Deploy and Use Galaxy With Examind WPS

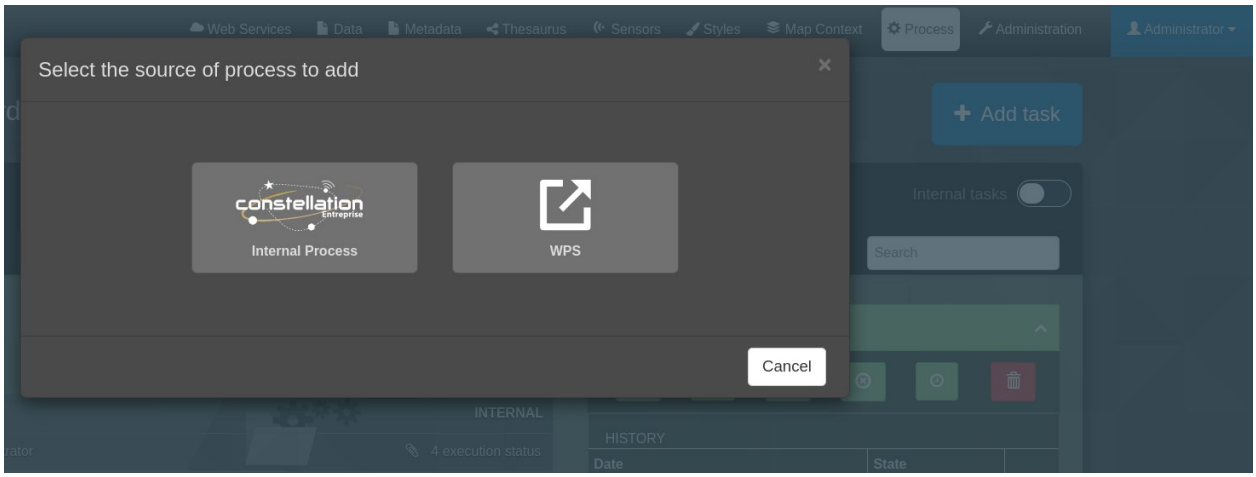
Needed :

- Examind community running somewhere (with docker for example)
- A file named processGalaxy.xml describing the galaxy workflow)
- A json with the parameters of the workflow

Steps :
- DEPLOYMENT

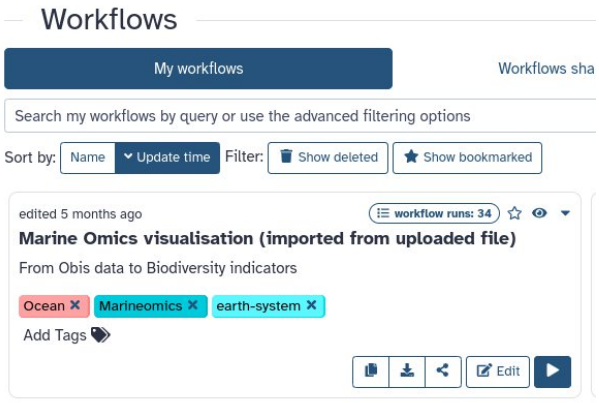
In category : « Process », click on « Add task »

Then click on « Internal Process », and in the category « examind », on « galaxy.deploy »



You will need to set a « Task Name », the id of your galaxy workflow.

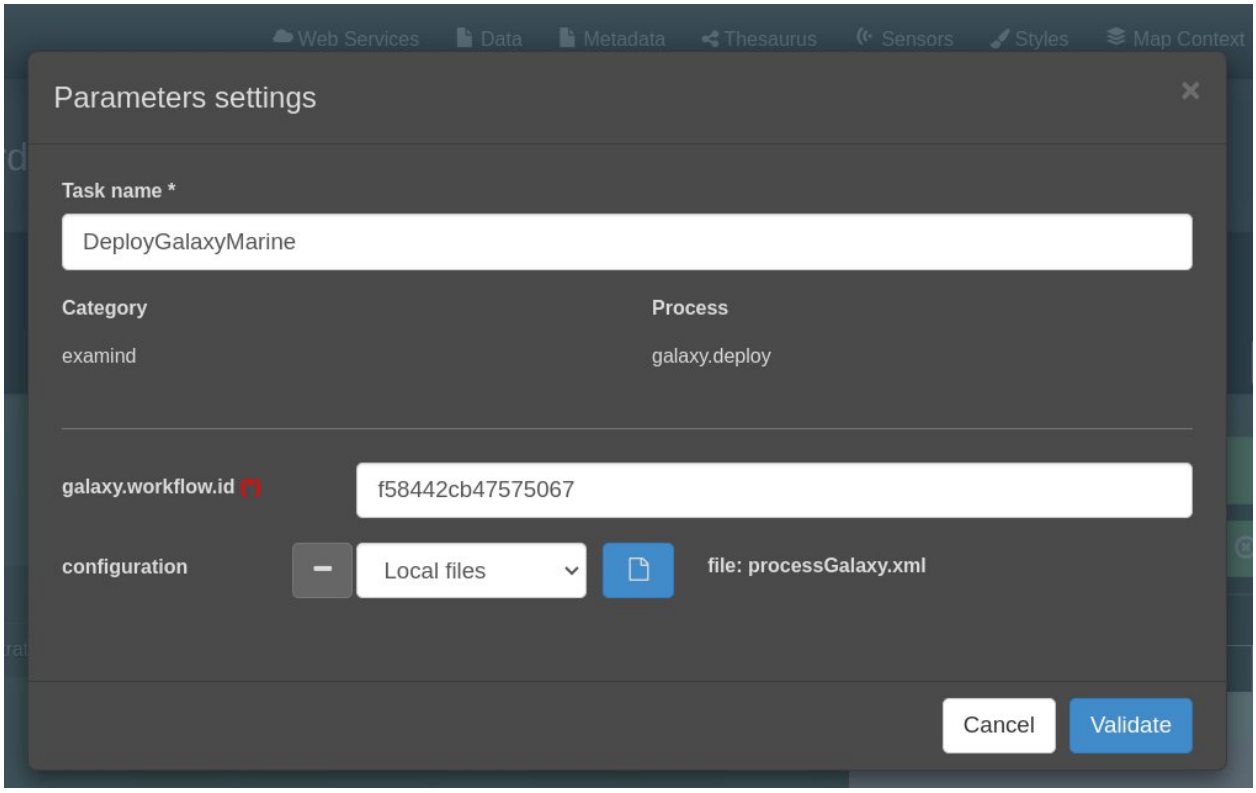
How to find the workflow id ?
Open galaxy in your browser and go in « Workflows », then click on Edit on your workflow.



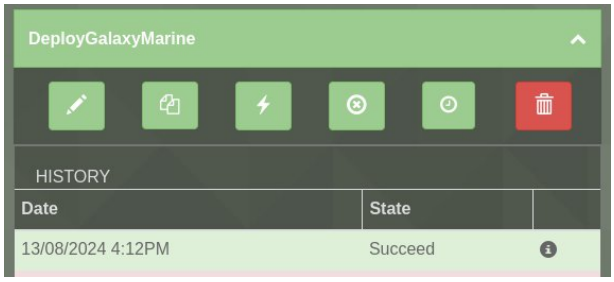
In the link of the page you will have the ID of the workflow, for example, for me the link is :

https://earth-system.usegalaxy.eu/workflows/edit?id=f58442cb47575067

Then, you need to open the processGalaxy.xml file and click on « Validate ».



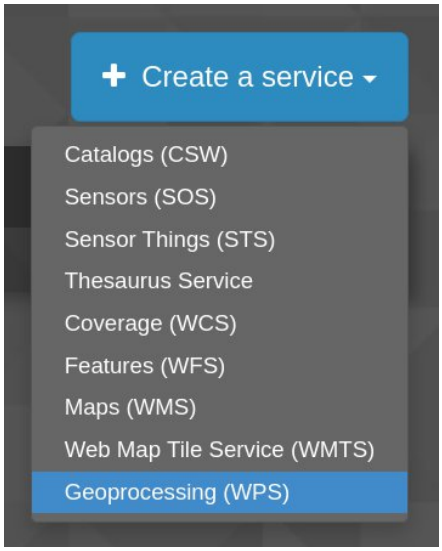
You need to click on the little thunder to run the deployment process, and if it’s all ok you will have a « Succeed » in green.



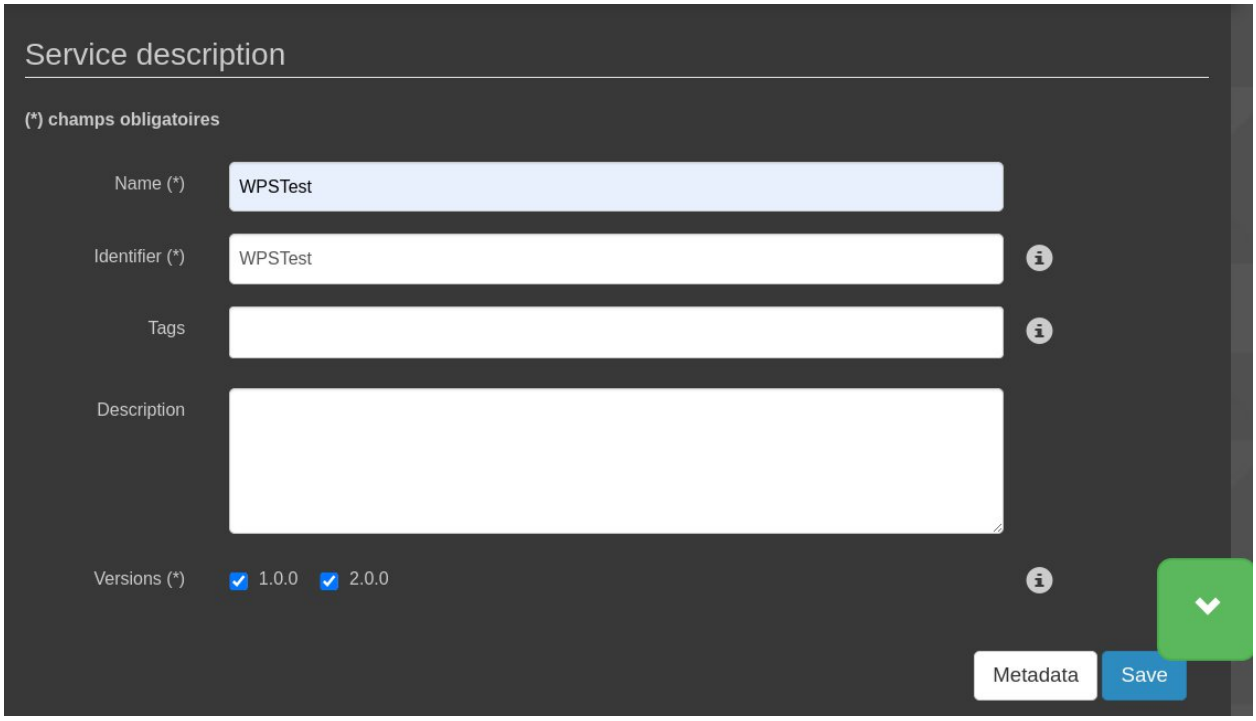
The process is deployed in EXAMIND !

- SERVICE CREATION

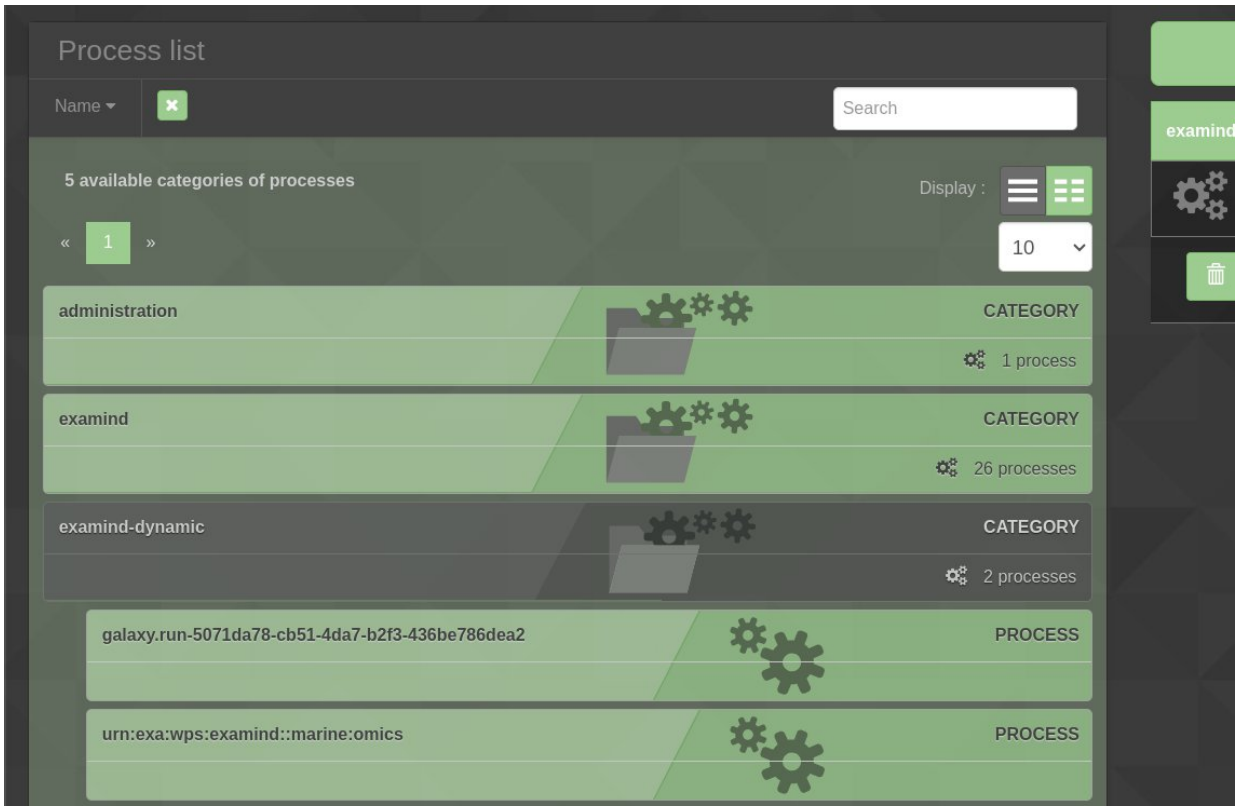
We need to create a WPS Service. You need to go in the category « Web Services », and add a WPS Service.



Set a name, an indentifier and CLICK ON THE TWO VERSIONS ! (important)



You can check if the galaxy process is here by clicking on Edit, you should see, below « examind-dynamic » something like that :



Run the service.

- **USAGE**

You can describe the process with : (« **DescribeProcess** » request)
http://localhost:8080/examind/WS/wps/WPSTest?service=WPS&version=2.0.0&request=DescribeProcess&Identifier=urn:exa:wps:examind::marine:omics

You can Execute the process with : (« **Execute** »request)
http://localhost:8080/examind/WS/wps/WPSTest?service=WPS&version=2.0.0&request=Execute&Identifier=urn:exa:wps:examind::marine:omics

(you need to set data in the request body, see the WPS doc for requests)

Note : you need to set the parameters for your process using Json

You can get the status of the invocation with : (« **GetStatus** »request)
http://localhost:8080/examind/WS/wps/WPSTest?service=WPS&version=2.0.0&request=GetStatus&Identifier=urn:exa:wps:examind::marine:omics

(you need to set data in the request body, see the WPS doc for requests)

You can get the result of the invocation with : (« **GetResult** » request)
http://localhost:8080/examind/WS/wps/WPSTest?service=WPS&version=2.0.0&request=GetResult&Identifier=urn:exa:wps:examind::marine:omics

(you need to set data in the request body, see the WPS doc for requests)

In the execute request, you need to send parameters and inputs for the workflow : to do this refers to :

1- How can I found the json (for parameters) for my workflow ?

2- How can I send files to my workflow using inputs ?

How to create a processGalaxy.xml for my workflow ?

If you want to have your own workflow in examind, you need to create a *processGalaxy.xml*.

It's en xml document used by examind to create the process template. You can reuse one of the existing *processGalaxy.xml* next to this document.

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In this document you need to change for you workflow :

- The Title (line 4)
- The Abstract (line 5)
- All the identifiers

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For examples identifiers are like :

`urn:exa:wps:examind::marine:omics:biosynthetic:gene:clusters`

You wan change this identifier by editing the part after `urn:exa:wps:examind::`

You can choos wathever you want, but all the identifiers of the document needs to use the same identifier. For example :

`urn:exa:wps:examind::marine:omics:biosynthetic:gene:clusters:input:inputs`

Will become :

`urn:exa:wps:examind::<your-workflow-identifier>:input:inputs`

How can I found the json (for parameters) for my workflow ?

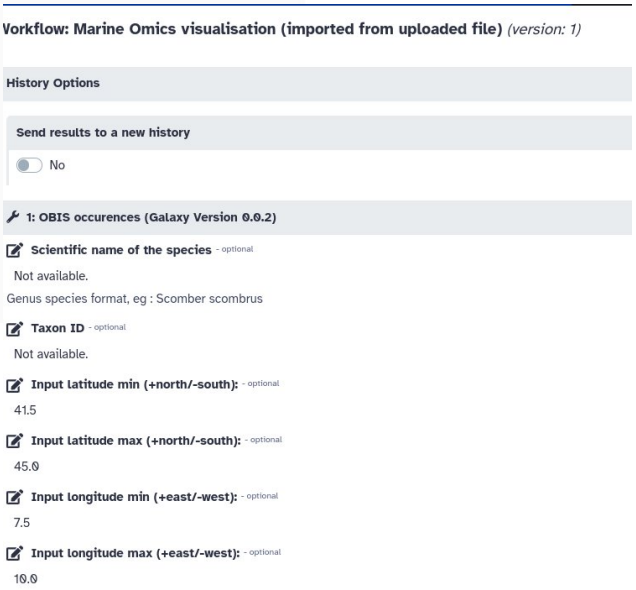
Unfortunately, there are no simple techniques for recovering the expected json formatting to send the parameters to your workflow.

1- You can either create a json format by hand (by entering for each step the list of expected parameters, to do this you can use the example provided in one of the example ExecuteRequest given next to this file).

For example with marine omics workflow :

Parameters Json input


```
{
    "0":{
        "species":null,
        "taxon":null,
        "lat_min":"40.5",
        "lat_max":"44",
        "long_min":"6.8",
        "long_max":"9.0"
    },
    "1":{
        "complement":"",
        "delimiter":"",
        "cut_type_options|cut_element":"-f",
        "cut_type_options|list":["1","7","8","44","78"]
    },
    "2":{
        "colnames":true,
        "separator":"t",
        "longitude":"3",
        "latitude":"2",
        "species":"4",
        "records":"5",
        "type":"0",
        "resolution":"9"
    }
}
```

For this technique you can use the Galaxy UI to find out what is expected in terms of parameters

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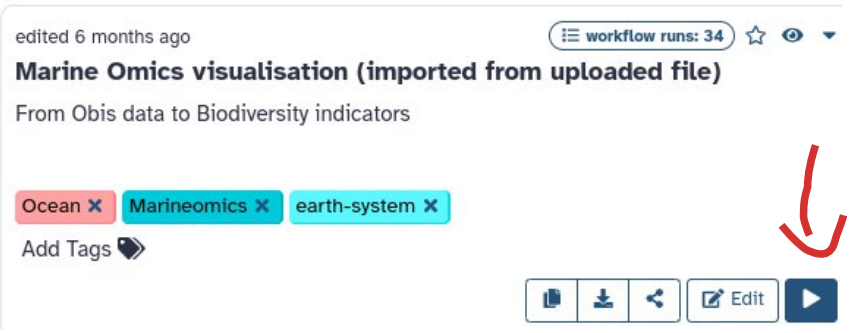
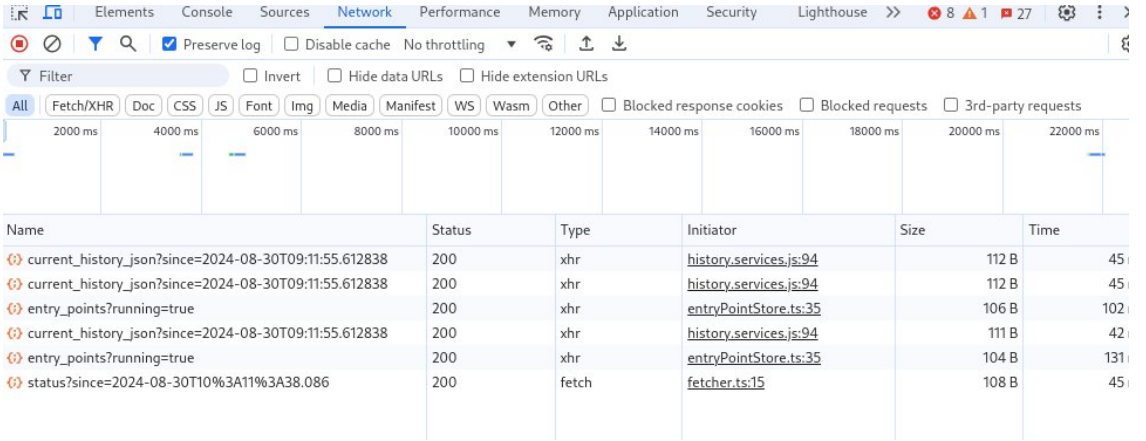
2- Or, you can use the devtools on the Galaxy tool to find out what Galaxy UI sends to the server when a workflow is launched. Here's a short tutorial on how to do it !

1. Open Galaxy UI, and select a workflow

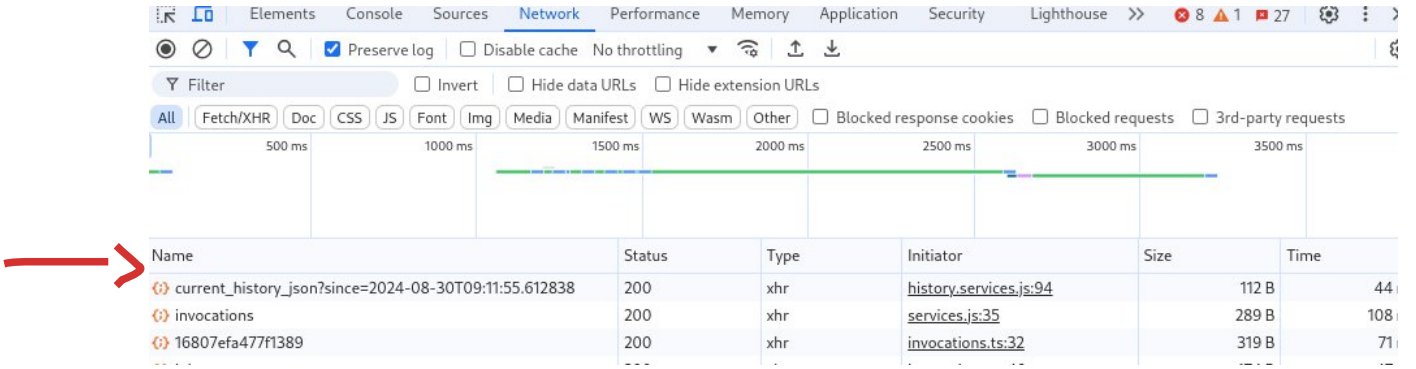
2. Then click on RUN



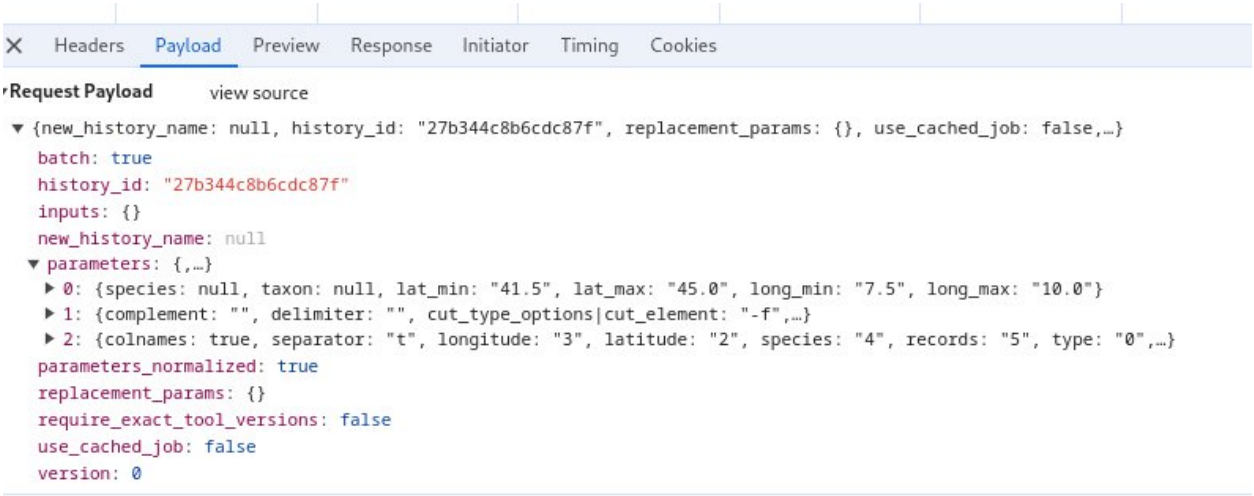
3. Click on « Expand to full workflow form. »
4. Press F12 on your keyboard to open Chrome's 'DevTools', and go in « Network » tab (in the devtools). You will have something like that



5. Now you can click on RUN WORKLOW in Galaxy
6. In the chrome DevTools you will have that (an « invocations » request)



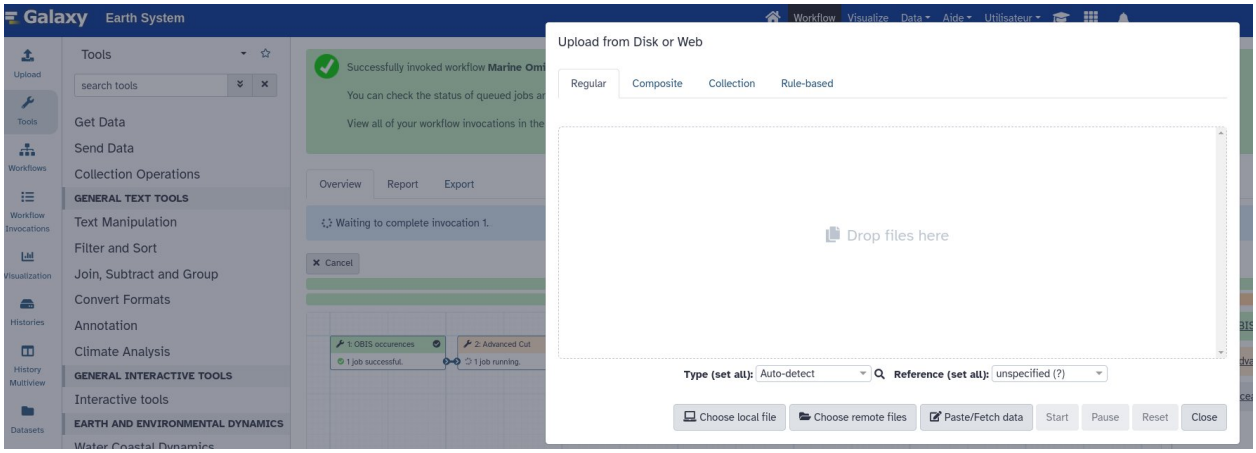
7. Click on it, and go to « Payload ». Open the ‘parameters’ json part and you'll have the json to enter in the ExecuteRequest!



How can I send files to my workflow using inputs ?

It is not currently possible to send files from Examind to Galaxy. We are working on this, but for the moment there's a temporary solution, which I will explain here.

1. Go to Galaxy UI, and click (on the left) on « Upload »
2. Upload the files needed as inputs for your workflow



3. Once it’s done, on the right (in history), for each file, you will have something like that : 

4. Click on the little eye, to open the « preview »
5. Once the preview is open, look at the url of the page you are on. You'll find the file ID there. Make a note of this identifier for each file. Ex of url with id : https://earth-system.usegalaxy.eu/datasets/4838ba20a6d8676508817867eb0a2776/preview
6. In the body of your ExecuteRequest for your workflow, in the input part, we are going to use ids to tell galaxy which file should be read at which point in the workflow
7. You need to write a json part in « inputs » like that :

```
<wps:Input>
    <ows:Identifier>urn:exa:wps:examind::marine:omics:biosynthetic:gene:clusters:input:inputs</ows:Identifier>
    <wps:Data>
        <wps:LiteralData>{
        "0": {
            "batch": false,
            "product": false,
            "values": [
            {
                "id": "4838ba20a6d8676508817867eb0a2776",
                "src": "hda",
                "map_over_type": null
            }
            ]
        }}</wps:LiteralData>
    </wps:Data>
</wps:Input>
```

In this example, we tell galaxy that at step 0 of the workflow, there is the file with id X as input.

If you have several files for a single step, simply add the other files to the table after ‘values’. If you have several files at different stages of the process, simply specify the stage number and follow the same procedure.

Note: the step number indicated on Galaxy is greater than 1 than the step number for the server. For example, if the step number on Galaxy UI is 2, then the json should be set to 1 (2 - 1 = 1).