



# Taverna Workflows a bio diversity example

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bttp://www.tovorpo.org.uk/



# **Bio-diversity research example**

- In this example we are going to use Taverna to help find the occurrences of Marmota marmot
- Optionally we will then show the locations using google earth.
- Alternatively a xpath service could be added to extract interesting data.





## Find the service in Biocatalogue

- Go to <a href="http://biocatalogue.org">http://biocatalogue.org</a>
- Search for occurrence
- Find the GBIF occurrence service and copy the address where the web page shows the 'base URL'
  - GBIF have several different REST services (or REST endpoints)
- (It should look like this:

#### http://data.gbif.org/ws/rest/occurrence)

- Hint: Sometime opening the base URL in a web browser will open a useful help page
  - We used this information to get the parameters used on the next slides





## Configure the Service

- In Taverna, paste the GBIF base URL into the REST pop-up window (this should already be open if not, right-click on the REST service in the workflow diagram and select 'Configure REST Service' in the drop-down menu).
- To the end of the address, add /list?scientificname={species\_name}
- Make sure the HTTP Method is set to 'GET', click 'apply' and close the pop up window.





Ctrl+V

### **Input & Output Ports**

Edit

Paste

Show details

Show validation report

Workflow input port

Nested workflow

Spreadsheet import

String constant

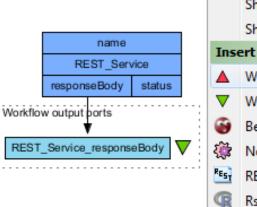
REST Rshell

XPath

Workflow output port

Add workflow input port

- In a blank area of the workflow diagram, right-click and select 'add workflow input port' and name it 'species'
- Link the new input to the REST service by clicking and dragging the arrow across
- Repeat the process to add an output port to the responseBody







#### **Test Run the Workflow**

- Save the workflow by going to 'file -> save'
- Run the workflow by going to 'file -> run'
- In the pop-up 'run workflow' window, click-on 'set value' and type 'Marmota marmota' where it says 'some data goes here'
- As the workflow runs, you can see the progress in the Results window, which you are automatically switched to
- View the results by clicking 'value' in the bottom left panel





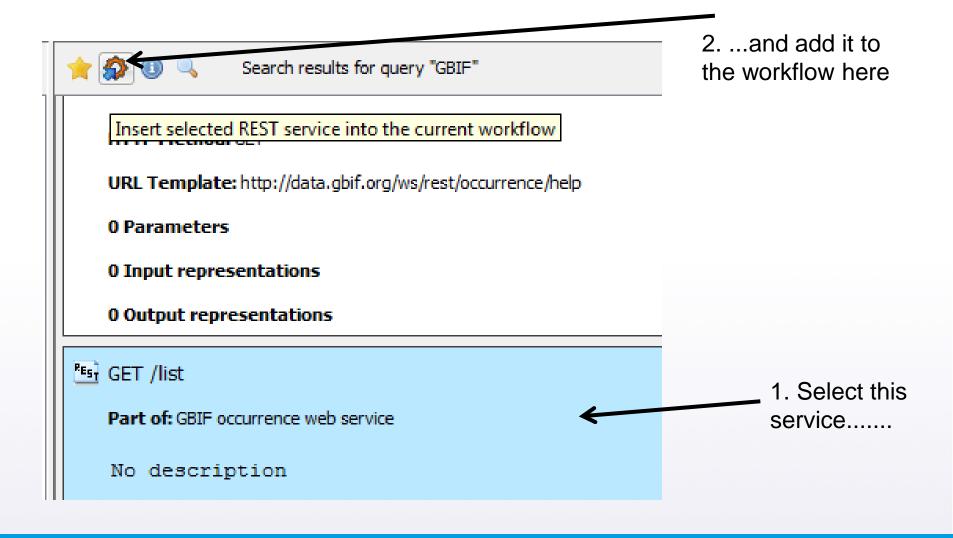
#### **Add More Parameters**

- These results show all the occurrence data. To restrict it to a particular geographical area, substitute the simple GBIF endpoint for one that will allow you to add latitude and longitude values.
- We do this by adding more parameters to the REST service address.
- You could find this by going to the BioCatalogue web page, or by going to the BioCatalogue plugin in Taverna.
- Go to the top of the workbench and click on 'Service Catalogue' and search for "occurrence" again.





#### **Add More Parameters**







## **Explore the Ports**

This is an easier way of adding new REST services, but it only works if they are registered in the BioCatalogue.

- Go back to the workflow window by clicking on the 'Design' tab and expand the workflow view to show all input and output ports
- Now you will see the new REST service.

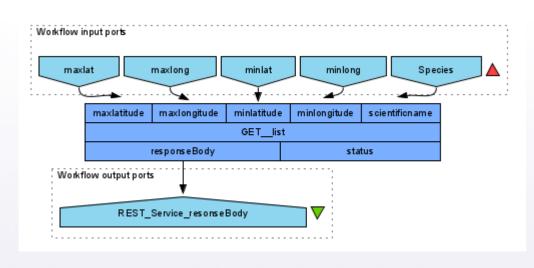






## Redesign the Workflow

- Delete the original REST service by right-clicking and selecting 'delete service'
- Connect the new service to the original input and output by dragging arrows between the boxes
- Make new input ports for the co-ordinates by right-clicking on the workflow diagram and selecting 'add new workflow inputs'
- Connect the new inputs to the REST service







#### **Provide co-ordinates**

- Run the workflow, entering Marmota marmota and the following co-ordinates:
  - -89 (for minlat)
  - 89 (for maxlat)
  - -179.9 (for minlong)
  - 179.9 (for maxlong)





- The service returns XML data. This is good for computers, but not easy to read.
- You can plot the data on Google earth to make it easier to interpret. We have already written a workflow that does this.
  - See the next 2 slides
- Alternatively try adding an Xpath service to extract some interesting data from the XML





## **Google Earth Plot**

- In Taverna, go to file -> 'Open workflow location' and copy the following link into the pop-up box:
  - http://www.myexperiment.org/workflows/2592/download?version=1
  - It is possible to load workflows from a file, or from a web link
- This workflow opens a local copy of Google Earth. If you don't, have it, please go to Google Earth and install it: <a href="http://www.google.com/earth">http://www.google.com/earth</a>
- For windows See also
  http://www.myexperiment.org/workflows/2592.html





## **Google Earth Plot**

- Run this workflow with the same parameters as you used in your own workflow (e.g. Marmota marmota and lat, long).
   NOTE: there are some example values in the workflow, but you may need to select or change them.
- You need to specify an additional parameter for the location of your local Google Earth program.
- This time, the results are plotted on Google Earth.
- Additionally, an interactive step allows you to modify lat/long values while the workflow is running.





## Test the Workflow with other Species

- The workflow you ran only has information from one species, but selecting species can be complex
- Re-run the workflow twice, once with the species Abraxas sylvatus, and once with Abraxas sylvata. Do you get different results?
- They both represent the same species, but one is simply a different spelling. You may need to discover all species names and synonyms and combine data before continuing with your modelling.