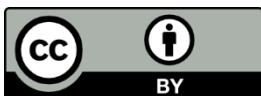
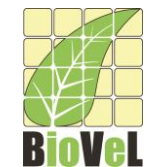




# Working with BioVeL Portal

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# Running your workflow in BioVeL

- Go to <http://portal.biovel.eu>
- Login or set up a user account
  - If you are not part of any of the listed projects or Institutions please select “Training” and “Others”
  - You will not be able to run workflows until approved.



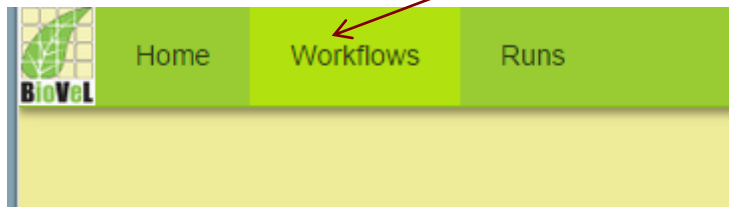
# Running your workflow in BioVeL

- In this short tutorial we will work with the BioVeL portal
- We will upload the Species\_Occurrence workflow which we created in the “Using BiodiversityCatalogue” tutorial and run it in the portal
  - Available from <http://www.myexperiment.org/workflows/4484.html>

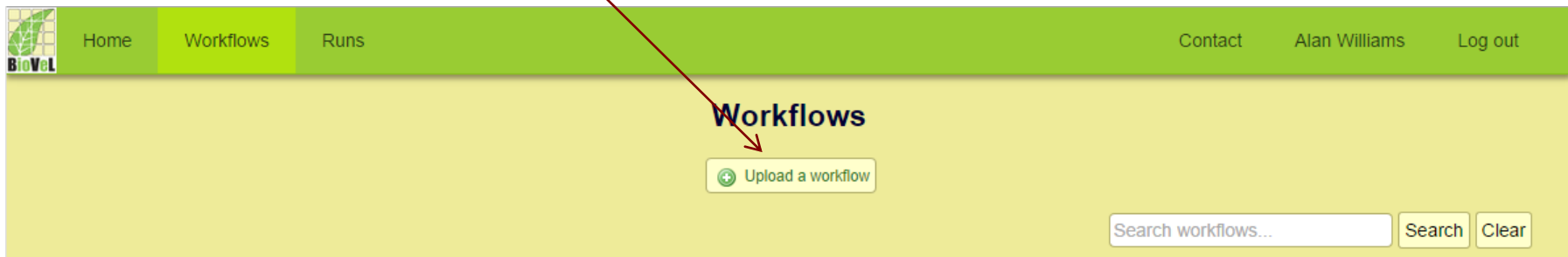


# Upload the workflow

- Click on the Workflows tab



- Then click Upload a workflow





# Upload the workflow

- You can upload a workflow from your local drive
- Select a suitable category such as “Other”
- Tick “Allow data sweeps” if you want to be able run the same workflow over multiple data values

The screenshot shows the 'New workflow' form in the BioVeL interface. The form includes the following fields:

- File:** A 'Choose file' button next to the text 'Species\_Occurrence.t2.pov'.
- Category:** A dropdown menu currently set to 'Taxonomic Refinement'.
- MyExperiment Link:** An empty text input field.
- Documentation Link:** An empty text input field.
- Allow data sweeps?:** A checkbox that is checked.

The BioVeL logo is visible in the top left and bottom left corners. The European Union flag is in the bottom center. The 'myGrid' logo is in the bottom right corner.



# Upload the workflow

- Workflows are associated with a project
- Select “Training” and then click “Associate with this Workflow”

The screenshot shows a web interface titled "Projects" with a yellow header bar. Below the header, it says "The following projects are associated with this workflow:". There is a blue bar containing the word "None". Below that is a dropdown menu currently set to "Training". At the bottom left of the interface is a button labeled "Associate with this Workflow" with a green plus icon. A red arrow points from the text "Associate with this Workflow" in the second bullet point of the list above to this button.

- If you joined the portal, in a project different to “Training” please use that one instead.



# Upload the workflow

- You can leave the Sharing as private
- Then click “Next”

**Sharing**

Here you can specify who can **view** the summary of, **get** access to the content of, and **edit** the workflow. [More info](#)

- Keep this workflow private (only visible to you)

**Or share it with...**

- Members of projects associated with this workflow:

[Advanced permissions](#)

or



# Upload the workflow

- We can now categorize the inputs and outputs, and specify the type their value has
- Set sciName's type to "Plain text document" and locatedOccurrences to XML document
- Click "Save Changes"

Workflow was successfully uploaded and saved.

### Input and Output Types

Please specify the purpose of each workflow input and output port, and the type that they accept or produce.  
Specifying the type of a port will help BioVeL Portal display workflow results and input data in an appropriate way.

Inputs	Data	Parameter	Type
sciName	<input checked="" type="radio"/>	<input type="radio"/>	Plain text document (.txt)

Outputs	Result	Error/Log	Type
locatedOccurrences	<input checked="" type="radio"/>	<input type="radio"/>	XML document (.xml)

Save Changes or Cancel





# Workflow information

- You can see the information about the workflow is now visible in the portal

## Species Occurrence

Run workflow Run data sweep Download workflow Add to Favourites Manage workflow Upload new version Publish Workflow

Visibility: Private

Retrieve the first 100 occurrences of a species in Darwin format

Inputs (1)

Data Inputs (1)

**sciName** (text/plain)

Description:  
The scientific name of the species

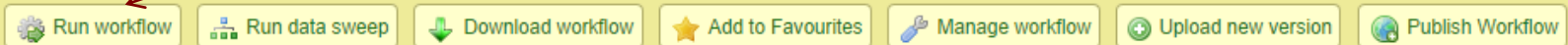
Example value:  
Marmota marmota

Related runs  
None



# Running a workflow

- Now we can run our uploaded workflow in the portal
- Click on “Run workflow”





# Running a workflow - 2

- You can now enter values for the inputs
- For the first run, use the example value
- Click “Start Run”

**New Workflow Run: Species Occurrence**

Run name:  
Species Occurrence (v1) run 24 Sep 2014 14:38:39 UTC

**Data**

sciName ⓘ

The example value is automatically entered in the box below. Click to edit or enter a new value directly or choose a file.

Marmota marmota

Or select a file...  
Choose file No file chosen

Start Run Cancel



# Running a workflow - 3

- And the workflow should run...
- When finished you will see the results in the browser page

Name:  Save

Visibility: Private

Workflow: Species Occurrence      Created at: 24 Sep 2014 14:41:58 UTC

Category: Taxonomic Refinement      Started at: 24 Sep 2014 14:41:59 UTC

Status: Finished      Finished at: 24 Sep 2014 14:42:15 UTC

Outputs

Jump to:

Results:

Results (1)

**locatedOccurrences** (application/xml)  Download value

```
<?xml version='1.0' encoding='UTF-8'?>
<?xml-stylesheet type="text/xsl" href="http://data.gbif.org/ws/rest/occurrence/stylesheet"?>
<gbif:gbifResponse xsi:schemaLocation="http://portal.gbif.org/ws/response/gbif http://data.gbif.org/ws/rest/occurrence/schema http://purl.org/dc/elements/1.1/ http://data.gbif.org/schema/dc.xsd http://purl.org/dc/terms/ http://data.gbif.org/schema/dcterms.xsd http://www.w3.org/1999/02/22-rdf-syntax-ns# http://data.gbif.org/schema/rdf.xsd http://www.w3.org/2002/07/owl# http://data.gbif.org/schema/owl.xsd http://rs.tdwg.org/ontology/voc/Common# http://data.gbif.org/schema/tcom.xsd http://rs.tdwg.org/ontology/voc/TaxonOccurrence# http://data.gbif.org/schema/TaxonOccurrence.xsd http://rs.tdwg.org/ontology/voc/TaxonConcept# http://data.gbif.org/schema/TaxonConcept.xsd http://rs.tdwg.org/ontology/voc/TaxonName# http://data.gbif.org/schema/TaxonName.xsd" xmlns:gbif="http://portal.gbif.org/ws/response/gbif" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#" xmlns:to="http://rs.tdwg.org/ontology/voc/TaxonOccurrence#" xmlns:tc="http://rs.tdwg.org/ontology/voc/TaxonConcept#" xmlns:tn="http://rs.tdwg.org/ontology/voc/TaxonName#" xmlns:dc="http://purl.org/dc/terms/">
  <gbif:header>
    <gbif:help>
      http://data.gbif.org/ws/rest/occurrence/help
    </gbif:help>
    <gbif:request>
      list
    </gbif:request>
    <gbif:statements>
```





# Running a workflow - 4

- You can download all the results in a zip file

Species Occurrence (v1) run 24 Sep 2014 14:38:39 UTC

[Download all results](#) [Data sweep based on this run](#) [Manage run](#) [Delete](#)

- Or download an individual result

Outputs

Jump to:

Results:

Results (1)

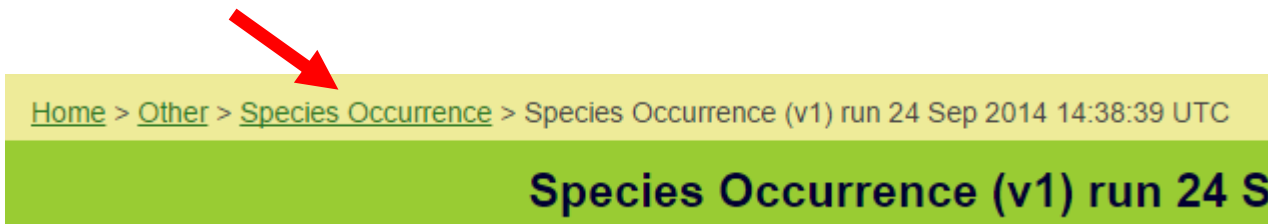
locatedOccurrences ⓘ (application/xml)

[Download value](#)

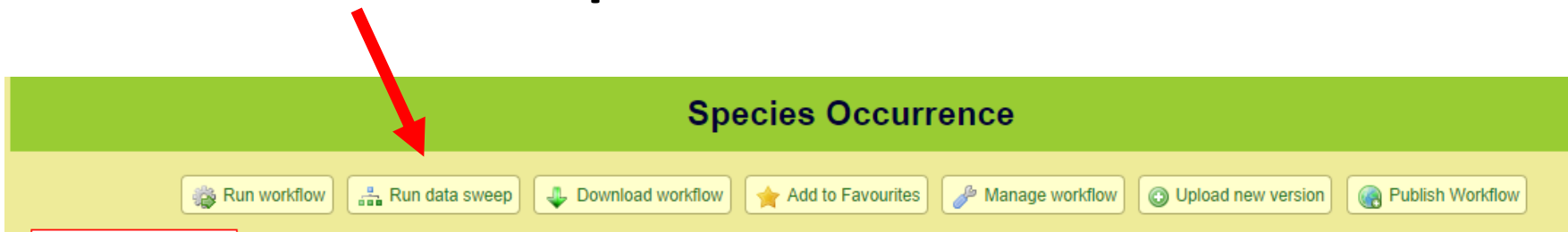


# Creating a sweep

- Go back to the workflow



- Click **Run data sweep**





# Sweep data

- For each workflow input, you can choose to iterate over it (change its value over the sweep) – otherwise you will give a fixed value for all iterations
- We are sweeping over *sciName* so leave it ticked
- For each iteration specify the input values
  - To create a new iteration click **Add Iteration**

Data

Iteration 1 (Remove)

sciName

Enter input here...

Or select a file...

Choose file No file chosen

Add Iteration



# Starting the sweep

- You can use any species names
- Create two additional iterations
- Use
  - *Limulus polyphemus*
  - *Kogia breviceps*
  - *Marmota marmot*as the three sciName values
- Warning: Make sure there is no space or newline after the values
- Warning: Don't press **Add Iteration** after entering the values of the last sweep or it will create an additional blank sweep
- Click **Start sweep**














# Running sweeps

- You will see the state of the sweep iterations
  - perhaps queued then
  - Running then
  - Finished

Runs




Search:

Run	Workflow	Category	State	Created	Finished	Actions
 Species Occurrence sweep - (1)	Species Occurrence	Other	Running 	less than a minute ago	-	 Cancel
 Species Occurrence sweep - (2)	Species Occurrence	Other	Running 	less than a minute ago	-	 Cancel
 Species Occurrence sweep - (3)	Species Occurrence	Other	Running 	less than a minute ago	-	 Cancel



# Viewing sweep results

- When a sweep iteration has finished you can click on the Run and view it (as we did before)
- You can view results from the Sweep page by clicking on (View) in the Sweep results table
- You can also pick which values to download

Run	locatedOccurrences <input checked="" type="checkbox"/>
 Species Occurrence sweep - (1)	<input checked="" type="checkbox"/> (View)
 Species Occurrence sweep - (2)	<input checked="" type="checkbox"/> (View)
 Species Occurrence sweep - (3)	<input checked="" type="checkbox"/> (View)
Download selected values	



# Portal summary

- You now know how to upload a workflow to the portal
- Describe the ports of the workflow
- Perform a single workflow run
- Use the workflow to sweep over data values