CodingLab3

May 11, 2025

Neural Data Science

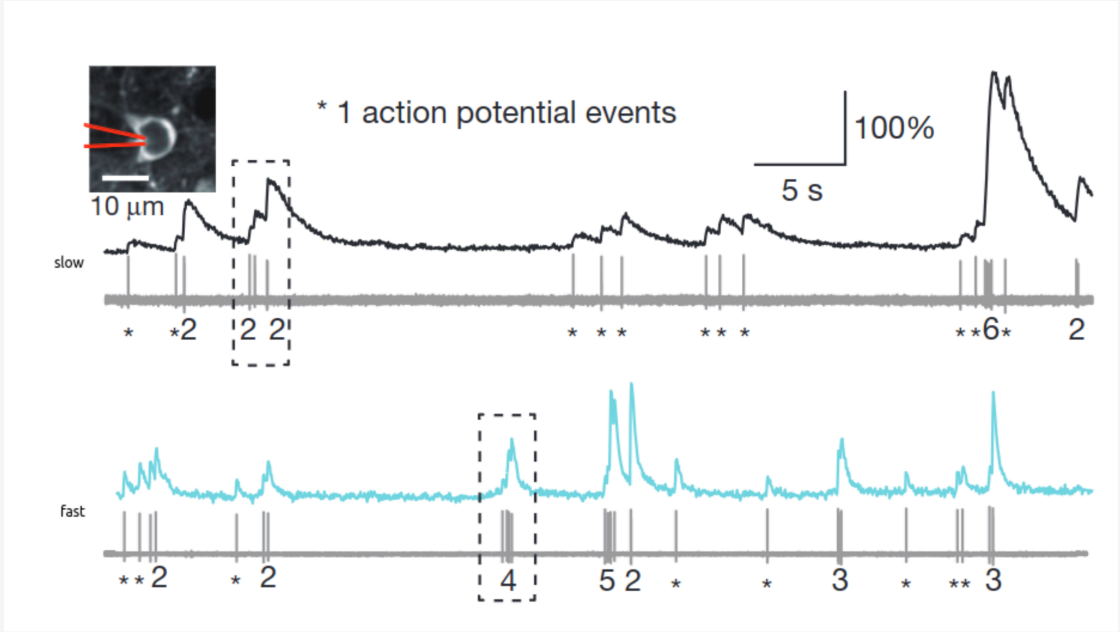
Lecturer: Dr. Jan Lause, Prof. Dr. Philipp Berens

Tutors: Jonas Beck, Fabio Seel, Julius Würzler

Summer term 2025

- Student names: Ahmed Eldably, Aakarsh Nair, Andreas Kotzur
- LLM Disclaimer: Chat GPT o3, Gemini, Copilot. For plotting and answer verification, and neuroscience context.

1 Coding Lab 3



In this notebook you will work with 2 photon calcium recordings from mouse V1 and retina. For details see Chen et al. 2013 and Theis et al. 2016. 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 easier analysis,

please resample it to 25 Hz. `scipy.signal.decimate` can help here, but note that it is only meant for continous signals.

Data: Download the data file `nds_cl_3_*.csv` from ILIAS and save it in a subfolder `../data/`. Note, some recordings were of shorter duration, hence their columns are padded.

[1]:
```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
from scipy import signal
from scipy.signal import decimate, lfilter
from __future__ import annotations
import logging


%matplotlib inline

%load_ext jupyter_black

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

```
Last updated: 2025-05-11 17:31:08CEST

Python implementation: CPython
Python version       : 3.10.13
IPython version      : 8.21.0

sklearn: 1.3.2

logging   : 0.5.1.2
numpy     : 1.26.2
pandas    : 2.2.3
scipy     : 1.11.4
matplotlib: 3.8.0
seaborn   : 0.13.0

Watermark: 2.5.0
```

[2]:
```
plt.style.use("../matplotlib_style.txt")
```

1.1 Load data

[3]:
```
# 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)
print(f"[OGB] calcium: {ogb_calcium.shape}, spikes: {ogb_spikes.shape}")

# 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)
print(f"[GCaMP] calcium: {gcamp_calcium.shape}, spikes: {gcamp_spikes.shape}")

# spike dataframe
ogb_spikes.head()
```

```
[OGB] calcium: (71986, 11), spikes: (71986, 11)
[GCaMP] calcium: (23973, 37), spikes: (23973, 37)
```

[3]:

	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

1.2 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. Align the traces by eye (add a small offset to the plot) such that a valid comparison is possible and zoom in on a small segment of tens of seconds.

Grading: 3 pts

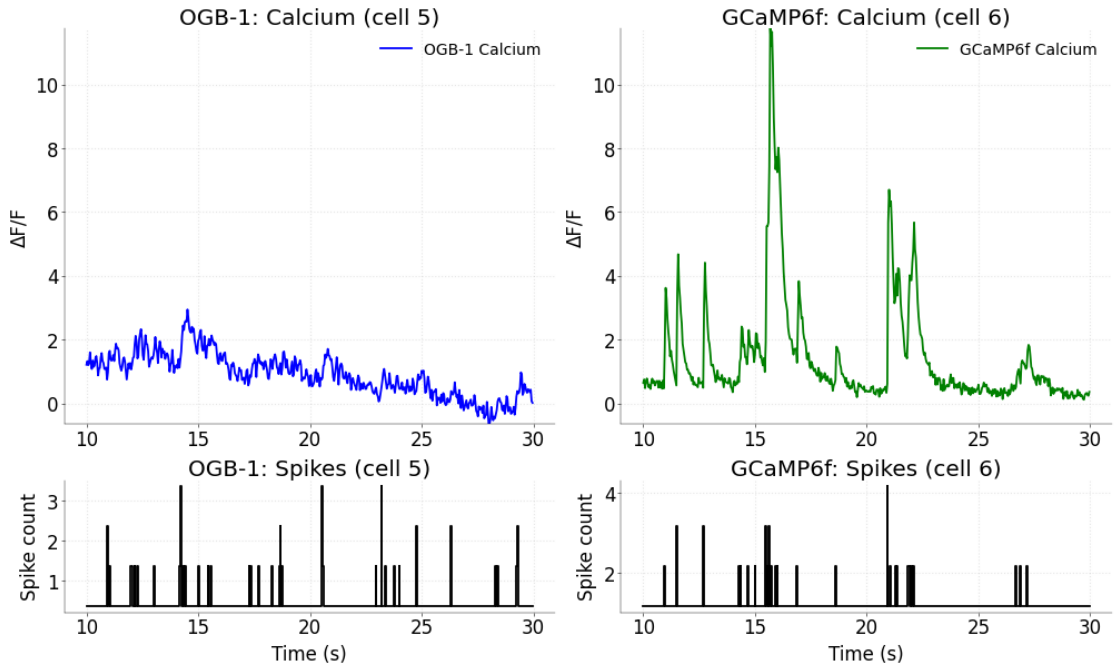
[4]:
```
# --------------------------------
# Resample and prepare data (1 pt)
# --------------------------------


# CLEAN: interpolate and fill any NaNs
def clean_df(df):
    return df.interpolate(axis=0).fillna(method="bfill").fillna(method="ffill")


ogb_cal = clean_df(ogb_calcium)
ogb_spk = clean_df(ogb_spikes)
```

```
gcamp_cal = clean_df(gcamp_calcium)
gcamp_spk = clean_df(gcamp_spikes)

# DOWNSAMPLING FUNCTIONS
DOWNSAMPLE_FACTOR = 4  # 100 Hz → 25 Hz


def downsample_calcium(df):
    """Zero-phase FIR decimation of each continuous trace."""
    return df.apply(
        lambda col: decimate(
            col.values, DOWNSAMPLE_FACTOR, ftype="fir", zero_phase=True
        ),
        axis=0,
        result_type="expand",
    ).set_axis(df.columns, axis=1)


def downsample_spikes(df):
    """Bin & sum integer spike counts into non-overlapping windows."""
    arr = df.values
    n_bins = arr.shape[0] // DOWNSAMPLE_FACTOR
    arr = arr[: n_bins * DOWNSAMPLE_FACTOR]
    binned = arr.reshape(n_bins, DOWNSAMPLE_FACTOR, arr.shape[1]).sum(axis=1)
    return pd.DataFrame(binned, columns=df.columns)


# APPLY DOWNSAMPLING
ogb_cal_ds = downsample_calcium(ogb_cal)
ogb_spk_ds = downsample_spikes(ogb_spk)
gcamp_cal_ds = downsample_calcium(gcamp_cal)
gcamp_spk_ds = downsample_spikes(gcamp_spk)

# DEFINE SEGMENT & TIME VECTOR
start_t, end_t = 10, 30  # seconds
sr_new = 25  # Hz after downsampling
start_idx = start_t * sr_new
end_idx = end_t * sr_new
time = np.linspace(start_t, end_t, end_idx - start_idx, endpoint=False)

cell_ogb, cell_gcamp = 5, 6

# EXTRACT SEGMENTS
ogb_cal_seg = ogb_cal_ds.iloc[start_idx:end_idx, cell_ogb]
ogb_spk_seg = ogb_spk_ds.iloc[start_idx:end_idx, cell_ogb]
gcamp_cal_seg = gcamp_cal_ds.iloc[start_idx:end_idx, cell_gcamp]
gcamp_spk_seg = gcamp_spk_ds.iloc[start_idx:end_idx, cell_gcamp]
```

```
# DYNAMIC OFFSETS FOR SPIKES
offset_ogb = 0.1 * (ogb_cal_seg.max() - ogb_cal_seg.min())
offset_gcamp = 0.1 * (gcamp_cal_seg.max() - gcamp_cal_seg.min())

# --------------------
# Plot OGB data (1 pt)
# --------------------


# ----------------------
# Plot GCamp data (1 pt)
# ----------------------


plt.rcParams.update(
    {
        "font.size": 12,
        "lines.linewidth": 1.3,
    }
)

fig, axs = plt.subplots(
    nrows=2,
    ncols=2,
    figsize=(10, 6),
    gridspec_kw={"height_ratios": [3, 1]},
    constrained_layout=True,
)

# Top-left: OGB-1 calcium (blue)
axs[0, 0].plot(time, ogb_cal_seg, color="blue", label="OGB-1 Calcium")
axs[0, 0].set_title("OGB-1: Calcium (cell 5)")
axs[0, 0].set_ylabel("ΔF/F")
axs[0, 0].legend(loc="upper right")

# Top-right: GCaMP6f calcium (green)
axs[0, 1].plot(time, gcamp_cal_seg, color="green", label="GCaMP6f Calcium")
axs[0, 1].set_title("GCaMP6f: Calcium (cell 6)")
axs[0, 1].set_ylabel("ΔF/F")
axs[0, 1].legend(loc="upper right")

# Match y-limits on both calcium panels
ymin = min(ogb_cal_seg.min(), gcamp_cal_seg.min())
ymax = max(ogb_cal_seg.max(), gcamp_cal_seg.max())
for ax in (axs[0, 0], axs[0, 1]):
    ax.set_ylim(ymin, ymax)
```

```python
# Bottom-left: OGB-1 spikes (black)
axs[1, 0].step(
    time, ogb_spk_seg + offset_ogb, where="mid", color="black",␣
↪label="_nolegend_"
)
axs[1, 0].set_title("OGB-1: Spikes (cell 5)")
axs[1, 0].set_xlabel("Time (s)")
axs[1, 0].set_ylabel("Spike count")

# Bottom-right: GCaMP6f spikes (black)
axs[1, 1].step(
    time, gcamp_spk_seg + offset_gcamp, where="mid", color="black",␣
↪label="_nolegend_"
)
axs[1, 1].set_title("GCaMP6f: Spikes (cell 6)")
axs[1, 1].set_xlabel("Time (s)")
axs[1, 1].set_ylabel("Spike count")

# Add subtle gridlines
for ax in axs.flatten():
    ax.grid(alpha=0.3, linestyle=":")

# Save & show
fig.savefig("task1_comparison.png", dpi=300, bbox_inches="tight")
plt.show()
```

```
/var/folders/76/g6ys7mkj75zg7zyn8m093rk40000gn/T/ipykernel_16004/928315864.py:8:
FutureWarning: DataFrame.fillna with 'method' is deprecated and will raise in a
future version. Use obj.ffill() or obj.bfill() instead.
  return df.interpolate(axis=0).fillna(method="bfill").fillna(method="ffill")
/var/folders/76/g6ys7mkj75zg7zyn8m093rk40000gn/T/ipykernel_16004/928315864.py:8:
FutureWarning: DataFrame.fillna with 'method' is deprecated and will raise in a
future version. Use obj.ffill() or obj.bfill() instead.
  return df.interpolate(axis=0).fillna(method="bfill").fillna(method="ffill")
/var/folders/76/g6ys7mkj75zg7zyn8m093rk40000gn/T/ipykernel_16004/928315864.py:8:
FutureWarning: DataFrame.fillna with 'method' is deprecated and will raise in a
future version. Use obj.ffill() or obj.bfill() instead.
  return df.interpolate(axis=0).fillna(method="bfill").fillna(method="ffill")
/var/folders/76/g6ys7mkj75zg7zyn8m093rk40000gn/T/ipykernel_16004/928315864.py:8:
FutureWarning: DataFrame.fillna with 'method' is deprecated and will raise in a
future version. Use obj.ffill() or obj.bfill() instead.
  return df.interpolate(axis=0).fillna(method="bfill").fillna(method="ffill")
```



1.3 Bonus Task (Optional): Calcium preprocessing

To improve the quality of the inferred spike trains, further preprocessing steps can undertaken. This includes filtering and smoothing of the calcium trace.

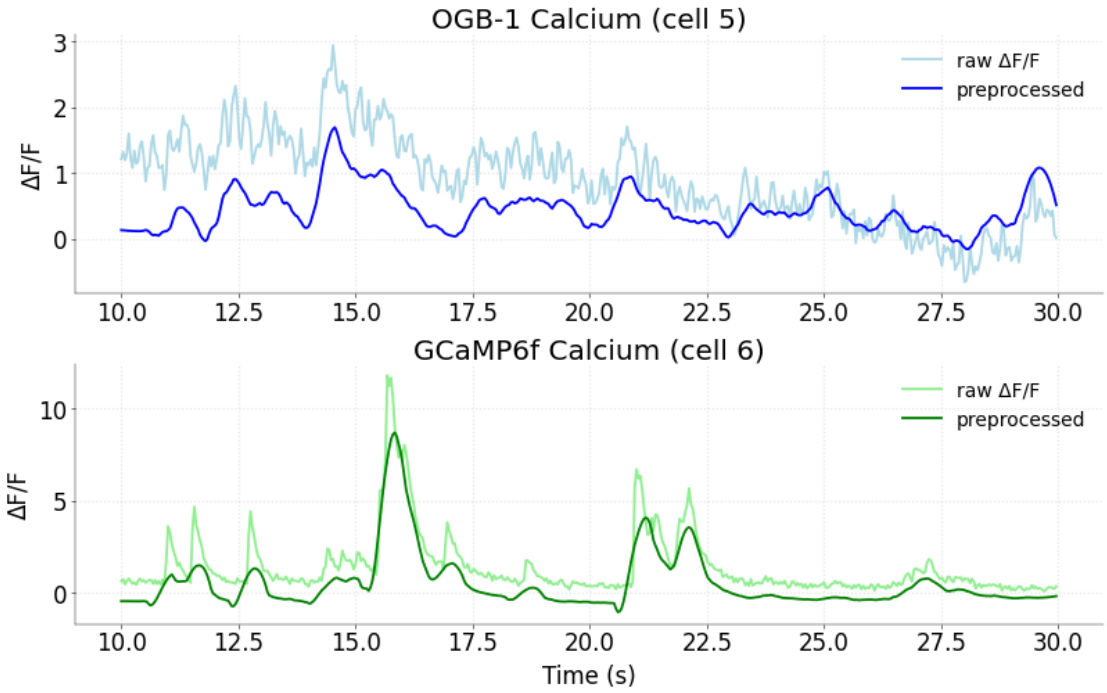
Implement a suitable filter and local averaging procedure as discussed in the lecture. Explain your choices and discuss how it helps!

Grading: 1 BONUS point

BONUS Points do not count for this individual coding lab, but sum up to 5% of your ***overall coding lab grade****. There are 4 BONUS points across all coding labs.*

[5]:
```python
from scipy.signal import butter, filtfilt, savgol_filter


# PARAMETERS
fs = 25  # Hz (after downsampling)
hp_cutoff = 0.01  # Hz, to remove very slow drifts
savgol_window = 21  # samples (~0.6 s window)
savgol_poly = 2  # quadratic fit for Savitzky-Golay

# DESIGN A HIGH-PASS BUTTERWORTH FILTER
b_hp, a_hp = butter(N=2, Wn=hp_cutoff / (fs / 2), btype="highpass")


def preprocess_calcium(trace: np.ndarray) -> np.ndarray:
```

```
    """
    (1) Zero-phase high-pass filter to strip slow drifts.
    (2) Savitzky-Golay smoothing to suppress high-frequency noise
        while preserving transient shape.
    """
    # remove DC offset
    centered = trace - np.nanmean(trace)
    # high-pass
    hp = filtfilt(b_hp, a_hp, centered)
    # Savitzky-Golay smoothing
    sg = savgol_filter(hp, savgol_window, polyorder=savgol_poly, mode="interp")
    return sg


# APPLY TO SEGMENTS
ogb_cal_filt = preprocess_calcium(ogb_cal_seg.values)
gcamp_cal_filt = preprocess_calcium(gcamp_cal_seg.values)

# PLOT RAW vs PREPROCESSED
fig, axs = plt.subplots(2, 1, figsize=(8, 5), constrained_layout=True)
t = time  # your 10-30 s time vector

# OGB-1 panel
axs[0].plot(t, ogb_cal_seg, color="lightblue", label="raw ΔF/F")
axs[0].plot(t, ogb_cal_filt, color="blue", label="preprocessed")
axs[0].set_title("OGB-1 Calcium (cell 5)")
axs[0].set_ylabel("ΔF/F")
axs[0].legend()
axs[0].grid(alpha=0.3, linestyle=":")

# GCaMP6f panel
axs[1].plot(t, gcamp_cal_seg, color="lightgreen", label="raw ΔF/F")
axs[1].plot(t, gcamp_cal_filt, color="green", label="preprocessed")
axs[1].set_title("GCaMP6f Calcium (cell 6)")
axs[1].set_xlabel("Time (s)")
axs[1].set_ylabel("ΔF/F")
axs[1].legend()
axs[1].grid(alpha=0.3, linestyle=":")
```



Implement a suitable filter and local averaging procedure as discussed in the lecture. Explain your choices and discuss how it helps! *Answer:* We chose the following filters, a Highpass filter to keep shart transients, and a Golay filter to smooth noise in the transients.

- High-pass Butterworth (0.01 Hz cutoff, 2nd order, zero-phase via filtfilt)
  - Removes very slow drifts (e.g. bleaching, baseline wander) without shifting event timing.
- Savitzky–Golay smoothing (window=21 samples 0.84 s, poly order=2)
  - Suppresses high-frequency noise (shot noise/electronic jitter) while preserving transient peak shape.
- Combined effect
  - Baseline stability + cleaner peaks → more reliable deconvolution and higher true-vs-inferred spike correlation.

1.4 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 ($\tau_{OGB} = 0.5s$, $\tau_{GCaMP} = 0.1s$). Note there can be no negative rates! 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. Explain your results and your choice of kernel.

Grading: 6 pts

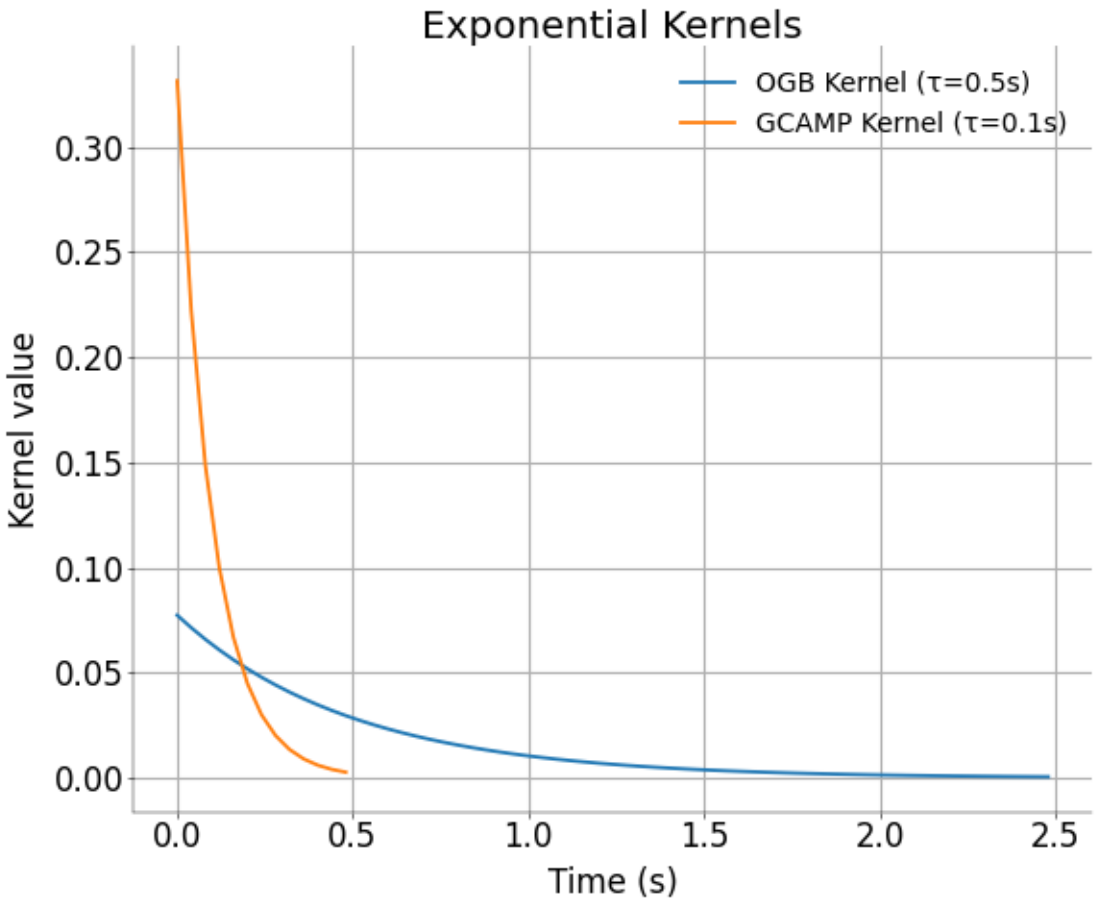
[6]:
```
def init_config():
    """Initialize the configuration for the analysis."""
    config = {
        "sampling_rate": 100,
        "new_sampling_rate": 25,
        "decimate_factor": 4,
        "start_time": 10,
        "end_time": 30,
        "tau_ogb": 0.5,
        "tau_gcamp": 0.1,
        "cell_ogb": 5,
        "cell_gcamp": 6,
        "deconvolution_plot_start_time": 10,
        "deconvolution_plot_end_time": 30,
    }
    # Downsample factor: 100 Hz → 25 Hz → factor = 4
    config["downsample_factor"] = config["sampling_rate"] //␣
↪config["new_sampling_rate"]
    config["dt"] = 1 / config["new_sampling_rate"]  # 0.04 s

    # plotting timestamps:
    config["deconvolution_plot_start_index"] = int(
        config["deconvolution_plot_start_time"] * config["new_sampling_rate"]
    )
    config["deconvolution_plot_end_index"] = int(
        config["deconvolution_plot_end_time"] * config["new_sampling_rate"]
    )
    start = config["deconvolution_plot_start_index"]
    end = config["deconvolution_plot_end_index"]

    config["deconvolution_plot_time_segment"] = (
        np.arange(start, end) / config["new_sampling_rate"]
    )  # Absolute time
    return config


config = init_config()


def get_exponential_decay_kernel(tau: float, dt: float) -> np.ndarray:
    """
    Generates an exponential decay kernel.

    Parameters
    ----------
    tau : float
        Decay constant of the kernel.
```

```
    dt : float
        Sampling interval.

    Returns
    -------
    np.ndarray
        The generated exponential decay kernel, normalized to have unit area.
    """
    # Define kernel duration to cover approximately 5 times the decay constant.
    # This ensures the kernel captures the significant part of the decay.
    kernel_len = int(np.ceil(5 * tau / dt))

    # Create a time vector for the kernel.
    # It starts from 0 and goes up to (kernel_len - 1) * dt.
    t = np.arange(kernel_len) * dt

    # Create the exponential decay kernel using the formula: exp(-t / tau).
    kernel = np.exp(-t / tau)

    # Normalize the kernel so that its sum is 1 (unit area).
    # This is important for deconvolution to preserve signal amplitude.
    if (
        kernel.sum() > 0
    ):  # Avoid division by zero if kernel is all zeros (e.g., tau is very␣
↪small)
        kernel /= kernel.sum()

    return kernel


def deconv_ca(ca: np.ndarray, tau: float, dt: float) -> np.ndarray:
    """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.

    Return
    ------
```

```
    sp_hat: np.array
    """

    # ------------------------------------------
    # apply devonvolution to calcium signal (1 pt)
    # ------------------------------------------

    # Create the exponential decay kernel using the provided tau and dt.
    # This kernel models the calcium signal decay.
    # The kernel is normalized to ensure it has unit area.
    # This is important for deconvolution to preserve signal amplitude.
    kernel = get_exponential_decay_kernel(tau, dt)
    logging.debug(f"Kernel shape: {kernel.shape}")

    # Use scipy to deconvolve
    sp_hat, _ = signal.deconvolve(ca, kernel)

    # Pad the output to match original size (deconvolve returns shorter output)
    sp_hat = np.pad(sp_hat, (0, ca.shape[0] - sp_hat.shape[0]), mode="constant")

    # Clip negative values
    sp_hat = np.clip(sp_hat, 0, None)

    return sp_hat


kernels = {
    "OGB": get_exponential_decay_kernel(config["tau_ogb"], config["dt"]),
    "GCaMP": get_exponential_decay_kernel(config["tau_gcamp"], config["dt"]),
}


# Plot the kernels
def plot_kernels(kernels: dict, config: dict):
    """
    Plots the exponential decay kernels for OGB and GCaMP.

    Parameters
    ----------
    kernels : dict
        Dictionary containing the kernel names and their corresponding values.
    config : dict
        Configuration dictionary containing parameters like dt and tau.
    """
    fig, ax = plt.subplots(figsize=(6, 5), layout="constrained")
    for name, kernel in kernels.items():
```

```
        t = np.arange(len(kernel)) * config["dt"]
        ax.plot(
            t,
            kernel,
            label=f"{name.upper()} Kernel (τ={config['tau_ogb'] if name ==␣
↪'OGB' else config['tau_gcamp']}s)",
        )
    ax.set_title("Exponential Kernels")
    ax.set_xlabel("Time (s)")
    ax.set_ylabel("Kernel value")
    ax.legend()
    ax.grid(True)
    plt.tight_layout()
    plt.show()


plot_kernels(kernels, config)
```

```
/var/folders/76/g6ys7mkj75zg7zyn8m093rk40000gn/T/ipykernel_16004/1559813834.py:1
51: UserWarning: The figure layout has changed to tight
  plt.tight_layout()
```



[7]:
```
# ------------------------
# Plot the 2 kernels (1 pt)
# ------------------------


# ------------------------
# Task 2: Simple deconvolution
# ------------------------

# 1) parameters (from your notebook)
sr_new = 25.0  # Hz after downsampling
dt = 1.0 / sr_new  # s per sample
tau_ogb = 0.5  # OGB-1 decay constant (s)
tau_gcamp = 0.1  # GCaMP6f decay constant (s)
t0, t1 = 10.0, 30.0  # seconds window to plot

cell_ogb = 5  # the column index you chose for OGB-1
cell_gcamp = 6  # the column index for GCaMP6f


# grab your full ΔF/F vectors
ca_full_ogb = ogb_cal_ds.iloc[:, cell_ogb].values
ca_full_gcamp = gcamp_cal_ds.iloc[:, cell_gcamp].values

# run deconvolution
s_full_ogb = deconv_ca(ca_full_ogb, tau_ogb, dt)
s_full_gcamp = deconv_ca(ca_full_gcamp, tau_gcamp, dt)

s_full_ogb.shape, s_full_gcamp.shape
```

[7]:
```
((17997,), (5994,))
```

[ ]:
```

```

Answer:

High-pass Butterworth (0.01 Hz cutoff, 2nd order, zero-phase via filtfilt): Removes very slow drifts (e.g. bleaching, baseline wander) without shifting event timing.

Savitzky–Golay smoothing (window=21 samples 0.84 s, poly order=2): Suppresses high-frequency noise (shot noise/electronic jitter) while preserving transient peak shape.

Combined effect: Baseline stability + cleaner peaks → more reliable deconvolution and higher true-vs-inferred spike correlation.

1.4.1 Questions (1 pt)

1) Explain how you constructed the kernels When a neuron fires an action potential, the calcium indicator shows a fluorescence increase which rises quickly after a spike and then decreases slowly. This pattern looks a lot like the decaying exponential.The decaying constants is 0.5s for OGB and 0.1s for GCAMP were given to us by the task, the higher value means a slower decay. These kernels were thus chosen for deconvolution when we wanted to see the spikes as more localized than the indicator allowed for.

We chose a kernel duration of approximately 5 times the decay constant as is common practice. We normalized the kernel so as to preserve the original signal amplitudes.

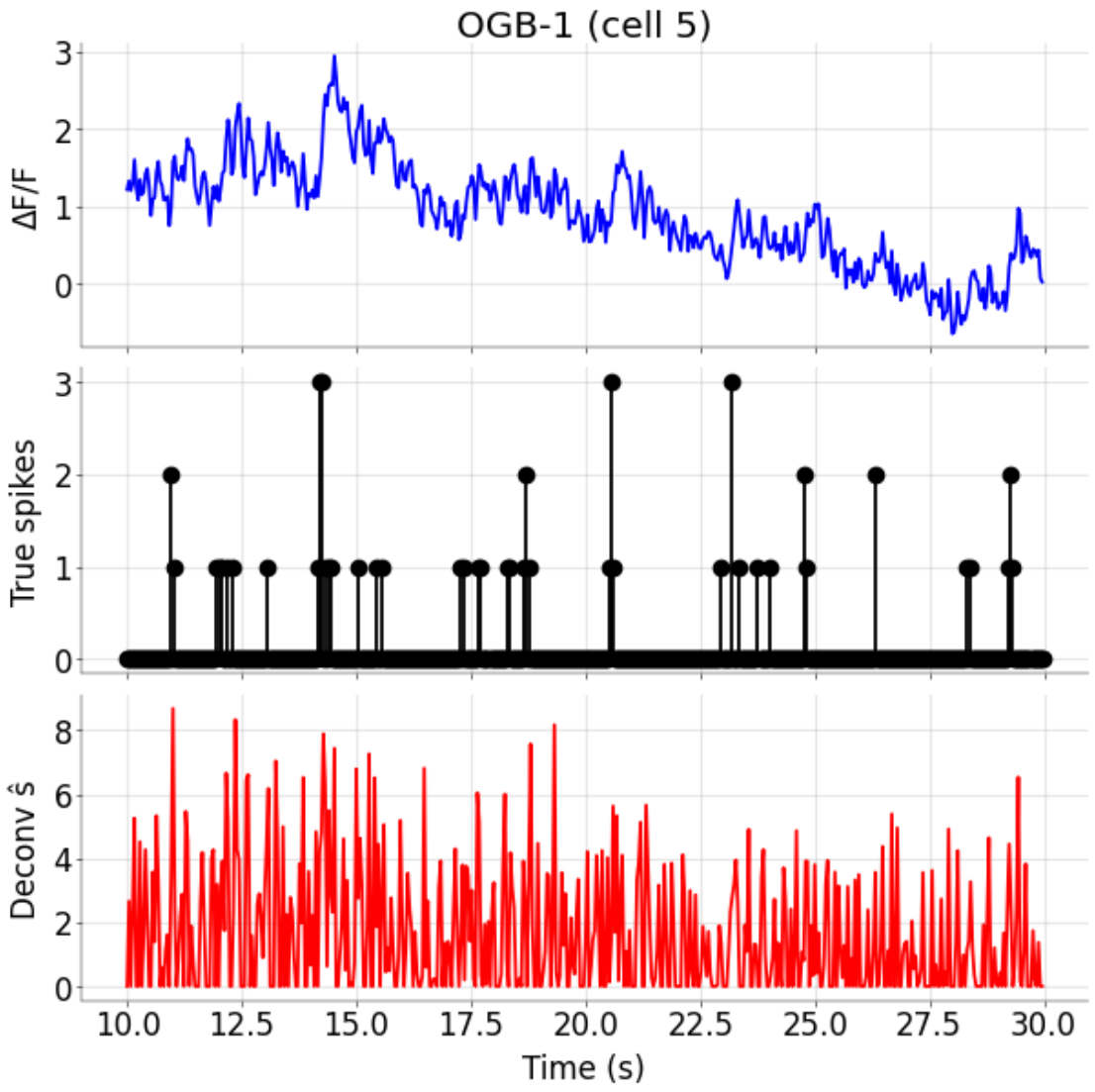
2) How do the indicators / kernels compare? Comparison for the indicators: * OGB - indicator has a slowly decaying indicator, as seen in its lower decaying constant. This makes spike detection on the signal more challenging; the indicator might be decaying while the next spike is arriving or noise in the signal, might result in multiple adjacent detection of the spikes. * GCAMP - is a relatively faster indicator, we find that even a simple kernel deconvolution is able to pick out spikes with much more ease than with the OGB signal. Consequently the kernel decays much faster and it can act more locally. Thus all else being equal we would prefer this indicator.

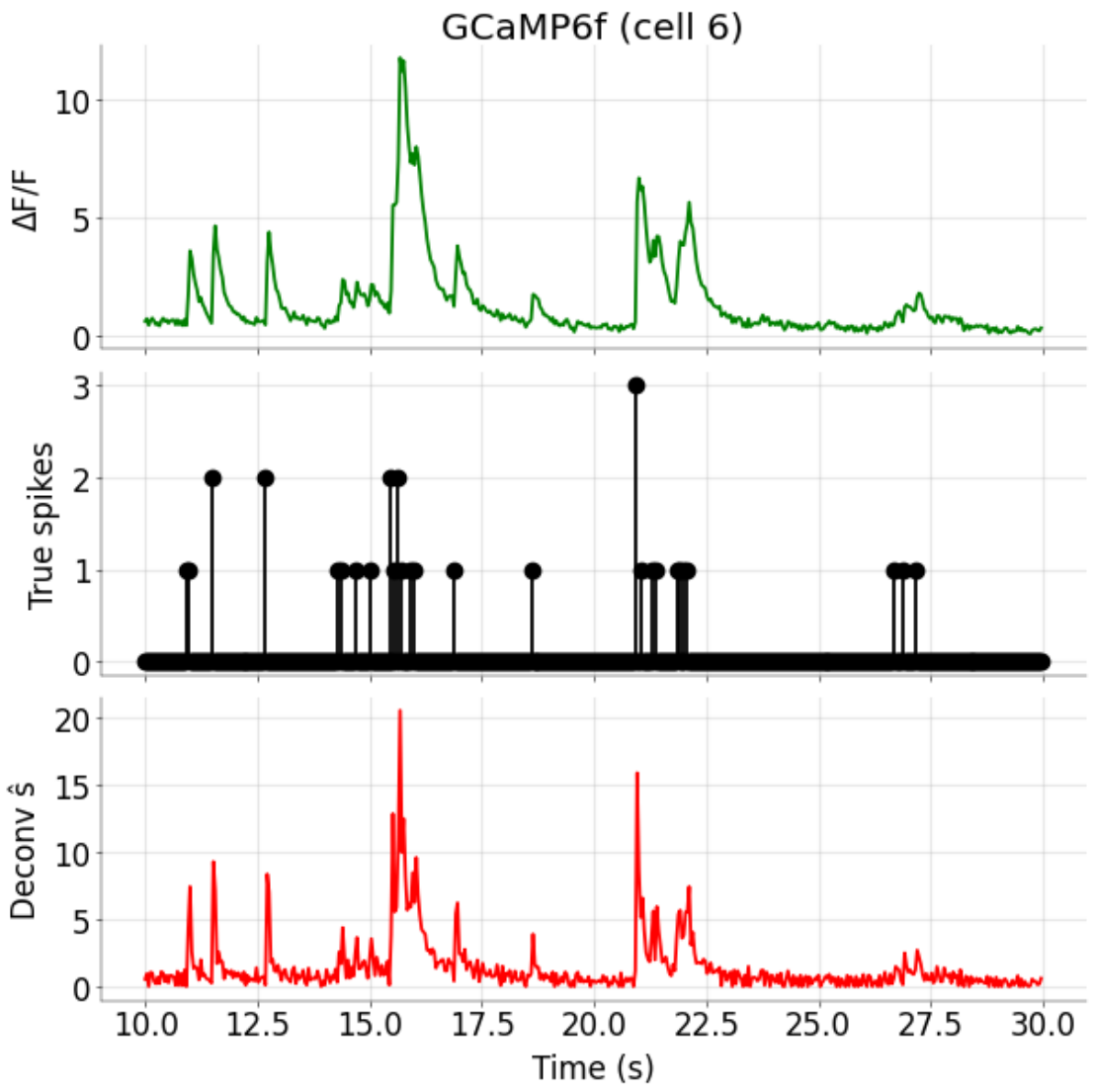
3) What are pros and cons of each indicator?

- **Imaging Duration**: GCAMP can be used for longterm imaging, whereas OGB is only for short term.
- **Signal Speed**: OGB has a faster signal speed than GCAMP
- **Targeting**: With GCAMP it is possible to target specific types of neuron; OGB labels all loaded cells (often random)
- **Spike Detection**: GCAMP fast decay allows for more localized spike detection than OGB.

[8]:
```
# ----------------------------------------------------------------------
# Compare true and deconvolved spikes rates for the OGB and GCamP cells.
# What do you notice? Why is that? (3 pts)
# ----------------------------------------------------------------------


# OGB Cell

# GCamp Cell
# slice out the 10-30 s window
i0 = int(t0 * sr_new)
i1 = int(t1 * sr_new)
time = np.linspace(t0, t1, i1 - i0, endpoint=False)

seg_cal_ogb = ca_full_ogb[i0:i1]
seg_spk_ogb = ogb_spk_ds.iloc[i0:i1, cell_ogb].values
seg_hat_ogb = s_full_ogb[i0:i1]

seg_cal_gc = ca_full_gcamp[i0:i1]
seg_spk_gc = gcamp_spk_ds.iloc[i0:i1, cell_gcamp].values
```

```
seg_hat_gc = s_full_gcamp[i0:i1]

# Plot OGB-1
fig, ax = plt.subplots(3, 1, figsize=(6, 6), sharex=True,␣
 ↪constrained_layout=True)
ax[0].plot(time, seg_cal_ogb, color="blue")
ax[0].set_ylabel("ΔF/F")
ax[0].set_title(f"OGB-1 (cell {cell_ogb})")

ax[1].stem(time, seg_spk_ogb, linefmt="k-", markerfmt="ko", basefmt=" ")
ax[1].set_ylabel("True spikes")

ax[2].plot(time, seg_hat_ogb, color="red")
ax[2].set_ylabel("Deconv ŝ")
ax[2].set_xlabel("Time (s)")

for a in ax:
    a.grid(alpha=0.3)


# 6) Plot GCaMP6f
fig, ax = plt.subplots(3, 1, figsize=(6, 6), sharex=True,␣
 ↪constrained_layout=True)
ax[0].plot(time, seg_cal_gc, color="green")
ax[0].set_ylabel("ΔF/F")
ax[0].set_title(f"GCaMP6f (cell {cell_gcamp})")

ax[1].stem(time, seg_spk_gc, linefmt="k-", markerfmt="ko", basefmt=" ")
ax[1].set_ylabel("True spikes")

ax[2].plot(time, seg_hat_gc, color="red")
ax[2].set_ylabel("Deconv ŝ")
ax[2].set_xlabel("Time (s)")

for a in ax:
    a.grid(alpha=0.3)
```


OGB-1 (cell 5)
ΔF/F
True spikes
Deconv ŝ
Time (s)
0
1
2
3
4
6
8
10.0
12.5
15.0
17.5
20.0
22.5
25.0
27.5
30.0



Compare true and deconvolved spike rates for OGB and GCAMP cells, What do you notice ? Why is that ? Answer: We notice that the deconvoluted spikes for GCAMP are more localized and thus results in more true spike detections. They have fewer false positives, and allow easier selection of thresholds for spikes. This is due to the slow decay of OGB which makes it harder to distinguish between subsequent spikes vs slow decaying signal from previous spike.

1.5 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: 3 pts

[9]:
```
# run this cell to download the oopsi.py file and put it in the same folder as␣
↪this notebook
# !wget https://raw.githubusercontent.com/liubenyuan/py-oopsi/master/oopsi.py
# import oopsi
```

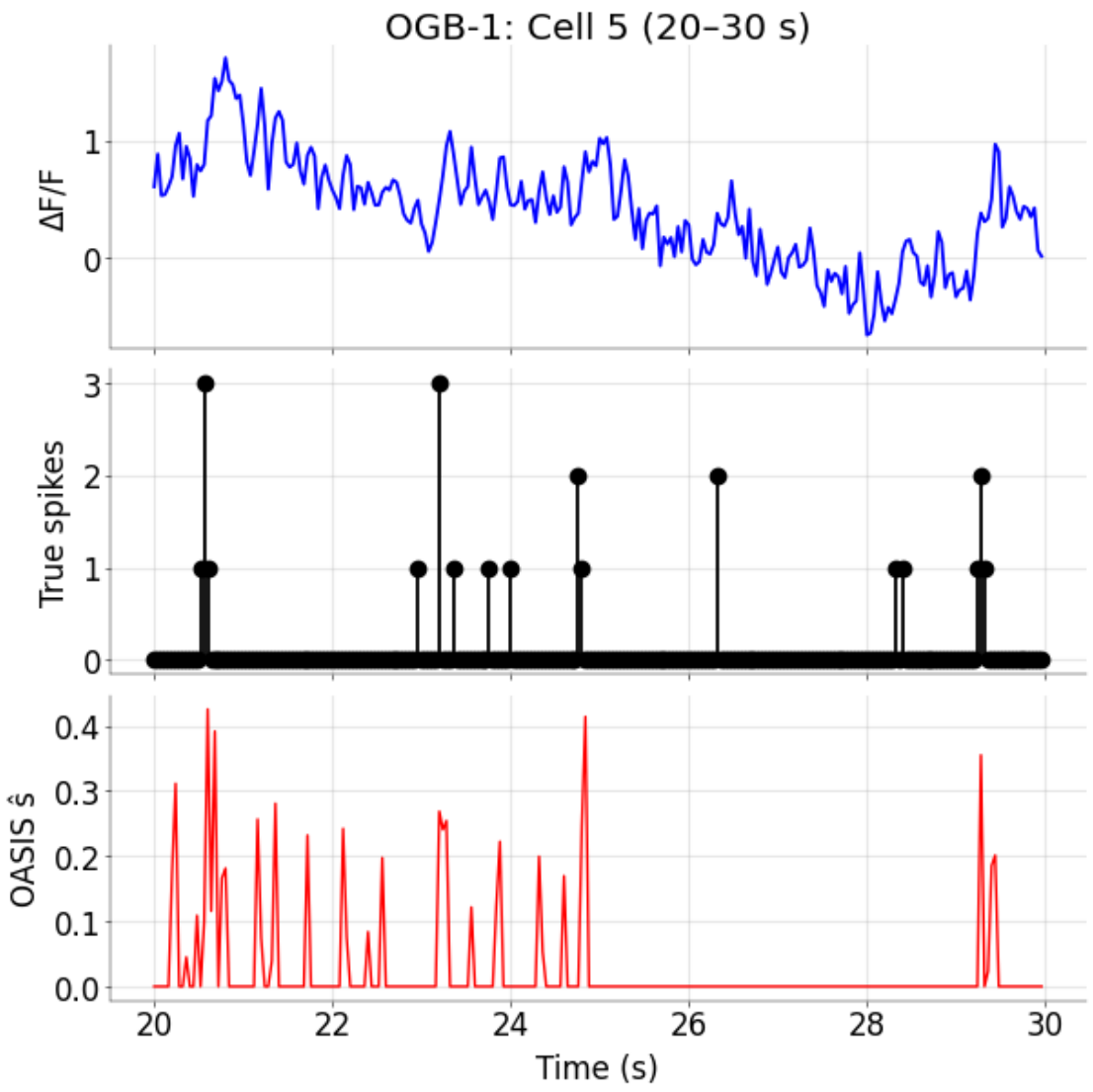
[10]:
```
# ------------------------------------------------------------------------
# Apply one of the advanced algorithms to the OGB and GCamp Cells (1 pt)
# ------------------------------------------------------------------------

import oasis.functions


# Define a simple Oasis wrapper
def run_oasis(trace, penalty=1.0):
    _, s, _, _, _ = oasis.functions.deconvolve(trace, penalty=penalty,␣
↪optimize_g=False)
    return s


# Parameters and indices
fs = 25  # sampling rate after downsampling (Hz)
t0, t1 = 20.0, 30.0  # window in seconds
i0, i1 = int(t0 * fs), int(t1 * fs)  # sample indices 500 → 750
time = np.linspace(t0, t1, i1 - i0, endpoint=False)  # 250 points

cell_ogb = 5  # example OGB cell index
cell_gcamp = 6  # example GCaMP cell index

# Grab full preprocessed ΔF/F and ground-truth spikes from Task 1
full_ca_ogb = ogb_cal_ds.iloc[:, cell_ogb].values
full_spk_ogb = ogb_spk_ds.iloc[:, cell_ogb].values

full_ca_gcamp = gcamp_cal_ds.iloc[:, cell_gcamp].values
full_spk_gcamp = gcamp_spk_ds.iloc[:, cell_gcamp].values

# Run OASIS deconvolution on the full traces
c_ogb_full, s_ogb_full, *_ = oasis.functions.deconvolve(
    full_ca_ogb, penalty=1.0, optimize_g=False
)
c_gcamp_full, s_gcamp_full, *_ = oasis.functions.deconvolve(
    full_ca_gcamp, penalty=1.0, optimize_g=False
)

c_ogb_full.shape, c_gcamp_full.shape
```

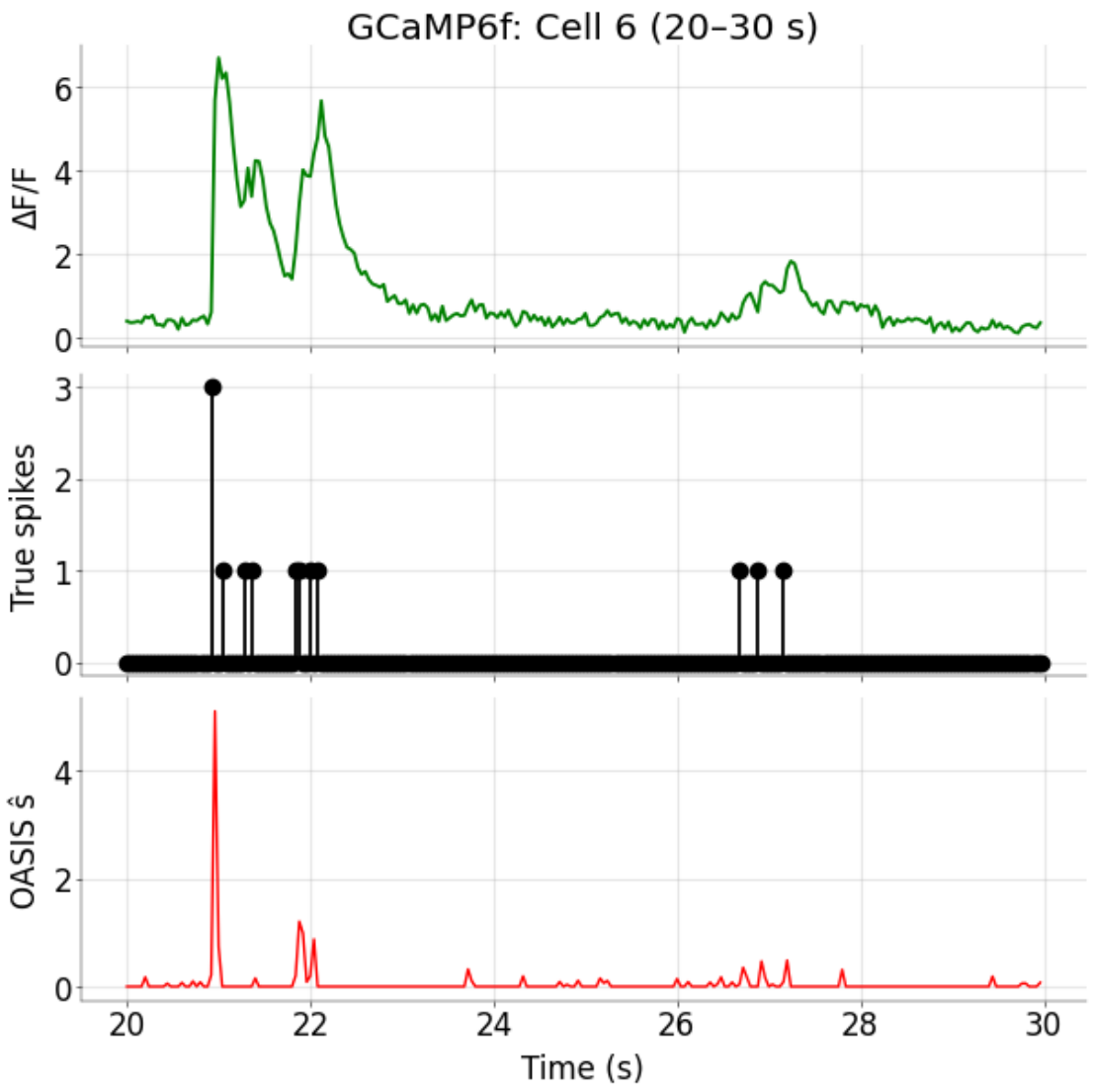
```
/Users/ahmedeldably/anaconda3/lib/python3.10/site-
packages/oasis/functions.py:13: UserWarning: Could not find cvxpy. Don't worry,
you can still use OASIS, just not the slower interior point methods we compared
to in the papers.
  warn("Could not find cvxpy. Don't worry, you can still use OASIS, " +
```

[10]:
```
((17997,), (5994,))
```

[11]:
```
#␣
 ↪------------------------------------------------------------------------------
# Plot the results for the OGB and GCamp Cells and describe the results (1+1␣
 ↪pts)
#␣
 ↪------------------------------------------------------------------------------

# OGB Cell

# GCamP Cell


#␣
 ↪------------------------------------------------------------------------------
# Plot the results for the OGB and GCamp Cells and describe the results (1+1␣
 ↪pts)
#␣
 ↪------------------------------------------------------------------------------

# 4) Slice out exactly 20-30 s (250 samples)
seg_ca_ogb = full_ca_ogb[i0:i1]
seg_true_ogb = full_spk_ogb[i0:i1]
seg_hat_ogb = s_ogb_full[i0:i1]

seg_ca_gcamp = full_ca_gcamp[i0:i1]
seg_true_gcamp = full_spk_gcamp[i0:i1]
seg_hat_gcamp = s_gcamp_full[i0:i1]

# Plot OGB-1 results (3×1)
fig, axs = plt.subplots(3, 1, figsize=(6, 6), sharex=True,␣
 ↪constrained_layout=True)
axs[0].plot(time, seg_ca_ogb, color="blue")
axs[0].set_ylabel("ΔF/F")
axs[0].set_title("OGB-1: Cell 5 (20-30 s)")

axs[1].stem(time, seg_true_ogb, linefmt="k-", markerfmt="ko", basefmt=" ")
axs[1].set_ylabel("True spikes")

# ← here's the only change: use plot() instead of stem()
```

```
axs[2].plot(time, seg_hat_ogb, color="red", linewidth=1)
axs[2].set_ylabel("OASIS ŝ")
axs[2].set_xlabel("Time (s)")

for ax in axs:
    ax.grid(alpha=0.3)
plt.show()


# Plot GCaMP6f results (3×1)
fig, axs = plt.subplots(3, 1, figsize=(6, 6), sharex=True,␣
 ↪constrained_layout=True)
axs[0].plot(time, seg_ca_gcamp, color="green")
axs[0].set_ylabel("ΔF/F")
axs[0].set_title("GCaMP6f: Cell 6 (20-30 s)")

axs[1].stem(time, seg_true_gcamp, linefmt="k-", markerfmt="ko", basefmt=" ")
axs[1].set_ylabel("True spikes")

# ← same change here
axs[2].plot(time, seg_hat_gcamp, color="red", linewidth=1)
axs[2].set_ylabel("OASIS ŝ")
axs[2].set_xlabel("Time (s)")

for ax in axs:
    ax.grid(alpha=0.3)
plt.show()
```


OGB-1: Cell 5 (20–30 s)
ΔF/F
1
0
True spikes
3
2
1
0
OASIS ŝ
0.4
0.3
0.2
0.1
0.0
20
22
24
26
28
30
Time (s)



1.6 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. Note these functions provide useful options for formatting the plots. See their documentation, i.e. `sns.boxplot?`.

Grading: 5 pts

First, evaluate on OGB data and create OGB dataframe. Then repeat for GCamp and combine the two dataframes.

[12]:
```
# ----------------------------------------------------------
# Evaluate the algorithms on the OGB and GCamp cells (2 pts)
# ----------------------------------------------------------


def run_deconvolution(
    calcium: np.ndarray, tau: float, dt: float, deconvolution_func=deconv_ca
) -> np.ndarray:
    """
    Run deconvolution on calcium data for all cells.

    Parameters
    ----------
    calcium : np.ndarray
        Calcium data of shape (time, n_cells).
    tau : float
        Decay constant for the algorithm.
    dt : float
        Sampling interval.

    Returns
    -------
    np.ndarray
        Inferred spike data of shape (time, n_cells).
    """
    inferred_spikes = np.zeros_like(calcium)
    for cell in range(calcium.shape[1]):  # Iterate over each cell
        inferred_spikes[:, cell] = deconvolution_func(calcium[:, cell],␣
 ↪tau=tau, dt=dt)
    return inferred_spikes
```

[13]:
```
# ----------------------------------------------------------
# Evaluate the algorithms on the OGB and GCamp cells (2 pts)
# ----------------------------------------------------------


def run_deconvolution(
    calcium: np.ndarray, tau: float, dt: float, deconvolution_func=deconv_ca
) -> np.ndarray:
    """
    Run deconvolution on calcium data for all cells.

    Parameters
```

```
    ----------
    calcium : np.ndarray
        Calcium data of shape (time, n_cells).
    tau : float
        Decay constant for the algorithm.
    dt : float
        Sampling interval.

    Returns
    -------
    np.ndarray
        Inferred spike data of shape (time, n_cells).
    """
    inferred_spikes = np.zeros_like(calcium)
    for cell in range(calcium.shape[1]):  # Iterate over each cell
        inferred_spikes[:, cell] = deconvolution_func(calcium[:, cell],␣
↪tau=tau, dt=dt)
    return inferred_spikes


# --------------------------------
# Construct the dataframe (1 pts)
# --------------------------------


def oasisAR1(trace, tau, dt):
    """AR(1) OASIS spike inference wrapper."""
    return run_oasis(trace)


def evaluate_algorithm(
    algorithm: str,
    calcium: np.ndarray,
    spikes: np.ndarray,
    tau: float,
    dt: float,
    indicator: str,  # Add this to label which dataset (OGB or GCaMP)
) -> pd.DataFrame:
    """
    Evaluate the algorithm on calcium and spike data for all
    cells.

    Parameters
    ----------
    calcium : np.ndarray
        Calcium data of shape (time, n_cells).
    spikes : np.ndarray
```

```
    Binned spike data of shape (time, n_cells).
algorithm : str
    Algorithm to use ("deconv" or "oopsi").
tau : float
    Decay constant for the algorithm.
dt : float
    Sampling interval.
indicator : str
    Indicator label (e.g. "OGB" or "GCaMP").

Returns
-------
pd.DataFrame
    DataFrame with correlation results for each cell.
"""
# Run the algorithm
if algorithm == "deconv":
    inferred_spikes = run_deconvolution(calcium, tau=tau, dt=dt)
elif algorithm == "oasisAR1":
    inferred_spikes = run_deconvolution(
        calcium, dt=dt, tau=tau, deconvolution_func=oasisAR1
    )
else:
    raise ValueError(f"Unsupported algorithm: {algorithm}")

# Ensure same shape
assert (
    inferred_spikes.shape == spikes.shape
), f"Shape mismatch: inferred {inferred_spikes.shape}, true {spikes.shape}"

# Compute correlation for each cell
results = []
for cell in range(spikes.shape[1]):
    true_cell = spikes[:, cell]
    inferred_cell = inferred_spikes[:, cell]

    # Optional: handle NaNs if any
    if np.isnan(true_cell).any() or np.isnan(inferred_cell).any():
        corr = np.nan
    else:
        corr = np.corrcoef(true_cell, inferred_cell)[0, 1]

    results.append(
        {
            "algorithm": algorithm,
            "correlation": corr,
            "indicator": indicator,
```

```
                "cell": cell,
            }
        )

    return pd.DataFrame(results)


def run_all_algorithms(
    indicators: list[str],
    calcium_data_map: dict,
    spike_data_map: dict,
    algorithm_map: dict,
    tau_map: dict,
    dt: float,
) -> pd.DataFrame:
    """
    Run all algorithms on the provided calcium and spike data.
    Parameters
    ----------
    indicators : list[str]
        List of indicators (e.g. ["OGB", "GCaMP"]).
    calcium_data : dict
        Dictionary mapping indicator names to their respective calcium data.
    spike_data : dict
        Dictionary mapping indicator names to their respective spike data.
    algorithm_map : dict
        Mapping of algorithm names to their respective functions.
    tau_map : dict
        Mapping of indicator names to their respective tau values.
    dt : float
        Sampling interval.
    Returns
    -------
    pd.DataFrame
        DataFrame with correlation results for each cell.
    """
    # List to store individual DataFrame results
    all_results_list = []

    for alg_name, alg_func in algorithm_map.items():
        for indicator in indicators:
            # Get the calcium and spike data for the current indicator
            calcium_data = calcium_data_map[indicator]
            spike_data = spike_data_map[indicator]
            tau = tau_map[indicator]

            logging.debug(
```

```
                f"\nEvaluating Algorithms: '{alg_name}' for Indicator:␣
↪'{indicator}'"
            )
            logging.debug(f"Initial calcium data shape: {calcium_data.shape}")
            logging.debug(f"Initial spike data shape: {spike_data.shape}")
            # Ensure calcium and spike data have the same number of time points␣
↪(rows)
            # This can be important if decimation and binning led to slight␣
↪length differences
            min_rows = min(calcium_data.shape[0], spike_data.shape[0])
            aligned_calcium = calcium_data[:min_rows, :]
            aligned_spikes = spike_data[:min_rows, :]
            logging.debug(
                f"Aligned calcium shape for evaluation: {aligned_calcium.shape}"
            )
            logging.debug(
                f"Aligned spikes shape for evaluation: {aligned_spikes.shape}"
            )

            # Call the evaluation function
            df_result = evaluate_algorithm(
                algorithm=alg_name,
                calcium=aligned_calcium,
                spikes=aligned_spikes,
                tau=tau,
                dt=dt,
                indicator=indicator,
            )
            all_results_list.append(df_result)
    # Concatenate all results into the final DataFrame
    if all_results_list:
        eval_results_df = pd.concat(all_results_list, ignore_index=True)
    else:
        eval_results_df = pd.DataFrame()  # Create an empty DataFrame if no␣
↪results
    return eval_results_df


# %%

full_ca_ogb = ogb_cal_ds.values
full_spk_ogb = ogb_spk_ds.values

full_ca_gcamp = gcamp_cal_ds.values
full_spk_gcamp = gcamp_spk_ds.values
```

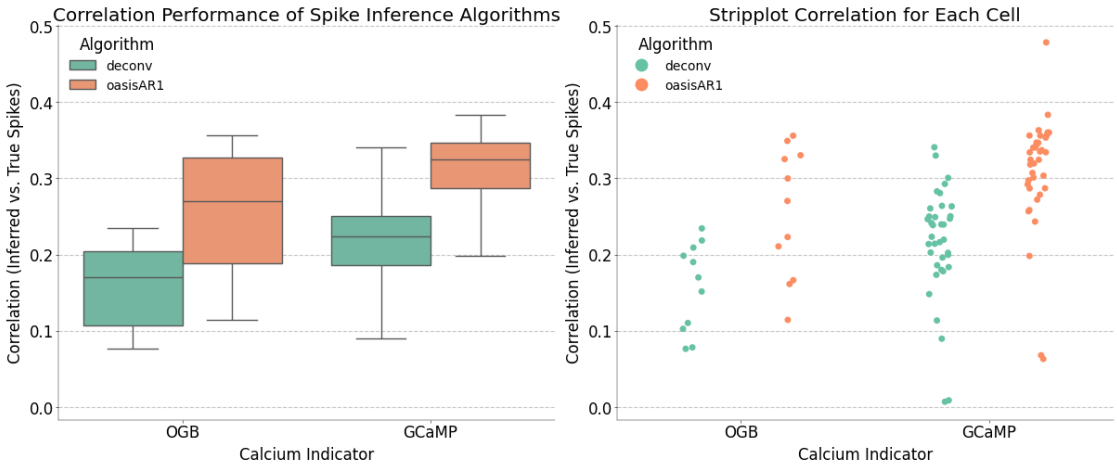
```
eval_results_df = run_all_algorithms(
    indicators=["OGB", "GCaMP"],
    calcium_data_map={"OGB": full_ca_ogb, "GCaMP": full_ca_gcamp},
    spike_data_map={"OGB": full_spk_ogb, "GCaMP": full_spk_gcamp},
    algorithm_map={
        "deconv": run_deconvolution,
        "oasisAR1": run_oasis,
    },
    tau_map={"OGB": config["tau_ogb"], "GCaMP": config["tau_gcamp"]},
    dt=config["dt"],
)
```

Combine both dataframes. Plot the performance of each indicator and algorithm. You should only need a single plot for this.

[14]:
```
# ------------------------------------------------------------------------
# Create Strip/Boxplot for both cells and algorithms Cell as described. (1 pt)
# Describe and explain the results briefly. (1 pt)
# ------------------------------------------------------------------------

# --- 5) plotting ---
fig, axes = plt.subplots(1, 2, figsize=(12, 5), constrained_layout=True)
sns.boxplot(
    x="indicator",
    y="correlation",
    hue="algorithm",
    data=eval_results_df,
    palette="Set2",
    fliersize=0,
    ax=axes[0],
)
axes[0].set_title("Boxplot of r (true vs. inferred)")
axes[0].grid(axis="y", alpha=0.3)

sns.stripplot(
    x="indicator",
    y="correlation",
    hue="algorithm",
    data=eval_results_df,
    dodge=True,
    jitter=True,
    palette="Set2",
    ax=axes[1],
    size=10,
)

for ax in axes:
```

```
    ax.grid(axis="y", alpha=0.3)
    ax.set_xlabel("Calcium Indicator")
    ax.set_ylabel("Correlation (Inferred vs. True Spikes)")
    ax.grid(axis="y", linestyle="--", alpha=0.7)
    ax.legend(title="Algorithm")  # Add a legend for the hue


axes[0].title.set_text("Correlation Performance of Spike Inference Algorithms")

axes[1].set_title("Stripplot Correlation for Each Cell")


# remove duplicate legends
handles, labels = axes[1].get_legend_handles_labels()

plt.show()
```

```
/Users/ahmedeldably/anaconda3/lib/python3.10/site-packages/seaborn/_base.py:948:
FutureWarning: When grouping with a length-1 list-like, you will need to pass a
length-1 tuple to get_group in a future version of pandas. Pass `(name,)`
instead of `name` to silence this warning.
  data_subset = grouped_data.get_group(pd_key)
/Users/ahmedeldably/anaconda3/lib/python3.10/site-
packages/seaborn/categorical.py:632: FutureWarning: SeriesGroupBy.grouper is
deprecated and will be removed in a future version of pandas.
  positions = grouped.grouper.result_index.to_numpy(dtype=float)
/Users/ahmedeldably/anaconda3/lib/python3.10/site-packages/seaborn/_base.py:948:
FutureWarning: When grouping with a length-1 list-like, you will need to pass a
length-1 tuple to get_group in a future version of pandas. Pass `(name,)`
instead of `name` to silence this warning.
  data_subset = grouped_data.get_group(pd_key)
/Users/ahmedeldably/anaconda3/lib/python3.10/site-
packages/seaborn/categorical.py:632: FutureWarning: SeriesGroupBy.grouper is
deprecated and will be removed in a future version of pandas.
  positions = grouped.grouper.result_index.to_numpy(dtype=float)
```



1.6.1 Describe and explain the results briefly. (1 pt)

Answer: We find that extracted spikes from GCaMP have a much better correlation than the extracted spikes for OGB. We note that this is due to the fast decay of the luminance signal which allows for much cleaner spike detection. Thus all else being equal one would prefer the fast indicator. We then ran the oasis algorithm on both sets of the datasets. We noted that runs of oasis resulted in better correlation with the true spikes even when operating on the OGB dataset. Thus oasis makes for a good candidate algorithm choice for both indicators.