Block course
Day 1: Github, python and [Ca] data binarization

Overview

1. Using Anaconda as an environment manager (quick intro)
2. Using Github as algorithm repository (quick intro)
3. Python (quick intro)
4. Binarizing Suite2p data using python

POll

How many people heard of programming languages?

What about python?

What about anaconda or virtual environments or containers?

What about git and github?

Anaconda

Anaconda Intro

Anaconda is several things

- Today we only discuss managing (coding) environments
- But what is an environment? (hint: what is a native environment?)

So we can make our own “container” that remembers:

- The version of python we install
- Versions of other packages that we install to work in python
- … and other settings

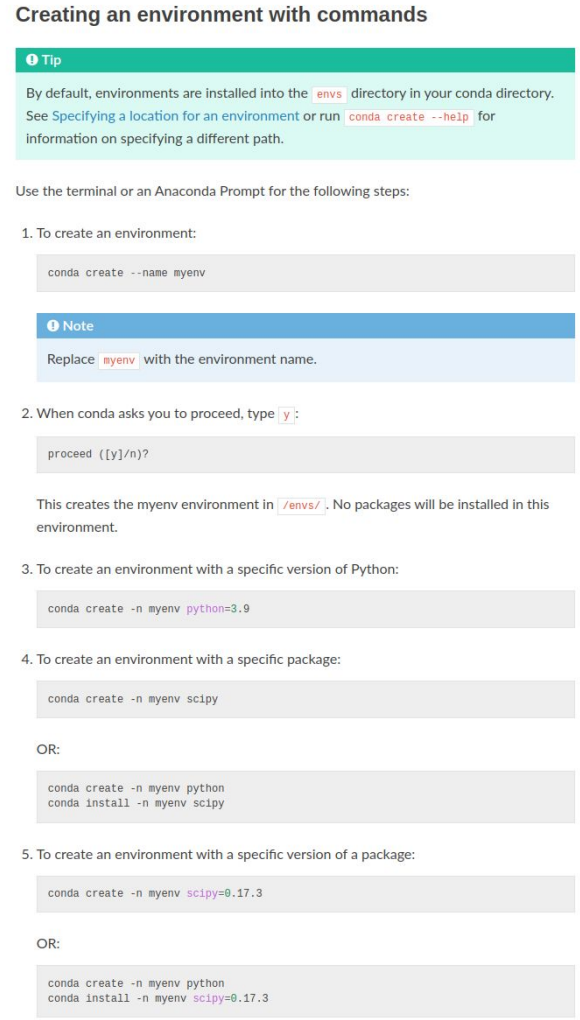
For today we already have our own environment for the course:

block_course

To load it

- We use windows anaconda command line and type:

  conda activate block_course



Creating an environment with commands

Tip

By default, environments are installed into the `envs` directory in your conda directory. See Specifying a location for an environment or run `conda create --help` for information on specifying a different path.

Use the terminal or an Anaconda Prompt for the following steps:

1. To create an environment:

```
conda create --name myenv
```

Note

Replace `myenv` with the environment name.

2. When conda asks you to proceed, type `y`:

```
proceed ([y]/n)?
```

This creates the myenv environment in `/envs/`. No packages will be installed in this environment.

3. To create an environment with a specific version of Python:

```
conda create -n myenv python=3.9
```

4. To create an environment with a specific package:

```
conda create -n myenv scipy
```

OR:

```
conda create -n myenv python
conda install -n myenv scipy
```

5. To create an environment with a specific version of a package:

```
conda create -n myenv scipy=0.17.3
```

OR:

```
conda create -n myenv python
conda install -n myenv scipy=0.17.3
```

Github

Github Intro

Github is also several things

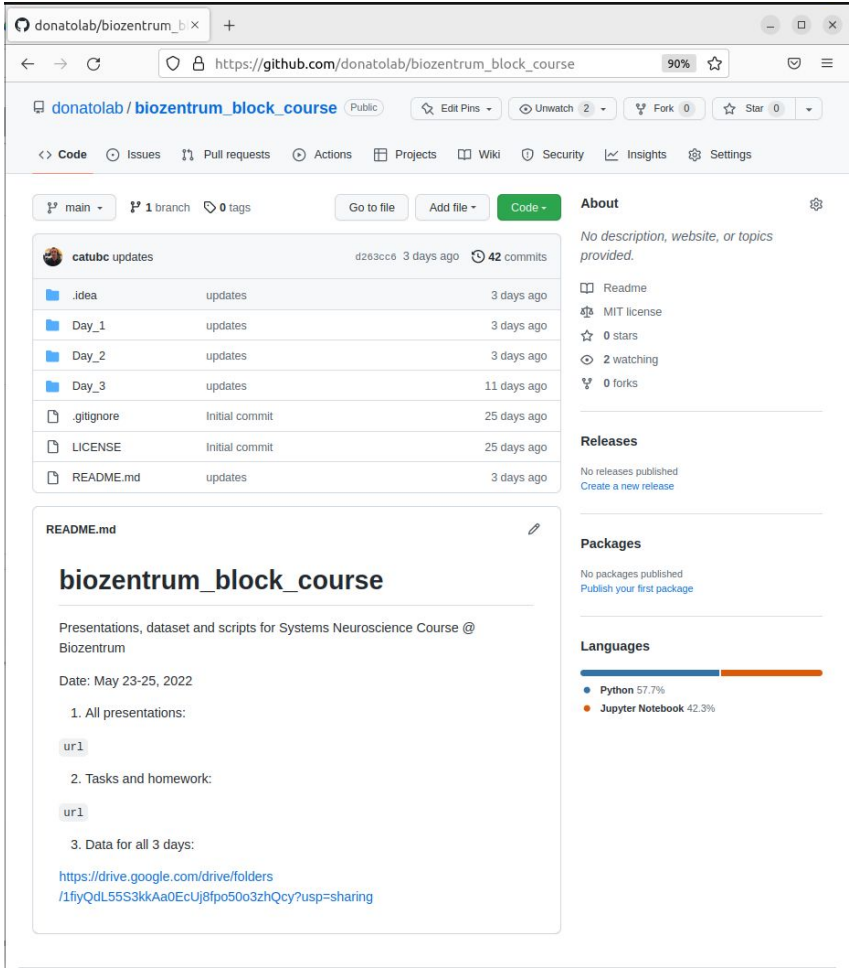
- Today we focus on repository storage and retrieving
- But what is a repository ?

Git vs. github

- Git is a “distributed version control system”
  - Allows teams of developers to write code together each contributing small parts
  - Allows retrieval and management of different version of the code (e.g. retrieving old code when made a mistake

- Git can be run locally on single computer (or group)

- Github is essentially a managed git service hosted publicly at github.com that can be accessed by anyone
  - Can have both public and private repos



Python

Python intro (1/3)

Interface for coding in python

- We use Jupyter-lab or Jupyter notebook which are dynamic/interactive
  - Quiz: What does “interactive” mean?
- We start jupyter-lab by calling it from the Windows command line once in the correct environment:
  jupyter lab

Variables

- String
  - fname = r”C:\Users\block_course.npy”
- Scalar
  - x = 5
- Vectors
  - x = [0,1,2,3,4]
- Matrices
  - x = [[0,1,2],
    [3,4,5],
    [6,7,8]]

Many intrinsic packages and functions (e.g. “numerical python”)

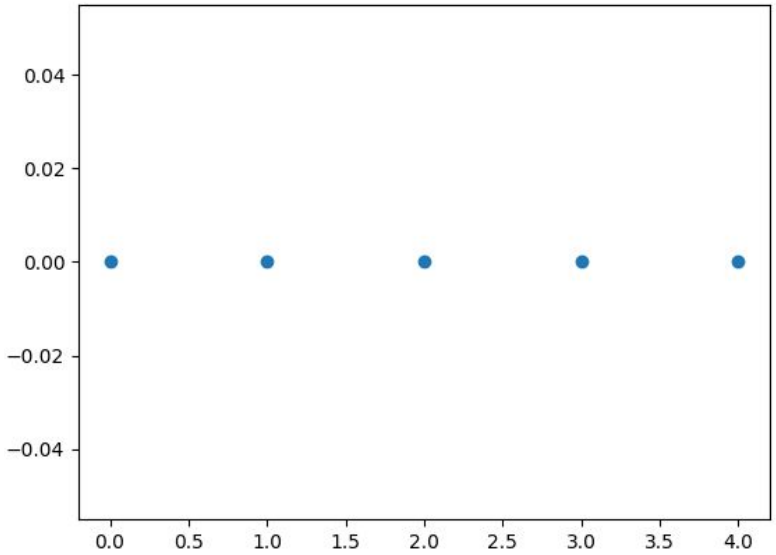
- import numpy
  - x = numpy.arange(5)
  - print (x)
    [0,1,2,3,4]

Plotting

- We use matplotlib package to plot a scatter plot

```
1  import matplotlib.pyplot as plt
2  import numpy as np
3
4  # generate a simple array
5  x = np.arange(5)
6  y = np.zeros(5)
7
8  #
9  print ("x: ", x)
10 print ("y: ", y)
11
12 # make a figure
13 plt.figure()
14
15 # scatter plot x vs. y
16 plt.scatter(x,y)
17
18 # show the image
19 plt.show()
```

```
x:  [0 1 2 3 4]
y:  [0. 0. 0. 0. 0.]
```



Python intro (3/3)

Using Python to make our own packages (or classes)

- E.g. Calcium class developed @Donatolab
  - We can load the Suite2p output

```
# initialize calcium object and load suite2p data
c = calcium.Calcium()
c.verbose = True                                # output
c.recompute_binarization = True                 # recomp
c.data_dir = data_dir
c.load_suite2p()
```

  - And we can run some algorithms on the data

```
################################################
########### RUN BINARIZATION STEP ##############
################################################
#
c.binarize_fluorescence()
```

Binarization

Using the Calcium() python class to convert Suite2p output to binarized rasters

1. Provide link to suite2p file location

2. Set parameters
   a. Threshold: usually 2.5 x std
   b. [ca] low pass filter: 0.5hz
   c. Detrend model degree: 1

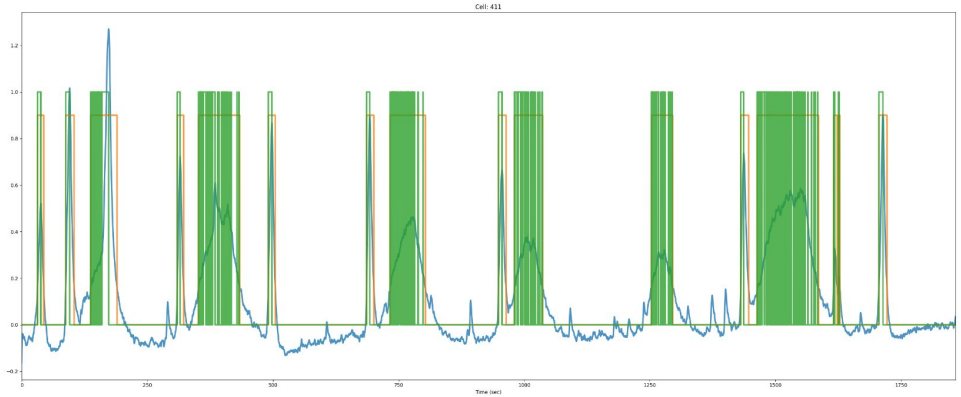
3. Output saved as .mat and .npz files

```
##############################################
######### LOAD SUITE2P AND BINARIZE ##########
##############################################

# input directory where Suite2p outputs matlab Fall.mat and all .npy files
# data_dir = '/media/cat/4TB/donato/steffen/DON-004366/20210228/'
# data_dir = '/media/cat/4TB/donato/steffen/DON-004366/20210301/'
data_dir = '/media/cat/4TB/donato/DON-003343/DON-003343_20210213/suite2p/plane0/'
# data_dir = '/media/cat/4TB/donato/nathalie/plane0'
# data_dir = '/media/cat/4TB/donato/renan/renan'
# data_dir = '/media/cat/4TB/donato/steffen/DON-004366/20210228'   # can also add suite2p/plane0/

# initialize calcium object and load suite2p data
c = calcium.Calcium()
c.verbose = True                          # outputs additional information during processing
c.recompute_binarization = True           # recomputes binarization and other processing steps; False: loads from previous saved locations
c.data_dir = data_dir
c.load_suite2p()

# set flags to save matlab and python data
c.save_python = True         # save output as .npz file
c.save_matlab = True         # save output as .mat file

##############################################
##### PARAMETERS FOR RUNNING BINARIZATION #####
##############################################
c.min_width_event_onphase = c.sample_rate//2 # set minimum withd of an onphase event; default: 0.5 seconds
c.min_width_event_upphase = c.sample_rate//4 # set minimum width of upphase event; default: 0.25 seconds

############# PARAMTERS TO TWEAK ##############
#     1. Cutoff for calling somthing a spike:
#        This is stored in: std_Fluorescence_onphase/uppohase: defaults: 1.5
#                                   higher -> less events; lower -> more events
#                                   start at default and increase if data is very noisy and getting too many noise-events
c.min_thresh_std_onphase = 2.5      # set the minimum thrshold for onphase detection; defatul 2.5
c.min_thresh_std_upphase = 2.5      # set the minimum thershold for uppohase detection; default: 2.5

#     2. Filter of [Ca] data which smooths the data significantly more and decreases number of binarzied events within a multi-second [Ca]
#        This is stored in high_cutoff: default 0.5 to 1.0
#        The lower we set it the smoother our [Ca] traces and less "choppy" the binarized traces (but we loose some temporal precision)
c.high_cutoff = 0.5

#     3. Removing bleaching and drift artifacts using polynomial fits
#        This is stored in detrend_model_order
c.detrend_model_order = 1 # 1-5 polynomial fit


##############################################
########## RUN BINARIZATION STEP #############
##############################################
#
c.binarize_fluorescence()
```

Visualizing the binarization code results

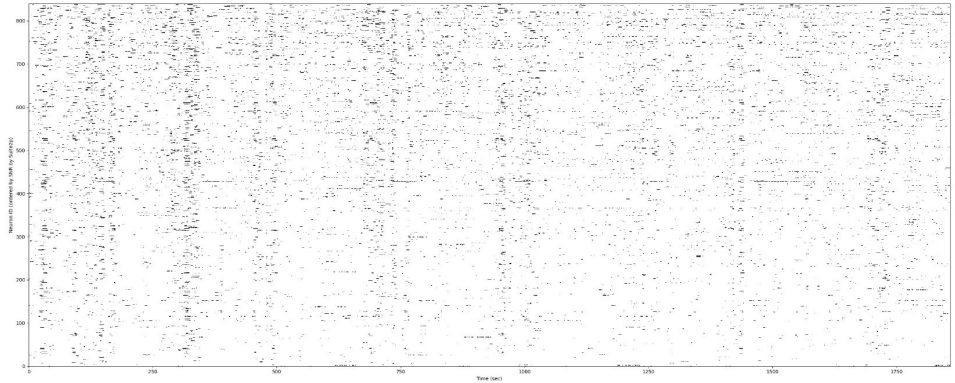
1. Visualize single cell binarization

```
#############################################################
######### LOAD BINARZIED DATA AND VISUALIZE CELL ACTIVITY #####
#############################################################
#fname = '/media/cat/4TB/donato/DON-003343/DON-003343_20210213/suite2p/plane0/bi
#fname = '/media/cat/4TB/donato/steffen/DON-004366/20210228/binarized_traces.npz
#fname = '/media/cat/4TB/donato/nathalie/plane0/binarized_traces.npz'
#fname = '/media/cat/4TB/donato/renan/renan/binarized_traces.npz'
#
fname = '/media/cat/4TB/donato/steffen/DON-004366/20210228/binarized_traces.npz'

c = calcium.Calcium()
c.fname = fname
c.load_binarization()

# pick a random cell to visuzlie
cell_id = 307
scale = 100

#
c.plot_cell_binarization(cell_id, scale)
```



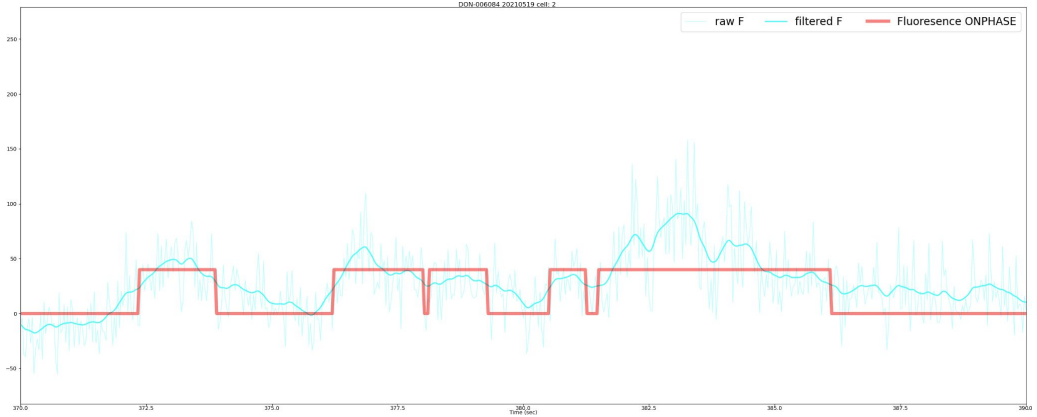
2. Look at entire raster

```
#########################################################
############# SHOW RASTERS ##############################
#########################################################
fname = '/media/cat/4TB/donato/DON-003343/DON-003343_20210213/suite2p/plane0/binarized_
data_dir = '/media/cat/4TB/donato/DON-003343/DON-003343_20210213/suite2p/plane0/'

c = calcium.Calcium()
c.data_dir = data_dir
c.fname = fname
c.recompute_binarization = False
c.load_binarization()

c.show_rasters()
```

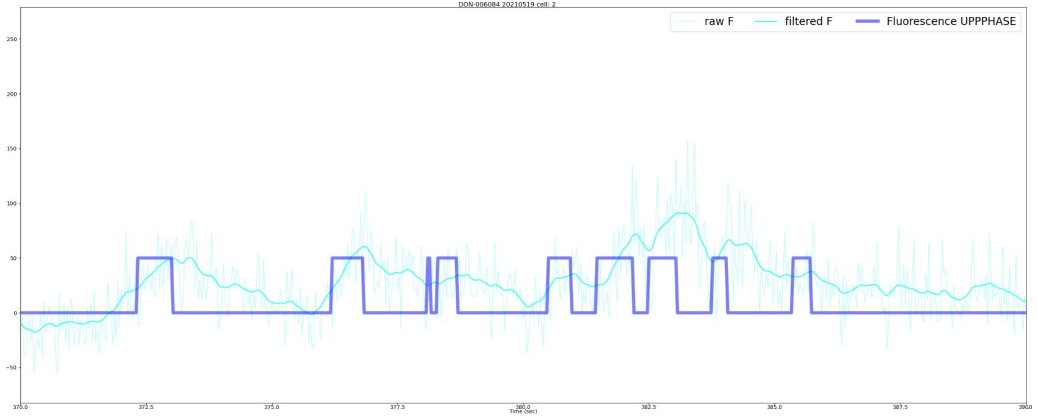


Binarization: converting [ca] activity into spiking/boolean data

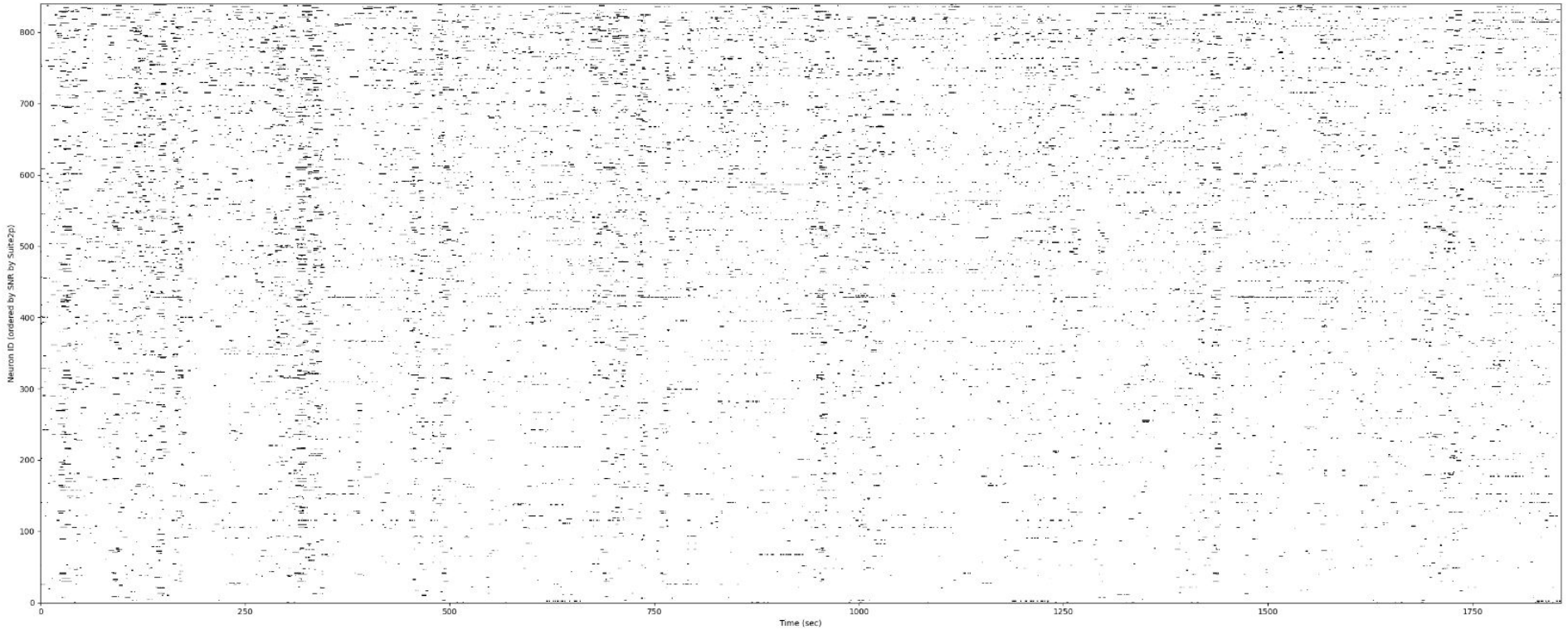
ON phase



UP phase

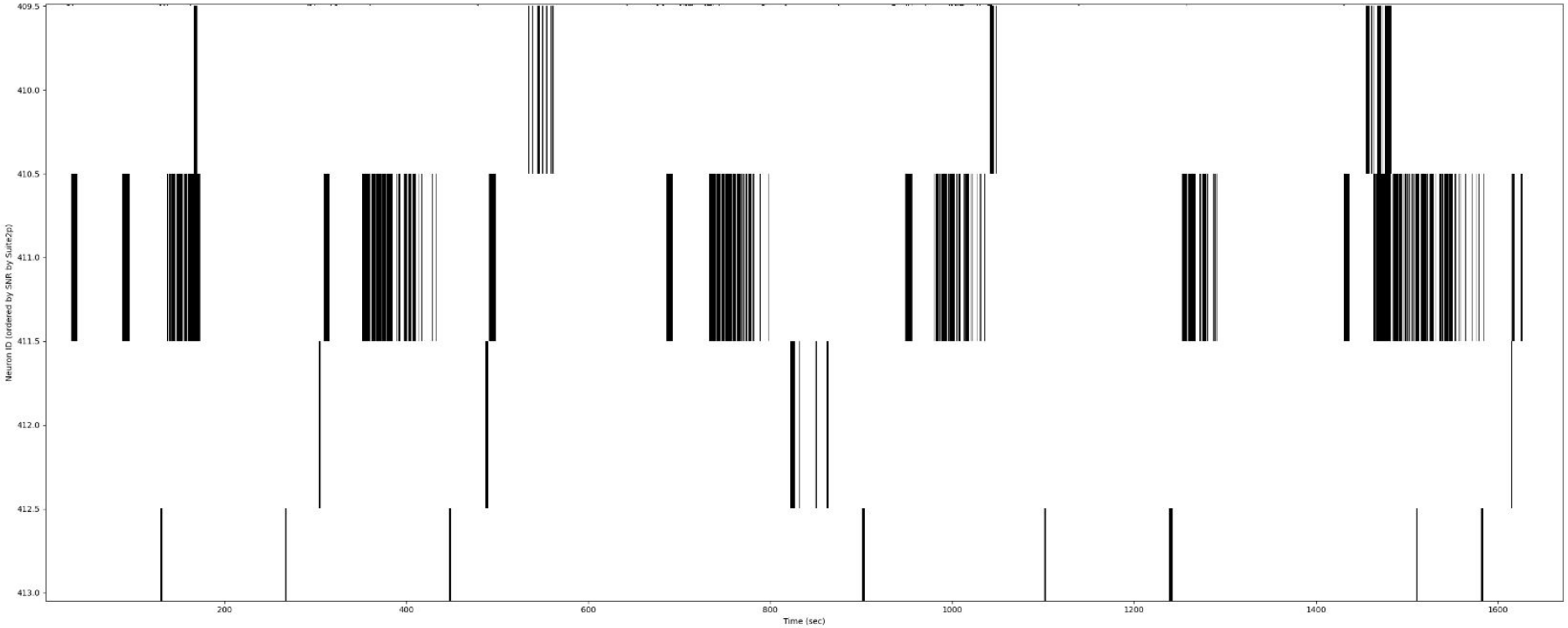


Dataset #1: Intrinsic activity - Steffen/Flavio dataset (mouse 3343)



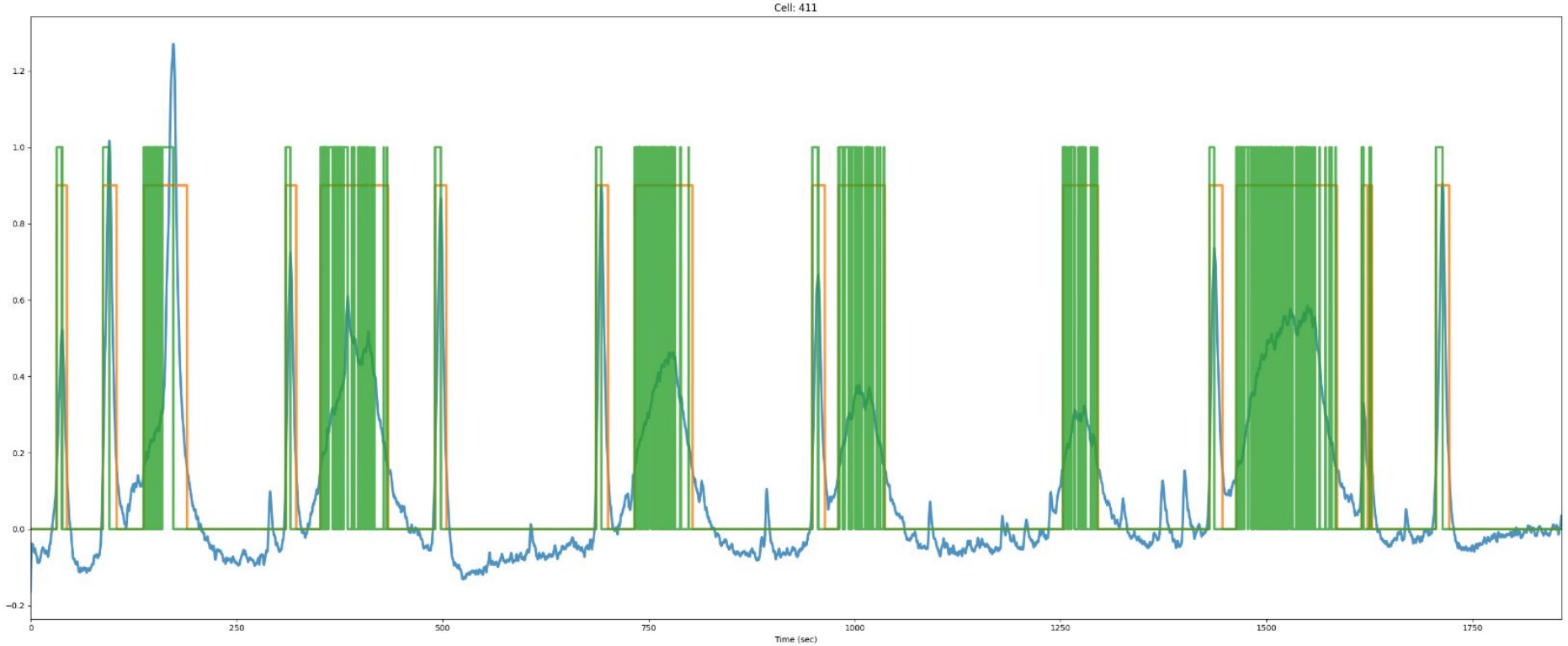
Q: Are there any weird / bad cells??

Zooming in on raster of potentially bad cell (using python

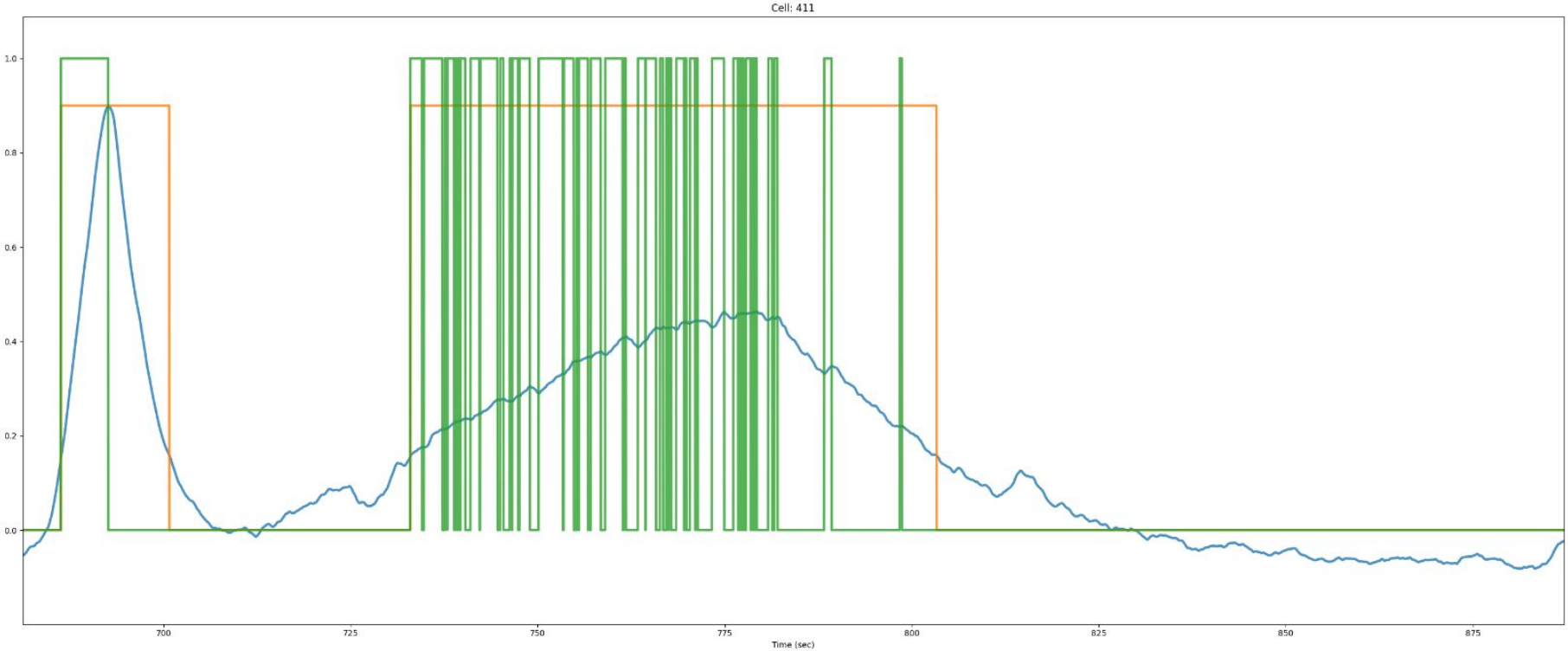


Q: what is the neuron id of the weird / bad cell?

We can then visualize the bad/weird cell

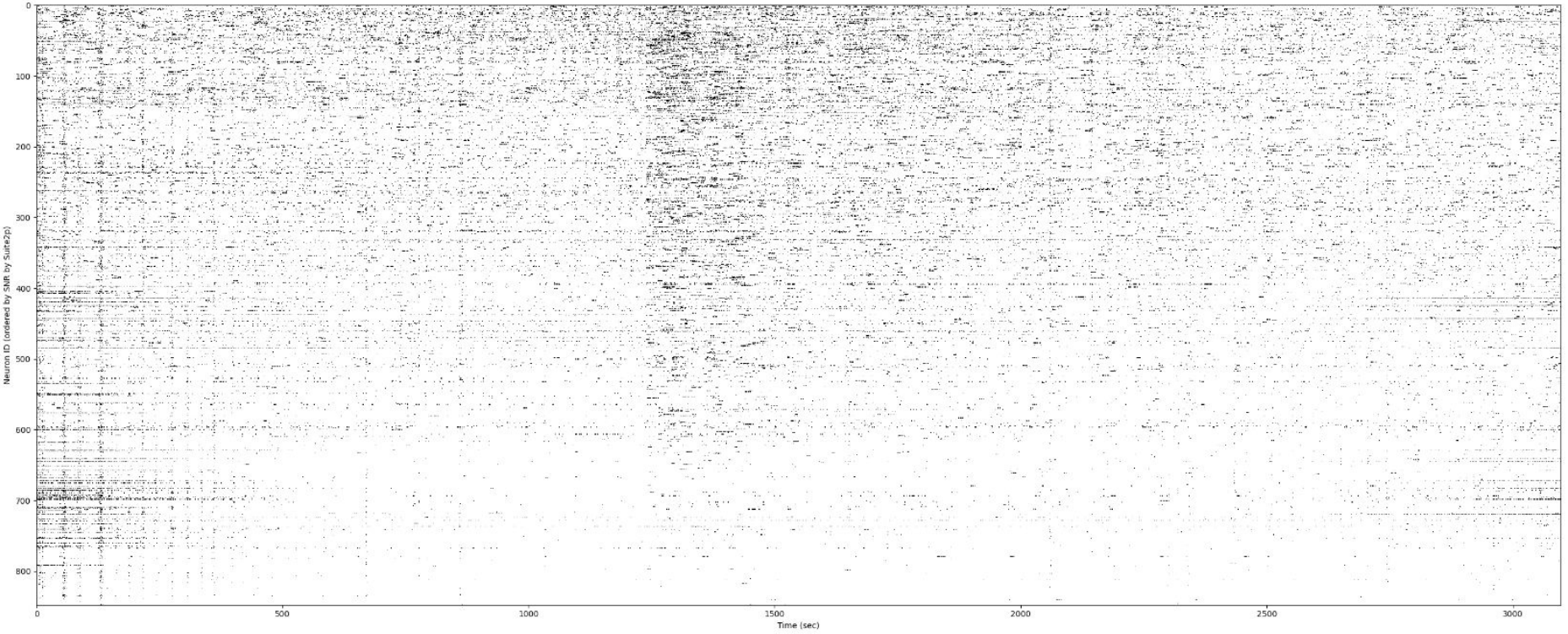


We can also zoom in even more to look at the UP-states found by our algorithm

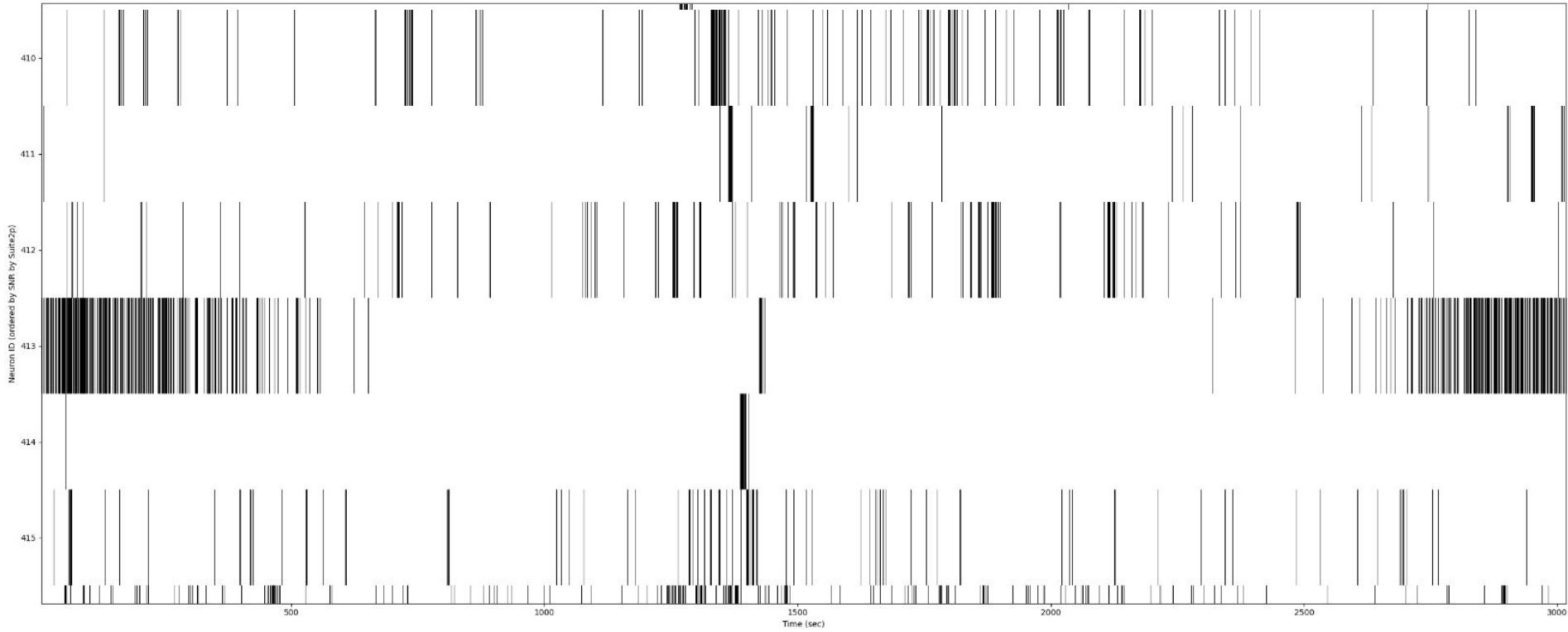


So cell… looks a bit bad

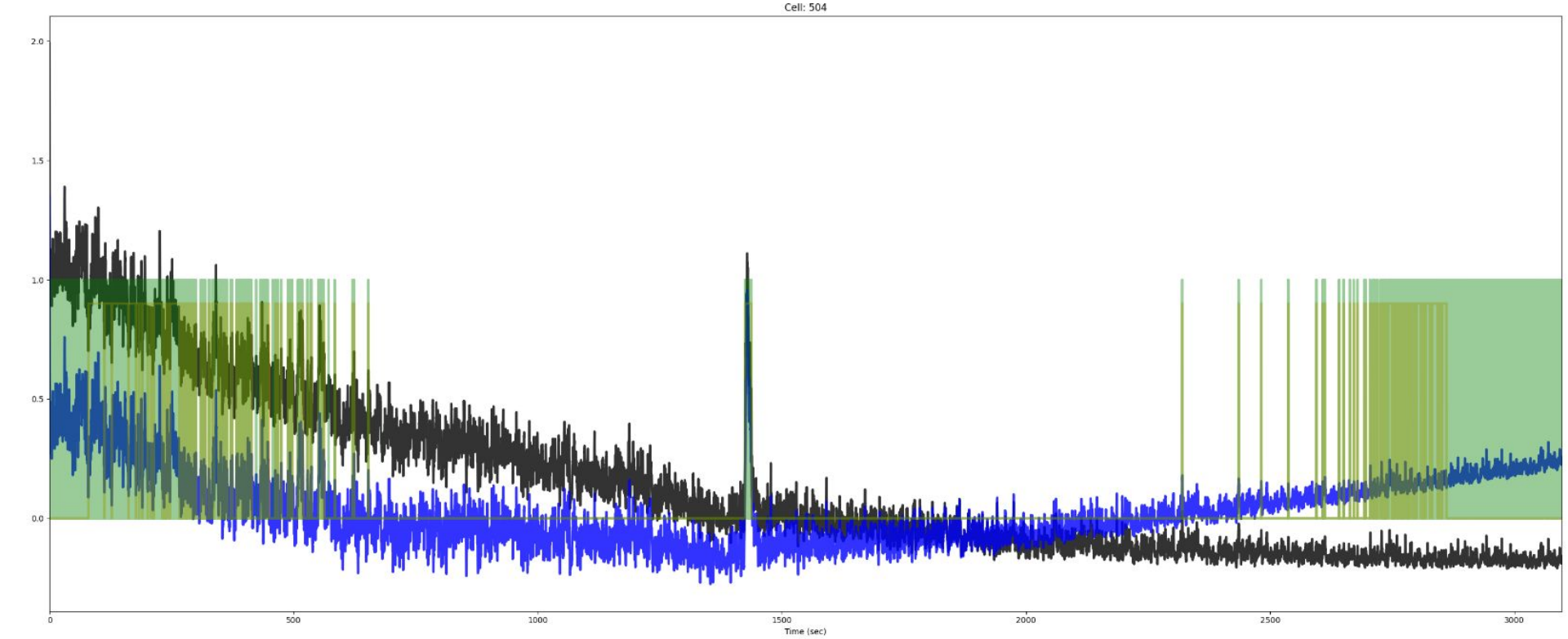
Steffen treadmill data



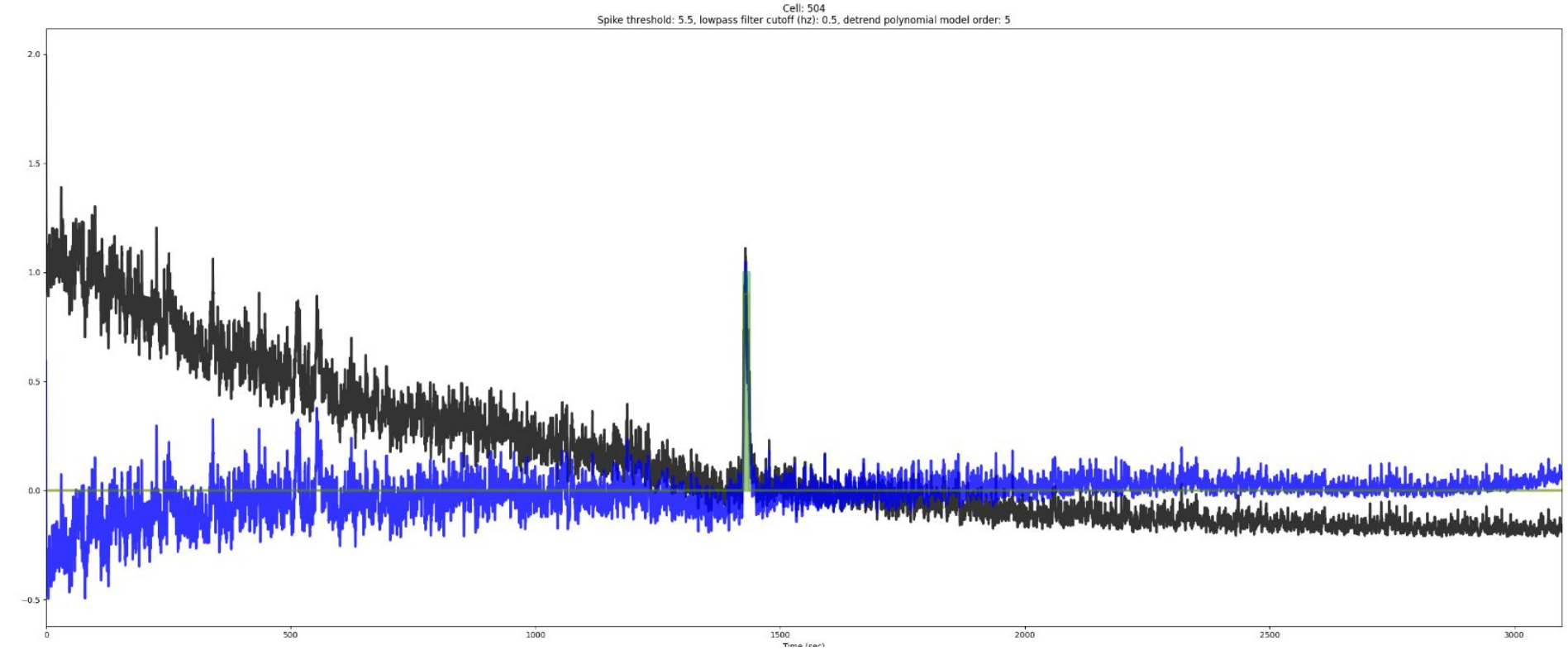
Steffen treadmill data



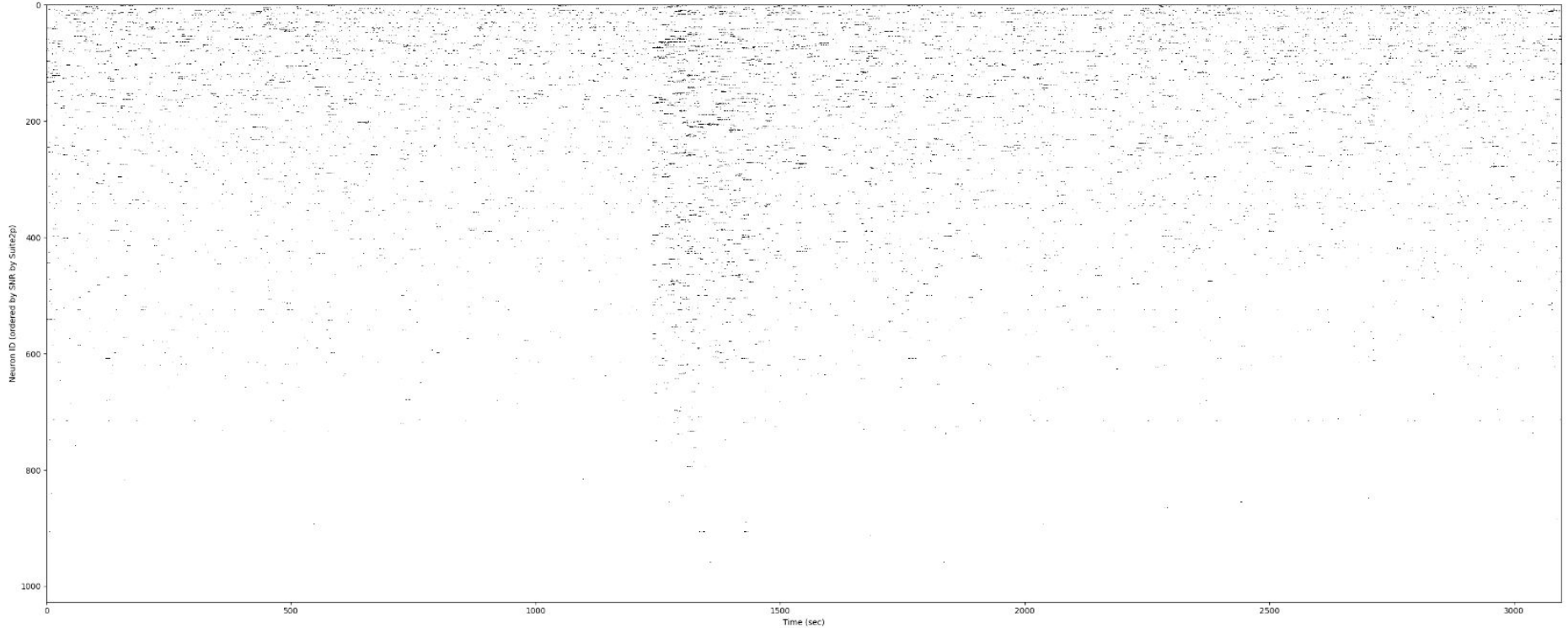
Steffen treadmill data



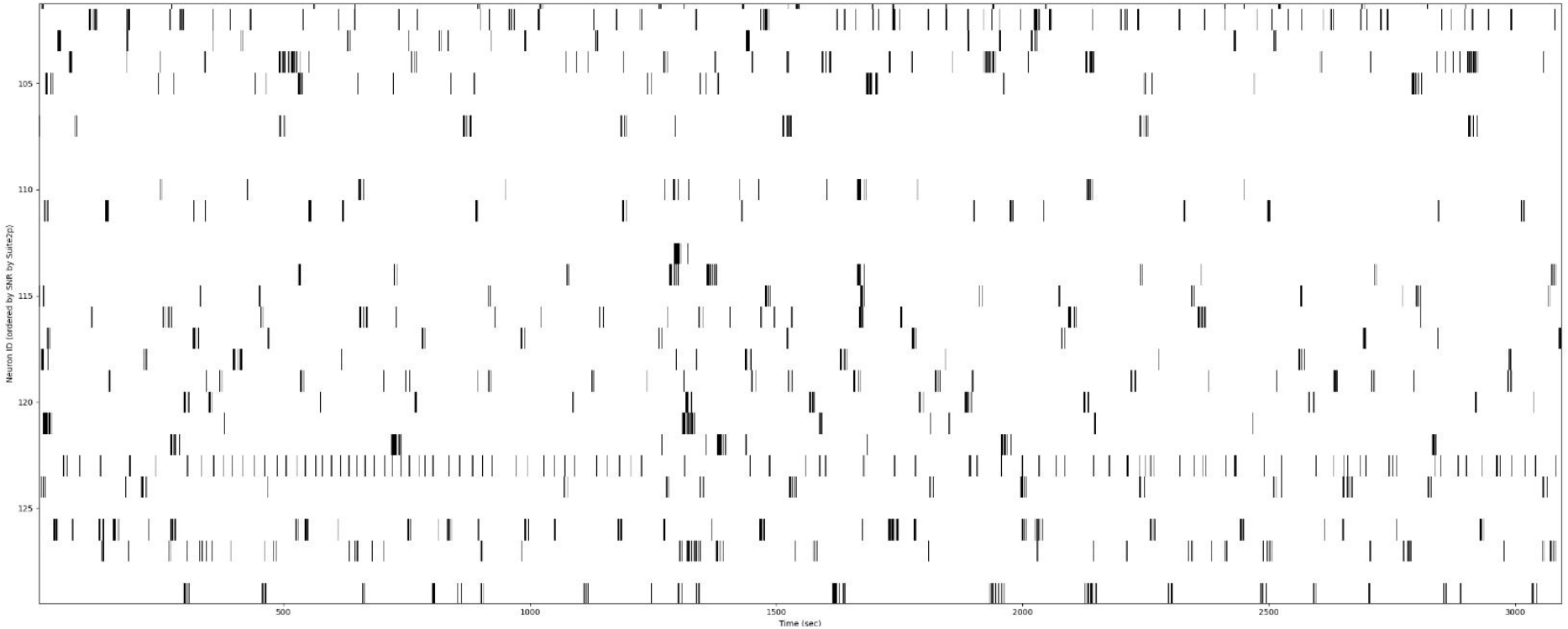
Cell 504 - using - polynomial fit

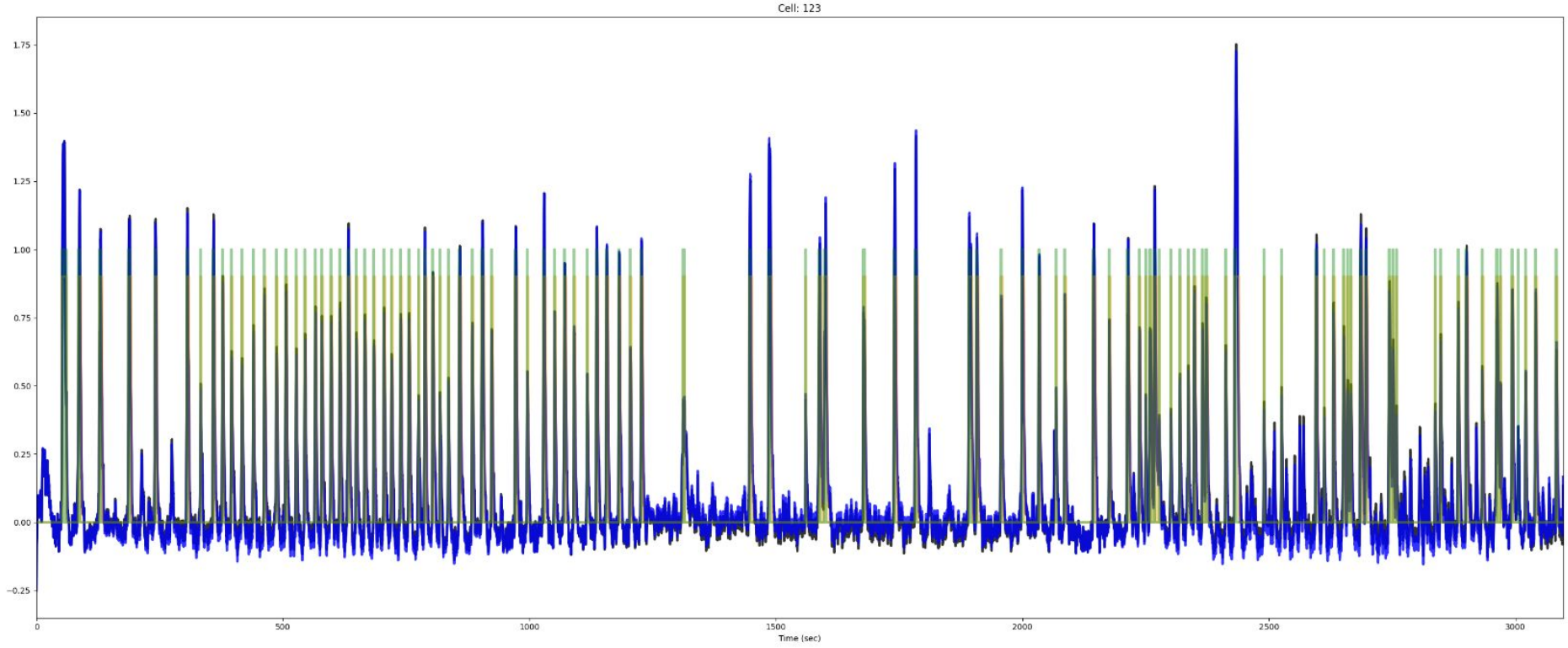


Steffen treadmill data - polynomial fit



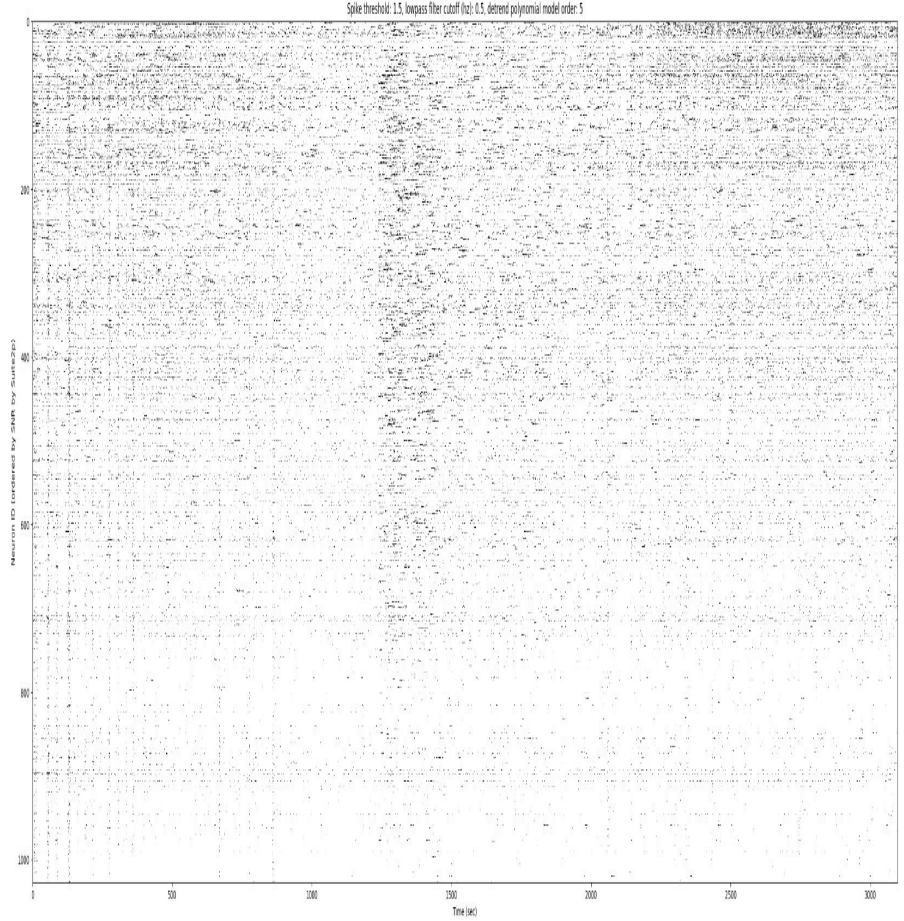
Look at some other cells



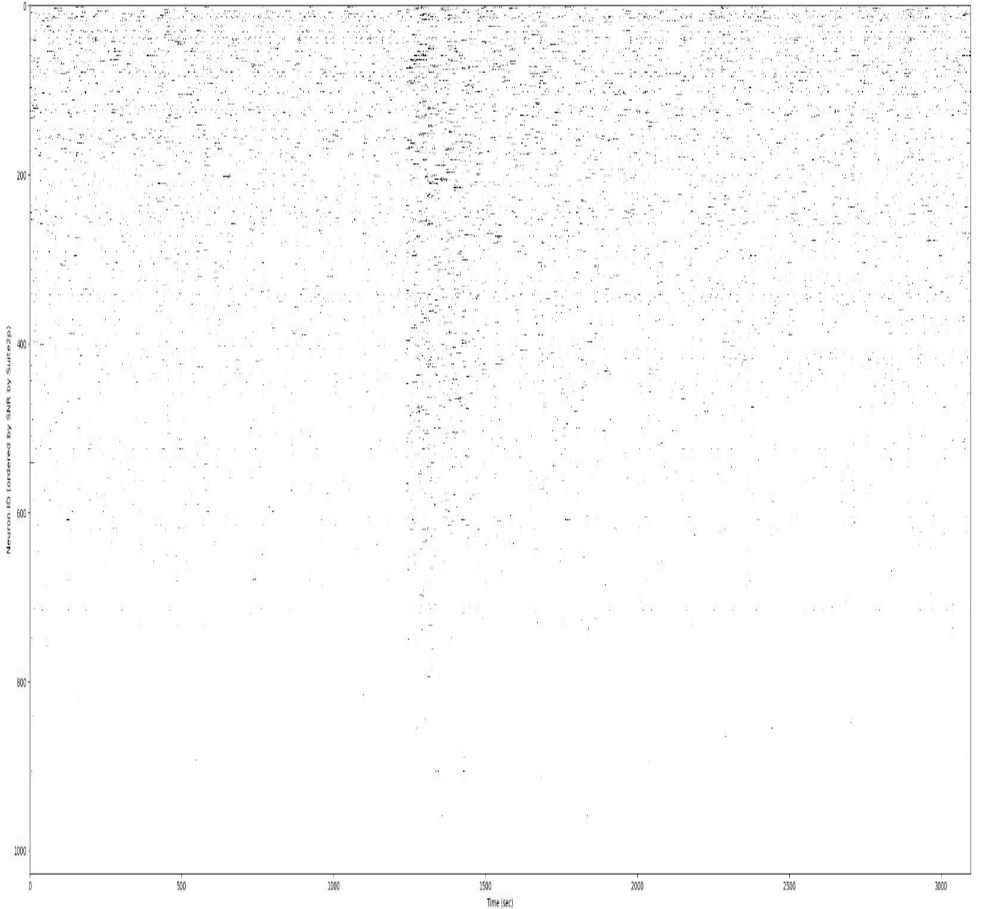

Cell: 123
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
−0.25
0
500
1000
1500
2000
2500
3000
Time (sec)

Side point: why do we have whole FOV vertical stripes in low thresholded data?

Thresh: 1.5



Thresh: 5.5



Open question: Are these stripes to guide us into setting good thresholds?