

Deploy and Use Galaxy With Examind WPS

Needed :

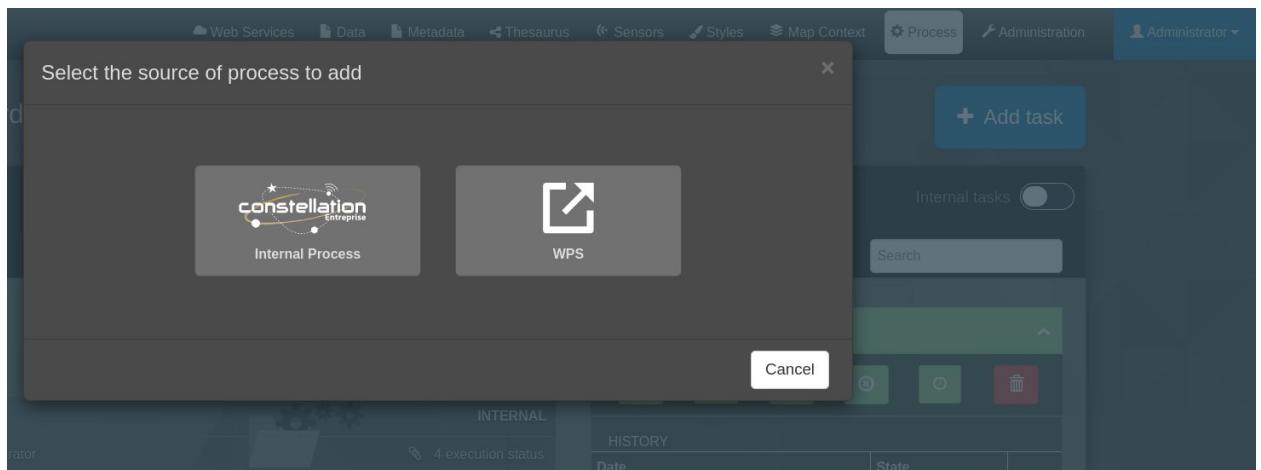
- Examind community running somewhere (with docker for example)
- [A file named processGalaxy.xml describing the galaxy workflow](#)
- [A json with the parameters of the workflow](#)

Steps :

- DEPLOYMENT

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

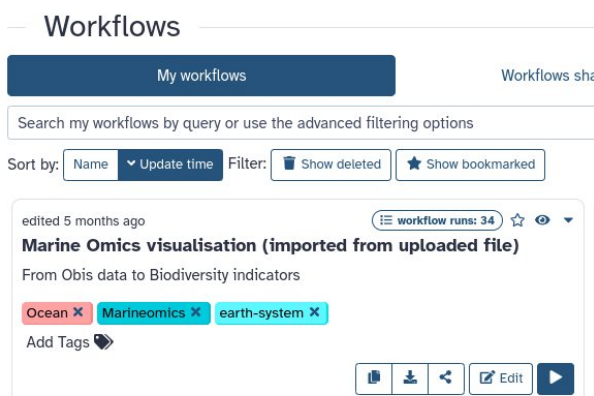
Then click on « Internal Process », and in the category « examind », on « galaxy.deploy »



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

How to find the workflow id ?

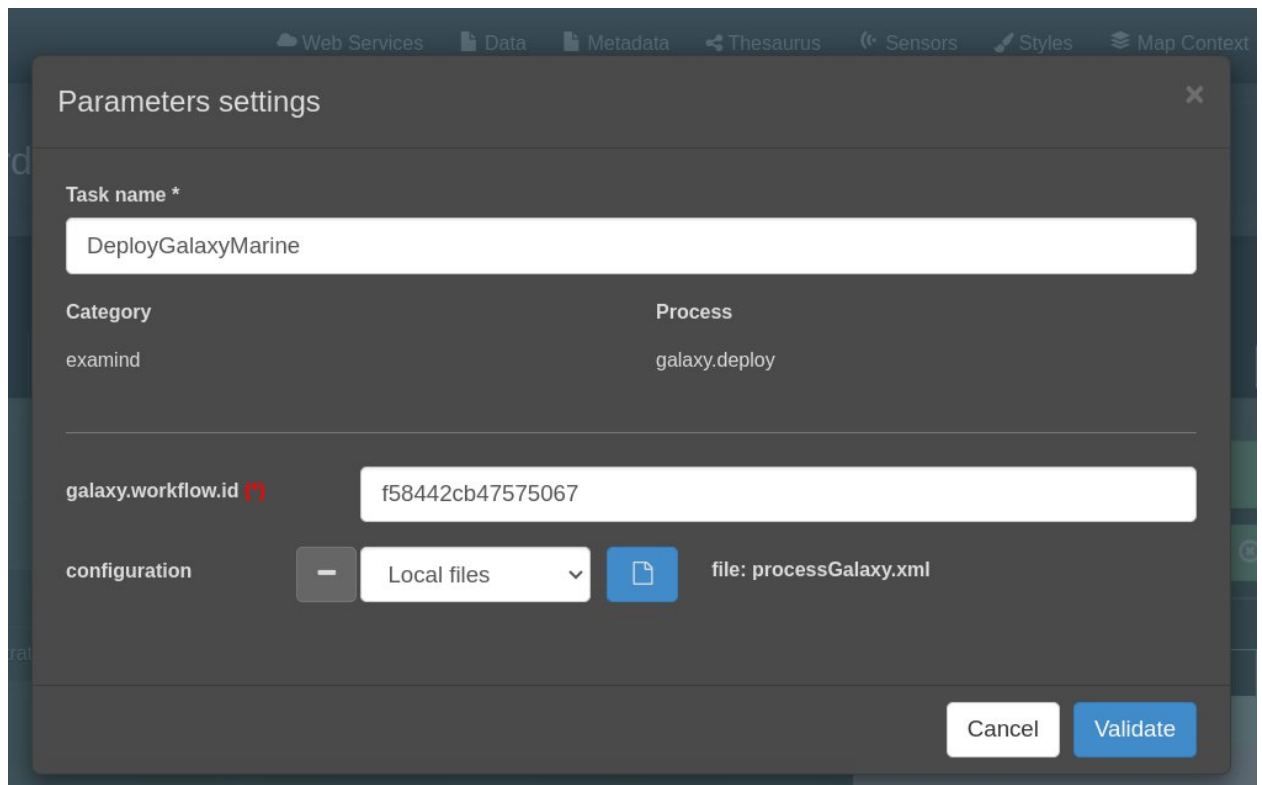
Open galaxy in your browser and go in « Workflows », then click on Edit on your workflow.



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 ».



Parameters settings

Task name *

DeployGalaxyMarine

Category

examind

Process

galaxy.deploy

galaxy.workflow.id

f58442cb47575067

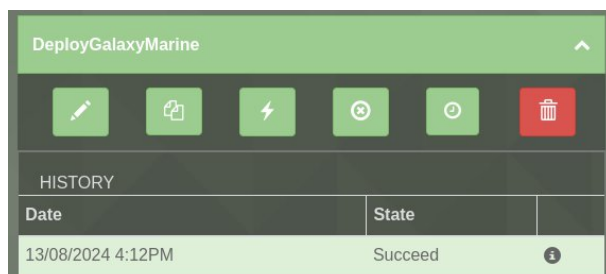
configuration

Local files

file: processGalaxy.xml

Cancel 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.

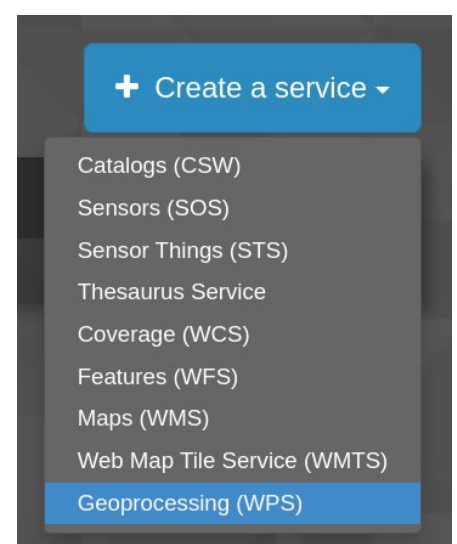


DeployGalaxyMarine	
HISTORY	
Date	State
13/08/2024 4:12PM	Succeed

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 identifier and CLICK ON THE TWO VERSIONS !
(important)

Service description


(*) champs obligatoires


Name (*) WPSTest

Identifier (*) WPSTest 

Tags 

Description


Versions (*) ☒ 1.0.0 ☒ 2.0.0 



Metadata Save



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









Process list

Name  Search

5 available categories of processes

« 1 »

Display :   10

administration		CATEGORY
		 1 process
examind		CATEGORY
		 26 processes
examind-dynamic		CATEGORY
		 2 processes
galaxy.run-5071da78-cb51-4da7-b2f3-436be786dea2		PROCESS
urn:exa:wps:examind::marine:omics		PROCESS

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

In this document you need to change for your workflow :

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

For examples identifiers are like :

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

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

You can choose whatever you want, but all the identifiers of the document need 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 find 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

```
1 {
2   "0":{
3     "species":null,
4     "taxon":null,
5     "lat_min":"40.5",
6     "lat_max":"44",
7     "long_min":"6.8",
8     "long_max":"9.0"
9   },
10  "1":{
11    "complement":"",
12    "delimiter":"",
13    "cut_type_options|cut_element":"-f",
14    "cut_type_options|list":["1","7","8","44","78"]
15  },
16  "2":{
17    "colnames":true,
18    "separator":"t",
19    "longitude":"3",
20    "latitude":"2",
21    "species":"4",
22    "records":"5",
23    "type":"0",
24    "resolution":"9"
25  }
26 }
```

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

Workflow: Marine Omics visualisation (imported from uploaded file) (version: 1)

History Options

Send results to a new history

☐ No

1: OBIS occurrences (Galaxy Version 0.0.2)

☒ Scientific name of the species - optional

Not available.

Genus species format, eg : Scomber scombrus

☒ Taxon ID - optional

Not available.

☒ Input latitude min (+north/-south): - optional

41.5

☒ Input latitude max (+north/-south): - optional

45.0

☒ Input longitude min (+east/-west): - optional

7.5

☒ Input longitude max (+east/-west): - optional

10.0

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

edited 6 months ago workflow runs: 34 ☆ 👁 ▼


Marine Omics visualisation (imported from uploaded file)

From Obis data to Biodiversity indicators

Ocean Marineomics earth-system

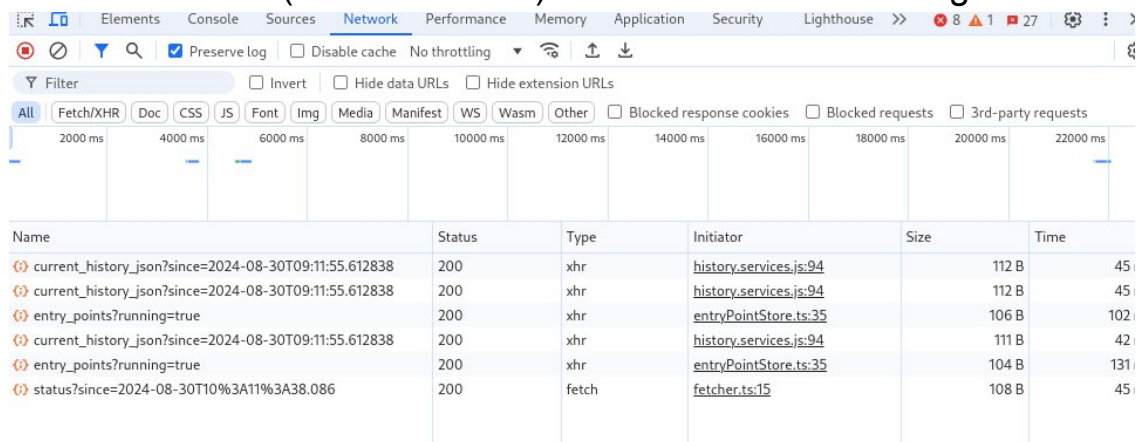
Add Tags 🔖

📄 📥 🔄 Edit ▶



3. Click on « Expand to full workflow form. »

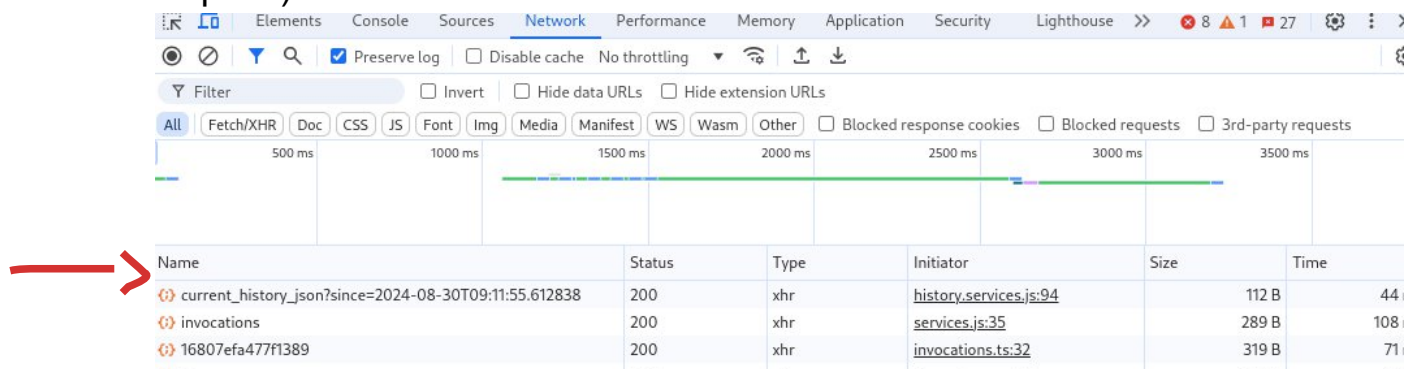
4. Press F12 on your keyboard to open Chrome's 'DevTools', and go in « Network » tab (in the devtools). You will have something like that



Name	Status	Type	Initiator	Size	Time
current_history_json?since=2024-08-30T09:11:55.612838	200	xhr	history.services.js:94	112 B	45
current_history_json?since=2024-08-30T09:11:55.612838	200	xhr	history.services.js:94	112 B	45
entry_points?running=true	200	xhr	entryPointStore.ts:35	106 B	102
current_history_json?since=2024-08-30T09:11:55.612838	200	xhr	history.services.js:94	111 B	42
entry_points?running=true	200	xhr	entryPointStore.ts:35	104 B	131
status?since=2024-08-30T10%3A11%3A38.086	200	fetch	fetcher.ts:15	108 B	45

5. Now you can click on RUN WORKFLOW in Galaxy

6. In the chrome DevTools you will have that (an « invocations » request)



Name	Status	Type	Initiator	Size	Time
current_history_json?since=2024-08-30T09:11:55.612838	200	xhr	history.services.js:94	112 B	44
invocations	200	xhr	services.js:35	289 B	108
16807efa477f1389	200	xhr	invocations.ts:32	319 B	71

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

X

Headers

Payload

Preview

Response

Initiator

Timing

Cookies

Request Payload

view source

▼

{new_history_name: null, history_id: "27b344c8b6cdc87f", replacement_params: {}, use_cached_job: false,...}

batch: true

history_id: "27b344c8b6cdc87f"

inputs: {}

new_history_name: null

▼ parameters: {,...}

▶ 0: {species: null, taxon: null, lat_min: "41.5", lat_max: "45.0", long_min: "7.5", long_max: "10.0"}

▶ 1: {complement: "", delimiter: "", cut_type_options|cut_element: "-f",...}

▶ 2: {colnames: true, separator: "t", longitude: "3", latitude: "2", species: "4", records: "5", type: "0",...}

parameters_normalized: true

replacement_params: {}

require_exact_tool_versions: false

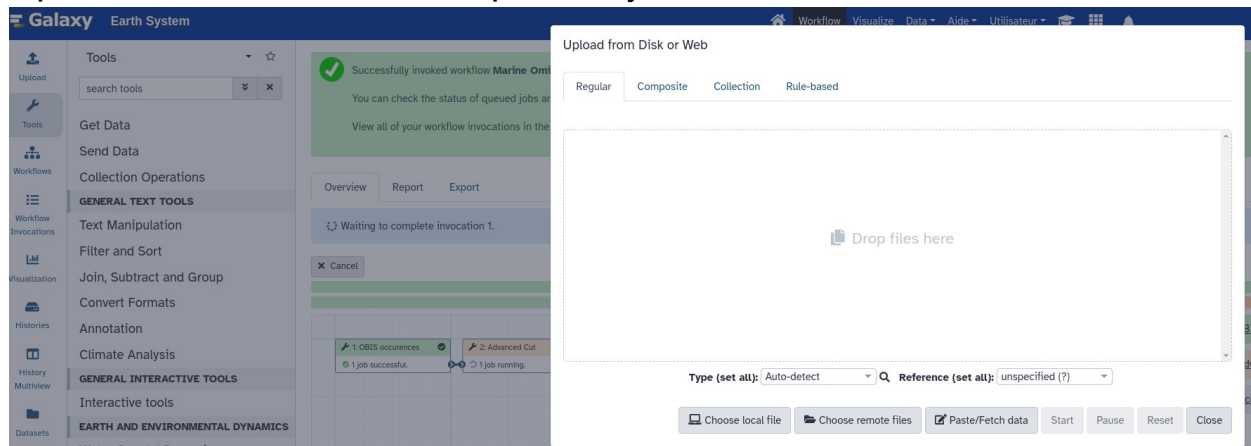
use_cached_job: false

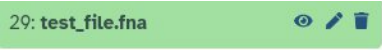
version: 0

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 ($2 - 1 = 1$).