
pangeo-binder Documentation

Pangeo Team

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CHAPTER 1

About Pangeo's Binder

Much like mybinder.org, the Pangeo's BinderHub deployment (binder.pangeo.io) allows users to create and share custom computing environments. The main distinction between the two BinderHubs is that Pangeo's BinderHub allows users to perform scalable computations using [Dask Gateway](#).

For more information on the Pangeo project, check out the [online documentation](#).

Using Pangeo's Binder

Preparing a repository for use with a BinderHub is quite simple. There are two components

1. The environment specification, typically a directory called `binder` with some configuration files (a `Dockerfile`, a `conda environment.yaml`, ...)
2. The content: notebooks, scripts, images, etc. that are present when the binder launches.

Users with fairly standard environment needs can focus solely on the content by using pangeo's "default binder" repository. This is a standard environment with the most commonly-used geoscience packages.

To use this environment with your content, you need to craft a URL. <https://jupyterhub.github.io/nbgitpuller/link?tab=binder&repo=https://github.com/pangeo-gallery/default-binder> provides a tool for creating these URLs (select the "binder" tab). For example, to use the content from <https://github.com/pangeo-data/pangeo-tutorial-gallery> with the default-binder environment on pangeo's binder:

- BinderHub URL: <https://binder.pangeo.io>
- Environment URL: <https://github.com/pangeo-gallery/default-binder>
- Content URL: <https://github.com/pangeo-data/pangeo-tutorial-gallery>

You might want to select a different User Interface, like JupyterLab.

nbgitpuller 0.1b documentation

Search the docs ...

Installation

Automatic Merging Behavior

Options in an nbgitpuller URL

nbgitpuller link generator

Theme by the Executable Book Project

nbgitpuller link generator

Use the following form to create your own **nbgitpuller** links.

[JupyterHub](#) [Launch from Canvas](#) [Binder](#)

`https://binder.pangeo.io/v2/gh/pangeo-gallery/default-binder/master?urlpath=git-pull%3Frepo%3Dhttps%253A%252F%252Fgithub.com%252Fpangeo-data%252Fpangeo-tutorial-gallery%26urlpath%3Dlab%252Ftree%252Fpangeo-tutorial-gallery%252FREADME.md%26branch%3Dmaster`

BinderHub URL

Git Environment Repository URL

The environment repository must have **nbgitpuller** installed.

Git Content Repository URL

File to open

This file or directory from within the repo will open when user clicks the link.

Application to Open

☐ Classic Jupyter Notebook

☒ JupyterLab

☐ RStudio

☐ Custom URL

Pre-populating some fields in the link generator

You can pre-populate some fields in order to make it easier for some users to create their own links. To do so, use the following URL parameters **when accessing this page**:

- hub** is the URL of a JupyterHub
- repo** is the URL of a github repository to which you're linking
- branch** is the branch you wish to pull from the Repository

For example, the following URL will pre-populate the form with the UC Berkeley DataHub as the JupyterHub:

`https://jupyterhub.github.io/nbgitpuller/link?hub=https://datahub.berkeley.edu`

Activating a tab when someone lands on this page

You can also activate one of the tabs in the form above by default when a user lands on this page. To do so, use the **tab=** REST parameter. Here are the possible values:

- ?tab=binder** - activates the Binder tab
- ?tab=canvas** - activates the Canvas tab.

[<< Options in an nbgitpuller URL](#)

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Which generates the final URL: `https://binder.pangeo.io/v2/gh/pangeo-gallery/default-binder/master?urlpath=git-pull%3Frepo%3Dhttps%253A%252F%252Fgithub.com%252Fpangeo-data%252Fpangeo-tutorial-gallery%26urlpath%3Dlab%252Ftree%252Fpangeo-tutorial-gallery%252FREADME.md%26branch%3Dmaster`

See <https://github.com/pangeo-gallery/default-binder> for more.

If pangeo's default image isn't sufficient, see below for building a custom image. For more information on building custom binder images, check out the [BinderHub documentation](#). The sections below outline some common configurations used on Pangeo's BinderHub deployment. Specifically, we'll provide examples of the `.dask/config.yaml` configuration file and the `binder/start` script.

2.1 Using the Pangeo-Binder Cookiecutter

We have put together a cookiecutter repo to help setup binder repositories that can take advantage of Pangeo. This automates the setup of some of the configuration (described in detail below). The usage for this tool is described below.

```
pip install -U cookiecutter
cookiecutter https://github.com/pangeo-data/cookiecutter-pangeo-binder.git
```

After running the cookiecutter command, simply follow the command line instructions to complete setting up your repository. Add some Jupyter Notebooks, configure your environment and push the whole thing to GitHub.

2.2 Configuring Dask

The Pangeo Binder is configured to include a Dask Gateway server, which allows users to create Dask Clusters for distributed computation. To create the clusters, we recommend depending on the `pangeo-notebook` metapackage. This metapackage brings in [several dependencies](#) including `dask-gateway` and `dask-labextension`.

```
# binder/environment.yml
channels:
  - conda-forge
dependencies:
  - pangeo-notebook
  # Additional packages for your analysis...
```

The version of `dask-gateway` pre-configured on the Binder must match the `dask-gateway` in the `environment.yml`. That's currently `dask-gateway=>0.8.0`.

With Dask Gateway installed, your notebooks can create clusters:

```
from dask_gateway import Gateway
from dask.distributed import Client

gateway = Gateway()
cluster = gateway.new_cluster()

client = Client(cluster)
```

You can use `dask_gateway.GatewayCluster.scale()` to scale the number of workers manually, or set the cluster to adaptive mode with `dask_gateway.GatewayCluster.adapt()` to scale up and down based on computational load.

2.3 start script

The start script (e.g. `binder/start`) provides a mechanism to update the user environment at run time. The start script should look roughly like the example below. A few key points about using the start script:

- The start script must end with the `exec "$@"` line.
- The start script should not do any major work (i.e. don't download a large dataset using this script)

```
#!/bin/bash

# Replace DASK_DASHBOARD_URL with the proxy location
sed -i -e "s|DASK_DASHBOARD_URL|/user/${JUPYTERHUB_USER}/proxy/8787|g" binder/
↪ jupyterlab-workspace.json
# Get the right workspace ID
sed -i -e "s|WORKSPACE_ID|/user/${JUPYTERHUB_USER}/lab|g" binder/jupyterlab-workspace.
↪ json

# Import the workspace into JupyterLab
jupyter lab workspaces import binder/jupyterlab-workspace.json \
  --NotebookApp.base_url=user/${JUPYTERHUB_USER}

exec "$@"
```

CHAPTER 3

Examples using Pangeo's Binder

- [Pangeo Example Notebooks](#)