

# SPATIAL TRANSCRIPTOMICS VIEWER v0.6.3 USER MANUAL

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## **Preface**

The Spatial Transcriptomics viewer (ST viewer) is a desktop application that allows users to securely access and visualize spatially distributed gene expression profile data with their respective tissue image. At the same time it allows users to analyze the data directly, or export it for their own analyses. The application can obtain the data from a secured server (configuration files will need to be updated for this) and/or from local files.

For installation instructions, please see the README.md file. This file describes the install instructions on Windows, OSX and Linux.



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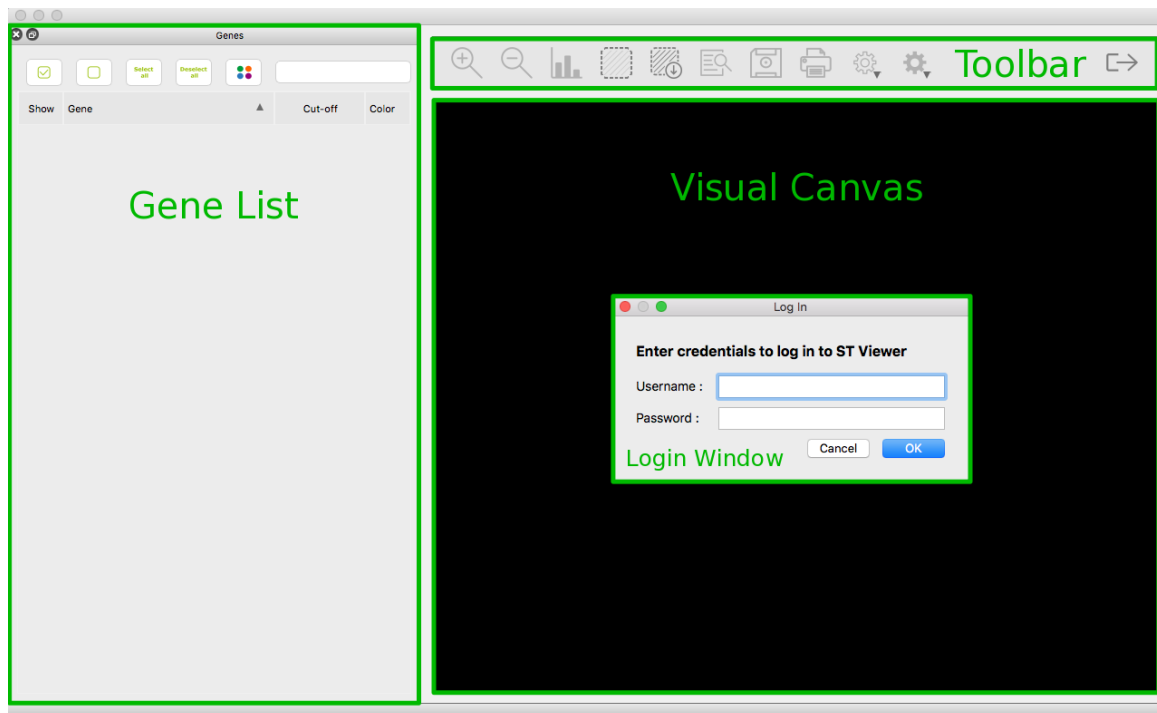


# Chapter 1

## Introduction

### 1.1 User Interface

When running the spatial transcriptomics viewer for the first time, you will be presented with an interface as shown in figure 1.1. If the viewer has been configured to access datasets through the ST API then the login window will be shown, otherwise it will not be shown.



**Figure 1.1:** The default interface presented when the ST viewer is run for the first time. The elements present are the gene list window on the left, the toolbar in the top right, the visual canvas on the right, and optionally the log in window (if the viewer is configured to access datasets through the ST API).

Once you have logged in (if applicable), your user name will be displayed in the toolbar, as shown in figure 1.2.



**Figure 1.2:** Toolbar showing username after logging in.

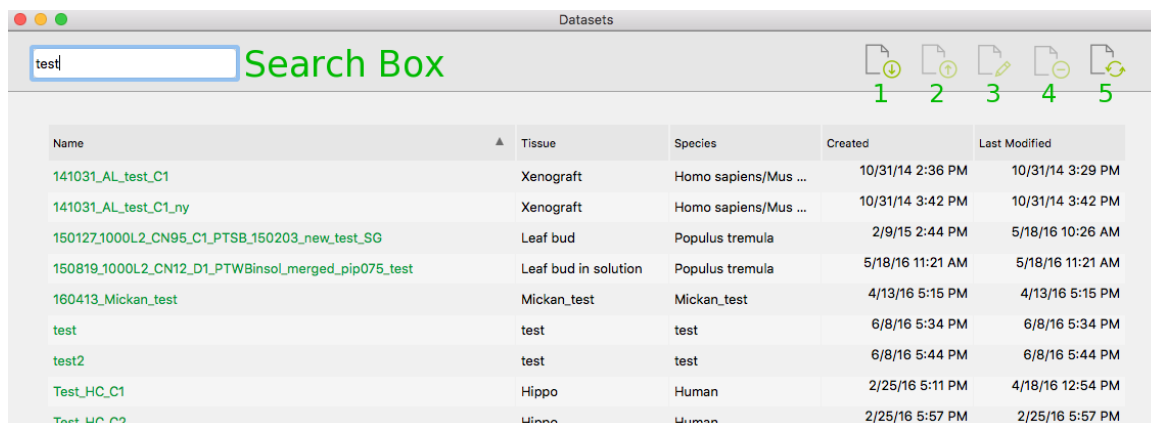
There are two other main windows in the ST viewer, datasets and selections. They can both be accessed from the views menu by clicking views → datasets and views → selections. The datasets window shows all the datasets that you have



access to. There is a search box that can be used to find a keyword in the dataset names to narrow down the list of datasets (see figure 1.3). There are five buttons to the right of the dataset search box (labelled 1 — 5). They are:

1. Import dataset from file (local file on your computer)
2. Open selected dataset (for datasets stored in the database)
3. Edit selected dataset (change name, add comments)
4. Delete selected dataset
5. Refresh list of datasets

The datasets displayed in the dataset view can also be sorted by each column (e.g. name or species).

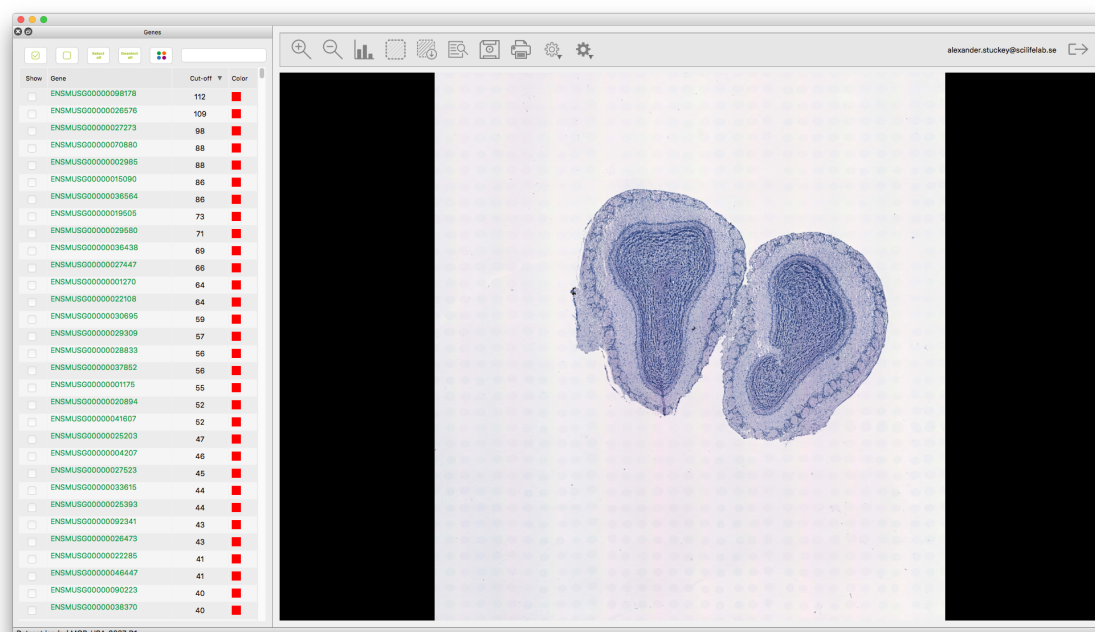


**Figure 1.3:** Datasets view. The search box is being used to display only the datasets that contain the word "test" in their name.

The selection view will be discussed further in a following chapter.

**Note:** Each dataset is associated with a substantial amount of data, which will be accessed after a dataset has been selected and opened. As such the transition between the views might require a few moments. It is worth noting that the data is cached, which implies that once it is downloaded, the next time the same dataset will open much quicker. This does not apply if the dataset is updated in the cloud in the meantime.

When a dataset is loaded, the gene list will populate with the list of all genes that are associated with the current dataset, and the visual canvas will display the image of the tissue section (see figure 1.4).

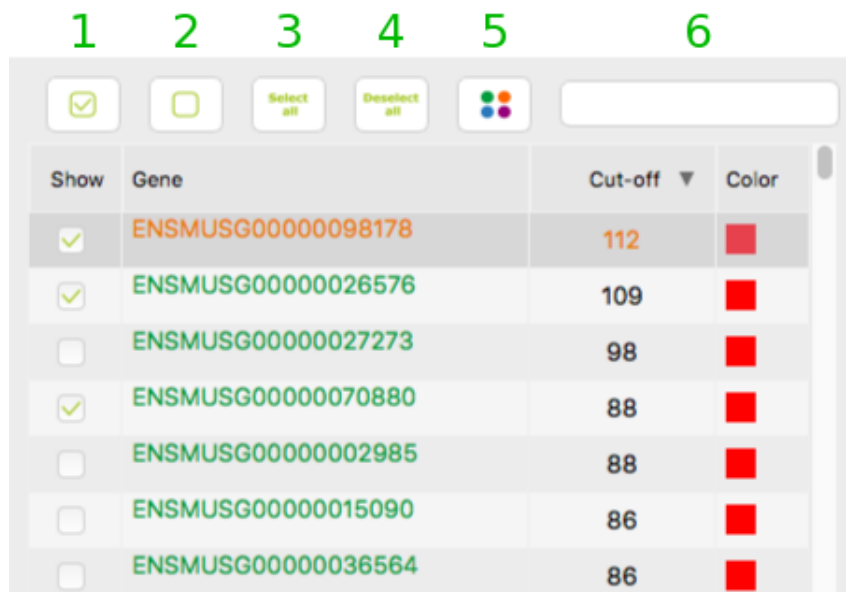


**Figure 1.4:** The default view after loading a dataset. The gene list is populated by all the genes in the data, and an image of the tissue section is presented on the visual canvas.

The gene list is headed by five buttons and a text box. The buttons are, in order:

1. Show selected
2. Hide selected
3. Select all
4. Deselect all
5. Set colour
6. Search box

The text box enables you to search the list of genes for genes that are of interest. Shown genes are marked with a checkmark in the box to the left of the gene name / ensemble ID. Selected genes have their names highlighted in orange instead of green, and have a darker grey background. Note that shown genes and selected genes may differ (as seen in figure 1.5). The gene list is also able to be sorted by gene name and cut-off value.



The interface shows a control bar at the top with five buttons and a search box. Below is a table with columns for 'Show', 'Gene', 'Cut-off', and 'Color'. The first row is highlighted in orange, indicating it is selected. The other rows have a lighter grey background. The 'Show' column contains checkboxes, and the 'Color' column contains small red squares.

Show	Gene	Cut-off	Color
<input checked="" type="checkbox"/>	ENSMUSG00000098178	112	■
<input checked="" type="checkbox"/>	ENSMUSG00000026576	109	■
<input type="checkbox"/>	ENSMUSG00000027273	98	■
<input checked="" type="checkbox"/>	ENSMUSG00000070880	88	■
<input type="checkbox"/>	ENSMUSG00000002985	88	■
<input type="checkbox"/>	ENSMUSG00000015090	86	■
<input type="checkbox"/>	ENSMUSG00000036564	86	■

**Figure 1.5:** Gene list