

# - STARDIST

## Installation

Installation steps detailed in ([stardist/stardist: StarDist - Object Detection with Star-convex Shapes](https://github.com/stardist/stardist) ([github.com](https://github.com)))

Versions I recommend:

- Conda environment - python 3.7
- tensorflow 1.15 in Windows // tensorflow 2.8 in Bioimaging VDI
  - Other versions of tensorflow gave errors
- Follow the special instructions for tensorflow1 specified in the instructions

Stardist also has the option to train a model yourself <https://github.com/stardist/stardist/tree/master/examples/2D>

## Jupyter notebook

There is a dedicated jupyter notebook in our github ([https://github.com/farkkilab/cycif-snippets/blob/master/Segmentation\\_STARDIST\\_multiple.ipynb](https://github.com/farkkilab/cycif-snippets/blob/master/Segmentation_STARDIST_multiple.ipynb)) to run Stardist in Python with a pre-trained model. It is recommended to use the bioimaging VDI to run it with >5GB images, it is also faster than to run it on your laptop. The notebook has two parts:

- One for processing an **individual slide** (inputs required are the path, image name and x,y number of tiles)
- One for processing **multiple slides** (input and output path required, x,y number of tiles). Adjust the number of tiles according to the dimensions of the biggest image you are processing.

In python, STARDIST can process big images, to define the right amount of tiles an image has been segmented with different numbers of tiles until finding the minimum one. That constant has been incorporated into the script so that the number of tiles is estimated for individual images, but this constant fails for some cases still, so manual adjustment based on that estimate with some margin added is recommended.

## Fiji plugin

The FIJI plugin crashes with big images, even when the number of tiles has been adjusted, it failed even with a quite small tCycif image (4GB) . The error was related to java heap space. This same procedure was carried out in a powerful computer and the error persisted, so that might be a bug from FIJI.



**Possible improvements:** automatic tile adjustment

### Issues solved:

Bioimaging VDI has initially presented problems in the output format of the mask (the image could not be opened by any program, and an error indicated that it had less than 2D). Making sure that the dtype of the array was "int32" solved the problem.