
TissUUmaps

Release 3.0

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This page hosts the documentation for TissUMaps 3.0.

For more information on the TissUMaps project, including video tutorials and demos, visit our website: <https://tissuums.github.io>.

Work in progress!

This page is mostly empty for now. We are working actively on writing this documentation, more content will be available soon!

INTRODUCTION

1.1 About TissUMaps

[TissUMaps](#) is a browser-based tool for GPU-accelerated visualization and interactive exploration of 10^7+ datapoints overlaying tissue samples. Users can visualize markers and regions, explore spatial statistics and quantitative analyses of tissue morphology, and assess the quality of decoding in situ transcriptomics data. TissUMaps provides instant multi-resolution image viewing, can be customized, shared, and also integrated in Jupyter Notebooks. We envision TissUMaps to contribute to broader dissemination and flexible sharing of large-scale spatial omics data.

Currently, microscopy data can be cumbersome to share: physically transferring the images is often necessary and dedicated software must be installed. Instead, researchers can now share their findings with a simple link to a website running TissUMaps. The images are loaded in real time, together with annotations, markers, and masks that may also be modified by the user. We also provide tools for quality control and image processing. The software is designed to display and interact with images at multiple resolutions and large numbers of markers, especially data from spatially resolved omics techniques and tissue atlases. TissUMaps is compatible with many different bioimage informatics tools, and provides new ways to develop insights when exploring and sharing data.

You can access the [TissUMaps project gallery](#) with interactive examples to explore data from in situ sequencing and spatial transcriptomics experiments and view localized quantification of cell and tissue morphology, including links to publications. For seeing examples of TissUMaps compatibility with other platforms you can access the [tutorials page](#).

1.2 Installation

[TissUMaps](#) is a browser-based tool for fast visualization and exploration of millions of data points overlaying a tissue sample. TissUMaps can be used as a web service or locally in your computer, and allows users to share regions of interest and local statistics.

1.2.1 Windows installation

1. Download the Windows Installer from [the last release](#) and install it. Note that the installer is not signed yet and may trigger warnings from the browser and from the firewall. You can safely pass these warnings.

1.2.2 PIP installation (for Linux and Mac)

1. Install libvips for your system: <https://www.libvips.org/install.html>

An easy way to install libvips is to use an [Anaconda](#) environment with libvips:

```
conda create -y -n tissuumaps_env -c conda-forge python=3.9 libvips
conda activate tissuumaps_env
```

2. Install the TissUMaps library using pip:

```
pip install "TissUMaps[full]"
```

3. Start the TissUMaps user interface:

```
tissuumaps
```

4. Or start TissUMaps as a local server:

```
tissuumaps_server path_to_your_images
```

And open <http://127.0.0.1:5000/> in your favorite browser.

1.3 Citing TissUMaps

Please cite our [preprint](#) on bioRxiv if using TissUMaps in your work:

TissUMaps 3: Interactive visualization and quality assessment of large-scale spatial omics data *Nicolas Pielawski, Axel Andersson, Christophe Avenel, Andrea Behanova, Eduard Chelebian, Anna Klemm, Fredrik Nysjö, Leslie Solorzano, Carolina Wählby* bioRxiv 2022.01.28.478131; doi: <https://doi.org/10.1101/2022.01.28.478131>

1.4 Changelog

1.4.1 3.0.8.5

- Minor fixes.

1.4.2 3.0.8.4

- Add tiling to viewport capture for higher resolution output
- Increase resolution of markers on high resolution devices
- Fix jumps on pan with mouse gesture (mobile)
- Add fix for bright image canvas on Safari
- Add an option to remove markers' outlines.

1.4.3 3.0.8.3

- Fix png artifact in Firefox, by generating jpg tiles.

1.4.4 3.0.8.2

- Add high resolution capture of viewport, up to 4096x4096 pixels.

1.4.5 3.0.8.1

- Fix multiple dataset alignment when no background image

1.4.6 3.0.8

- Fix black images generated by VIPS
- Fix Linux and Mac open of captures
- Auto save datasets as buttons when saving tmap projects
- Add mpp (microns per pixel) option in tmap files, to add scale bar to viewer
- Make region line thickness depend on zoom level
- Add compatibility with JupyterLab
- Add opacity per marker option

1.4.7 3.0.7

- Add menu to load plugins through an update-site

1.4.8 3.0.6

- Fix multiple plugins opening always last plugin
- Move to OpenSeadragon 3.0.0
- Add tooltip format in Advanced Settings
- Add drag and drop to open CSV files and images
- Add “Add layer” button for flask version
- Add viewport capture

1.4.9 3.0.5

- Move csv loading to Papa Parse streaming, to allow better memory management

1.4.10 3.0.4

- Add filtering of markers

1.4.11 3.0

- Add tissuumaps.jupyter module

GETTING STARTED

2.1 Images

2.1.1 Supported image formats

TissUMaps can read whole slide images in any format recognized by the OpenSlide library:

- Aperio (.svs, .tif)
- Hamamatsu (.ndpi, .vms, .vmu)
- Leica (.scn)
- MIRAX (.mrxs)
- Philips (.tiff)
- Sakura (.svslide)
- Trestle (.tif)
- Ventana (.bif, .tif)
- Generic tiled TIFF (.tif)

TissUMaps will automatically convert any other format into a pyramidal tiff (in a temporary `.tissumaps` folder created in the original image folder) using `vips`.

If your image fails to open, try converting it to `tif` format using an external tool.

2.1.2 Load images

2.1.3 Apply filters

2.2 Markers

2.2.1 Supported marker format

TissUMaps can read CSV (Comma Separated Values) files with a header row, and at least spatial coordinate columns (X and Y). CSV files are not limited in the number of columns or number of rows. Other columns can contain information for displaying markers (key to group markers, color, size, shape, piecharts, etc.)

CSV files can be exported from any spreadsheet program, or any programming language (Python, R, etc.)

2.2.2 Load markers

2.2.3 Markers settings

File and coordinates

Render options

Advanced options

Table of markers

2.3 Regions

2.3.1 Supported region formats

TissUUmapi can read and write region files in the [GeoJSON](#) format.

Only a subset of the GeoJSON format is supported, as TissUUmapi uses only polygonal regions:

Main types:

- Feature
- FeatureCollection
- GeometryCollection

Geometries:

- Polygon
- Multipolygon

The coordinate system must be the same as the image and marker coordinate systems.

2.3.2 Draw Regions

2.3.3 Analyze Regions

2.3.4 Load Regions

2.3.5 Export Regions

2.4 Projects

2.4.1 Saving and loading projects

2.4.2 The tmap file format

2.5 Exporting screenshots

2.6 Plugins

2.6.1 Load plugins

2.6.2 Make your own plugin

Download the Plugin Template python and javascript files from the [Plugin Update Site](#) and put them in your local folder `$USER_PATH/.tissuums/plugins/`.

Javascript file

You can access the javascript API [here](#).

Python file

You only need to use the Python file if your plugin needs to do processing on the server side. For pure javascript plugins, you can leave this file empty.

SHARING PROJECTS

3.1 Apache server

TissUMaps projects can be exported into static webpages, that can be uploaded to any Apache server.

1. Save your project from TissUMaps (menu > File > Save project)
2. Export to static page (menu > File > Export to static webpage)
3. Copy the exported folder on your Apache server

3.2 Docker container

1. Start the docker container `cavenel/tissuums:latest` from Docker Hub:

```
docker run -it -p 56733:80 --name=tissuums -v /path/to/local/images:/mnt/data cavenel/  
↪tissuums:latest
```

1. Place your images in the local folder `/path/to/local/images/share`.
2. Open <http://127.0.0.1:56733/> in your favorite browser.

ADVANCED USAGE

4.1 Jupyter notebooks

TissUMaps can easily be used inside a Jupyter Notebook or Jupyter Lab.

Simple example to load an image in TissUMaps:

```
import tissumaps.jupyter as tj
viewer = tj.loaddata(["image.png"])

viewer.screenshot()
```

4.1.1 tissumaps.jupyter

Module used to run TissUMaps from a Jupyter Notebook or from Jupyter Lab.

`tissumaps.jupyter.opentmap(path, port=5100, host='localhost', height=700)`

Open a tmap project

Parameters

- **path** (*str*) – The path to a tmap file
- **port** (*int*) – The port to run the TissUMaps server
- **host** (*str*) – The host to run the TissUMaps server
- **height** (*int*) – The height of the jupyter iframe

Returns The TissUMaps viewer

Return type *TissUMapsViewer*

```
tissumaps.jupyter.loaddata(images=[], csvFiles=[], xSelector='x', ySelector='y', keySelector=None,
                             nameSelector=None, colorSelector=None, piechartSelector=None,
                             shapeSelector=None, scaleSelector=None, fixedShape=None, scaleFactor=1,
                             colormap=None, compositeMode='source-over', boundingBox=None,
                             port=5100, host='localhost', height=700, tmapFilename='_project',
                             plugins=[])
```

Load data in TissUMaps

Parameters

- **images** (*list* | *str*) – List of images or single image to display
- **csvFiles** (*list* | *str*) – List of csv files or single csv file to display

- **xSelector** (*str*) – Name of the csv column defining the X coordinates
- **ySelector** (*str*) – Name of the csv column defining the Y coordinates
- **keySelector** (*str*) – Name of the csv column defining the grouping key
- **nameSelector** (*str*) – Name of the csv column defining the group name
- **colorSelector** (*str*) – Name of the csv column defining the group color
- **piechartSelector** (*str*) – Name of the csv column defining pie-charts
- **shapeSelector** (*str*) – Name of the csv column defining markers' shape
- **scaleSelector** (*str*) – Name of the csv column defining markers' scale
- **fixedShape** (*int*) – Name of the markers' shape
- **scaleFactor** (*int*) – Global scale of markers
- **colormap** (*str*) – Name of the colormap used if colorSelector is set
- **compositeMode** – (*str*): Composite mode used for images
- **boundingBox** (*list*) – [X,Y,W,H] of the bounding box to display
- **port** (*int*) – The port to run the TissUMaps server
- **host** (*str*) – The host to run the TissUMaps server
- **height** (*int*) – The height of the jupyter iframe
- **tmapFilename** (*str*) – Name of the project file that will be created
- **plugins** (*list*) – List of plugins to add to the tmap project

Returns The TissUMaps viewer

Return type *TissUMapsViewer*

```
class tissumaps.jupyter.TissUMapsViewer(server, image, height=700)
```

Class representing a TissUMaps viewer instance

```
screenshot()
```

Capture the TissUMaps viewport and display image in the Notebook.

```
class tissumaps.jupyter.TissUMapsServer(slideDir, port=5000, host='0.0.0.0')
```

Class representing a TissUMaps server instance

4.2 Napari

Napari features an important hub containing 118 plugins at the time of writing, many of them expanding further the capabilities of Napari when dealing with biomedical imaging. We thus created our own plugin to allow users to work in Napari, benefit from the tools, scripting and existing plugins, and easily visualize and share the output of their research through TissUMaps.

The [Napari-TissUMaps plugin](#) is available on Napari Hub which makes the installation trivial: from the Napari install/uninstall plugins menu, the `napari-tissumaps` appears in the list and can be installed with a single click. Alternatively, the plugin can be installed with the Python package manager: `pip install napari-tissumaps`.

The plugin can export all standard Napari layers, such as images, labels, points, and shapes and preserves the metadata (opacity, visibility), but also the objects parameters (e.g.: label colors, marker colors and symbols, etc...). To export a TissUMaps project, care must be taken to save all layers of interest and type in a name with the extension `.tmap`, e.g.: `myProject.tmap`. This is important for Napari to delegate the saving of the files to the plugin. A folder is created

and contains all the necessary files and can be loaded in the TissUMaps server, software, Jupyter Notebook, or shared with the community.

The project folders generated by the plugin contain the metadata in a `main.tmap` file, along with folders for each Napari layer types: images, labels, points and regions. Images and labels are saved as plain tif images, points are saved as CSV files, and shapes are saved as GeoJSON. We hope that the use of a simple structure and widespread file formats can simplify the modifying and updating of the TissUMaps project when prototyping with e.g. Jupyter Notebooks. The source code is available at <https://github.com/TissUMaps/napari-tissuums> under the permissive MIT license. A demonstration of the Cellpose plugin of Napari being exported to the TissUMaps web viewer is available at: <https://tissuums.github.io/tutorials/#napari>.

4.3 AnnData

Work in progress

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