# ACROBAT annotation protocol – annotator 1 - public

This document describes the process of creating landmark annotations for the ACROBAT challenge. The tool is hosted at MEB in Karolinska Institute, Sweden and all annotations outside KI are made over remote connection. We recommend reading this document to the end before starting annotations.

# 1. Before starting

## 2. Open remote connection

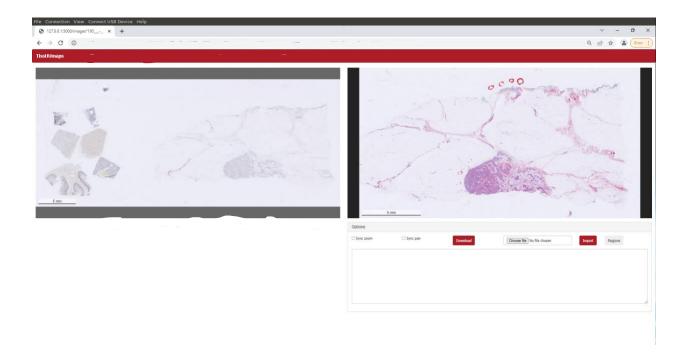
#### 3. Download files

# 4. Starting the annotation tool

Now there should be an excel sheet in the Documents directory showing the slides to annotate. Open it and it should look something like this

	ihc	wsi_he	wsi_ihc	filename_he	filename_ihc	link	done
0	PGR	/mnt/chimera	/mnt/chimera	ABC-ABC-ABC	ABC-ABC-ABC	http://127.0.0.1:5	0
1	ER	/mnt/chimera	/mnt/chimera	ABC-ABC-ABC	ABC-ABC-ABC	http://127.0.0.1.5	0
2	ER	/mnt/chimera	/mnt/chimera	ABC-ABC-ABC	ABC-ABC-ABC	http://127.0.0.1:5	0
2	DCD.	/	/man+/ah:maana	ADC ADC ADC	ADC ADC ADC	L++//127 0 0 1.E	0

You can copy a link from the sheet and open it in **Google Chrome browser**. You should see the following screen.



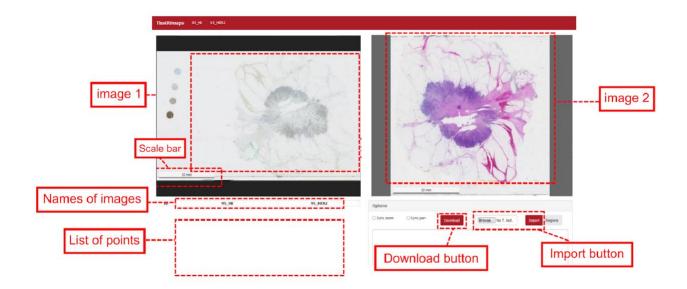
We can type in our browser or click on the link in the excel file and go to:

localhost:3000/95 HE.ndpi\*\*95 HER2.ndpi

Everything after the / tells our tool where and which are the two images. The images are separated by a double asterisk \*\*, and any single asterisk is there to replace a / in a longer path, for example an image at a folder called images will be seen in the url as "images\*95\_HE.ndpi\*\*images\*95\_HER2.ndpi" which translates to, show the image located at images/95\_HE.ndpi in the left; and image images/95\_HER2.ndpi in the right.

#### 5. User interface

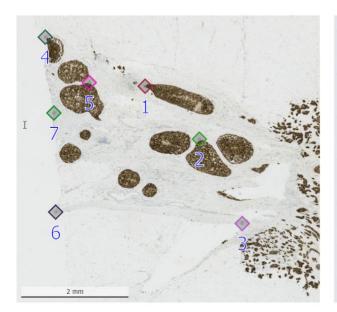
The picture below shows all components of the annotation tool. You can also see in the bottom part, a location where the list of points will appear once you start annotating. Also a button to save the points you annotate, these will be saved to your computer, you can also share them with annotators and load them back with the import button. The scale bar also shows the level you are looking at.

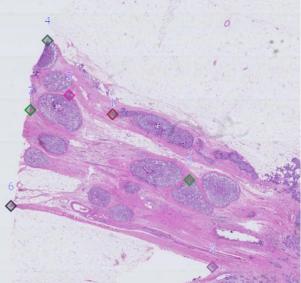


A VERY IMPORTANT NOTE: Do not refresh the browser (Ctrl-R or by while annotating as that will erase all points unless you have saved them using the "Download" button. Make sure to download annotations at regular intervals while annotating. If you refresh by accident, you can restore annotations from the most recently downloaded annotation file by selecting the file and pressing "import".

## 6. Example annotation

The objective of the annotations is to find and mark corresponding points, first in the left image and then in the right image. The output of the annotations should look approximately like this:





To set a point, zoom into both images and find a structure that you can identify in both views. When you find a structure present in both images, make sure the zoom level is **at least 250 microns**. Then, click on this point in the left image. A point with a number will be placed at this position in the left image. A point with a corresponding number now also appears in the right image. It may be in a different location, so you may have to zoom out to find it. Drag and drop it to the corresponding position in the right image. You will see in the bottom a list of added points and their location in the image (in pixels). We will try to improve the proximity of the default point in the H&E WSI shortly to speed up the annotation process. In each image pair, **place 50 landmarks**. The majority of points should be placed in non-fatty tissue regions, with only a few points in the contour of the fat tissue and inside the fatty tissue.

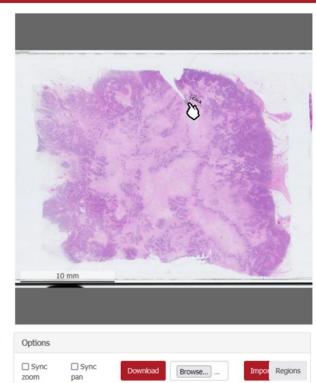
You can use this URL to familiarize yourself with the tool:

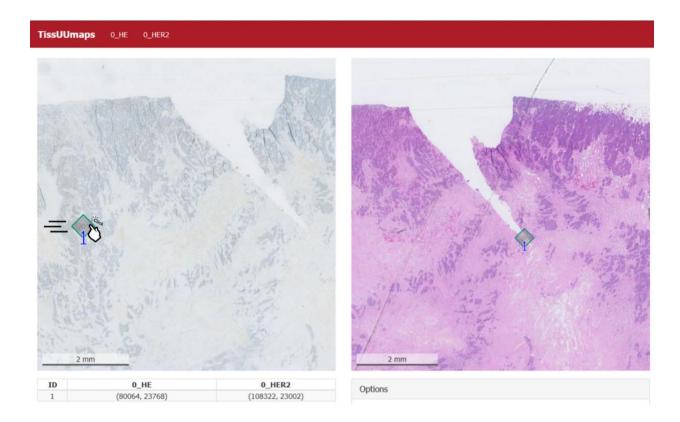
localhost:3000/0 HE.ndpi\*\*0 HER2.ndpi











In the image viewers, you will notice the following interaction buttons to help if needed.









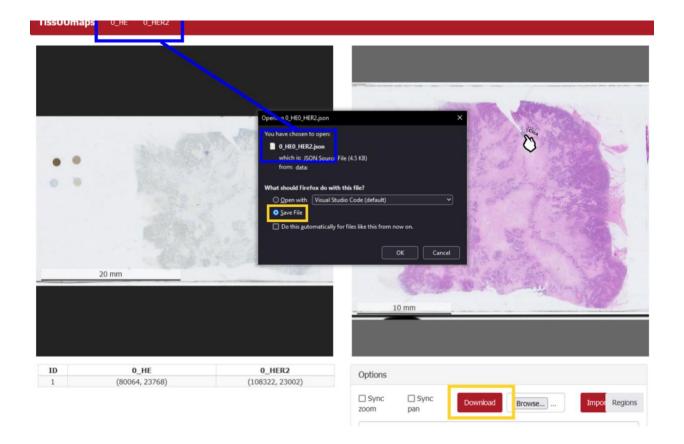




In particular the last two arrows are there to help you rotate the image in case it is needed. There are some images that are rotated 180 degrees and this makes it easier to annotate.

## 7. Saving annotations

Once you have annotated a couple of points, you can click the button: **Download** and a file with the combined name of the two images will be saved. If you are usings the Google Chrome browser, the file will be automatically downloaded to the 'Downloads' directory. If it for some reason asks you where to save it, tell it to do so in the Downloads directory. You can also tell it to always save it in 'Downloads'.



# 8. Annotation guidelines

Once you are somewhat familiar with the tool, here are the instructions on how each image pair from the excel file should be annotated. These are step by step instructions of the most important points to keep in mind. These can be glanced every now and then to make sure you are on the right path.

### Annotating a pair of H&E and IHC images

- 1. Click the link from the list of all annotation pairs (The excel file). An IHC image should open to the left pane and an H&E image should open to the right pane.
- 2. Find common structure in both images. While some landmarks should be placed on contours and if possible inside fatty tissue, focus on distributing the majority of landmarks in non-fatty tissue regions. Avoid placing annotations based on image intensities or tiny objects such as cells that are not the same object in adjacent sections. Use preferably tissue section boundaries and boundaries between tissue types such as fat tissue versus non-fat tissue or larger morphological structures like glands and ducts.
- 3. Zoom into the found structure and **insert a point only if the scale bar shows 250 micrometers or less**. This is important to have consistency across different annotators.

- 4. Click on a structure first in the IHC image (left pane) and move the corresponding point in the H&E image (right pane) to a matching location.
- 5. Every now and then press "Download" to download the annotations, just in case.
- 6. Repeat steps 2-5 until 50 points have been placed in both images.
- 7. Once you have annotated all the points, insert the number of annotations into the 'Done' column. Also, if there was anything peculiar in either of the images, you can add a comment about that into the 'Comment' column. Remember to save the file.

## 10. After annotations are done

Thank you very much for your contribution!