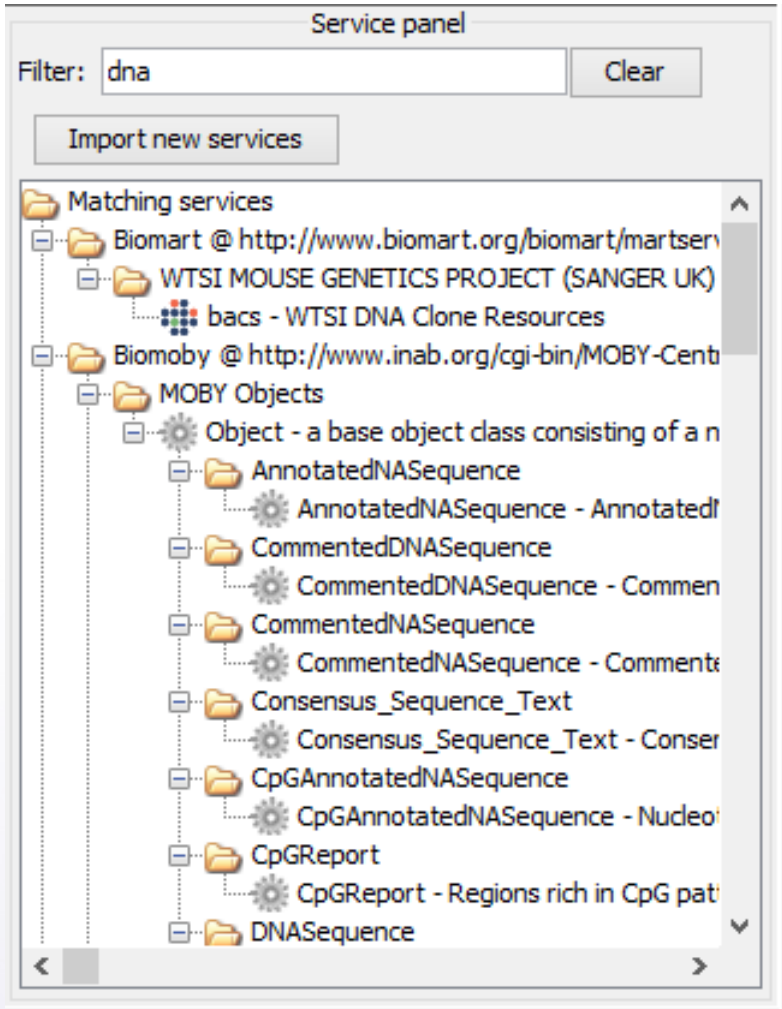
Lots of services…

- Provided by third parties:
  - EMBOSS / SOAPlab - UK
  - BioMOBY - Canada/Germany/Australia etc
  - BioMART / EBI - UK
  - NCBI and PathPort - US
  - KEGG - Japan
  - SeqHound / BIND – Canada
- The catch – services are not designed to work together



Building Workflows

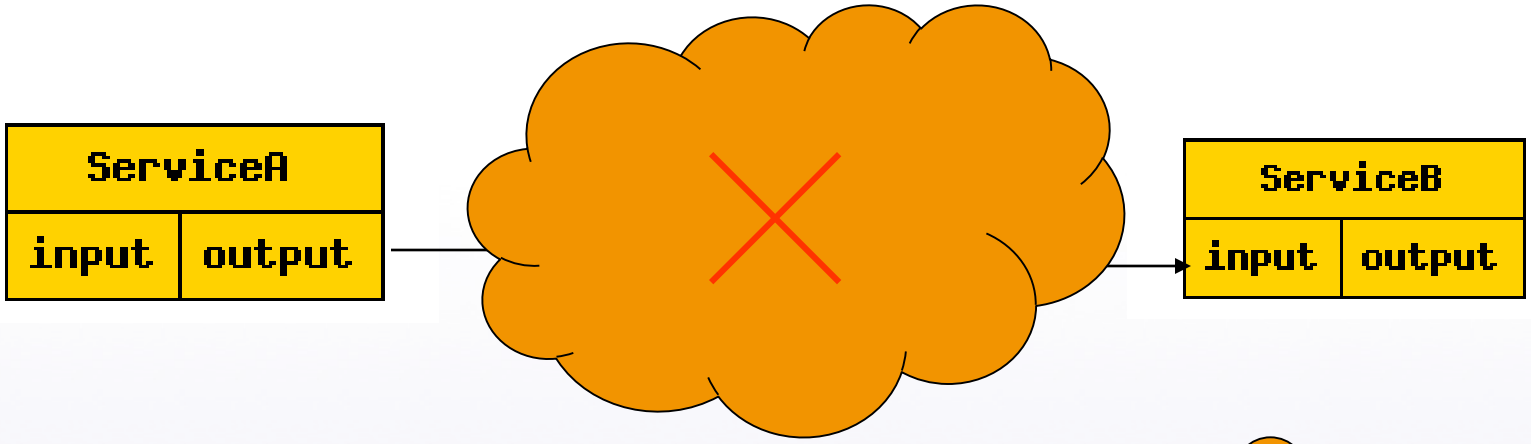
A two-stage process

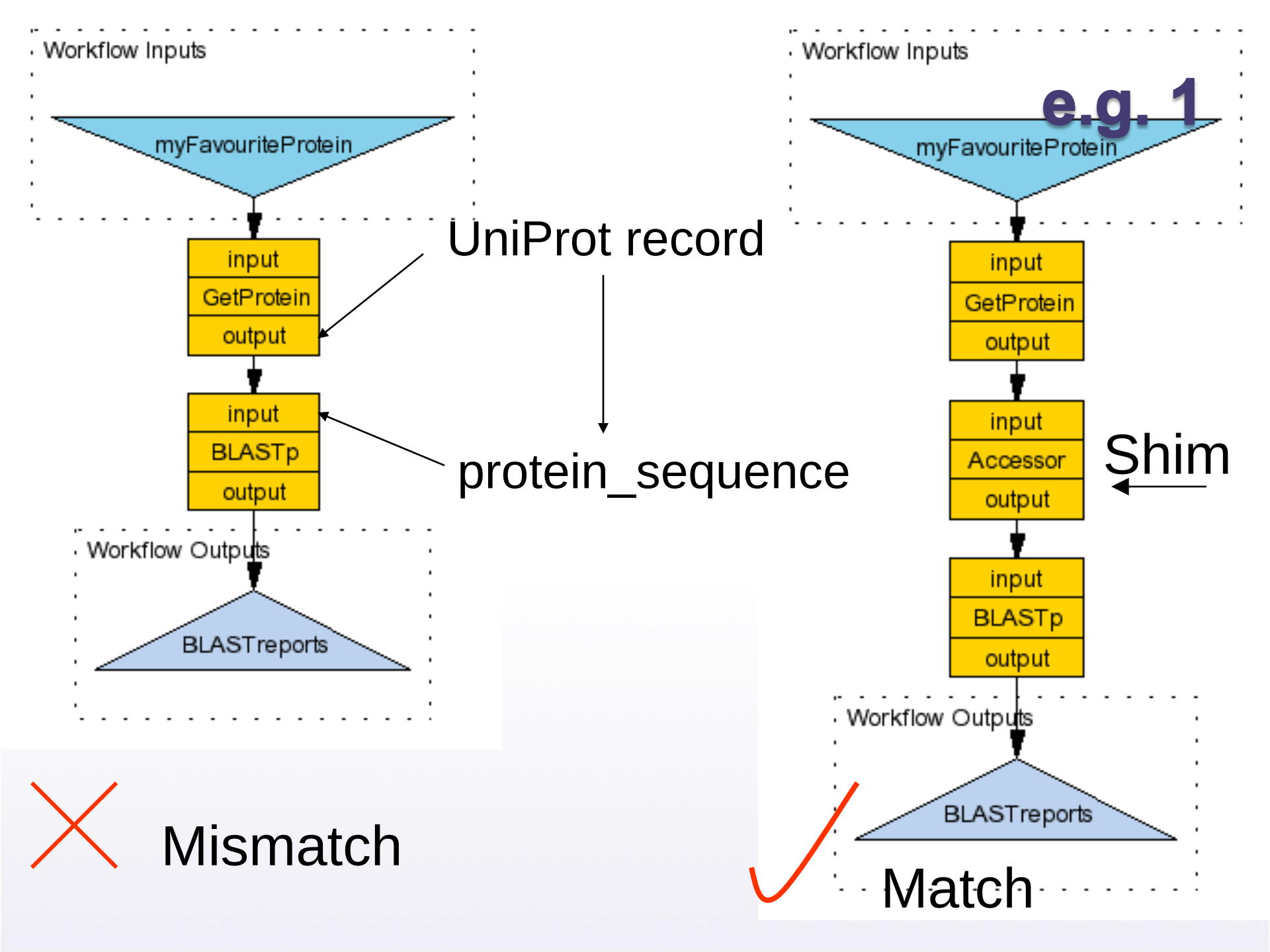
1. Assembly – identifying services that perform the scientific functions needed for the experiment
2. Gluing – identifying how (or more usually, if) theses services are compatible

If they are incompatible – we need services that convert data formats and act as connectors – we call these services Shims (or helper services)

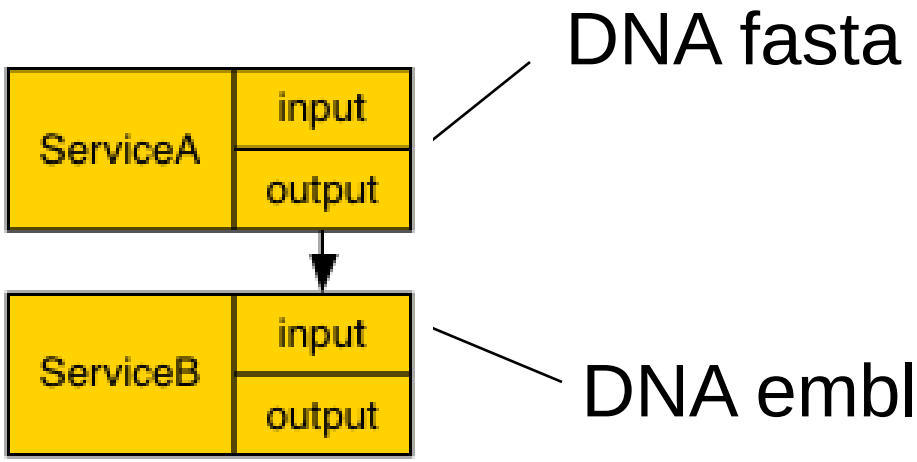
The Reality

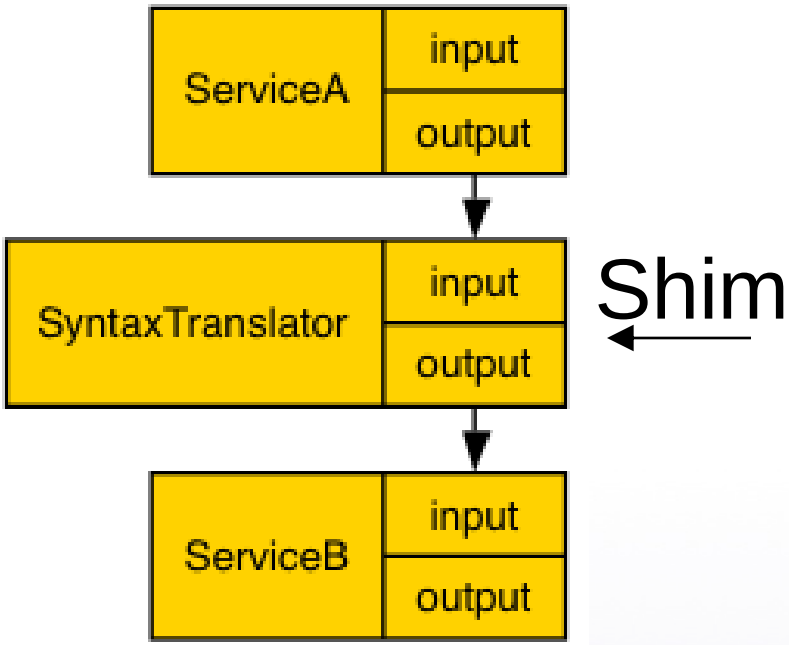
- Lots of services don't match: A into B doesn't go
- Lots of services are poorly described – can you even tell if A goes into B?




Workflow Inputs
myFavouriteProtein
input
GetProtein
output
input
BLASTp
output
Workflow Outputs
BLASTreports
UniProt record
protein_sequence
Mismatch
Workflow Inputs
e.g. 1
myFavouriteProtein
input
GetProtein
output
input
Accessor
output
Shim
input
BLASTp
output
Workflow Outputs
BLASTreports
Match

e.g. 2: syntax





Mismatch

Match

What if the service doesn't exist?

- If you're lucky someone will have already created a service that does what you want and will have described / annotated it in a way that lets you find it
- …if no service exists, one way to solve the problem is to create a lightweight BeanShell script (essentially a "lighter" version of Java) that runs on your local machine (not on a server like the services do)
- These come in two flavours: Ready made "Local Java Widgets" and roll-your-own "Local Services'',

Finding Shims

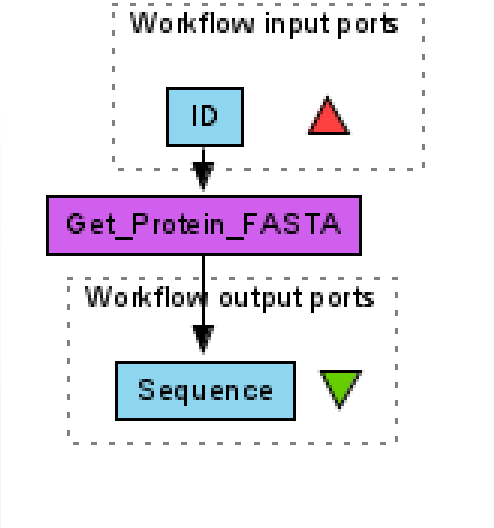
- BioCatalogue – some shims are regular WSDL or REST services
- myExperiment – look for all workflows containing the scientific services. Has anyone linked them together before?

Exploring Shims

- A shim is a service that doesn't perform an experimental function, but acts as a connector, or glue, when 2 experimental services have incompatible outputs and inputs
- A shim can be any type of service – WSDL, soaplab etc. Many are simple Beanshell scripts
- We have already used many shims in these exercises

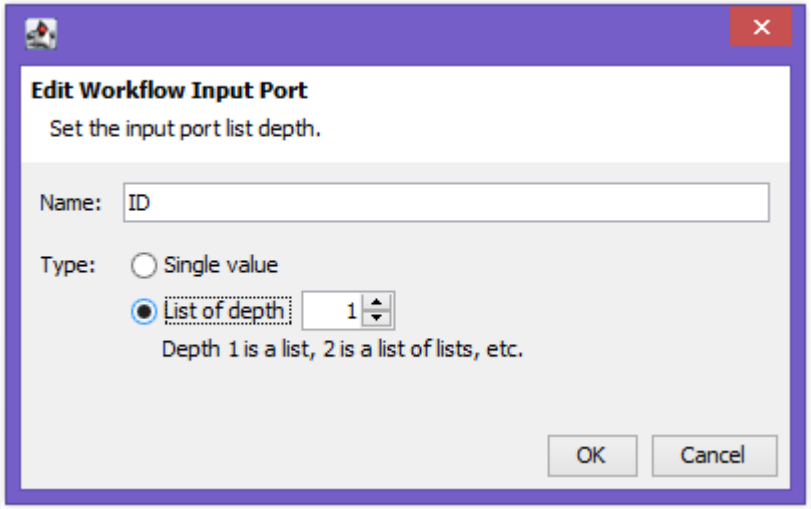
Shims for Data Input

- We will use the simple workflow that we build in the introductory tutorial
- So far, we have only added a few input values to our workflows. Normally, you would have a much larger data set. The “GetProteinFasta” activity can only handle one ID at a time.



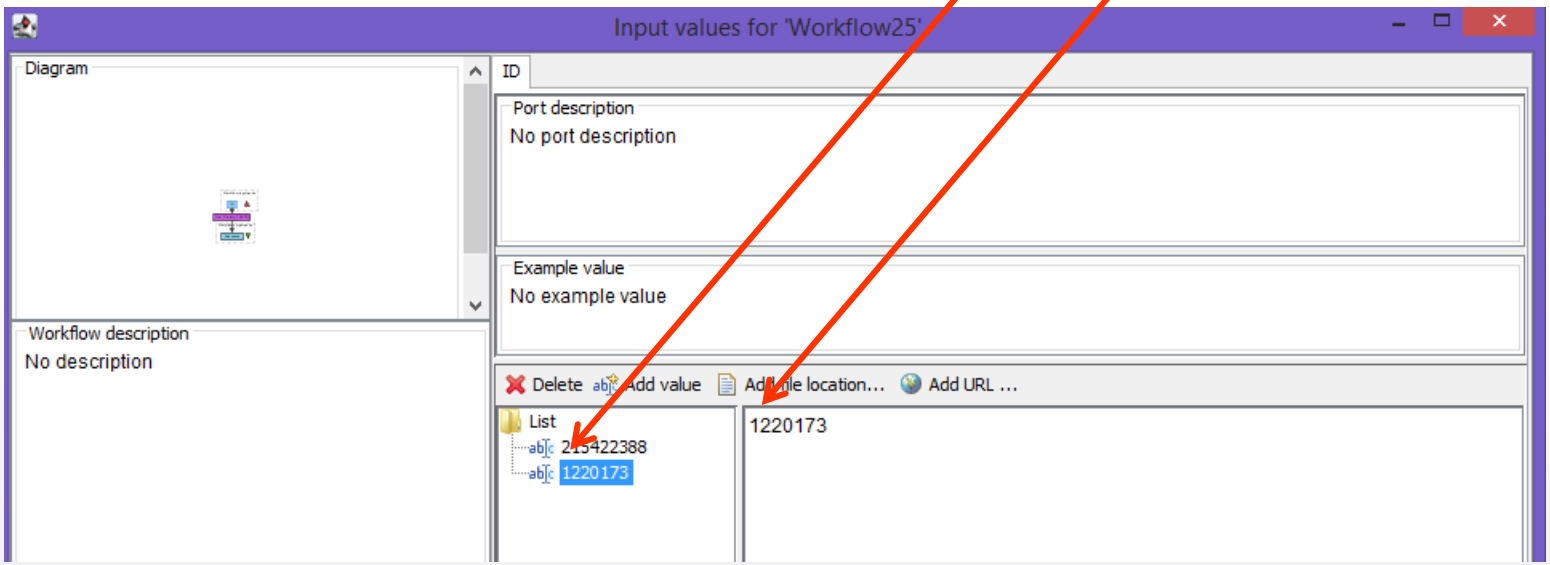
Shims for Data Input

- You can add a list of IDs by configuring the input port
- Right-click on the ID input and select ‘Edit workflow input port’ and change the depth to 1 (a list).
- Now, when you run the workflow, you can add multiple ID values



Shims for Data Input

- Try running it with 215422388 and 1220173
  - Press “Add value” to add each new value.
- If you have hundreds of IDs, however, this is not very practical. Instead, we need an extra service to split a list of data items into individual values

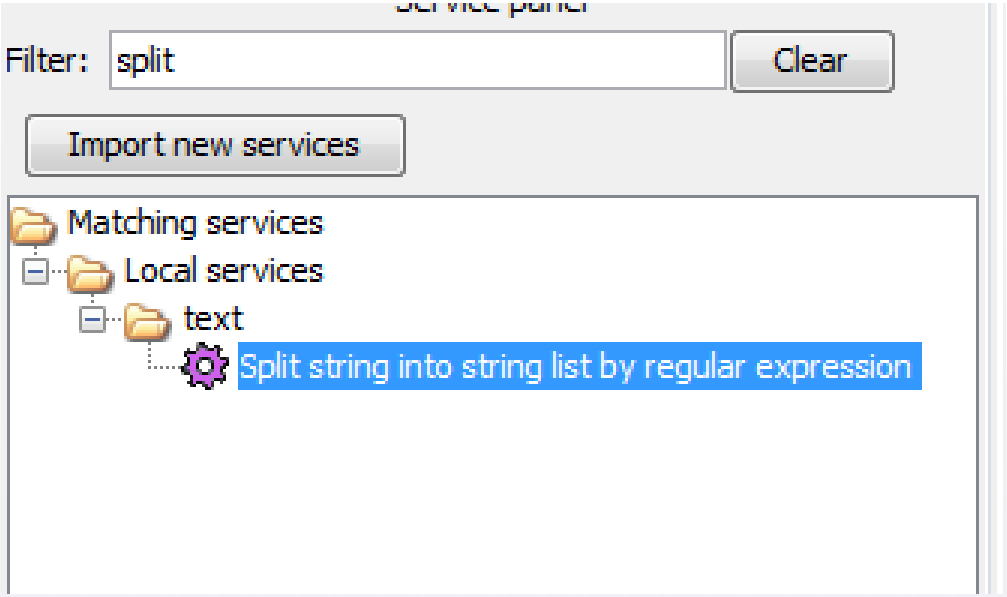


Shims for Data Input

- In the services panel, search for “split”
- Select “Split string into string list by regular expression” (a purple local java service) and drag it into the workflow
- Delete the data link between the “ID” input and “GetProteinFasta” by selecting and right-clicking on the diagram
- Connect “ID” to the “string” port of the new “split” activity
  - Hint: Press To Display all Service ports
- Add “\n” as a constant value to the “regex” input on “split…” by right-clicking and selecting “Set constant value”

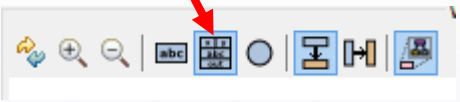
Shims for Data Input

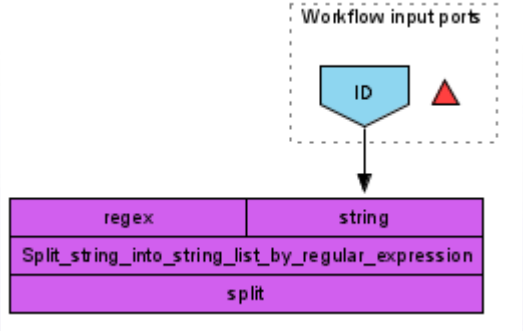
- In the services panel, search for “split”
- Select “split_string_into_string_list_by_regular_expression” (a purple local java service) and drag it into the workflow



Shims for Data Input

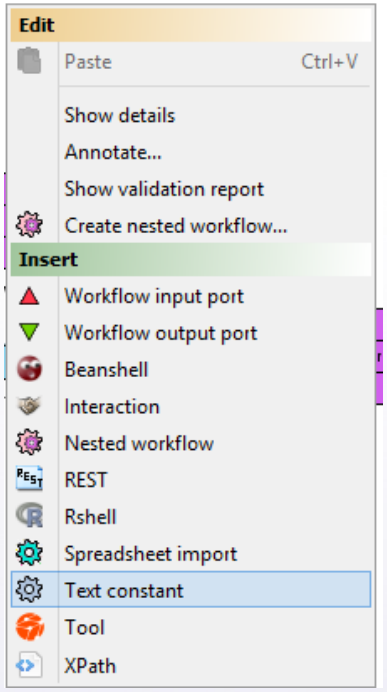
- Delete the data link between the “ID” input and “GetProteinFasta” by selecting and right-clicking on the diagram
- Connect “ID” to the “string” port of the new “split” activity
- Hint: If you don’t see the “string” port press the “Display all Service ports” button

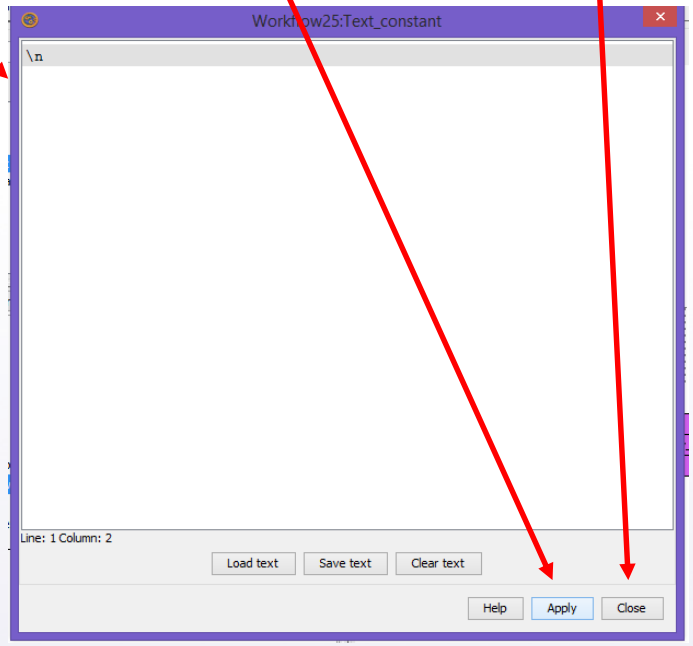




Shims for Data Input

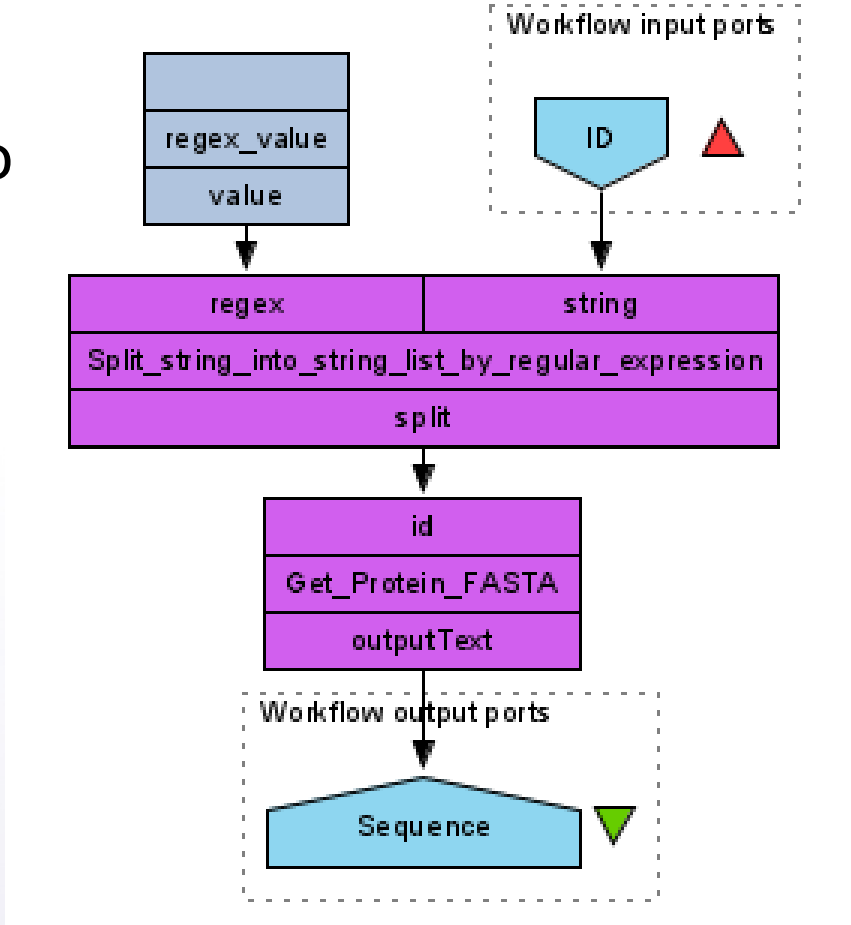
- Add a text constant. (Hint rightclick a blank part of the workflow and select “Text constant”)
- Set the value to “\n” and press “Apply” and “Close”
- Rename the service “regex_value” (Hint: rightclick the Text_constant” service and select Rename Service)





Shims for viewing data

- Connect the “regex_value” to the “regex” port.
- Connect the “split” output port to Get_protein_Fasta (“ID” input port)

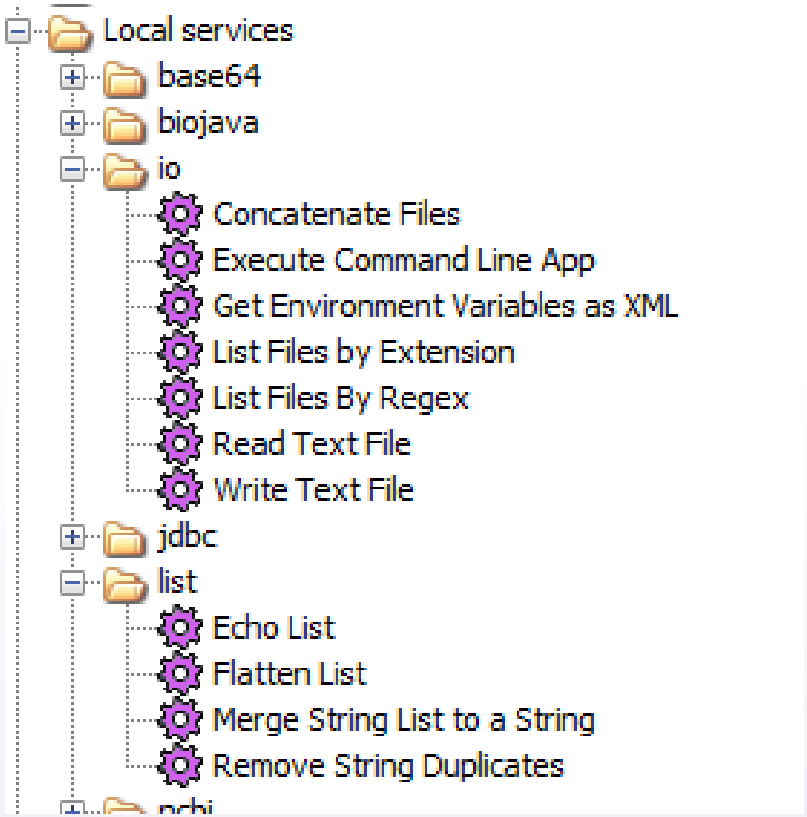


Shims for Data Input

- Run the workflow
- This time, instead of adding individual IDs add a file of IDs. If you don't have one to hand, there is one to download here:
- http://www.myexperiment.org/files/1267/download
- You can download and add the file, or you can add the URL from the input window
- As the workflow runs, you will see it iterate over the IDs in the file

Pre-configured Shims

- The local workers are ‘pre-configured’ shims. Have a look at the different categories on offer.

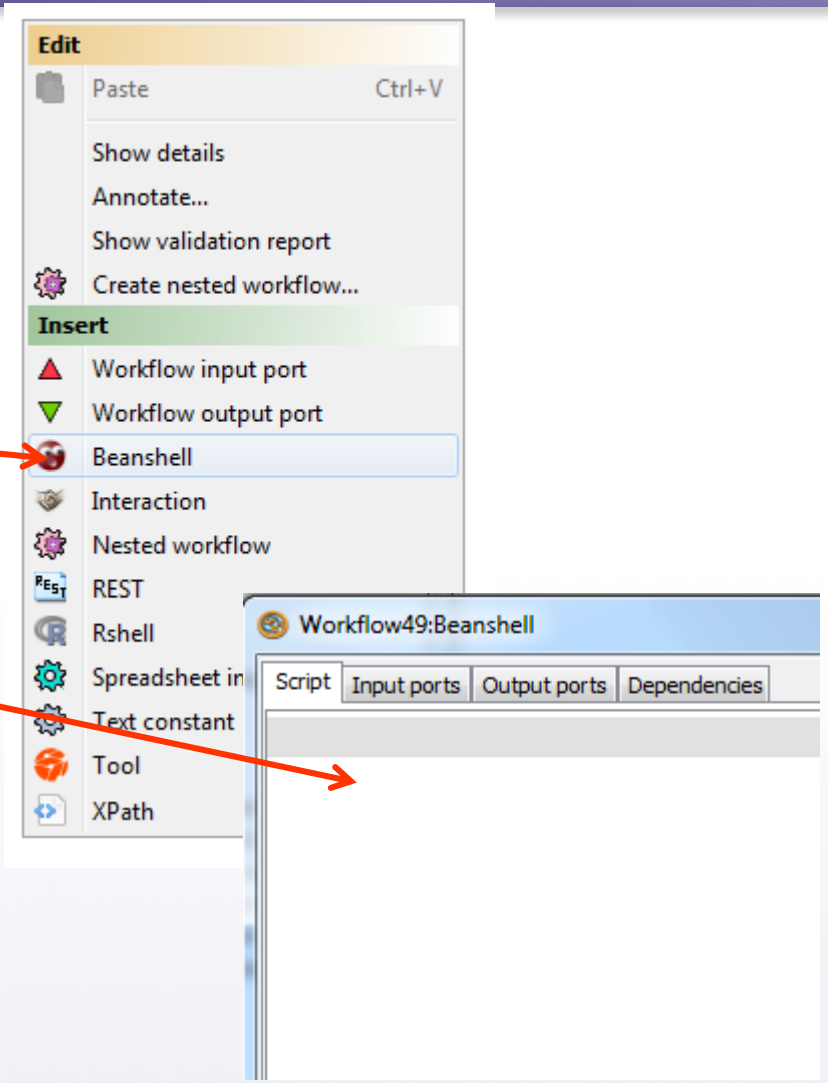


Writing your own shim services - Beanshells

- Many shims are actually Beanshell scripts.
- Beanshell scripts allow you to add simple data transformation steps into your workflow in an easy way.
- We will take a brief look at writing Beanshells

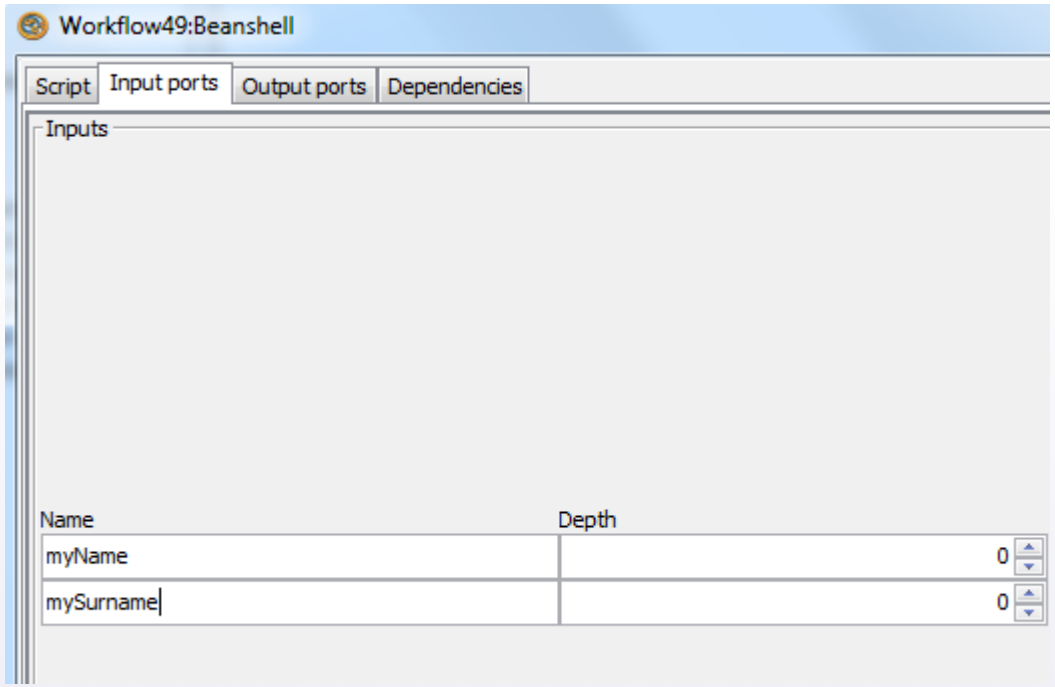
Writing your Own Beanshell

- Create a new workflow by selecting ‘file’ and ‘New Workflow’
- Add a new Beanshell
  - Hint (right click on blank part of the workflow)
- A configure window will pop-up



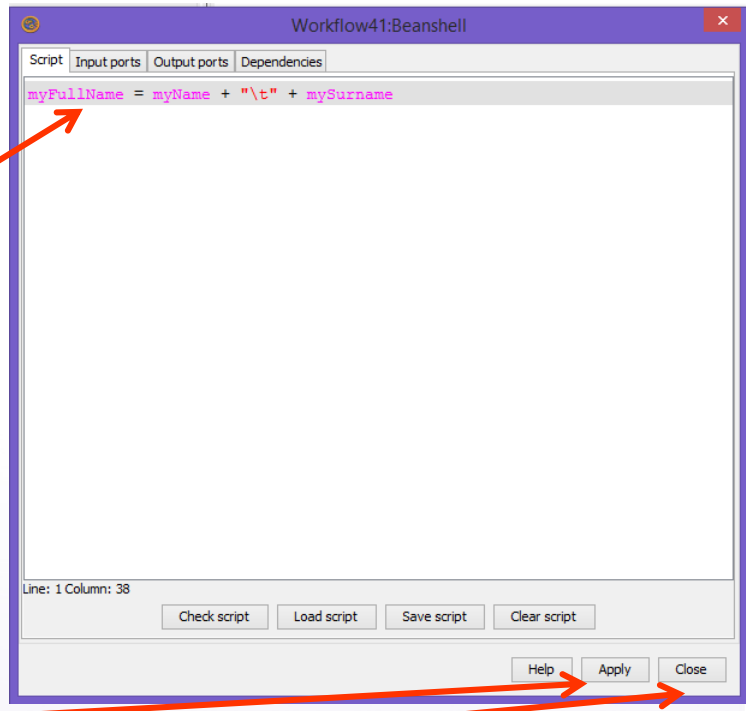
Writing your Own Beanshell

- Create 2 input ports named: “myName” and mySurname
  - Hint: Press “Add Port” after selecting the ‘Input Ports’ tab
- Cretate 1 output port named: myFullname



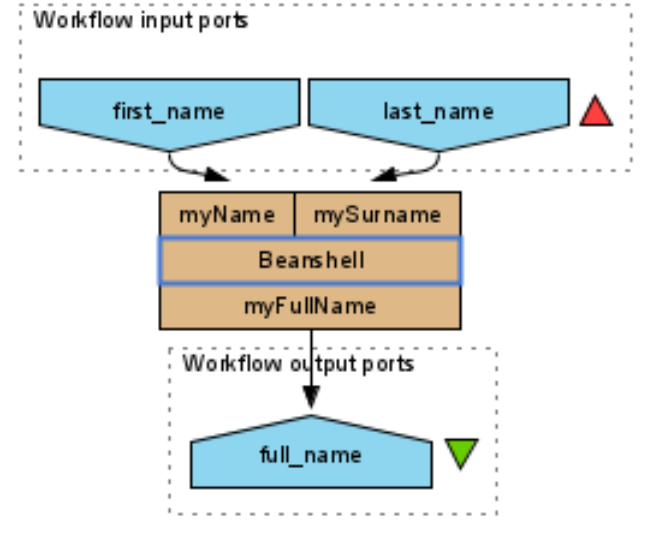
Writing your Own Beanshell

- Select the script tab and Paste the following script
- *myFullname = myName + "\t" + mySurname*
- *The variable names must match exactly the names of the input and output ports*
  - *Hint: They are shown in purple when correctly matching*
- *Then "Apply" and "Close" the "Beanshell" Window*



Writing your Own Beanshell

- Create 2 workflow inputs and 1 workflow output and connect them to the configured beanshell service.
  - Hint: The names of the input and output ports do not need to be the same as the names used in the script.



Writing your Own Beanshell

- Run the workflow
- You should get your full name printed in the output.

This is a very simple example of using helper services to format results from your workflow