Neural Data Science

Lecturer: Prof. Dr. Philipp Berens

Tutors: Jonas Beck, Ziwei Huang, Rita González Márquez

Summer term 2023

Student name: Kathrin Root, Alexander Wendt, Patrick Weygoldt

Coding Lab 3

- **Data**: Download the data file `nds_cl_3_*.csv` from ILIAS and save it in a subfolder `../data/`.
- **Dependencies**: You don't have to use the exact versions of all the dependencies in this notebook, as long as they are new enough. But if you run "Run All" in Jupyter and the boilerplate code breaks, you probably need to upgrade them.

Two-photon imaging is widely used to study computations in populations of neurons. In this exercise sheet we will study properties of different indicators and work on methods to infer spikes from calcium traces. All data is provided at a sampling rate of 100 Hz. For analysis, please resample it to 25 Hz using `scipy.signal.decimate`.

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
from scipy import signal
from scipy.io import loadmat
from __future__ import annotations

%matplotlib inline

%load_ext jupyter_black

%load_ext watermark
%watermark --time --date --timezone --updated --python --iversions --watermark -p sklearn
```

```
The jupyter_black extension is already loaded. To reload it, use:
  %reload_ext jupyter_black
The watermark extension is already loaded. To reload it, use:
  %reload_ext watermark
```

```
Last updated: 2023-05-09 19:56:04CEST

Python implementation: CPython
Python version       : 3.11.3
IPython version      : 8.11.0

sklearn: 0.0.post1

oasis     : 0.2.0
matplotlib: 3.7.1
seaborn   : 0.12.2
numpy     : 1.24.3
scipy     : 1.10.1
pandas    : 1.5.3

Watermark: 2.3.1
```

```
plt.style.use("../matplotlib_style.txt")
```

Load data

```
# ogb dataset from Theis et al. 2016 Neuron
ogb_calcium = pd.read_csv("../data/nds_cl_3_ogb_calcium.csv", header=0)
ogb_spikes = pd.read_csv("../data/nds_cl_3_ogb_spikes.csv", header=0)

# gcamp dataset from Chen et al. 2013 Nature
gcamp_calcium = pd.read_csv("../data/nds_cl_3_gcamp2_calcium.csv", header=0)
gcamp_spikes = pd.read_csv("../data/nds_cl_3_gcamp2_spikes.csv", header=0)
```

```
ogb_calcium.shape, ogb_spikes.shape, gcamp_calcium.shape, gcamp_spikes.shape
```

```
((71986, 11), (71986, 11), (23973, 37), (23973, 37))
```

```
ogb_spikes.head()
ogb_calcium.head()
```

	0	1	2	3	4	5	6	7	8	9
0	-0.234928	0.689186	2.578560	0.636770	-0.015140	0.819771	2.442105	0.391310	0.223523	1.557
1	-0.182441	0.869132	2.868601	0.596164	0.022464	0.831411	2.930201	0.490213	0.116095	1.628
2	-0.049257	0.949273	2.784989	0.711875	0.040028	0.877191	3.065872	0.610873	0.154437	1.479
3	-0.032876	0.848802	2.430735	0.940943	0.038616	0.975941	3.051014	0.714453	0.335288	1.302
4	-0.125313	0.665088	2.064211	1.168007	0.014035	1.156689	2.967063	0.737085	0.550485	1.234

```
ogb_spikes.head()
```

	0	1	2	3	4	5	6	7	8	9	10
0	0	0	0.0	0.0	0	0	0	0.0	0	0.0	0
1	0	0	0.0	0.0	0	1	0	0.0	0	0.0	0
2	0	0	0.0	0.0	0	0	0	0.0	0	0.0	0
3	0	0	0.0	0.0	0	1	0	0.0	0	0.0	0
4	0	0	0.0	0.0	0	0	0	0.0	0	0.0	0

Task 1: Visualization of calcium and spike recordings

We start again by plotting the raw data - calcium and spike traces in this case. One dataset has been recorded using the synthetic calcium indicator OGB-1 at population imaging zoom (~100 cells in a field of view) and the other one using the genetically encoded indicator GCamp6f zooming in on individual cells. Plot the traces of an example cell from each dataset to show how spikes and calcium signals are related. A good example cell for the OGB-dataset is cell 5. For the CGamp-dataset a good example is cell 6. Zoom in on a small segment of tens of seconds and offset the traces such that a valid comparison is possible.

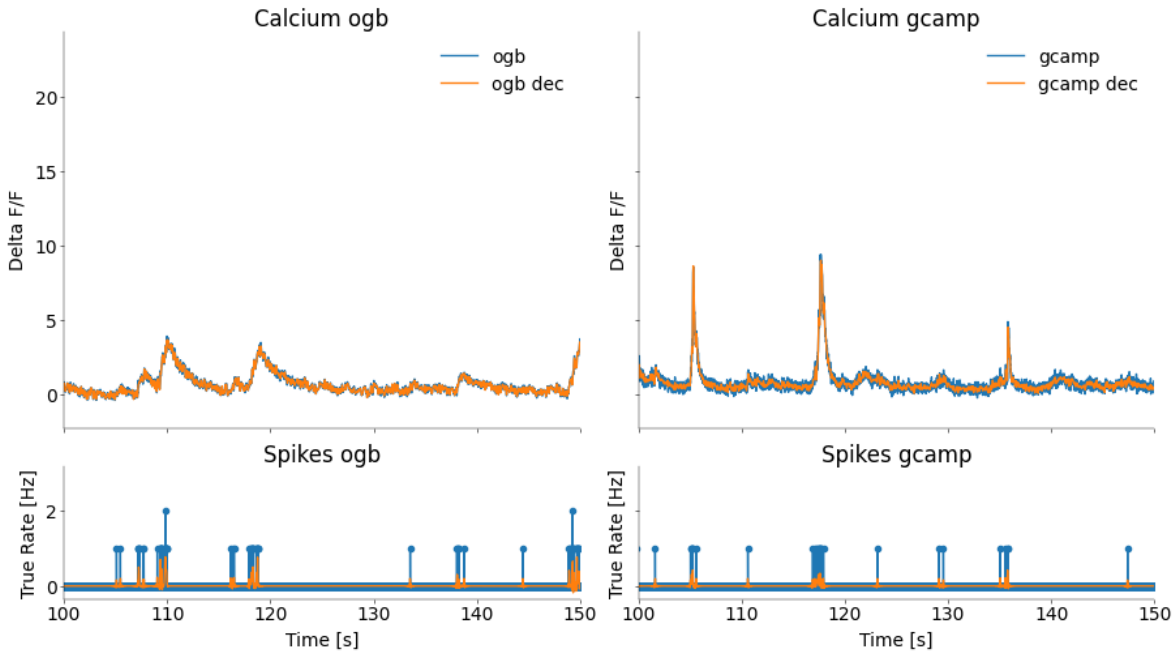
Grading: 2 pts

```
good_cell_ogb = 4
good_cell_gcamp = 5

samplerate = 25
downsaple_factor = 100 / samplerate

# Calcium data
calcium_ogb_cell = ogb_calcium[f"{good_cell_ogb}"].to_numpy()
calcium_ogb_cell_dec = signal.decimate(calcium_ogb_cell, int(downsaple_factor))

calcium_gcamp_cell = gcamp_calcium[f"{good_cell_gcamp}"].to_numpy()
```

```
calcium_gcamp_cell_dec = signal.decimate(calcium_gcamp_cell, int(downsaple_factor))


# Spike data
spike_ogb_cell = ogb_spikes[f"{good_cell_ogb}"].to_numpy()
spike_ogb_cell_dec = signal.decimate(spike_ogb_cell, int(downsaple_factor))

spike_gcamp_cell = gcamp_spikes[f"{good_cell_gcamp}"].to_numpy()
spike_gcamp_cell_dec = signal.decimate(spike_gcamp_cell, int(downsaple_factor))


# -------------------------
# make new time axis

time_ogb = np.arange(0, len(calcium_ogb_cell)) / 100
time_ogb_dec = np.arange(0, len(calcium_ogb_cell_dec)) / samplerate
time_gcamp = np.arange(0, len(calcium_gcamp_cell)) / 100
time_gcamp_dec = np.arange(0, len(calcium_gcamp_cell_dec)) / samplerate

fig, axs = plt.subplots(
    2,
    2,
    figsize=(9, 5),
    height_ratios=[3, 1],
    layout="constrained",
    sharex=True,
    sharey="row",
)
xlims_ogb = [100, 150]
xlims_gcamp = [100, 150]
axs[0, 0].plot(time_ogb, calcium_ogb_cell, label="ogb")
axs[0, 0].plot(time_ogb_dec, calcium_ogb_cell_dec, label="ogb dec")
axs[0, 0].set_title("Calcium ogb")
axs[0, 0].set_xlim(xlims_ogb)
axs[0, 0].set_ylabel("Delta F/F")
axs[0, 0].legend()


axs[0, 1].plot(time_gcamp, calcium_gcamp_cell, label="gcamp")
axs[0, 1].plot(time_gcamp_dec, calcium_gcamp_cell_dec, label="gcamp dec")
axs[0, 1].set_title("Calcium gcamp")
```

```
axs[0, 1].set_ylabel("Delta F/F")
axs[0, 1].set_xlim(xlims_gcamp)
axs[0, 1].legend()

axs[1, 0].plot(time_ogb, spike_ogb_cell)
axs[1, 0].plot(time_ogb_dec, spike_ogb_cell_dec)
axs[1, 0].set_title("Spikes ogb")
axs[1, 0].set_xlim(xlims_ogb)
axs[1, 0].scatter(time_ogb, spike_ogb_cell)
axs[1, 0].set_ylabel("True Rate [Hz]")
axs[1, 0].set_xlabel("Time [s]")

axs[1, 1].plot(time_gcamp, spike_gcamp_cell)
axs[1, 1].plot(time_gcamp_dec, spike_gcamp_cell_dec)
axs[1, 1].scatter(time_gcamp, spike_gcamp_cell)
axs[1, 1].set_title("Spikes gcamp")
axs[1, 1].set_xlim(xlims_gcamp)
axs[1, 1].set_ylabel("True Rate [Hz]")
axs[1, 1].set_xlabel("Time [s]")


# plot raw gcamp data
```

```
Text(0.5, 0, 'Time [s]')
```



Task 2: Simple deconvolution

It is clear from the above plots that the calcium events happen in relationship to the spikes. As a first simple algorithm implement a deconvolution approach like presented in the lecture in the function `deconv_ca`. Assume an exponential kernel where the decay constant depends on the indicator ($\tau_{OGB} = 0.5s$, $\tau_{GCaMP} = 0.1s$). As we know that there can be no negative rates, apply a heavyside function to the output. Plot the kernel as well as an example cell with true and deconvolved spike rates. Scale the signals such as to facilitate comparisons. You can use functions from `scipy` for this.

Grading: 3 pts

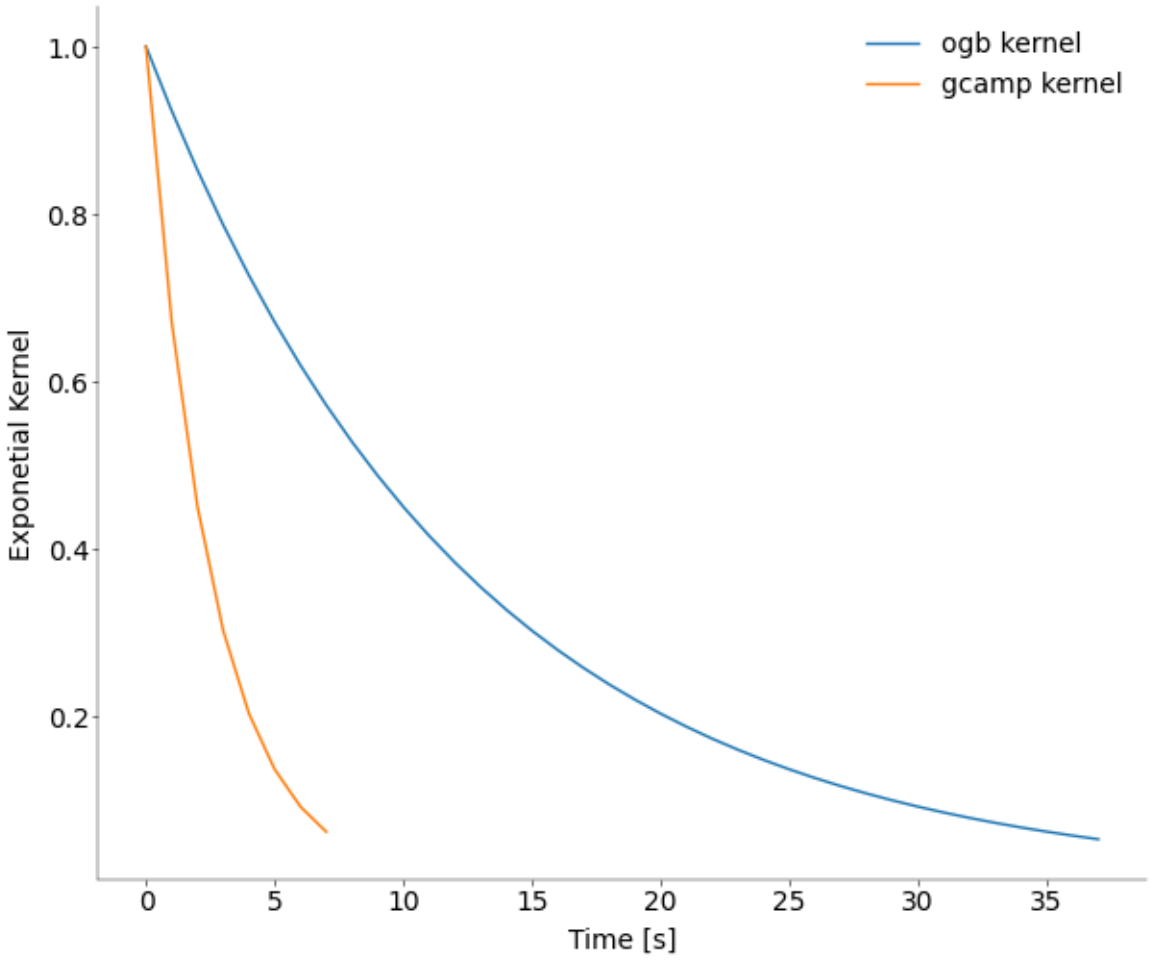
```
def deconv_ca(ca, tau, dt):
    """Compute the deconvolution of the calcium signal.

    Parameters
    ----------

    ca: np.array, (n_points,)
        Calcium trace

    tau: float
```

```
    decay constant of conv kernel

dt: float
    sampling interval. 1/samplerate

Return
------

sp_hat: np.array
kernel: np.array
"""

# get the filter coefficients
coeffs = signal.butter(4, 0.3, "lowpass", fs=dt, output="sos")
# pass the filter coefficients  and the data to the filter function
filtered_data = signal.sosfiltfilt(sos=coeffs, x=ca)

# initialize the smoothing algorithm
n = 0
while n < 5000:
    # find all peaks in the filtered data
    all_peaks = signal.find_peaks(filtered_data)[0]
    diff_peaks = np.abs(np.diff(filtered_data[all_peaks]))
    # search for the smallest difference between peaks
    p_min = np.argmin(diff_peaks)
    # set the datapoints around the peak to the mean of the segment
    datapoints = 25
    mean_segment = np.mean(
        filtered_data[
            np.arange(all_peaks[p_min] - datapoints, all_peaks[p_min] + datapoints)
        ]
    )
    # replace the datapoints with the mean
    filtered_data[
        np.arange(all_peaks[p_min] - datapoints, all_peaks[p_min] + datapoints)
    ] = mean_segment

    p_min = diff_peaks[p_min]
    # if the difference between peaks is larger than 1, break the loop
    if p_min > 1:
        break
    n += 1
```

```
    kernel = np.exp(-np.arange(0, 3 * tau, 1 / dt) / tau)
    # deconvolve the filtered data with the kernel
    sp_hat, _ = signal.deconvolve(filtered_data, kernel)
    # heavy side function
    sp_hat[sp_hat < 0] = 0
    # pad the array with zeros
    sp_hat = np.pad(sp_hat, (0, len(filtered_data) - len(sp_hat)), "constant")

    return sp_hat, kernel


deconv_calcium_ogb_cell, ogb_kernel = deconv_ca(calcium_ogb_cell_dec, 0.5, samplerate)
deconv_calcium_gcamp_cell, gcamp_kernel = deconv_ca(
    calcium_gcamp_cell_dec, 0.1, samplerate
)
```

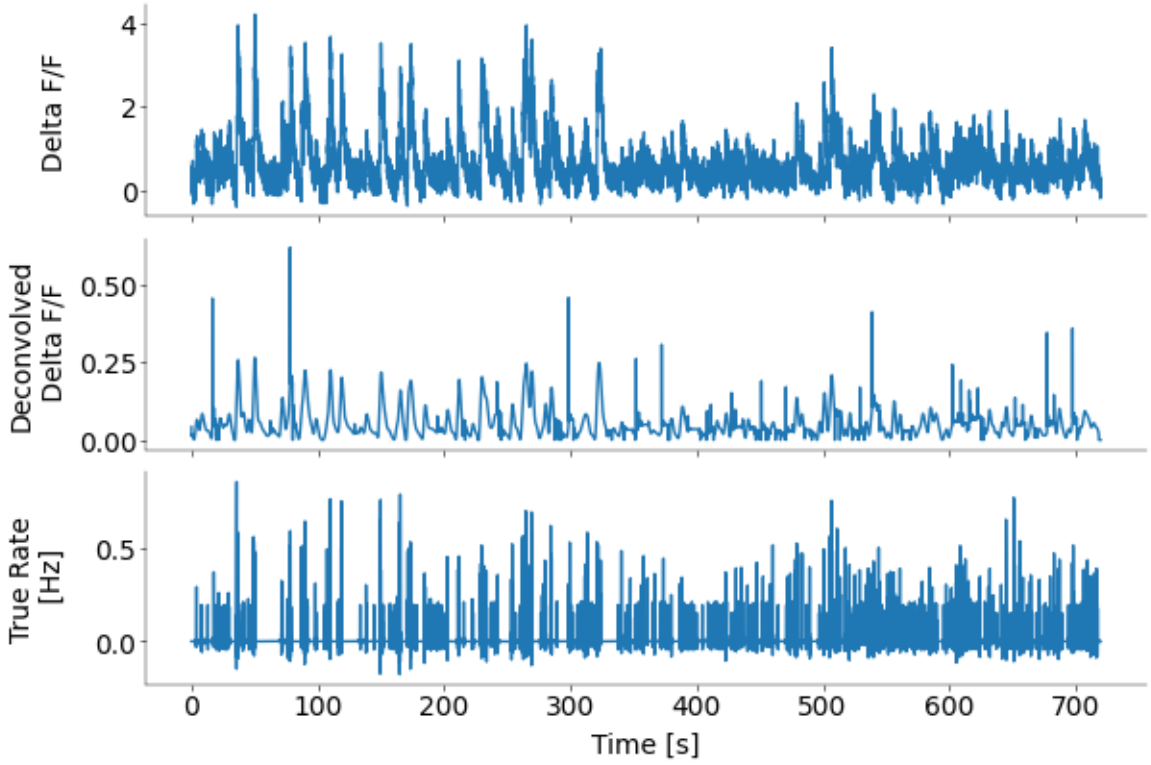
```
fig, ax = plt.subplots(figsize=(6, 5), layout="constrained")

ax.plot(ogb_kernel, label="ogb kernel")
ax.plot(gcamp_kernel, label="gcamp kernel")
ax.set_xlabel("Time [s]")
ax.set_ylabel("Exponetial Kernel")
ax.legend()
```

```
<matplotlib.legend.Legend at 0x281c54790>
```



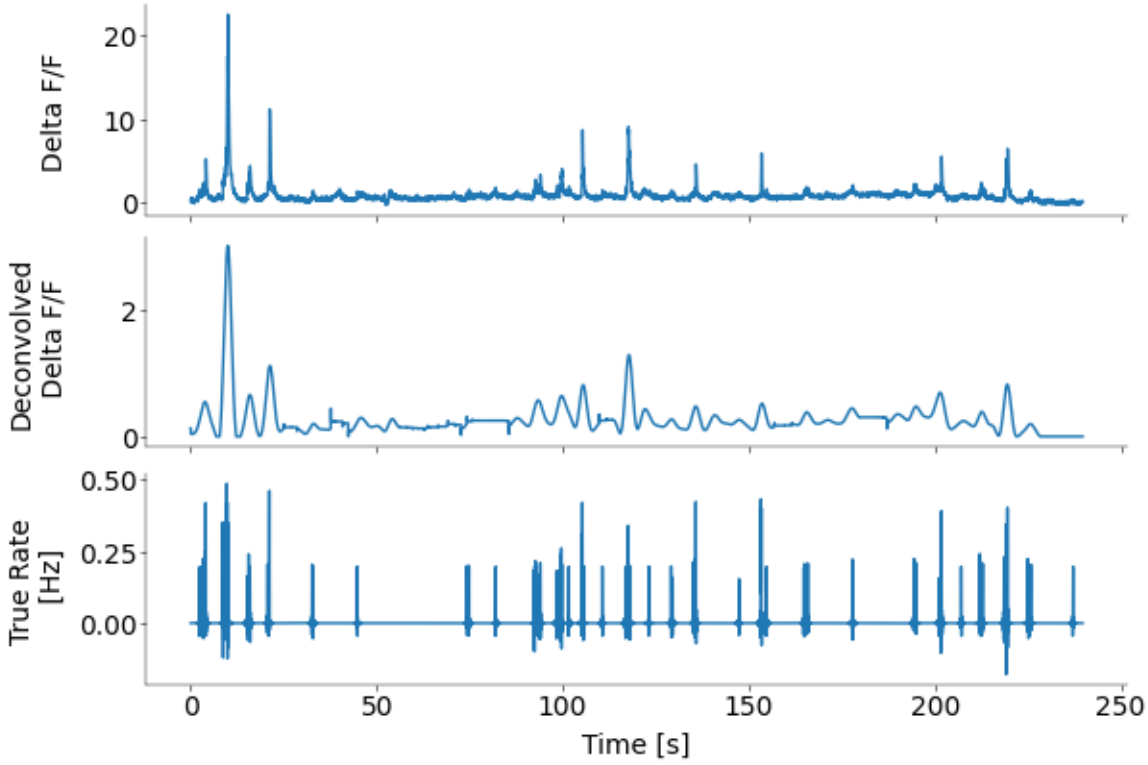

```
# OGB
fig, axs = plt.subplots(
    3,
    1,
    figsize=(6, 4),
    height_ratios=[1, 1, 1],
    gridspec_kw=dict(hspace=0),
    sharex=True,
)

axs[0].plot(time_ogb_dec, calcium_ogb_cell_dec, label="ogb")
axs[1].plot(time_ogb_dec, deconv_calcium_ogb_cell, label="ogb dec")
axs[2].plot(time_ogb_dec, spike_ogb_cell_dec, label="ogb spike")
```

```
axs[2].set_xlabel("Time [s]")
axs[0].set_ylabel("Delta F/F")
axs[1].set_ylabel("Deconvolved\n Delta F/F")
axs[2].set_ylabel("True Rate\n [Hz]")
fig.align_labels()
```




```
# GCAMP
fig, axs = plt.subplots(
    3,
    1,
    figsize=(6, 4),
    height_ratios=[1, 1, 1],
    gridspec_kw=dict(hspace=0),
    sharex=True,
)
axs[0].plot(time_gcamp_dec, calcium_gcamp_cell_dec, label="ogb")
axs[1].plot(time_gcamp_dec, deconv_calcium_gcamp_cell, label="ogb dec")
```

```
axs[2].plot(time_gcamp_dec, spike_gcamp_cell_dec, label="ogb spike")
axs[2].set_xlabel("Time [s]")
axs[0].set_ylabel("Delta F/F")
axs[1].set_ylabel("Deconvolved\n Delta F/F")
axs[2].set_ylabel("True Rate\n [Hz]")
fig.align_labels()
```



Task 3: Run more complex algorithm

As reviewed in the lecture, a number of more complex algorithms for inferring spikes from calcium traces have been developed. Run an implemented algorithm on the data and plot the result. There is a choice of algorithms available, for example:

- Vogelstein: oopsi
- Theis: c2s
- Friedrich: OASIS

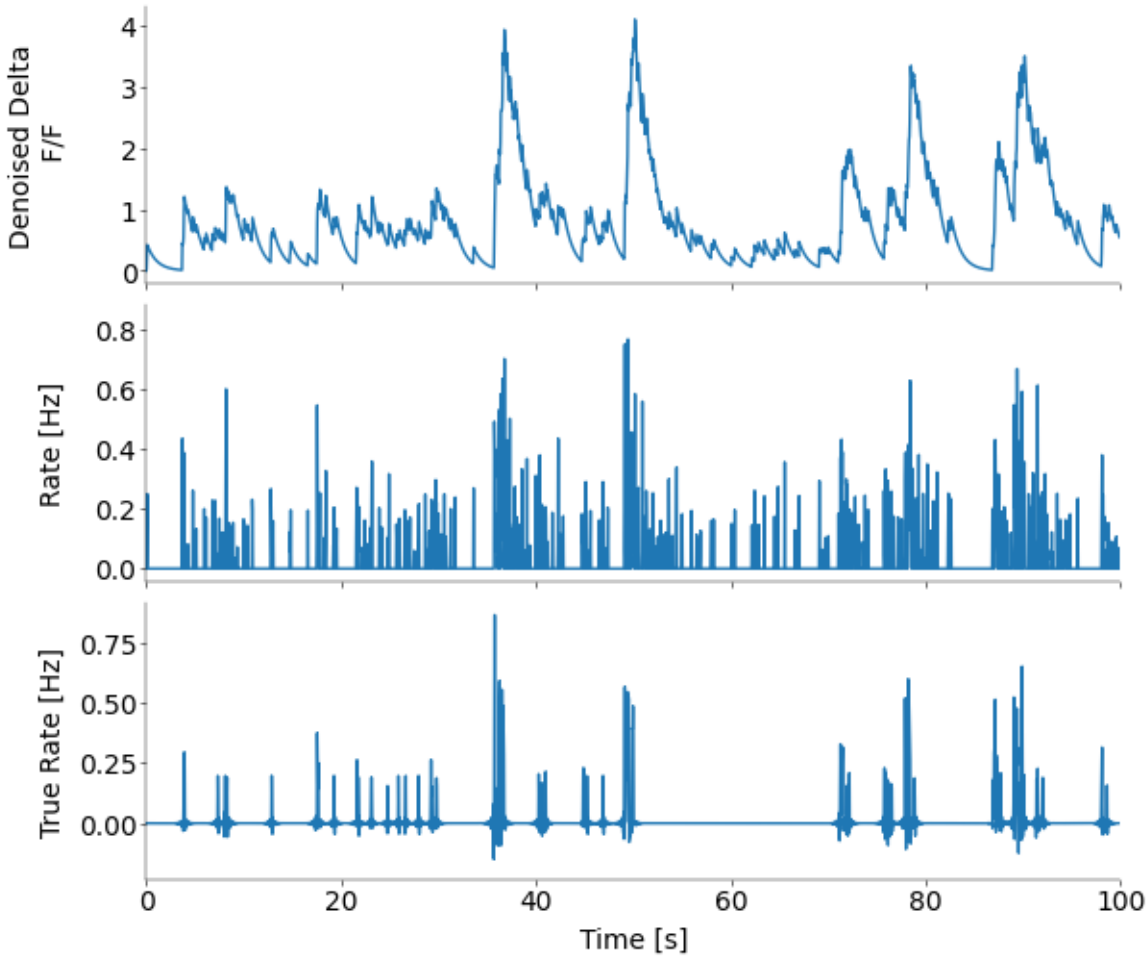
Grading: 2 pts

```
# run this cell to download the oopsi.py file if you haven't already mannually downloaded
# and put it in the same folder as this notebook
!wget https://raw.githubusercontent.com/liubenyuan/py-oopsi/master/oopsi.py
```

```
zsh:1: command not found: wget
```

```
import oasis

c, s, b, g, lam = oasis.functions.deconvolve(calcium_ogb_cell_dec)
```

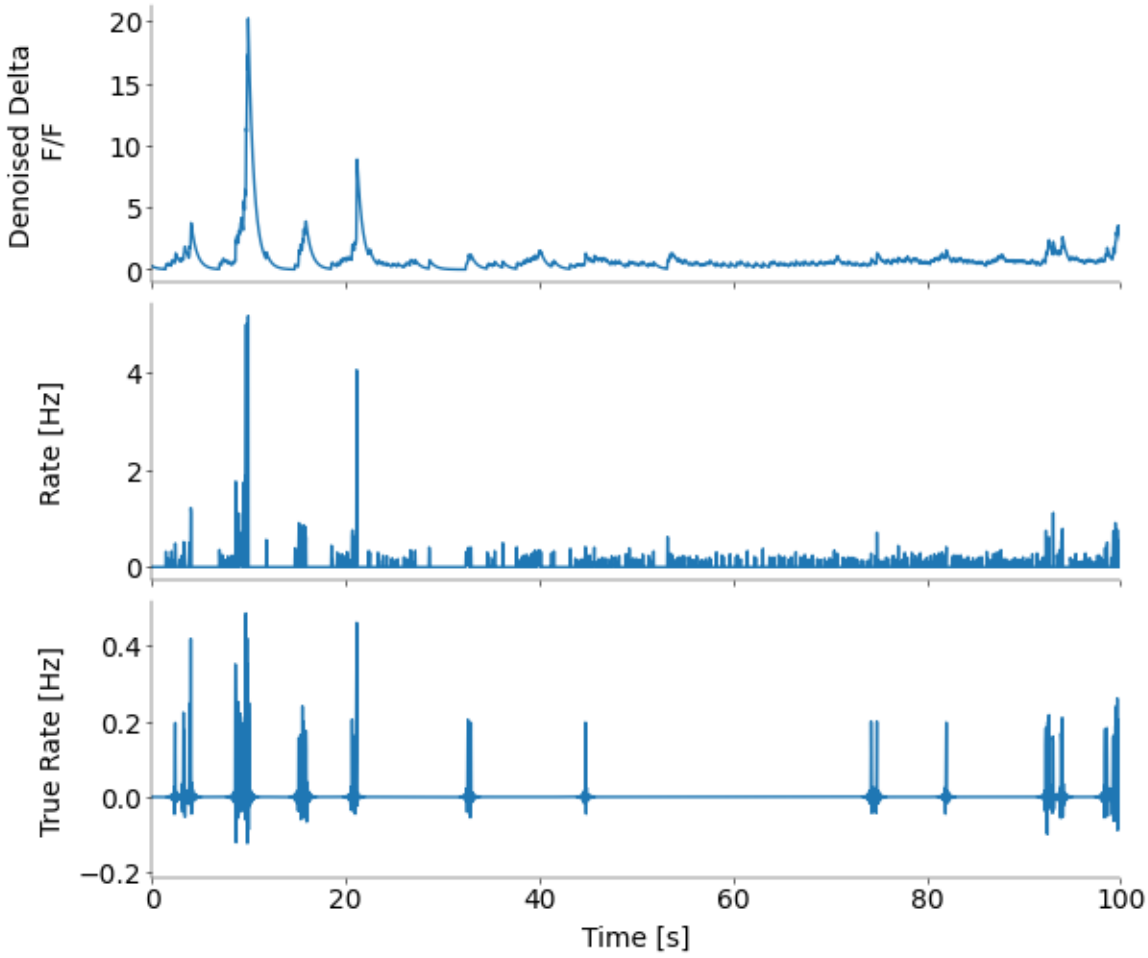
```
fig, axs = plt.subplots(
    3,
    1,
    figsize=(6, 5),
    height_ratios=[1, 1, 1],
    gridspec_kw=dict(hspace=0),
    sharex=True,
)

axs[0].plot(time_ogb_dec, c, label="ogb_oasis")
axs[1].plot(time_ogb_dec, s, label="spike_oasis")
axs[2].plot(time_ogb_dec, spike_ogb_cell_dec, label="ogb spike")
axs[2].set_xlabel("Time [s]")
axs[0].set_ylabel("Denoised Delta\n F/F")
axs[1].set_ylabel("Rate [Hz]")
axs[2].set_ylabel("True Rate [Hz]")
axs[2].set_xlim(0, 100)
fig.align_labels()
# OGB Cell
```




```
c, s, b, g, lam = oasis.functions.deconvolve(calcium_gcamp_cell_dec)
```

```
fig, axs = plt.subplots(
    3,
    1,
    figsize=(6, 5),
    height_ratios=[1, 1, 1],
    gridspec_kw=dict(hspace=0),
    sharex=True,
)

axs[0].plot(time_gcamp_dec, c, label="gcamp_oasis")
```

```
axs[1].plot(time_gcamp_dec, s, label="spike_oasis")
axs[2].plot(time_gcamp_dec, spike_gcamp_cell_dec, label="gcamp spike")
axs[2].set_xlabel("Time [s]")
axs[0].set_ylabel("Denoised Delta\n F/F")
axs[1].set_ylabel("Rate [Hz]")
axs[2].set_ylabel("True Rate [Hz]")
axs[2].set_xlim(0, 100)
fig.align_labels()
```



Task 4: Evaluation of algorithms

To formally evaluate the algorithms on the two datasets run the deconvolution algorithm and the more complex one on all cells and compute the correlation between true and inferred spike

trains. `DataFrames` from the `pandas` package are a useful tool for aggregating data and later plotting it. Create a dataframe with columns

- algorithm
- correlation
- indicator

and enter each cell. Plot the results using `stripplot` and/or `boxplot` in the `seaborn` package.

Grading: 3 pts

Evaluate on OGB data

```
algo = []
c = []
indicator = []

for cell in range(ogb_calcium.shape[1]):
    # get the current cell out of the dataframe
    cell_calcium_data = ogb_calcium[f"{cell}"].to_numpy()[
        ~np.isnan(ogb_calcium[f"{cell}"].to_numpy())
    ]
    cell_spike_data = ogb_spikes[f"{cell}"].to_numpy()[
        ~np.isnan(ogb_spikes[f"{cell}"].to_numpy())
    ]
    # decimate the data
    gcamp_calcium_dec = signal.decimate(cell_calcium_data, int(downsaple_factor))
    spike_gcamp_cell_dec = signal.decimate(cell_spike_data, int(downsaple_factor))
    # caluclate the time array
    time_gcamp_dec = np.arange(0, len(gcamp_calcium_dec)) / samplerate

    # deconvolve the data with our function
    deconv_calcium_gcamp_cell, ogb_kernel = deconv_ca(
        gcamp_calcium_dec, 0.5, samplerate
    )
    # deconvolve the data with oasis
    ca, s, b, g, lam = oasis.functions.deconvolve(gcamp_calcium_dec)

    # calulate the correlation between spike_ogb_cell_dec and deconv_calcium_ogb_cell
    c.append(np.corrcoef(spike_gcamp_cell_dec, deconv_calcium_gcamp_cell)[0, 1])
    algo.append("Our_Algorithm")
    indicator.append("OGB")
```

```
    # calulate the correlation between spike_ogb_cell_dec and oasis
    c.append(np.corrcoef(spike_gcamp_cell_dec, s)[0, 1])
    algo.append("Oasis")
    indicator.append("OGB")
```

Create OGB dataframe

```
df_ogb = pd.DataFrame({"algorithm": algo, "correlation": c, "indicator": indicator})
df_ogb.head()
```

	algorithm	correlation	indicator
0	Our_Algorithm	0.162190	OGB
1	Oasis	0.473556	OGB
2	Our_Algorithm	0.140082	OGB
3	Oasis	0.166155	OGB
4	Our_Algorithm	0.073209	OGB

Evaluate on GCamp data

```
algo = []
c = []
indicator = []

for cell in range(gcamp_calcium.shape[1]):
    # get the current cell out of the dataframe
    cell_calcium_data = gcamp_calcium[f"{cell}"].to_numpy()[
        ~np.isnan(gcamp_calcium[f"{cell}"].to_numpy())
    ]
    cell_spike_data = gcamp_spikes[f"{cell}"].to_numpy()[
        ~np.isnan(gcamp_spikes[f"{cell}"].to_numpy())
    ]
    # decimate the data
    gcamp_calcium_dec = signal.decimate(cell_calcium_data, int(downsaple_factor))
    spike_gcamp_cell_dec = signal.decimate(cell_spike_data, int(downsaple_factor))

    # deconvolve the data with our function
    deconv_calcium_gcamp_cell, ogb_kernel = deconv_ca(
        gcamp_calcium_dec, 0.5, samplerate
    )
    # deconvolve the data with oasis
```

```
    ca, s, b, g, lam = oasis.functions.deconvolve(gcamp_calcium_dec)

    # calulate the correlation between spike_ogb_cell_dec and deconv_calcium_ogb_cell
    c.append(np.corrcoef(spike_gcamp_cell_dec, deconv_calcium_gcamp_cell)[0, 1])
    algo.append("Our_Algorithm")
    indicator.append("gCamp")

    # calulate the correlation between spike_ogb_cell_dec and oasis
    c.append(np.corrcoef(spike_gcamp_cell_dec, s)[0, 1])
    algo.append("Oasis")
    indicator.append("gCamp")
```

Create GCamp dataframe

```
df_gcamp = pd.DataFrame({"algorithm": algo, "correlation": c, "indicator": indicator})
df_gcamp.head()
```

	algorithm	correlation	indicator
0	Our_Algorithm	0.428090	gCamp
1	Oasis	0.605176	gCamp
2	Our_Algorithm	0.234758	gCamp
3	Oasis	0.637547	gCamp
4	Our_Algorithm	0.374901	gCamp

Combine both dataframes and plot

```
df = pd.concat([df_ogb, df_gcamp])
df
```

	algorithm	correlation	indicator
0	Our_Algorithm	0.162190	OGB
1	Oasis	0.473556	OGB
2	Our_Algorithm	0.140082	OGB
3	Oasis	0.166155	OGB
4	Our_Algorithm	0.073209	OGB
...	...	...	...
69	Oasis	0.622005	gCamp
70	Our_Algorithm	0.312708	gCamp
71	Oasis	0.592172	gCamp

	algorithm	correlation	indicator
72	Our_Algorithm	0.223233	gCamp
73	Oasis	0.561245	gCamp

```
fig, axs = plt.subplots(figsize=(10, 5), sharey=True)
sns.stripplot(
    data=df,
    y=df["indicator"],
    x=df["correlation"],
    hue=df["algorithm"],
    dodge=True,
    size=15,
)
```

```
<Axes: xlabel='correlation', ylabel='indicator'>
```