plot_top_n

December 8, 2022

```
[ ]: %reload_ext autoreload
     %autoreload 2

     import matplotlib.pyplot as plt
     import numpy as np
     import sys
     sys.path.append(r'C:\Users\matt_analysis\Documents\GitHub\caImageAnalysis')


     from fish import LegacyFish as Fish
     from pathutils import pathcrawler
     from constants import invStimDict, monocular_dict, baseBinocs
     import volumes
```

1 find the paths

```
[2]: fishpaths = {3 : pathcrawler(r'D:\Data\Imaging\2022\Nov82022_3dpf', set(), [],␣
      ↪"fish"),
                  4 : pathcrawler(r'D:\Data\Imaging\2022\Nov92022_4dpf', set(), [],␣
      ↪"fish"),
                  5 : pathcrawler(r'D:\Data\Imaging\2022\Nov102022_5dpf', set(), [],␣
      ↪"fish"),}
```

2 make class objects per path

```
[3]: fish = {i : [] for i in fishpaths.keys()}
     for k in fishpaths.keys():
         for p in fishpaths[k]:
             f = Fish(p, stimkey='output')
             f.stimulus_df_condensed.loc[:, 'stim_nameINV'] = f.
      ↪stimulus_df_condensed.stim_name.map(invStimDict)
             fish[k].append(f)
```

```
C:\Soft_Kitty\Anaconda3\envs\caiman\lib\site-
packages\pandas\core\generic.py:5516: SettingWithCopyWarning:
```

```
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-
docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  self[name] = value
C:\Soft_Kitty\Anaconda3\envs\caiman\lib\site-
packages\pandas\core\indexing.py:1667: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-
docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  self.obj[key] = value
```

3 process a few example fish

[4]:

```
allthresholds = 0.75
zerobool = True # this will inflate correlations -- unsure if to my benefit or not will filter Off-responses&thelike

inds = {3: 0, 4: 0, 5: 0}
used_fish = {k : fish[k][v] for k,v in inds.items()}

for f in used_fish.values():
    f.zdiff_stimdicts()
    f.zdiff_booldf(threshold=allthresholds, zero_arr=zerobool)
```

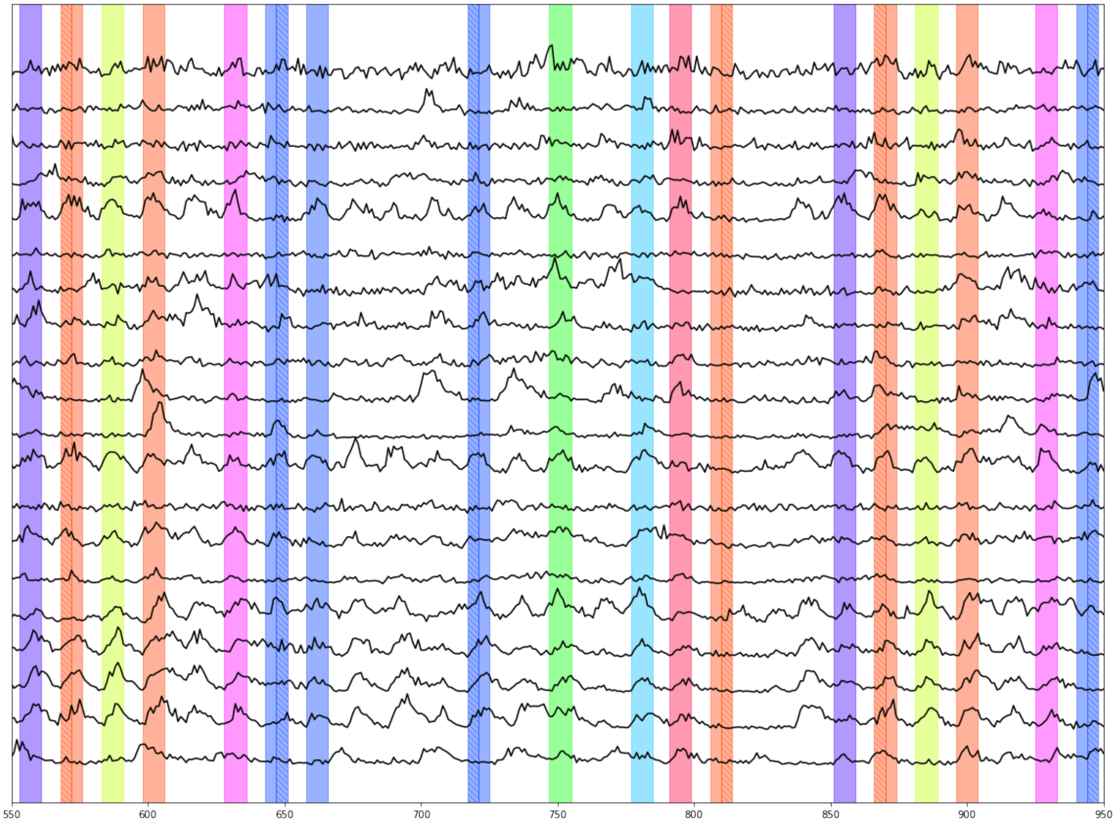
```
C:\Soft_Kitty\Anaconda3\envs\caiman\lib\site-
packages\pandas\core\indexing.py:1773: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-
docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  self._setitem_single_column(ilocs[0], value, pi)
100%|
     | 5/5 [00:07<00:00,  1.56s/it]
 60%|
| 3/5 [00:04<00:03,  1.53s/it]C:\Soft_Kitty\Anaconda3\envs\caiman\lib\site-
packages\numpy\lib\function_base.py:2691: RuntimeWarning: invalid value
encountered in true_divide
  c /= stddev[:, None]
C:\Soft_Kitty\Anaconda3\envs\caiman\lib\site-
packages\numpy\lib\function_base.py:2692: RuntimeWarning: invalid value
encountered in true_divide
  c /= stddev[None, :]
```

```
100%|
     | 5/5 [00:07<00:00,  1.41s/it]
100%|
     | 5/5 [00:08<00:00,  1.62s/it]
100%|
     | 5/5 [00:07<00:00,  1.45s/it]
100%|
     | 5/5 [00:09<00:00,  1.97s/it]
100%|
     | 5/5 [00:08<00:00,  1.80s/it]
```

4 plot top N (20) right neurons @ 3dpf

[5]:

```
nemo = used_fish[3]
stimChoice = 'right'

stim_offset = 5

nrns = volumes.grabPeakNeurons(nemo, stimChoice, 20)

plt.figure(figsize=(20,15))

for z in range(20):
    plt.plot(np.arange(len(nrns[z])), nrns[z] + z, color='black')

monoc_stims = nemo.stimulus_df_condensed[(nemo.stimulus_df_condensed.
 ↪stim_nameINV.isin(monocular_dict.keys()))|
                                         (nemo.stimulus_df_condensed.
 ↪stim_nameINV.isin(baseBinocs))]
frames = monoc_stims['0_frame'].values
stimmies = monoc_stims['stim_nameINV'].values

for s, stimmy in zip(frames,stimmies):
    if stimmy in monocular_dict.keys():
        plt.axvspan(s-1, s+stim_offset+2, color=monocular_dict[stimmy], alpha=0.
 ↪4)

    if stimmy in baseBinocs:
        begin =  s-1
        end = s+stim_offset+2
        midpt = begin + (end - begin)//2

        if stimmy == 'lateral_left':
            plt.axvspan(begin, midpt, color=monocular_dict['left'], alpha=0.4,␣
 ↪hatch=r'\\\\')
            plt.axvspan(midpt, end, color=monocular_dict['left'], alpha=0.4)
        if stimmy == 'medial_left':
            plt.axvspan(begin, midpt, color=monocular_dict['left'], alpha=0.4)
            plt.axvspan(midpt, end, color=monocular_dict['left'], alpha=0.4,␣
 ↪hatch=r'\\\\')

        if stimmy == 'lateral_right':
            plt.axvspan(begin, midpt, color=monocular_dict['right'], alpha=0.4)
            plt.axvspan(midpt, end, color=monocular_dict['right'], alpha=0.4,␣
 ↪hatch=r'\\\\')
        if stimmy == 'medial_right':
            plt.axvspan(begin, midpt, color=monocular_dict['right'], alpha=0.4,␣
 ↪hatch=r'\\\\')
            plt.axvspan(midpt, end, color=monocular_dict['right'], alpha=0.4)


plt.xlim(550, 950)
plt.yticks([])
plt.show()
```

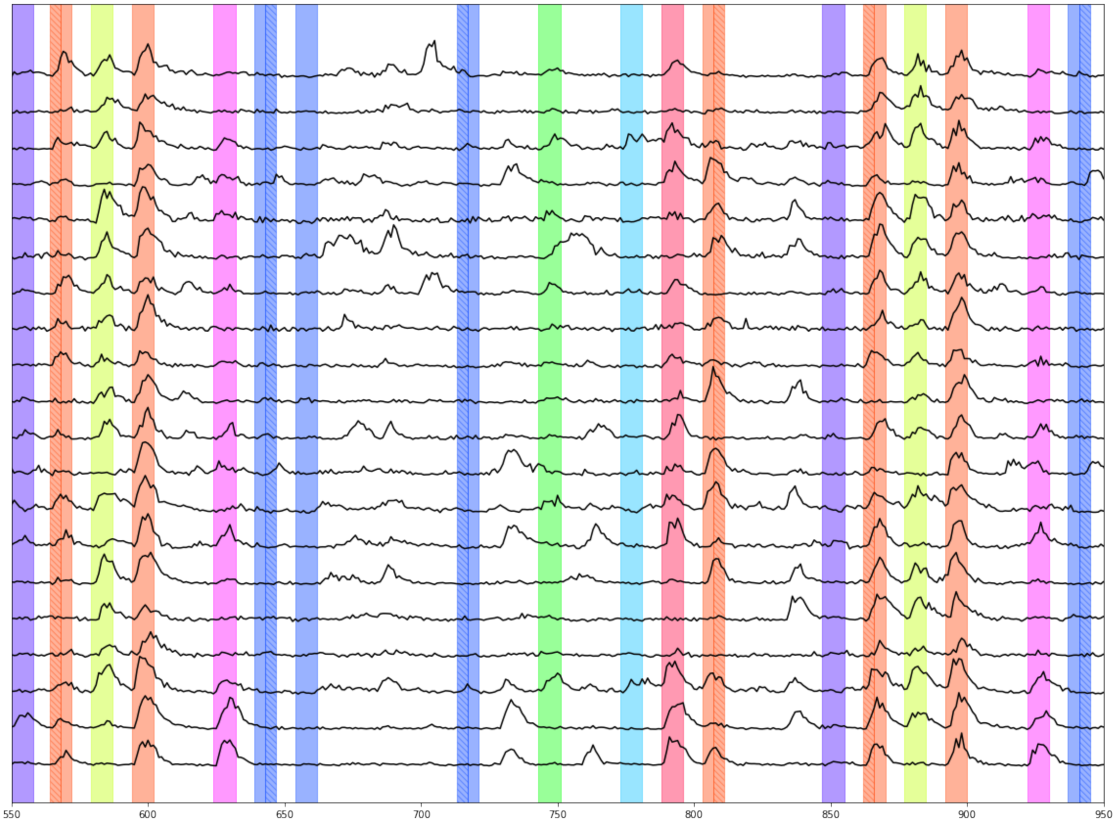


5 plot top N (20) right neurons @ 5dpf

[6]:

```
nemo = used_fish[5]
stimChoice = 'right'

stim_offset = 5

nrns = volumes.grabPeakNeurons(nemo, stimChoice, 20)

plt.figure(figsize=(20,15))

for z in range(20):
    plt.plot(np.arange(len(nrns[z])), nrns[z] + z, color='black')

monoc_stims = nemo.stimulus_df_condensed[(nemo.stimulus_df_condensed.
 ↪stim_nameINV.isin(monocular_dict.keys()))|
                                         (nemo.stimulus_df_condensed.
 ↪stim_nameINV.isin(baseBinocs))]
frames = monoc_stims['0_frame'].values
stimmies = monoc_stims['stim_nameINV'].values

for s, stimmy in zip(frames,stimmies):
    if stimmy in monocular_dict.keys():
        plt.axvspan(s-1, s+stim_offset+2, color=monocular_dict[stimmy], alpha=0.
 ↪4)

    if stimmy in baseBinocs:
        begin =  s-1
        end = s+stim_offset+2
        midpt = begin + (end - begin)//2

        if stimmy == 'lateral_left':
            plt.axvspan(begin, midpt, color=monocular_dict['left'], alpha=0.4,␣
 ↪hatch=r'\\\\')
            plt.axvspan(midpt, end, color=monocular_dict['left'], alpha=0.4)
        if stimmy == 'medial_left':
            plt.axvspan(begin, midpt, color=monocular_dict['left'], alpha=0.4)
            plt.axvspan(midpt, end, color=monocular_dict['left'], alpha=0.4,␣
 ↪hatch=r'\\\\')

        if stimmy == 'lateral_right':
            plt.axvspan(begin, midpt, color=monocular_dict['right'], alpha=0.4)
            plt.axvspan(midpt, end, color=monocular_dict['right'], alpha=0.4,␣
 ↪hatch=r'\\\\')
        if stimmy == 'medial_right':
            plt.axvspan(begin, midpt, color=monocular_dict['right'], alpha=0.4,␣
 ↪hatch=r'\\\\')
```

```
            plt.axvspan(midpt, end, color=monocular_dict['right'], alpha=0.4)


plt.xlim(550, 950)
plt.yticks([])
plt.show()
```



[ ]:

```
```