

Electron Microscopy Image Segmentation using Nipype and OpenCV on an HPC

Torsten Bullmann, Alexander Woodward

Objective: Create electron microscopy image processing pipeline on the SAKI HPC at the Neuroinformatics Japan Center

Method: Jupyter Notebook using OpenCV and Nipype. Batch processing via SunGridEngine. Notebook running on HPC and interfaced via VDI virtual machine running Ubuntu Linux.

Result: Installation of Python libraries, OpenCV, Nipypye etc., via Conda. Setting up Jupyter Notebook on the HPC and port forwarding to access from the VDI virtual machine.

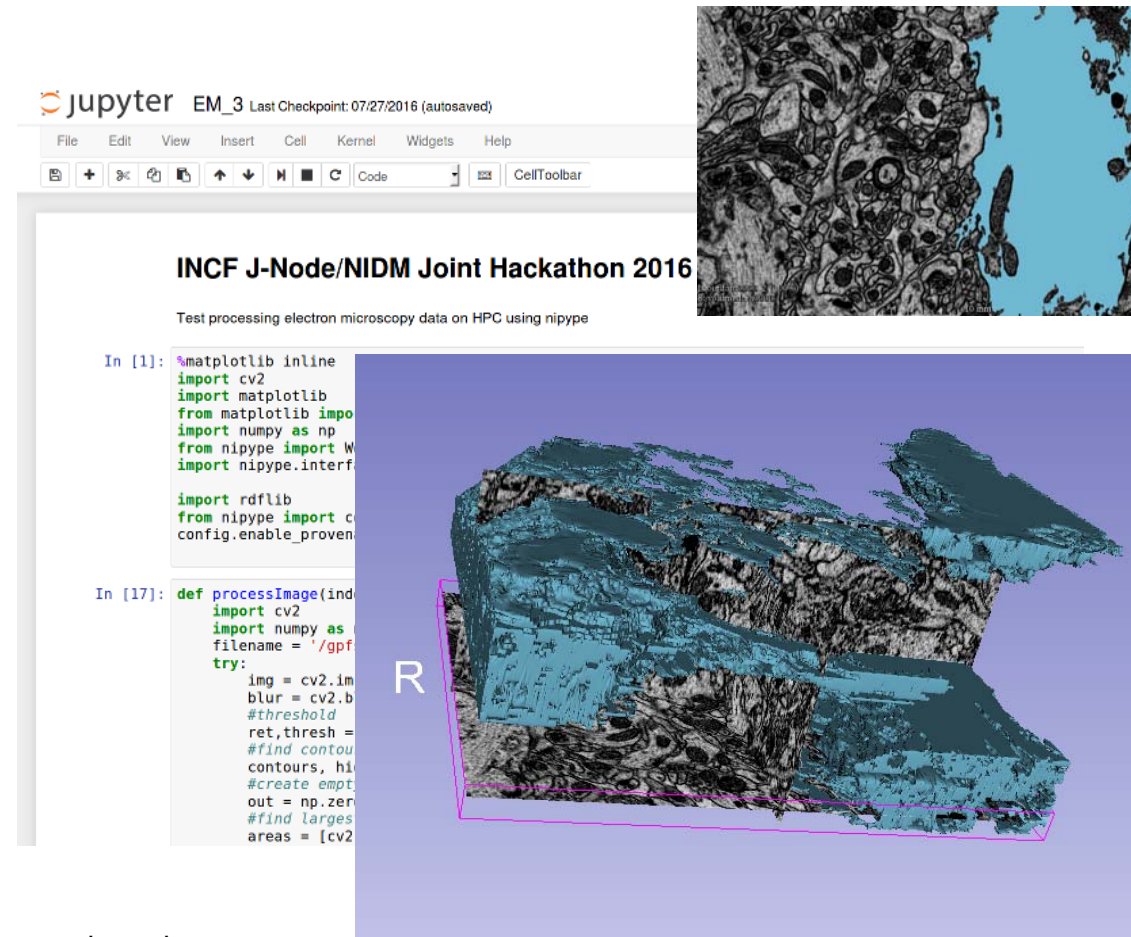
Created example workflow for segmentation of an EM image stack on the SAKI server at Neuroinformatics Japan.

References:

Conda: <http://conda.pydata.org/docs/intro.html>

Nipypye:

<http://nipype.readthedocs.io/en/latest/documentation.html>



The image shows a Jupyter Notebook interface with the following content:

- Header: **jupyter** EM_3 Last Checkpoint: 07/27/2016 (autosaved)
- Menu: File, Edit, View, Insert, Cell, Kernel, Widgets, Help
- Toolbar: +, -, ↺, ↻, ↵, ⏪, ⏩, 🔄, 📄, Code, 🗑️, CellToolBar
- Title: **INCF J-Node/NIDM Joint Hackathon 2016**
- Text: Test processing electron microscopy data on HPC using nipype
- Code Cell [1]:

```
%matplotlib inline
import cv2
import matplotlib
from matplotlib import pyplot as plt
import numpy as np
from nipype import Workflow, Node, Task
import nipype.interfaces

import rdflib
from nipype import config
config.enable_provenance = True
```
- Code Cell [17]:

```
def processImage(input_filename):
    import cv2
    import numpy as np
    filename = input_filename
    try:
        img = cv2.imread(filename)
        blur = cv2.GaussianBlur(img, (5, 5), 0)
        #threshold
        ret, thresh = cv2.threshold(blur, 127, 255, cv2.THRESH_BINARY)
        #find contours
        contours, hierarchy = cv2.findContours(thresh, cv2.RETR_TREE, cv2.CHAIN_APPROX_SIMPLE)
        #create empty list
        out = np.zeros_like(img)
        #find largest contour
        areas = [cv2.contourArea(c) for c in contours]
```
- Image: A 3D visualization of the segmented electron microscopy data, showing a complex, porous structure. A red box highlights a specific region of the structure. A white letter 'R' is visible on the left side of the image.