

SOP details

Title	Installing all necessary software and setup environment
Description	This SOP describes installing the software that is required to run TopoChip Data analysis templates and provides references for learning materials
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1 Purpose

To install Anaconda Navigator on a PC and to download the compressed folder 'DataAnalysis.zip' to your workstation.

2 Principle

This SOP describes the software that is used for analysis of the TopoChip screens and provides a guide to install Anaconda Navigator and install the python environment needed to run the TopoChip data analysis.

3 Important to know before starting

- The TopoChip screen data analysis scripts used at BiS are written in the Python programming language and implemented in Jupyter Notebook. Jupyter Notebook is a web-based interactive programming environment.
- The Python scripts make use of so-called packages. A package is a collection of functions and algorithms, maintained by a community and imported to your script as you need them.
- In order to start using the Jupyter Notebooks, it is advisable to install Anaconda Navigator, a free Python distribution, <https://www.anaconda.com/>. Anaconda automatically installs Jupyter Notebook, Python and most of the Python packages required to run the TopoChip screen data analysis.
- Anaconda Navigator makes use of environments, allowing you to run different versions of Python. We supplied an *environment.yml* file to make sure the dependencies of the TopoChipAnalysis package will not conflict in future updates of Python and any modules.

4 Required materials

4.1 Workplace

This SOP can be performed on your Laptop/Desktop.

4.2 Equipment

(Official requirements from Anaconda website)

- Laptop or desktop with Operating system: Windows 8 or newer, 64-bit macOS 10.13+, or GNU/Linux, including distributions such as Ubuntu and others.
- System architecture: Windows- 64-bit x86, 32-bit x86; MacOS- 64-bit x86; Linux- 64-bit x86, 64-bit Power8/Power9.
- Minimum 5 GB disk space to download and install.
- **To check your system architecture on Windows:** click on *Start* → *Settings* → *System* → *About*. You will find the system architecture under *System Type*.

4.3 Software Resources

Anaconda <https://www.anaconda.com/>

5 Procedure

5.1 Install MATLAB

1. MATLAB can be downloaded from the [TU/e MATLAB page](#).
2. Sign in with your TU/e credentials and follow the installation procedure. During installation don't forget to install the *Image Processing Toolbox*.

5.2 Install Anaconda Individual Edition

1. Visit installation section of the Anaconda official website: <https://docs.anaconda.com/anaconda/install/>
2. Click on the installation link corresponding to your operating system (OS)
3. Follow the official Installation instructions as described on the webpage.

5.3 Getting started with Jupyter notebooks and Python:

1. Start the application “*Anaconda Navigator*” from the application menu via *Start*.
2. The main *Anaconda Navigator* has two main features important to run the TopoScreen data analysis workflow. First, we use a Python 3.8 environment which should be defined under *Environments*:
 - a. Click on *Environments* and find and click the button *Import* at the bottom of the interface.
 - b. When prompted, enter the name for the TopoChip screening environment: *TopoChipAnalysis*.
 - c. For the specification file, click on the folder icon to open the file explorer. Navigate to the TopoChipAnalysis folder and select the *environment.yml* file. Click on ‘open’ and finally click on the ‘import’ button.
 - d. Before launching Jupyter Notebook, make sure that the *Applications on* drop-down menu is set to the TopoChipAnalysis environment you just imported.
3. To start working with *Jupyter Notebooks*, launch the *Jupyter Notebook web environment* (Figure 1B). This will launch your default internet browser and takes you to main page of the *Jupyter Notebook Interface*.

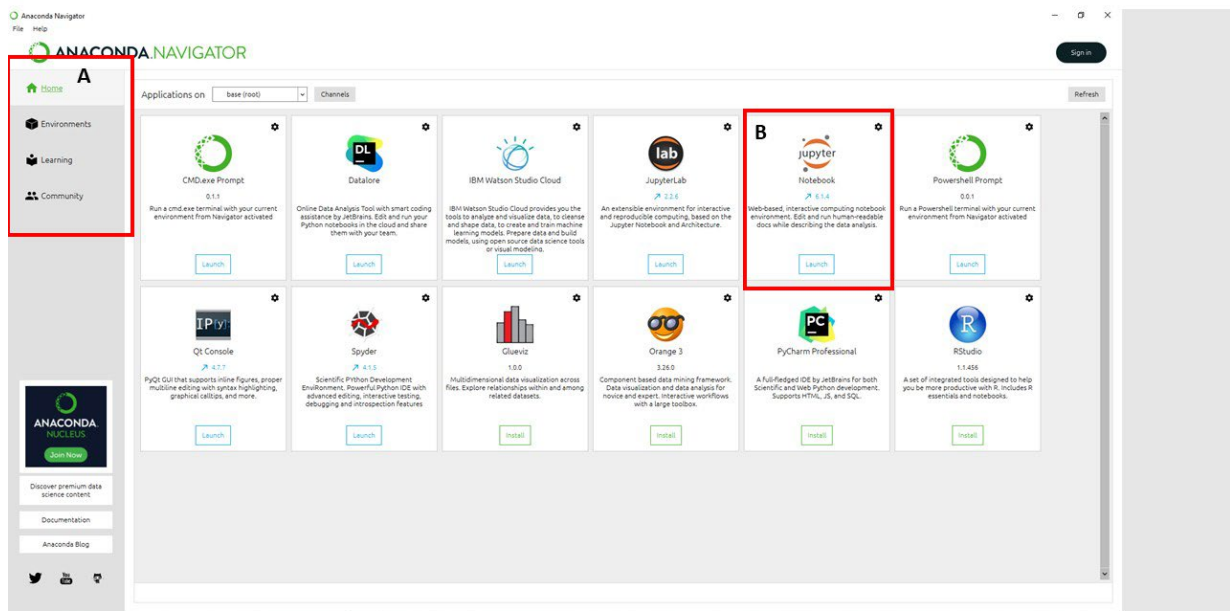


Figure 1: Anaconda menu with the installed applications and the menu navigation, including the environments tab (Red square A). *Jupyter Notebook Interface* can be launched by clicking the launch button (Red square B).

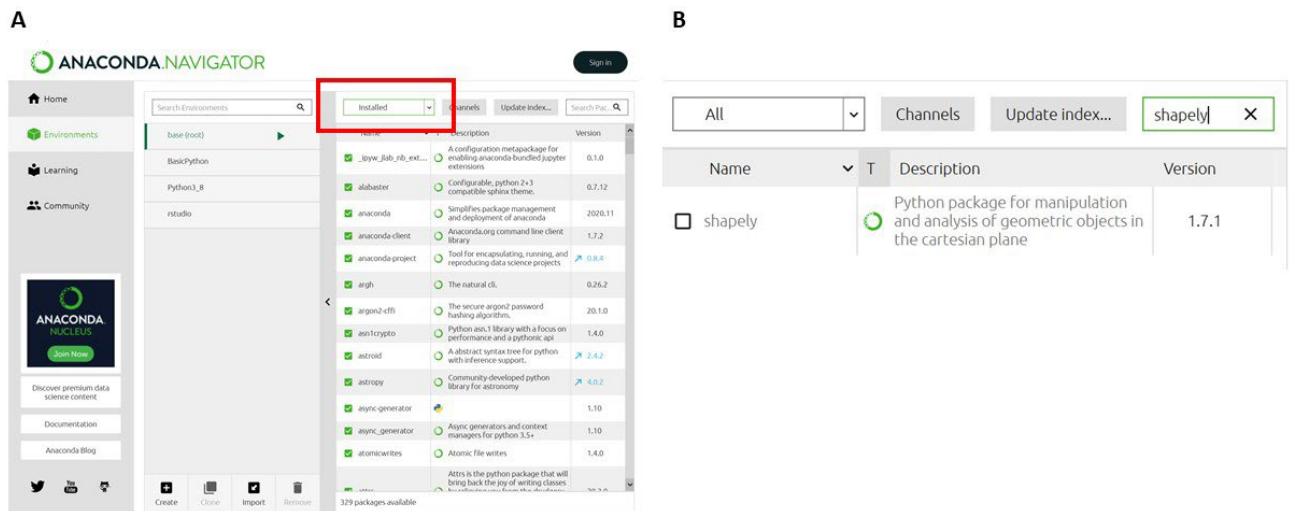


Figure 2: The environments tab with the installed environments (note these differ per user). **A:** the installed packages for the base (root) environment can be viewed by filtering the packages with the 'installed' option (red square). **B:** When a package is not installed, you can search all packages and install the ones you need.

5.4 Download and install NIS Viewer

1. NIS viewer is the commercial software package (Nikon) to view the acquired microscope images.
2. Visit <https://www.microscope.healthcare.nikon.com/products/software/nis-elements/viewer> and download the Windows or iOS installer.
3. After the download is complete, launch and follow the steps in the Nikon NIS Elements Installer.

5.5 Download and install CellProfiler

4. Visit <https://cellprofiler.org/> and download the Windows or iOS installer for CellProfiler 4.1.3.
5. After the download is complete, launch and follow the CellProfiler installer.

5.6 Download and setup the data analysis workflow

1. The data analysis workflow is a folder structure which provides all Jupyter notebooks, Python functions and annotation files needed to analyze the CellProfiler results. The Jupyter notebooks reads and writes the input and output from this folder.
2. **For people from BiS:** Navigate to `\\bmtfiler\Biointerface Science\1 BIS\Research supportive info\TopoChip\01_Topochip screen SOP\BiS TopoChip SOPs\4-analysis\Topochip analysis scripts\` and copy the compressed file (TopoChipAnalysis.zip) to your PC.
For external use: navigate to <https://github.com/cbite/TopoChipAnalysis> and copy the compressed file (TopoChipAnalysis.zip) to your PC.
3. Unzip the folder (right click on the compressed folder and select 7-Zip → extract to) and place the content in your location of choice. For example, the document folder of your project.
4. The data analysis workflow has a predesigned folder structure to make the analysis of the TopoChip as easy as possible. In figure 3, we see the folders and the *Jupyter notebooks* used to analyze your images. It is important to keep this folder structure and to not change any folder names.
5. Before you can start your analysis, you have to place the raw images in the folder “/RawImages/. By default, “/RawImages/” only contains *Chip_1* (Figure 4A). For any additional chips in the screen, new folders have to be created. Here it is important to follow the structure “*Chip_#*” with # the chip number (Figure 4B).
6. Now you have finished the setup for the data analysis workflow and can continue to SOP 4.2.

AnnotationFiles	04/05/2021 15:34	File folder	
DataAnalysis	20/05/2021 15:38	File folder	
RawImages	20/05/2021 11:17	File folder	
SegmentatedImages	20/05/2021 11:17	File folder	
1_alignFeatureIdx20210504.ipynb	20/05/2021 15:56	IPYNB File	7 KB
2_IdentifyOutliers_20210504.ipynb	20/05/2021 15:56	IPYNB File	7 KB
3_RankFeatures_20210512.ipynb	20/05/2021 15:56	IPYNB File	9 KB
4_Train_MLModel_18052021.ipynb	18/05/2021 07:18	IPYNB File	4 KB
AlignFeatureFunctions.py	11/05/2021 15:47	Python File	5 KB
rankFeaturesFunctions.py	20/05/2021 15:44	Python File	12 KB
removeOutliers.py	04/05/2021 12:11	Python File	2 KB
visualizeTopoChip.py	20/05/2021 13:09	Python File	9 KB

Figure 3: The content of the TopoChipAnalysis folder. Here you see the different subfolders, python files, and the Jupyter notebooks (ipynb) used to analyze the raw images obtained from the screening.

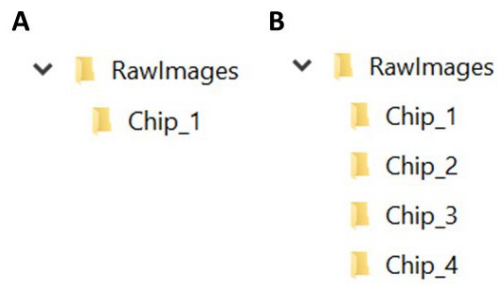


Figure 4: **A:** if you only have one chip, create a folder with the name “Chip_1” and place your raw images in this folder. **B:** If you have multiple chips, create multiple folders per chip and place the raw images to the corresponding folder.