Human-Augmenting Labeling Interface (HALI)

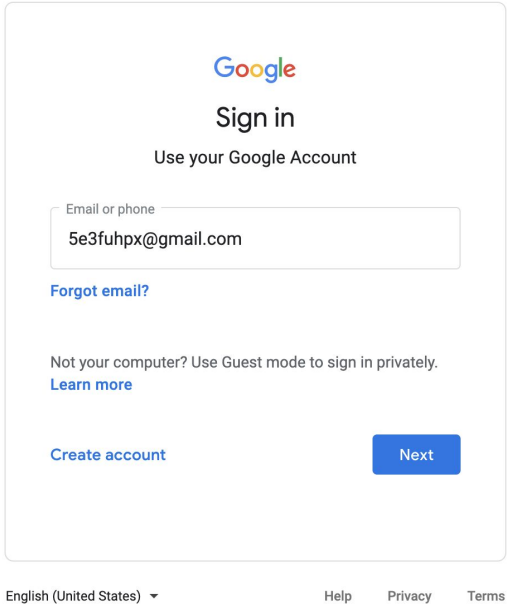
README

- This software is in a rough research state, and was developed strictly for the purposes of experimentation. It is not ready for widespread use.
- This software is run through a virtual machine (VM), on the web, and requires no installation.
- Google Chrome must be used as the web browser

Setup instructions

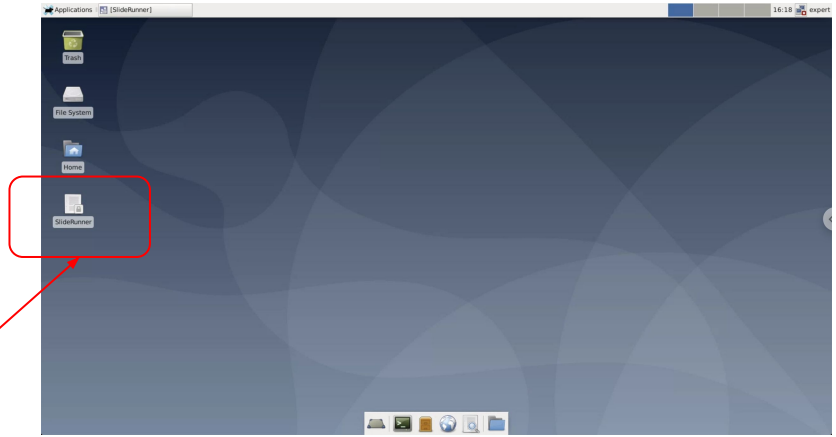
(1) Sign out of your Google account, and sign in with the following account:

- Username: 5e3fuhpx@gmail.com
  Password: $dBf3qe2j-PbK??z



Setup instructions

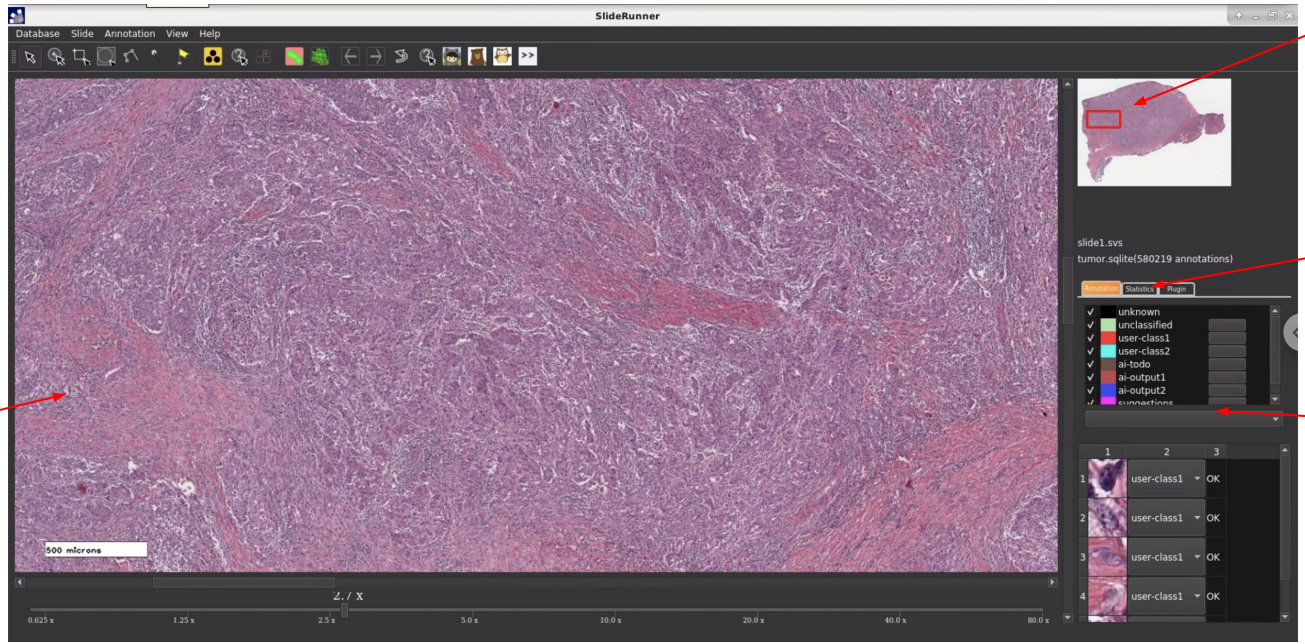
(2) Go to https://remotedesktop.google.com/access



- Click on the remote device assigned to you (e.g reviewer-1, reviewer-2, reviewer-3 ,etc.)
- Enter PIN: 123456
- On the desktop: click on the Sliderunner app
- In the menu bar click on Database → open remote. Then click OK without changing the server ip and then select the desired use-case from the dropdown menu and press OK.
- In the menu bar click on Slide → open Remote and press OK.

Setup instructions

The following should appear, for database “tumor”:



Your location relative to entire slide

Click on the “Statistics” tab to show the number of annotations per class

Labeling Panel

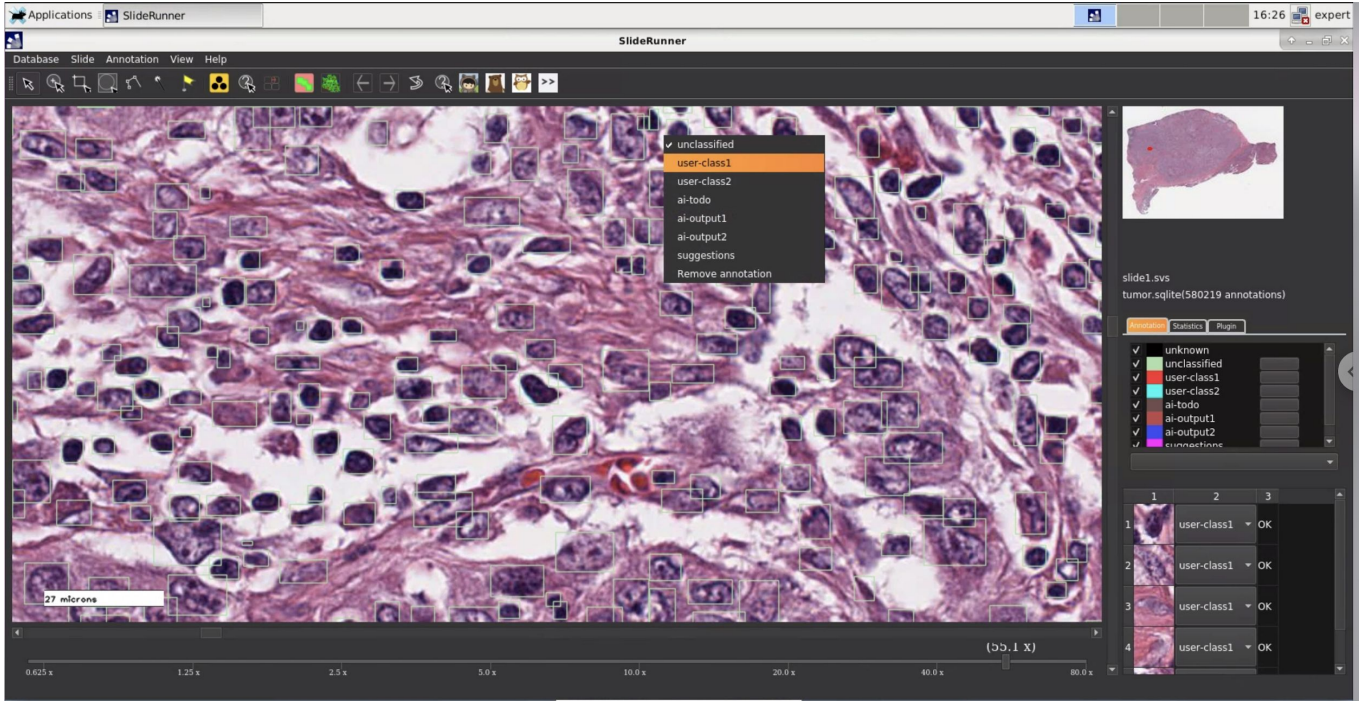
Labels annotated by the user and AI will have colored defined here

Important notes

- If you want to switch between use-cases, fully close the SlideRunner program and click on the desktop icon again.
- For ki67: Cells in the tissue microarrays on the left part of the slide can not be labelled.
- For eosinophils, tumor cells and lymphocytes: to keep the tool responsive, only cells on the left side of the slide are available to label.
- When requesting the AI to label all cells currently visible, this takes about 30 seconds. The actual prediction is very swift (< 1 second), but the process is bottlenecked by the database. In production this would be much faster.

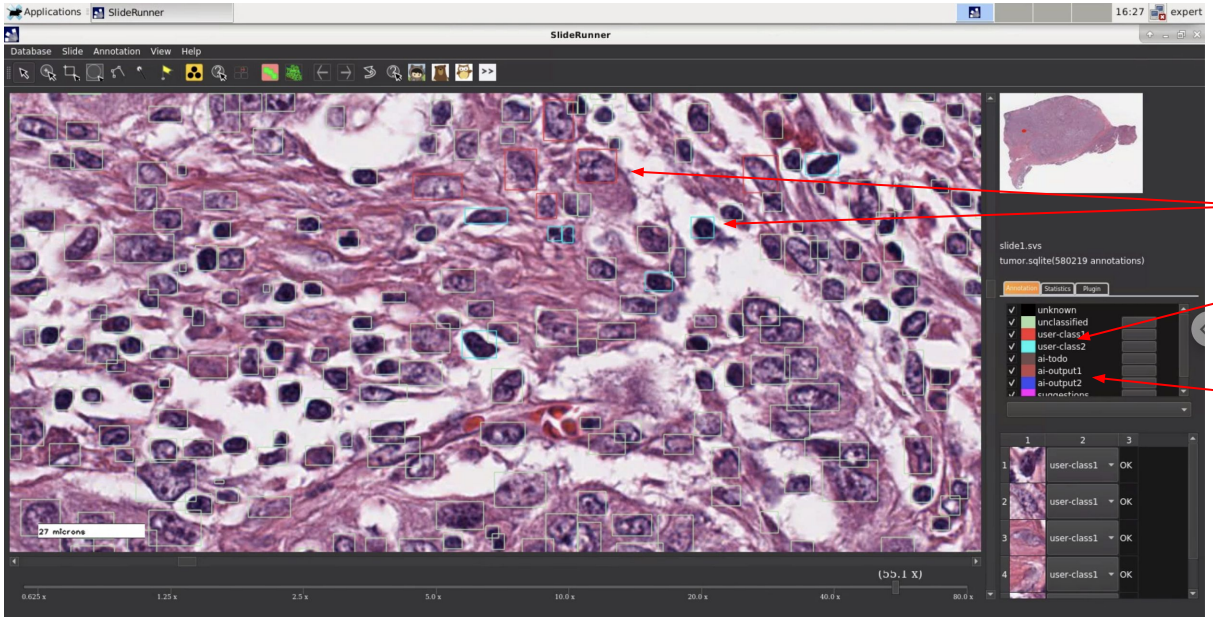
Demo: Labeling with and without the AI

- To annotate cells, zoom into the tissue using the slider at the bottom until green bounding boxes appear around cells, then right click to annotate cells by type.



Demo: Labeling with and without the AI

- Annotating cells will change the color of their containing bounding boxes (e.g. bright-red)
- Label cells as either user-class1 or user-class2. You can pick what kind of cells each class represents, the AI is trained from scratch.



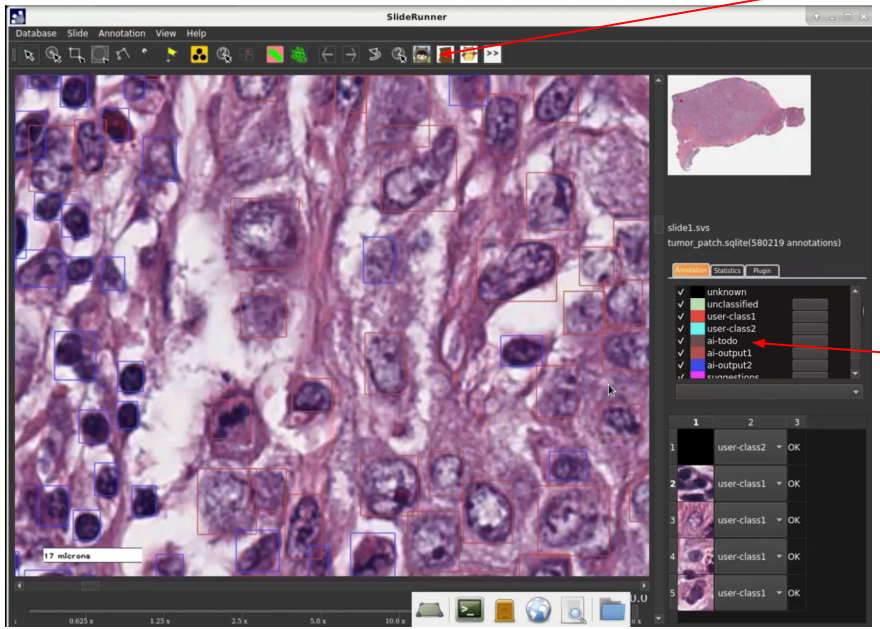
Notice that colors change when you select labels

User labels are called “user-class1”, “user-class2”, etc.

Anything the AI predicts is call “ai-output1”, “ai-output2”, etc.

Demo: Labeling with and without the AI

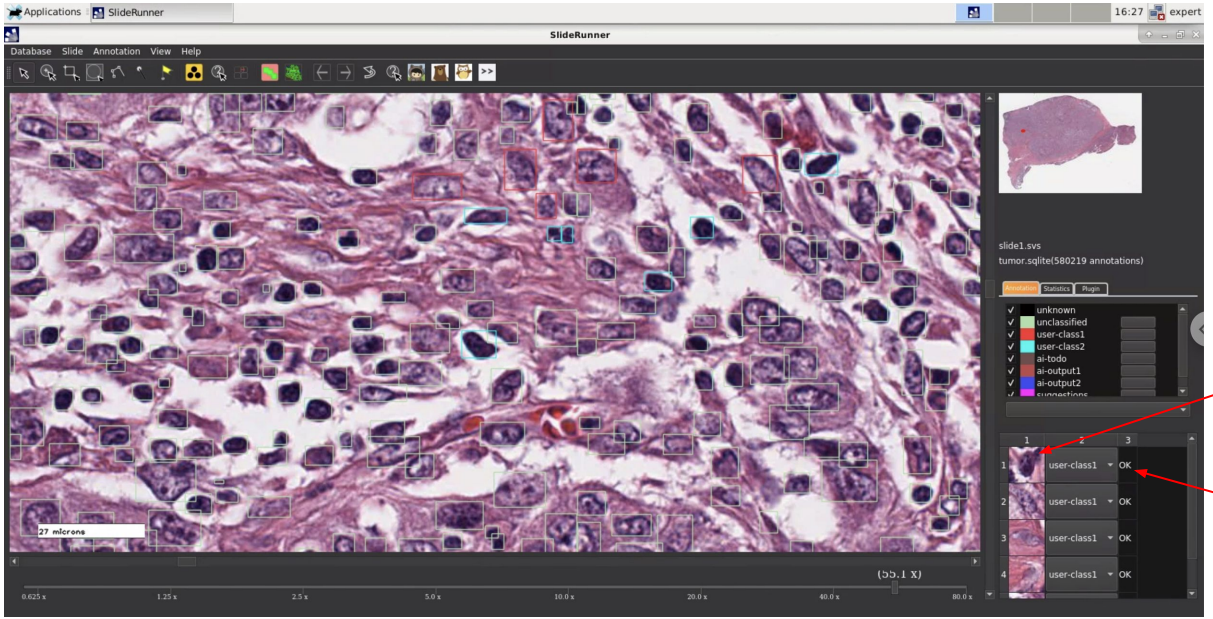
- Once enough cells are annotated for each class (~20/class, more or less for complex classes), the AI will begin training in the background, and keep re-training as more labels are provided.
- To ask the AI to annotate the entire field-of-view, click on the icon of a cartoon racoon() in the top toolbar. After ~30 seconds, bounding box colors will change. AI outputs will be in similar colors to user labels (e.g. brown-red).



Dark brown bounding boxes signify cells that are being processed: “ai-todo”

Demo: Labeling with and without the AI

- The active learning suggestions are displayed in the table on the bottom right. You can click on the thumbnail to move the main window to the location of the cell. Please note: suggestions will be meaningless until sufficient example images are provided (see previous slides).



Labeling your own images

It is possible to annotate your own microscopy or histopathology slide, but some setup is required by the authors. Please reach out if you would like to do this.