

When using an existing biaflows workflow as template, make sure to update it to the latest versions of both Cytomine-python client and biaflows-utilities (formerly neubiaswg5-utilities) before compiling your Docker image.

These libraries are essential components packaging the functions necessary to download images from a biaflows server, upload annotations from workflow results and compute metrics.

The current versions to use are: Cytomine-python-client 2.7.3 and biaflows-utilities 0.9.1.

To transition to these versions:

1) In the Dockerfile

- **Update** `"cd /Cytomine-python-client && git checkout vxxx"` to `"cd /Cytomine-python-client && git checkout v2.7.3"`
- **Search and replace** `"neubiaswg5-utilities"` > `"biaflows-utilities"`
- **Update** `"cd /biaflows-utilities/ && git checkout tags/vxxx"` to `"cd /biaflows-utilities/ && git checkout tags/v0.9.1"`

2) In the wrapper.py

- **Update imports** `"from neubiaswg5 import ..."` > `"from biaflows import ..."`
- **update class name** `"NeubiasJob"` > `"BiaflowsJob"`

3) For very old workflows: ensure that the Dockerfile initially sets a fixed base image for Python + OS distribution. For instance: **FROM** python:3.6.9-stretch