

# TissueMAPS

BIO325: Systems dynamics in cell and developmental biology

Joel Lüthi & Riccardo Murri

## Administration

Divide into two groups for the course:

- ▶ Group 1 goes to the Pelkmans Lab first
- ▶ Group 2 goes to the Brunner Lab first:
- ▶ Group 2 is further divided into sub-groups Fly & Yeast

## Learning Objectives

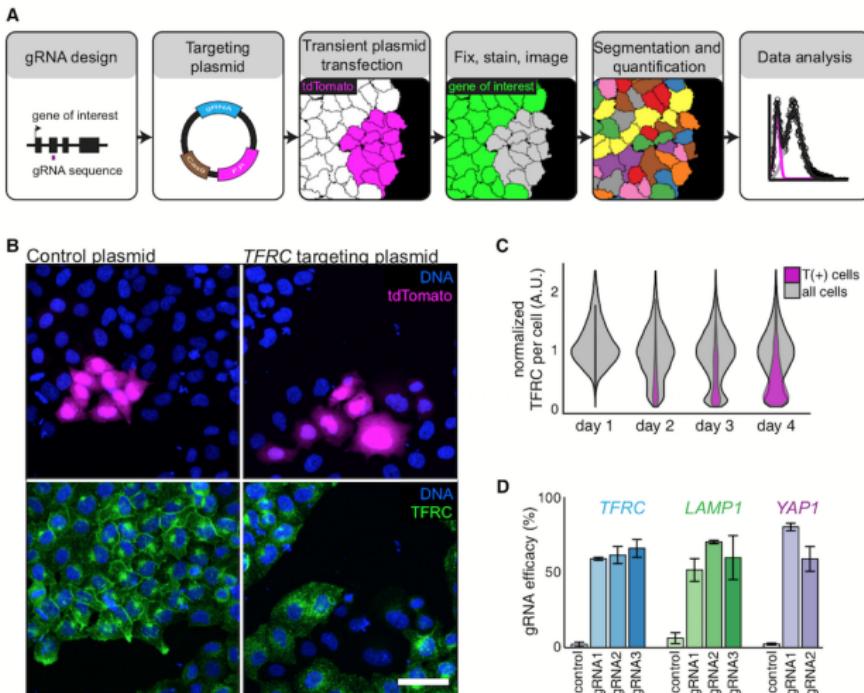
At the end of the day, you will be able to:

1. Understand the use-case for TissueMaps
2. Use TissueMaps to process your image data
3. Process single cell measurements using python
4. Create plots of your data using python

## What Will We Do Today?

- ▶ 9:20 - 10:00 Upload data to TissueMaps & start processing it
- ▶ 10:20 - 11:30 Image processing & cell segmentation in TissueMaps
- ▶ 12:30 - 13:15 Using machine learning & downloading data
- ▶ 13:15 - 13:45 Intro to Python
- ▶ 14:00 - 14:45 Data processing
- ▶ 14:45 - 15:00 Discussing data processing
- ▶ 15:15 - 16:00 Plotting data
- ▶ 16:00 - 16:30 Discussing plotting & wrap up

# Motivation for Doing Image Analysis



de Groot et al., 2018

# What is TissueMaps

- ▶ Cloud platform for image viewing & analysis
- ▶ Scalable & interactive
- ▶ Accessible by web browser

# Your Jupyter Notebook & TissueMaps Server

Get one sheet with instructions & passwords per 2 people.

# Connect to Jupyter Notebook

`http://172.23.X.Y:2000/`

The screenshot shows the Jupyter Notebook web interface. At the top, there is a header with the Jupyter logo and navigation links for 'Logout' and 'Control Panel'. Below the header, there are tabs for 'Files', 'Running', and 'Clusters', with 'Files' being the active tab. A sub-header allows selecting items to perform actions on them, with buttons for 'Upload', 'New', and a refresh icon. The main area displays a list of files and folders in a table format. The columns are 'Name' (with a dropdown arrow) and 'Last Modified'. The table contains the following data:

Name	Last Modified
0	
bio325-intro-to-tissuemaps	un minuto fa
Medium_Yap	21 giorni fa
seaborn-data	11 ore fa
TissueMAPS	un giorno fa

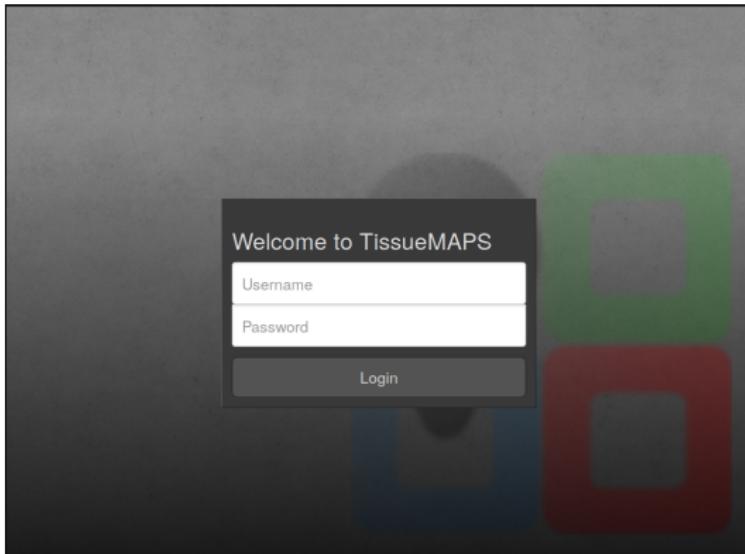
# Start a terminal (to be used later)

The screenshot shows the Jupyter Notebook interface. At the top, there is a navigation bar with the Jupyter logo, 'Logout', and 'Control Panel'. Below the navigation bar, there are three tabs: 'Files' (selected), 'Running', and 'Clusters'. A message 'Select items to perform actions on them.' is displayed above the file tree. The file tree shows a directory structure with the root folder '/'. Inside '/' are five items: '0', 'bio325-intro-to-tissuemaps', 'Medium\_Yap', 'seaborn-data', and 'TissueMAPS'. To the right of the file tree, a context menu is open, listing options for creating new notebooks: 'Upload', 'New', and a dropdown menu with 'Notebook:' (Bash, Python 2, Python 3, R) and 'Other:' (Text File, Folder, Terminal). The URL '172.23.88.49:2009/user/tissuemaps/tree#' is visible at the bottom of the browser window.

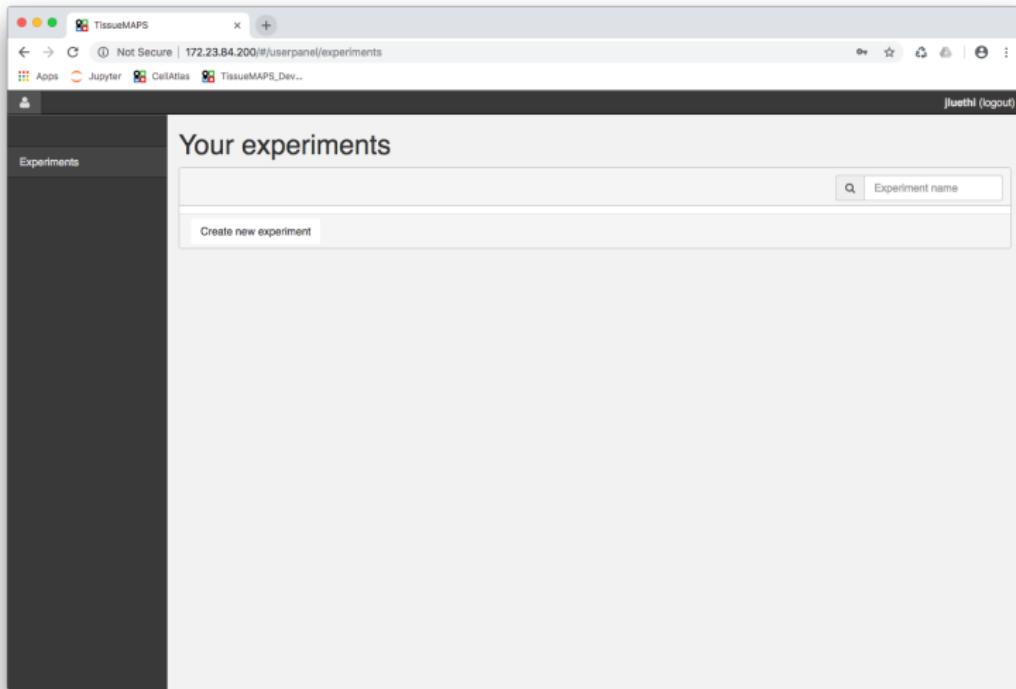
## Connect to TissueMAPS

`http://172.23.X.Y:1000/`

(Same address as Jupyter, but with :1000 at the end.)



# Creating a New Experiment in TissueMaps



# Name Your Experiment

The screenshot shows a web browser window titled "TissueMAPS" with the URL "Not Secure | 172.23.84.200#/userpanel/experiments/create". The page is titled "Create experiment". It contains several input fields:

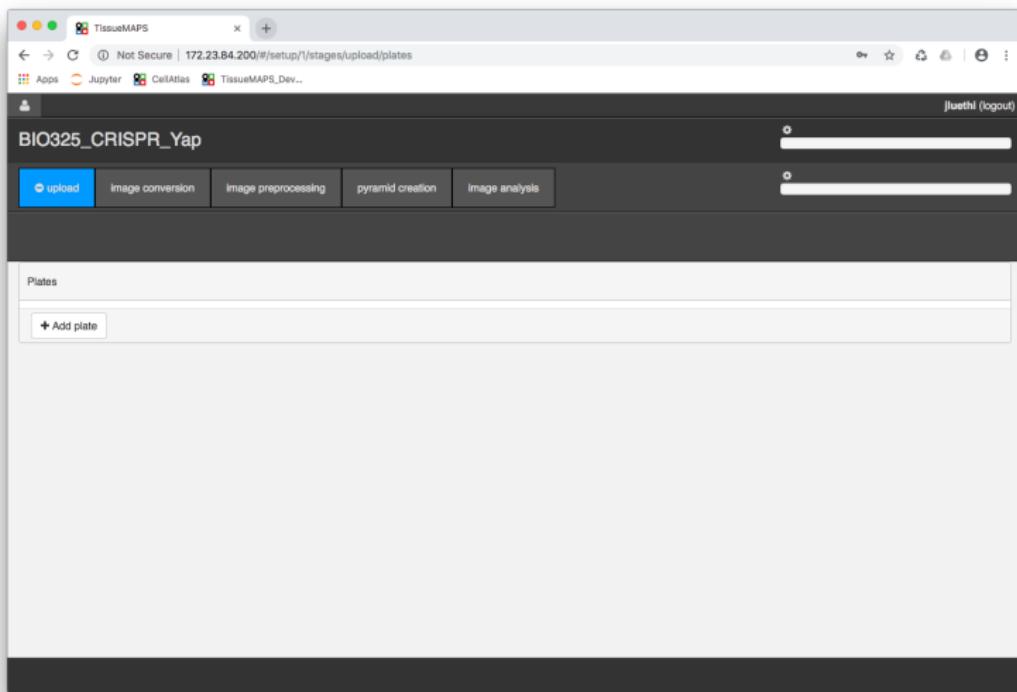
- Experiment name:** BIO325\_CRISPR\_Yap
- Description:** (Empty text area)
- Workflow type:** canonical  
Please specify which workflow type should be used for processing the experiment.
- Plate format:** 384  
Please specify the number of wells per plate. A plate represents a container with multiple reservoirs for different samples (wells) that might be stained independently, but imaged under the same conditions. For consistency, a slide is considered a plate with one well.
- Plate acquisition mode:** basic  
Please specify how images were acquired by the microscope. When "multiplexing", sequential acquisitions are interpreted as different channels, while when "basic" they are treated as time points.
- Microscope type:** celvoyager  
Please specify which microscope was used to acquire the images for this experiment.

A blue "Create experiment" button is located at the bottom left of the form.

# You Made a TissueMaps Experiment!

The screenshot shows a web browser window for the TissueMaps application. The title bar reads "TissueMAPS". The address bar says "Not Secure | 172.23.84.200/#/userpanel/experiments". The top navigation bar includes links for "Apps", "Jupyter", "CellAtlas", and "TissueMAPS\_Dev...". On the right, there is a user icon and the name "Juethi (logout)". The main content area is titled "Your experiments". It features a search bar with a magnifying glass icon and the placeholder "Experiment name". Below the search bar is a list containing one item: "BIO325\_CRISPR\_Yap". To the right of this item are three buttons: a red "Delete" button, a green "View" button, and a blue "Modify" button. At the bottom of the list is a link "Create new experiment".

# Modify Your Experiment



# Create a Plate

The screenshot shows a web-based application window titled "TissueMAPS" with the URL "Not Secure | 172.23.84.200/#/setup/1/stages/upload/plates/create". The top navigation bar includes links for "Apps", "Jupyter", "CellAtlas", and "TissueMAPS\_Dev...". On the right, there is a user profile icon and the name "Juethi (logout)". Below the header, the project name "BIO325\_CRISPR\_Yap" is displayed. A horizontal menu bar contains five tabs: "uploaded" (highlighted in blue), "Image conversion", "Image preprocessing", "pyramid creation", and "Image analysis". The main content area is titled "Create new plate". It features two input fields: "Name" with the value "b1" and "Description" with the placeholder "An optional description of this plate.". A "Create" button is located at the bottom left of this section.

# Create an Acquisition

The screenshot shows a web browser window for the TissueMAPS application. The title bar reads "TissueMAPS". The address bar shows the URL "Not Secure | 172.23.84.200/#/setup/1/stages/upload/plates/1/acquisitions/create". The navigation bar includes links for "Apps", "Jupyter", "CellAtlas", and "TissueMAPS\_Dev...". On the right side of the header, there is a user icon and the name "Juethl (logout)". Below the header, the page title is "BIO325\_CRISPR\_Yap". A horizontal menu bar contains five items: "uploaded" (highlighted in blue), "Image conversion", "Image preprocessing", "pyramid creation", and "Image analysis". The main content area displays the following message: "Plate: p1 (NOT READY FOR PROCESSING)". Below this, there is a section titled "Create new acquisition" with two input fields: "Name" containing "a1" and "Description" containing an empty field. A "Create" button is located at the bottom left of this section.

# Getting Data into TissueMaps

```
jluethi@pelkmanslab-slurm-master-001:~$ tm_client -h
Joel — ssh cluster — 127x39
jluethi@pelkmanslab-slurm-master-001:~$ tm_client -h
usage: tm_client [-h] [-H HOST] [-P PORT] [-u USERNAME] [-p PASSWORD] [-v]
                  {tools,workflow,jtproject,experiment,plate,well,site,acquisition,microscope-file,channel,object-type,feature,feature-values,segmentation,channel-image}
                  ...
TissueMAPS REST API client (version: 0.3.3).

optional arguments:
  {tools,workflow,jtproject,experiment,plate,well,site,acquisition,microscope-file,channel,object-type,feature,feature-values,segmentation,channel-image}
      resources
      tools          tools resources
      workflow       workflow resources
      jtproject     jterator project resources
      experiment    experiment resources
      plate         plate resources
      well          well resources
      site          site resources
      acquisition   acquisition resources
      microscope-file microscope file resources
      channel        channel resources
      object-type   object type resources
      feature       feature resources
      feature-values feature values resources
      segmentation  segmentation resources
      channel-image channel image resources

optional arguments:
  -h, --help            show this help message and exit
  -H HOST, --host HOST  TissueMAPS server host (default: localhost)
  -P PORT, --port PORT  TCP port number on which the server listens (default: 80)
  -u USERNAME, --user USERNAME
                        name of TissueMAPS user (default: jluethi)
  -p PASSWORD, --password PASSWORD
                        password of TissueMAPS user (default is the value of
                        environmental variable TM_PASSWORD)
  -v, --verbosity       increase logging verbosity
```

# Tell TmClient Who You are

```
jluethi@pelkmanslab-slurm-master-001:~$ tm_client -H 172.23.XX.YY -u clever_student -p myPassword
microscope-file -h
usage: tm_client microscope-file [-h] --EXPERIMENT {ls,upload,register} ...

Access microscope file resources.

positional arguments:
  {ls,upload,register}  access methods
    ls                list microscope files
    upload            upload microscope files
    register         register microscope files

optional arguments:
  -h, --help          show this help message and exit
  -e EXPERIMENT, --experiment EXPERIMENT
                      name of the experiment
jluethi@pelkmanslab-slurm-master-001:~$
```

# Tell TmClient What You Want to Do

```
jluethi@pelkmanslab-slurm-master-001:~$ tm_client -H 172.23.XX.YY -u clever_student -p myPassword microscope-file -e BIO325_CRISPR_Yap upload -h
usage: tm_client microscope-file upload [-h] -p PLATE -a ACQUISITION
                                         [--convert [FMT]] [--delete]
                                         [--directory] [--parallel [NUM]]
                                         [--retries NUM] [--no-retry]
                                         path

Upload microscope image and metadata files.

positional arguments:
  path                  path to file or directory to upload

optional arguments:
  -h, --help            show this help message and exit
  -p PLATE, --plate PLATE
                        name of the plate
  -a ACQUISITION, --acquisition ACQUISITION
                        name of the acquisition
  --convert [FMT]        Convert files to the specified format during upload.
                        The format is specified by giving the converted file's
                        extension, e.g., `png`, `jpeg`, etc. If `--convert` is
                        given without specifying a format, images files will
                        be converted to PNG. The conversion process depends on
                        the availability of ImageMagick's `convert` program --
                        if it cannot be executed, file upload will fail.
  --delete              Delete files after uploading. USE WITH CAUTION!
  --directory           Unused. Retained for backwards-compatibility only.
  --parallel [NUM]       Use NUM parallel processes for upload (default: 1). If
                        NUM is omitted or 0, the degree of parallelism is
```

# Tell TmClient Where the Images Are



```
jluethi@pelkmanslab-slurm-master-001:~$ tm_client -H 172.23.XX.YY -u clever_student -p myPassword microscope-file -e BIO325_CRISPR_Yap upload -p p1 -a a1 --directory ~/BIO325_Yap_Data -h
usage: tm_client microscope-file upload [-h] -p PLATE -a ACQUISITION
                                         [--convert [FMT]] [--delete]
                                         [--directory] [--parallel [NUM]]
                                         [--retries NUM] [--no-retry]
                                         path

Upload microscope image and metadata files.

positional arguments:
  path                  path to file or directory to upload

optional arguments:
  -h, --help            show this help message and exit
  -p PLATE, --plate PLATE
                        name of the plate
  -a ACQUISITION, --acquisition ACQUISITION
                        name of the acquisition
  --convert [FMT]        Convert files to the specified format during upload.
                        The format is specified by giving the converted file's
                        extension, e.g., 'png', 'jpeg', etc. If '--convert' is
                        given without specifying a format, images files will
                        be converted to PNG. The conversion process depends on
                        the availability of ImageMagick's 'convert' program --
                        if it cannot be executed, file upload will fail.
  --delete              Delete files after uploading. USE WITH CAUTION!
  --directory           Unused. Retained for backwards-compatibility only.
```

# Upload Completed

The screenshot shows a web-based application window titled "TissueMAPS". The address bar indicates the URL is "Not Secure | 172.23.84.200/#/setup/1/stages/upload/plates/1". The top navigation bar includes links for "Apps", "Jupyter", "CellAtlas", and "TissueMAPS\_Dev...". On the right side, there is a user profile icon and the text "Juethil (logout)". Below the header, the project name "BIO325\_CRISPR\_Yap" is displayed. A progress bar at the top right shows the status as "TERMINATED". A horizontal menu bar contains five items: "uploaded" (highlighted in blue), "Image conversion", "Image preprocessing", "pyramid creation", and "Image analysis". The main content area is titled "Plate: p1 (READY FOR PROCESSING)". It contains a section for "Acquisitions" with a single entry: "a1 (COMPLETE) - 400 files". To the right of this entry is a red "Delete" button. Below the acquisition list is a button labeled "+ Add acquisition".

# Add Metadata about the Experiment

The screenshot shows a web-based application window titled "TissueMAPS" with the URL "Not Secure | 172.23.84.200/#/setup/1/stages/image\_conversion/steps/metaconfig". The top navigation bar includes links for "Apps", "Jupyter", "CellAtlas", and "TissueMAPS\_Dev...". A user icon and "Juethil (logout)" are also present. Below the header, the experiment name "BIO325\_CRISPR\_Yap" is displayed. A horizontal menu bar contains several tabs: "upload", "image conversion" (which is highlighted in blue), "image preprocessing", "pyramid creation", "image analysis", "metaextract" (disabled), "metaconfig" (highlighted in blue), and "imextract".

**Configuration of image metadata**

Configuration of extracted OMEXML metadata and integration with additional microscope-specific information about the image acquisition process.

**Batch arguments**  
Arguments that control how data is partitioned into computational jobs.

**mip**  perform maximum intensity projection along z axis

**n\_horizontal**  
number of images along the horizontal axis of the stitched well overview mosaic image  
(optional)

**n\_vertical**  
number of images along the vertical axis of the stitched well overview mosaic image  
(optional)

**regex**

**Submission arguments**  
Arguments that control how computational jobs are submitted to the cluster.

**cores**  
number of cores that should be allocated to each "run" job (may be increased in case memory requirements of a job exceed resources of a single core)

**duration**  
walltime that should be allocated to a each "run" job in the format "HH:MM:SS" (may need to be adapted depending on the choice of batch size)

**memory**  
amount of memory in megabytes that should be allocated to each "run" job

**Buttons:** Submit, Resume, Resubmit, Kill, Save

# Define settings for the Pyramid / Image Browser

BIO325\_CRISPR\_Yap

pyramid creation

illuminate

batch\_size  
number of image files that should be processed per job  
100

clip   
whether images intensities should be clipped

clip\_percent  
threshold percentile at which image intensities should be clipped  
99.9

clip\_value  
threshold value at which image intensities should be clipped (defaults to 99.99th percentile; the set value overwrites calculated percentile)  
(optional)

illumcorr   
whether images should be corrected for illumination artifacts

illumcorr\_exceptions

Submit    Resume    Resubmit    Kill    Save

# Submit the Pipeline & Enjoy Your Break

BIO325\_CRISPR\_Yap

upload image conversion image preprocessing pyramid

Pyramid image builder

Creation of pyramids for interactive, web-based visualization of images.

**Batch arguments**

Arguments that control how data is partitioned into computational jobs.

**align**  whether images should be aligned between multiplexing cycles

**batch\_size** number of image files that should be processed per job  
100

**clip**  whether images intensities should be clipped

**clip\_percent** threshold percentile at which image intensities should be clipped  
99.9

**Submission arguments**

Arguments that control how computational jobs are submitted to the cluster.

**cores** number of cores that should be allocated to each "run" job (may be increased in case memory requirements of a job exceed resources of a single core)  
1

**duration** walltime that should be allocated to a each "run" job in the format "HH:MM:SS" (may need to be adapted depending on the choice of batch size)  
06:00:00

**memory** amount of memory in megabytes that should be allocated to each "run" job  
3133

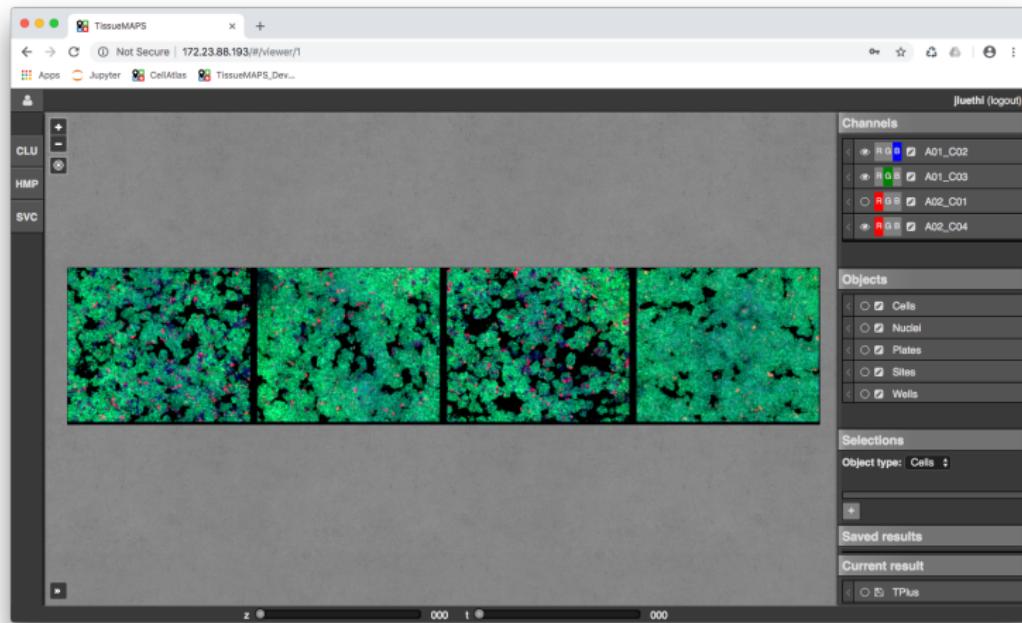
Submit Resume Resubmit Kill Save

Warning

Do you really want to submit the workflow?

Cancel Ok

# The Image Viewer Gives You an Overview of Your Experiment



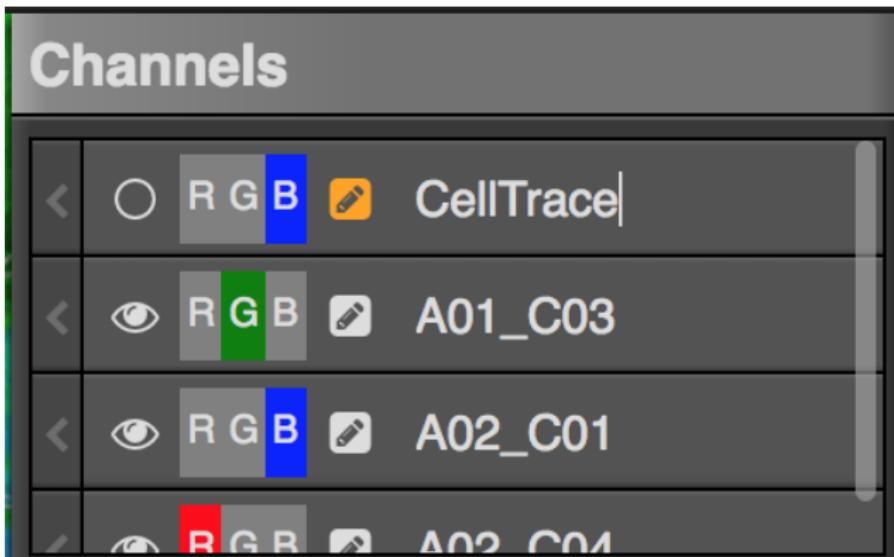
## Rename Your Channels

A01\_C02 → CellTrace

A02\_C01 → DAPI

A01\_C03 → Yap

A02\_C04 → Plasmid



# Go into the Image Processing Pipeline

The screenshot shows a web browser window titled "TissueMAPS" with the URL "Not Secure | 172.23.88.193/#/setup/l/stages/image\_analysis/steps/iterator". The page displays a pipeline engine interface for a project named "BIO325\_CRISPR\_Yap". The pipeline consists of several steps: "upload", "image conversion", "image preprocessing", "pyramid creation", "image analysis", and "iterator". The "image analysis" step is currently selected. Each step has a status indicator: "TERMINATED" with a green bar. The "iterator" step is highlighted in blue. On the right side, there is a user profile for "Jluethi (logout)". Below the pipeline, there are two sections: "Batch arguments" and "Submission arguments". The "Batch arguments" section contains a "batch\_size" input field set to "10" with an "Edit Pipeline" button. A red arrow points to the "Edit Pipeline" button. The "Submission arguments" section contains a "cores" input field set to "1" and a "duration" input field set to "06:00:00". At the bottom, there are buttons for "Submit", "Resume", "Resubmit", "Kill", and "Save".

# A Good Pipeline for Today

Input	
Select <b>channels</b> that should be available in the pipeline:	
DAPI	
Correct illumination <input checked="" type="checkbox"/>	
CellTrace	
Correct illumination <input checked="" type="checkbox"/>	
Yap	
Correct illumination <input checked="" type="checkbox"/>	
Transfection	
Correct illumination <input checked="" type="checkbox"/>	
<input type="button" value="+ Add"/>	<input type="button" value="Remove"/>
<input type="button" value="List jobs"/>	

Pipeline	
Define the <b>modules</b> and the order in which they should be processed:	
<input checked="" type="checkbox"/>	smooth_DAPI
<input checked="" type="checkbox"/>	threshold_otsu
<input checked="" type="checkbox"/>	filter_nuclei
<input checked="" type="checkbox"/>	separate_clumps
<input checked="" type="checkbox"/>	label_nuclei
<input checked="" type="checkbox"/>	register_objects
<input checked="" type="checkbox"/>	segment_secondary
<input checked="" type="checkbox"/>	register_objects_Cells
<input checked="" type="checkbox"/>	measure_intensity_DAPI
<input checked="" type="checkbox"/>	measure_intensity_CellTrace
<input checked="" type="checkbox"/>	measure_intensity_2_Yap
<input checked="" type="checkbox"/>	measure_intensity_3_Transfection
<input checked="" type="checkbox"/>	measure_morphology_Cells
<input checked="" type="checkbox"/>	measure_morphology_1_Nuclei
<input checked="" type="checkbox"/>	measure_texture_Transfection

Output	
Select <b>objects</b> that should be saved:	
Nuclei	
Represent as polygons <input checked="" type="checkbox"/>	
Cells	
Represent as polygons <input checked="" type="checkbox"/>	

# Resubmission

- ▶ Batch Size 15
- ▶ Resubmit from image\_analysis

The screenshot shows the TissueMAPS software interface. At the top, there's a navigation bar with tabs like 'upload', 'Image conversion', 'Image analysis', and 'Iterator'. The 'Iterator' tab is currently selected, indicated by a blue background. A red arrow points to the 'batch\_size' input field in the 'Batch arguments' section, which contains the value '15'. In the center, a modal dialog titled 'Resubmit' is open. It has a dropdown menu labeled 'Stage from which workflow should be resubmitted:' with 'image\_analysis' selected. Another red arrow points to this dropdown. Below the dropdown are 'Cancel' and 'OK' buttons. In the bottom right corner of the main window, there's a status bar showing 'Jluethi (logout)'.

BIO325\_CRISPR\_Yap

Resubmit

Stage from which workflow should be resubmitted:  
image\_analysis

Cancel OK

Batch arguments

Arguments that control how data is partitioned into computational jobs.

batch\_size  
number of sites that should be processed per job  
15

Submission arguments

Arguments that control how computational jobs are submitted to the cluster.

cores  
number of cores that should be allocated to each "run" job (may be increased in case memory requirements of a job exceed resources of a single core)  
1

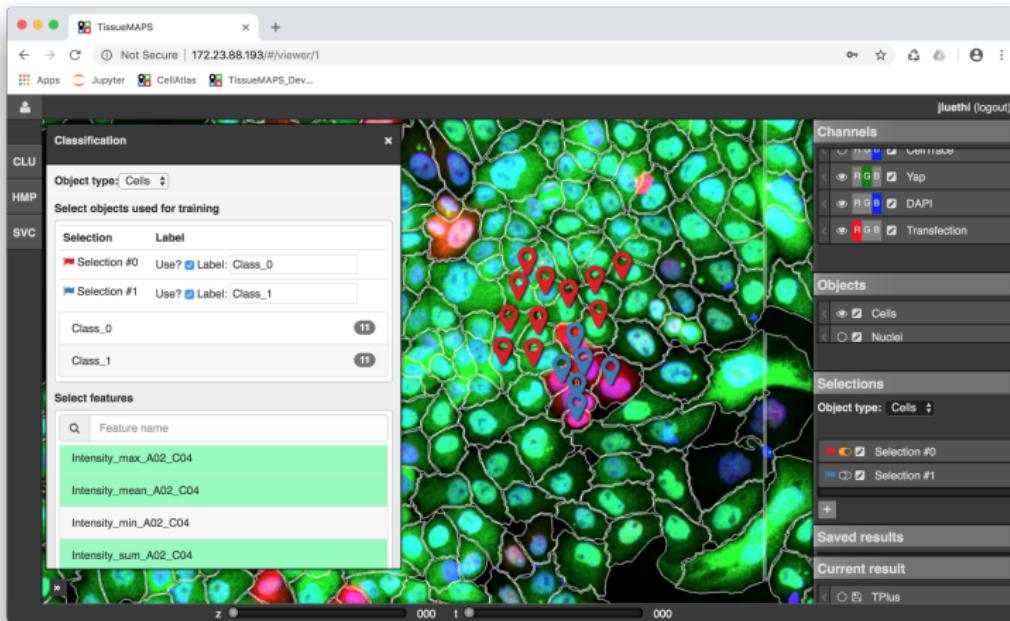
duration  
walltime that should be allocated to each "run" job in the format "HH:MM:SS" (may need to be adapted depending on the choice of batch size)  
06:00:00

Submit Resume Resubmit Kill Save

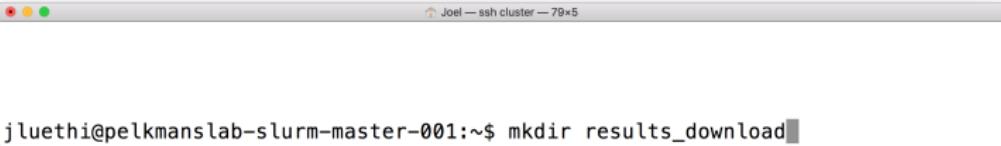
## What Will We Do Today?

- ▶ 9:20 - 10:00 Upload data to TissueMaps & start processing it
- ▶ 10:20 - 11:30 Image processing & cell segmentation in TissueMaps
- ▶ 12:30 - 13:15 Using machine learning & downloading data
- ▶ 13:30 - 14:00 Intro to Python
- ▶ 14:00 - 14:45 Data processing
- ▶ 14:45 - 15:00 Discussing data processing
- ▶ 15:15 - 16:00 Plotting data
- ▶ 16:00 - 16:30 Discussing plotting & wrap up

# Training a Classifier to Separate Transfected from Non-Transfected Cells



# Make a Directory for Your Results on Your Jupyter Machine



A screenshot of a terminal window titled "Joel — ssh cluster — 79x5". The window has a standard OS X title bar with red, yellow, and green buttons. The main area of the terminal shows a command being entered: "jluethi@pelkmanslab-slurm-master-001:~\$ mkdir results\_download". The cursor is positioned at the end of the command line.

# Download Results on Your Jupyter Machine

```
jluethi@pelkmanslab-slurm-master-001:~$ tm_client -H 172.23.XX.YY -u clever_student -p myPassword  
feature-values -e BIO325_CRISPR_Yap download -o Cells --directory ~/results_download -h  
usage: tm_client feature-values download [-h] -o OBJECT-TYPE  
                                         [--directory DIRECTORY]  
                                         [--parallel [NUM]]  
  
Download feature values for segmented objects as well as the corresponding  
metadata.  
  
optional arguments:  
  -h, --help            show this help message and exit  
  -o OBJECT-TYPE, --object-type OBJECT-TYPE  
                        name of the objects type  
  --directory DIRECTORY  
                        directory where download should be stored (defaults to  
                        temporary directory)  
  --parallel [NUM]      Use NUM parallel processes for download (default: 1).  
                        If NUM is omitted or 0, the degree of parallelism is  
                        proportional to the number of available CPUs.  
jluethi@pelkmanslab-slurm-master-001:~$
```