CodingLab4

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Neural Data Science

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LLM Disclaimer: *Did you use an LLM to solve this exercise? If yes, which one and where did you use it? Chat GPT 4o, Google Gemini - Task Tracking, Template Code, Background Knowledge, Plotting

1 Coding Lab 4

In this notebook you will work with preprocessed 2 photon calcium recordings, that have already been converted into spike counts for a population of cells from the Macaque V1. During the experiment the animal has been presented with several drifting grating stimuli, in response to which the neural activity was recorded. In this exercise sheet we will study how you can visualize the activity of multiple neural spike trains and assess whether a neuron is selective to a specific stimulus type.

Download the data files `nds_cl_4_*.csv` from ILIAS and save it in the subfolder `../data/`. We recommend you to use a subset of the data for testing and debugging, ideally focus on a single cell (e.g. cell number x). The spike times and stimulus conditions are read in as pandas data frames. You can solve the exercise by making heavy use of that, allowing for many quite compact computations. See documentation and several good tutorials on how to do this. Of course, converting the data into classical numpy arrays is also valid.

[1]:
```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import matplotlib as mpl
import numpy as np
import scipy.optimize as opt

from scipy import signal as signal
from typing import Tuple

import itertools
```

```
import logging

%matplotlib inline

%load_ext jupyter_black

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

```
Last updated: 2025-05-18 22:27:17CEST

Python implementation: CPython
Python version       : 3.11.11
IPython version      : 9.2.0

sklearn: not installed

seaborn   : 0.13.2
matplotlib: 3.9.4
numpy     : 1.26.4
pandas    : 2.2.3
scipy     : 1.15.2
logging   : 0.5.1.2

Watermark: 2.5.0
```

[2]:
```
# %%
logging.basicConfig(
    format="%(asctime)s - %(levelname)s - %(message)s",
    level=logging.DEBUG,
)
logger = logging.getLogger(__name__)
logger.setLevel(logging.WARN)
logger.info("Starting the script...")


# --- Add these lines to suppress Matplotlib's DEBUG messages ---
mpl_logger = logging.getLogger("matplotlib")
mpl_logger.setLevel(logging.WARNING)  # Or logging.INFO, logging.ERROR
# You can also target specific noisy submodules if needed:
# logging.getLogger('matplotlib.font_manager').setLevel(logging.WARNING)
# logging.getLogger('matplotlib.pyplot').setLevel(logging.WARNING)
# --- End of added lines ---
```

[ ]:
```
import warnings
import matplotlib.pyplot as plt

warnings.filterwarnings("ignore", category=UserWarning)
warnings.filterwarnings("ignore", category=FutureWarning)
```

[4]:
```
plt.style.use("../matplotlib_style.txt")
```

1.1 Load data

[5]:
```
spikes = pd.read_csv("../data/nds_cl_4_spiketimes.csv")  # neuron id, spike time
stims = pd.read_csv("../data/nds_cl_4_stimulus.csv")  # stimulus onset in ms,␣
 ↪direction

stimDur = 2000.0  # in ms
nTrials = 11  # number of trials per condition
nDirs = 16  # number of conditions
deltaDir = 22.5  # difference between conditions

stims["StimOffset"] = stims["StimOnset"] + stimDur
```

We require some more information about the spikes for the plots and analyses we intend to make later. With a solution based on dataframes, it is natural to compute this information here and add it as additional columns to the `spikes` dataframe by combining it with the `stims` dataframe. We later need to know which condition (`Dir`) and trial (`Trial`) a spike was recorded in, the relative spike times compared to stimulus onset of the stimulus it was recorded in (`relTime`) and whether a spike was during the stimulation period (`stimPeriod`). But there are many options how to solve this exercise and you are free to choose any of them.

[6]:
```
# you may add computations as specified above
spikes["Dir"] = np.nan
spikes["relTime"] = np.nan
spikes["Trial"] = np.nan
spikes["stimPeriod"] = np.nan

dirs = np.unique(stims["Dir"])
trialcounter = np.zeros_like(dirs)

for i, row in stims.iterrows():
    trialcounter[dirs == row["Dir"]] += 1

    i0 = spikes["SpikeTimes"] > row["StimOnset"]
    i1 = spikes["SpikeTimes"] < row["StimOffset"]

    select = i0.values & i1.values

    spikes.loc[select, "Dir"] = row["Dir"]
    spikes.loc[select, "Trial"] = trialcounter[dirs == row["Dir"]][0]
```

```
    spikes.loc[select, "relTime"] = spikes.loc[select, "SpikeTimes"] -␣
 ↪row["StimOnset"]
    spikes.loc[select, "stimPeriod"] = True

spikes = spikes.dropna()
```

[7]:
```
spikes.head()
```

[7]:

	Neuron	SpikeTimes	Dir	relTime	Trial	stimPeriod
514	1	15739.000000	270.0	169.000000	1.0	True
515	1	15776.566667	270.0	206.566667	1.0	True
516	1	15808.466667	270.0	238.466667	1.0	True
517	1	15821.900000	270.0	251.900000	1.0	True
518	1	15842.966667	270.0	272.966667	1.0	True

[8]:
```
stims.head()
```

[8]:

	StimOnset	Dir	StimOffset
0	15570	270.0	17570.0
1	19022	45.0	21022.0
2	22592	112.5	24592.0
3	26095	225.0	28095.0
4	29431	180.0	31431.0

1.2 Task 1: Plot spike rasters

In a raster plot, each spike is shown by a small tick at the time it occurs relative to stimulus onset. Implement a function `plotRaster()` that plots the spikes of one cell as one trial per row, sorted by conditions (similar to what you saw in the lecture). Why are there no spikes in some conditions and many in others?

If you opt for a solution without a dataframe, you need to change the interface of the function.

Grading: 3 pts

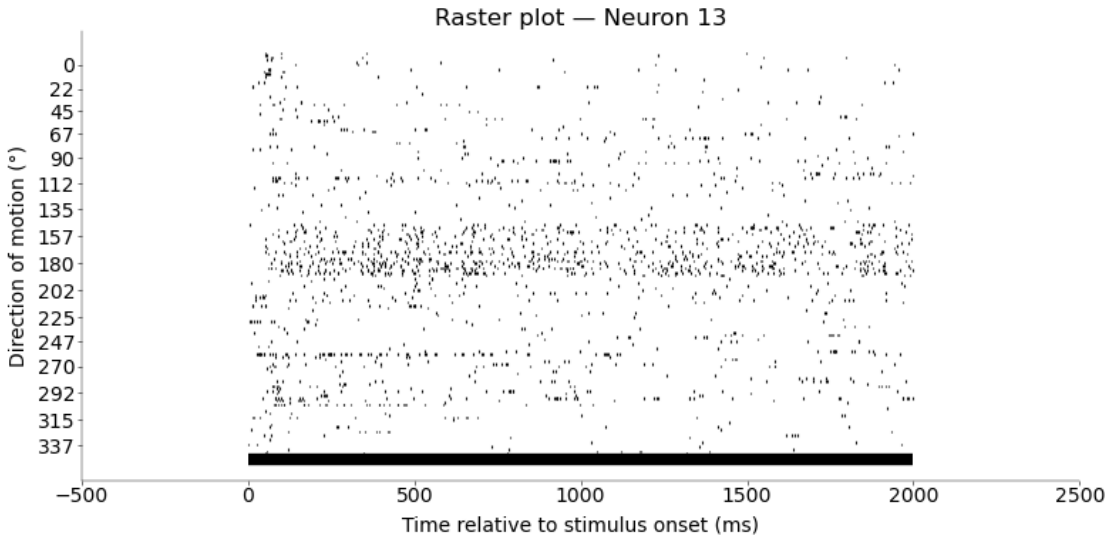
[9]:
```
def plotRaster(spikes: pd.DataFrame, neuron: int):
    """plot spike rasters for a single neuron sorted by condition

    Parameters
    ----------

    spikes: pd.DataFrame
        Pandas DataFrame with columns
            Neuron | SpikeTimes | Dir | relTime | Trial | stimPeriod

    neuron: int
        Neuron ID
```

```
    Note
    ----

    this function does not return anything, it just creates a plot!
    """

    # ------------------------------------------------
    # Write a raster plot function for the data (2 pts)
    # ------------------------------------------------
    df = spikes[(spikes["Neuron"] == neuron) & (spikes["stimPeriod"])]
    directions = np.sort(df["Dir"].unique())

    fig, ax = plt.subplots(figsize=(8, 4))
    y = 0
    yticks, ylabels = [], []

    for d in directions:
        sub = df[df["Dir"] == d]
        trials = np.sort(sub["Trial"].unique())
        # remember the center for this direction block
        yticks.append(y + len(trials) / 2)
        ylabels.append(int(d))
        for t in trials:
            times = sub[sub["Trial"] == t]["relTime"]
            ax.vlines(times, y, y + 1, linewidth=0.8, color="k")
            y += 1
        # small gap between direction blocks
        y += 0.5

    # stimulus-on bar
    ax.hlines(y + 0.5, xmin=0, xmax=stimDur, linewidth=6, color="k")

    ax.set_yticks(yticks)
    ax.set_yticklabels(ylabels)
    ax.set_xlabel("Time relative to stimulus onset (ms)")
    ax.set_ylabel("Direction of motion (°)")
    ax.set_title(f"Raster plot - Neuron {neuron}")

    # show some pre- and post-stimulus window
    ax.set_xlim(-500, stimDur + 500)

    # if you want 0° at bottom, 360° at top:
    ax.invert_yaxis()

    plt.tight_layout()
    plt.show()
```

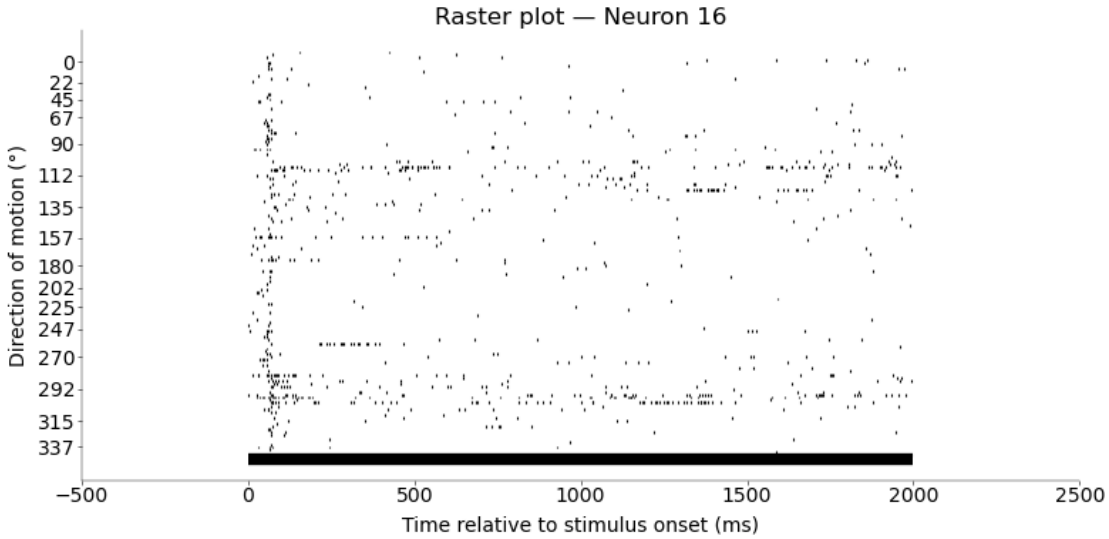
[10]:
```
# ---------------------------------
# Find and explain examples? (1 pt)
# ---------------------------------
# average over the full 0-stimDur window, per trial
rates = (
    spikes.query("stimPeriod")
    .groupby(["Neuron", "Dir", "Trial"])
    .size()  # spike count
    .reset_index(name="count")
    .assign(rate=lambda df: df["count"] / (stimDur / 1000))
    .groupby(["Neuron", "Dir"])["rate"]
    .mean()  # mean across trials
    .unstack()  # rows=Neuron, cols=Dir
)
dsis = {}
osis = {}
for nm, row in rates.iterrows():
    pref = row.max()
    pref_dir = row.idxmax()
    null_dir = (pref_dir + 180) % 360
    perp_dirs = [(pref_dir + 90) % 360, (pref_dir - 90) % 360]

    R_null = row[null_dir]
    R_perp = row[perp_dirs].mean()

    dsis[nm] = (pref - R_null) / (pref + R_null + 1e-6)
    osis[nm] = (pref - R_perp) / (pref + R_perp + 1e-6)

# then:
# Using hueristic thresholds, permutation tests used later provide more robust␣
 ↪and accurate results
# to determine the selectivity of the neuron
dir_sel = [n for n in dsis if dsis[n] > 0.5]  # [9, 13, 27]
ori_sel = [n for n in osis if osis[n] > 0.5 and dsis[n] < 0.2]  # [6, 7, 12]
non_sel = [n for n in dsis if abs(dsis[n]) < 0.1 and abs(osis[n]) < 0.1]  # [1,␣
 ↪4]

print("Direction-selective examples:", dir_sel)
print("Orientation-selective examples:", ori_sel)
print("Non-selective examples:", non_sel)

for neuron in [dir_sel[1], ori_sel[3], non_sel[0]]:
    print(f"\nNeuron {neuron}:\n")
    plotRaster(spikes, neuron)
```

```
Direction-selective examples: [9, 13, 27, 29, 32, 37, 38]
Orientation-selective examples: [6, 7, 12, 16, 17, 21]
Non-selective examples: [1, 4]
```

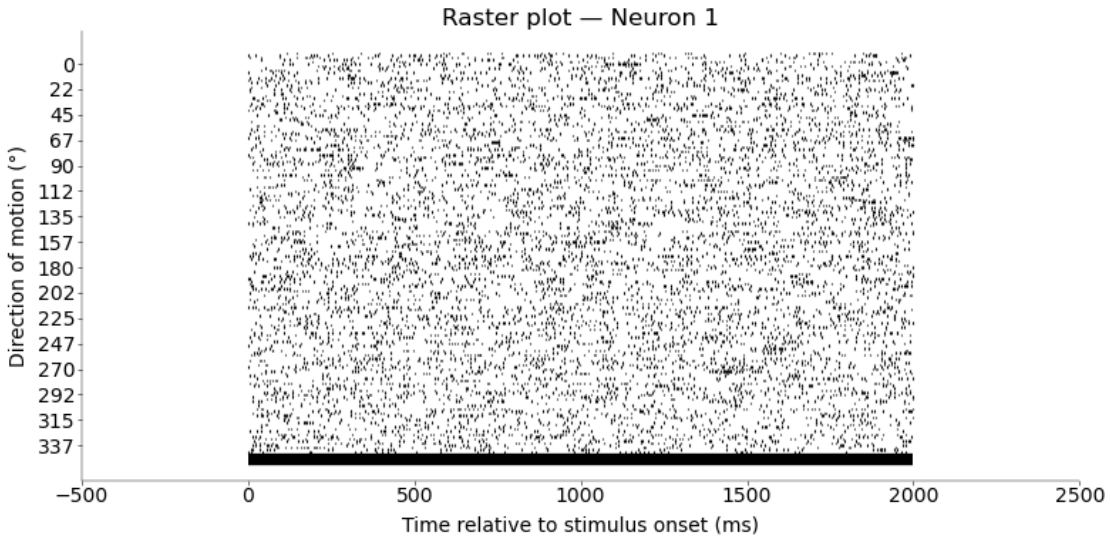
Neuron 13:



Neuron 16:



Neuron 1:



Why are there no spikes in some conditions and many in others? **Answer:** The primary reason why an individual neuron shows many spikes in some conditions and few or no spikes in others is because neurons themselves are intrinsically selective for specific stimulus features, such as particular orientations and directions of motion.

Each neuron in a sensory area like V1 is often 'tuned' to respond most strongly to its preferred stimulus. When a presented stimulus aligns with a neuron's preference, it fires vigorously (many spikes). When the stimulus does not match its preference, it fires weakly or not at all (few or no spikes).

In the experiment we are sub-sampling a population, and the specific neurons we happen to record will determine the range of preferences we observe in our dataset.

Find examples and and explain your choices:

1. A direction selective neuron:

Answer: We chose Neuron 13 as a possible example of a direction selective neuron. Observing the firing rate we find that there is a band between 140-180 degrees where the neuron is firing at a higher rate without a corresponding second direction to which it is selective.

2. An orientation selective neuron

Answer: We chose Neuron 16 as a possible example of orientation selective neuron. Observing that it fires for two directions roughly 180 degrees apart.

3. neither

Answer: We chose Neuron 1 as a possible example of a neuron which is not tuned to direction or orientation. It fires equally for all angles following stimulus.

1.3 Task 2: Plot spike density functions

Compute an estimate of the spike rate against time relative to stimulus onset. There are two ways: * Discretize time: Decide on a bin size, count the spikes in each bin and average across trials. * Directly estimate the probability of spiking using a density estimator with specified kernel width.

For full points, the optimal kernel- or bin-width needs to be computed.

Implement one of them in the function `plotPSTH()`. If you dont use a dataframe you may need to change the interface of the function.

Grading: 4 pts

[11]:
```
from scipy.stats import norm

nTrials = 11  # number of trials per direction


def select_optimal_binwidth(
    rel_times, T, n_trials, delta_min=1.0, delta_max=None, n_deltas=200
):
    """
    Shimazaki & Shinomoto (2007) algorithm to pick histogram bin width Δ,
    with log-spaced search capped at T/10 and a Freedman-Diaconis fallback.

    Parameters
    ----------
    rel_times : array-like (ms)
        all spike times within [0, T]
    T : float (ms)
        total observation window
    n_trials : int
        number of repeated trials
    delta_min : float (ms)
        smallest bin width to try
    delta_max : float (ms), optional
        largest bin width to try; defaults to T/10
    n_deltas : int
        number of candidate widths in the log-spaced grid

    Returns
    -------
    Δ_opt_ms : float
        optimal bin width (ms)
    """
    # convert to seconds
    rel_s = np.asarray(rel_times) / 1000.0
    T_s = T / 1000.0
```

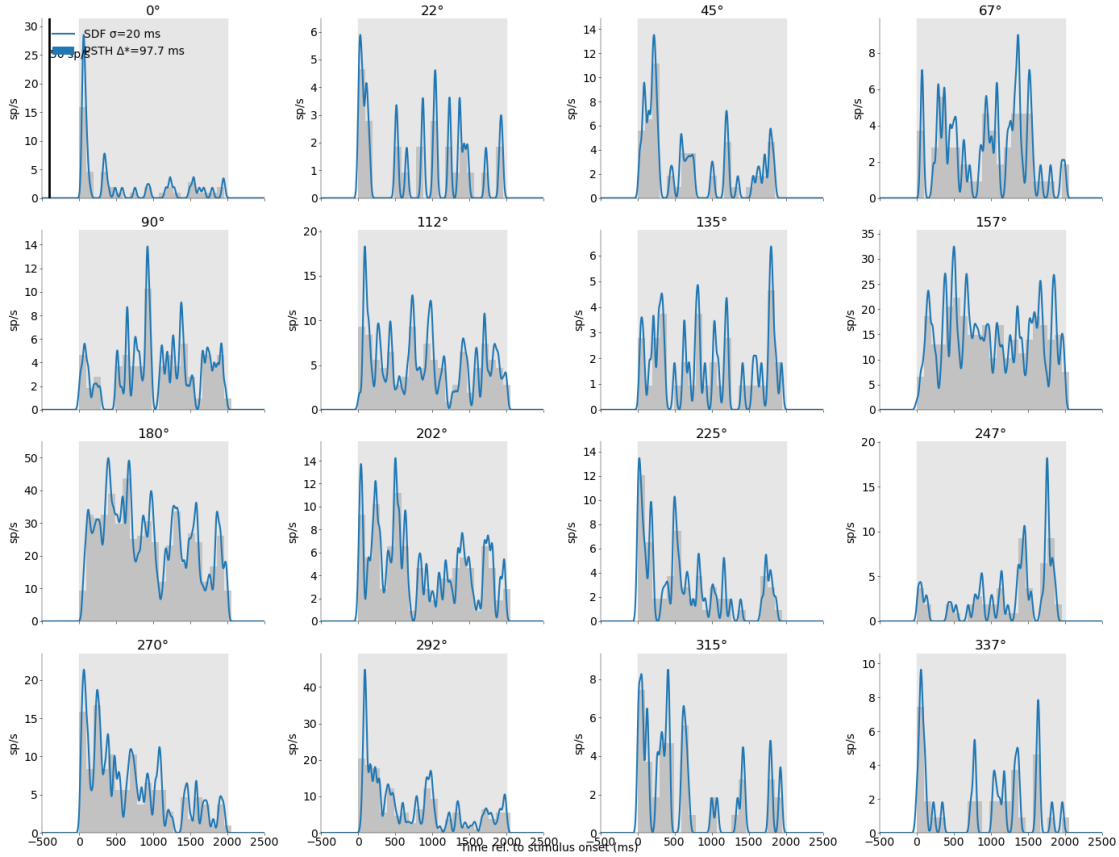
```
    # cap delta_max at T/10 if not provided
    if delta_max is None:
        delta_max = T / 20.0
    else:
        delta_max = min(delta_max, T / 20.0)

    # endpoints in seconds
    del_min_s = delta_min / 1000.0
    del_max_s = delta_max / 1000.0

    # log-spaced candidate Δ_s
    deltas_s = np.logspace(np.log10(del_min_s), np.log10(del_max_s), n_deltas)

    # compute Shimazaki-Shinomoto cost for each Δ_s
    costs = np.zeros_like(deltas_s)
    for i, Δ_s in enumerate(deltas_s):
        edges = np.arange(0, T_s + Δ_s, Δ_s)
        kis, _ = np.histogram(rel_s, bins=edges)
        kis = kis.astype(float) / n_trials
        k_bar = kis.mean()
        v = ((kis - k_bar) ** 2).mean()
        costs[i] = (2 * k_bar - v) / (Δ_s**2)

    # pick the Δ_s that minimizes the cost
    idx = np.argmin(costs)
    Δ_opt_ms = deltas_s[idx] * 1000.0

    # if the minimum is at the boundary, fallback to Freedman-Diaconis
    if idx == 0 or idx == len(deltas_s) - 1:
        x = np.asarray(rel_times)
        iqr = np.subtract(*np.percentile(x, [75, 25]))
        Δ_fd = 2 * iqr * (x.size ** (-1 / 3))
        Δ_opt_ms = np.clip(Δ_fd, delta_min, delta_max)

    return Δ_opt_ms


def plotPSTH(spikes: pd.DataFrame, neuron: int, stimDur=2000.0, n_trials=11):
    """Plot PSTH for a single neuron sorted by condition

    Parameters
    ----------

    spikes: pd.DataFrame
        Pandas DataFrame with columns
            Neuron | SpikeTimes | Dir | relTime | Trial | stimPeriod
```

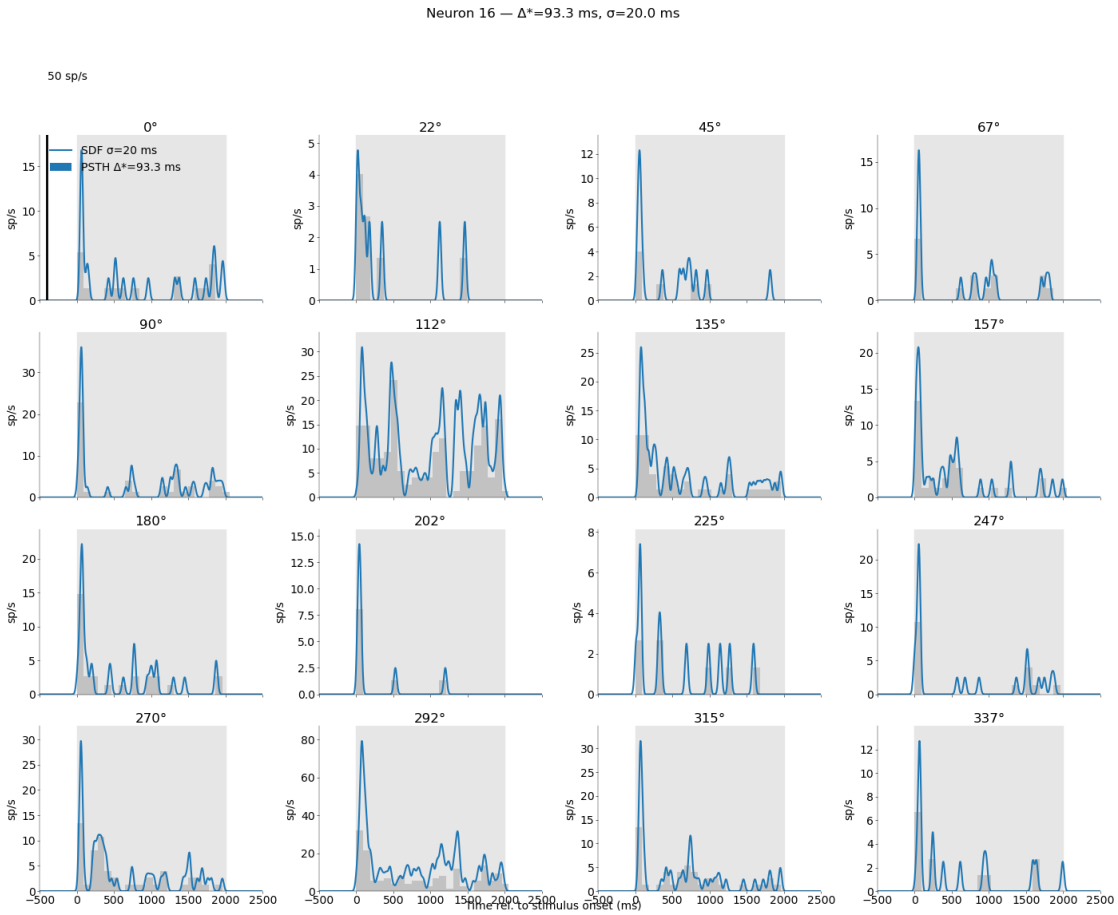
```
    neuron: int
        Neuron ID


    Note
    ----

    this function does not return anything, it just creates a plot!
    """

    # ------------------------------------------------
    # Implement one of the spike rate estimates (3 pts)
    # ------------------------------------------------
    # filter data
    df = spikes[(spikes.Neuron == neuron) & spikes.stimPeriod]
    dirs = np.sort(df.Dir.unique())
    n_trials = df.groupby("Dir").Trial.nunique().iloc[0]

    # compute optimal PSTH bin width Δ*
    Δ = select_optimal_binwidth(df.relTime.values, stimDur, n_trials)

    # PSTH edges & centers
    psth_edges = np.arange(0, stimDur + Δ, Δ)
    psth_centers = psth_edges[:-1] + Δ / 2

    # time vector for SDF (±500 ms)
    bg, ag = 500, 500
    tvec = np.arange(-bg, stimDur + ag + 1)

    # Gaussian kernel  =20 ms
    sigma = 20.0
    kt = np.arange(-3 * sigma, 3 * sigma + 1)
    gauss = norm.pdf(kt, 0, sigma)
    gauss /= gauss.sum()

    # 3) set up 4×4 grid
    ncols = 4
    nrows = int(np.ceil(len(dirs) / ncols))
    fig, axes = plt.subplots(nrows, ncols, sharex=True, figsize=(14, 3 * nrows))
    axes = axes.flatten()

    for ax, d in zip(axes, dirs):
        sub = df[df.Dir == d]

        # PSTH → spikes/sec
        trial_counts = []
        for t in range(1, n_trials + 1):
```

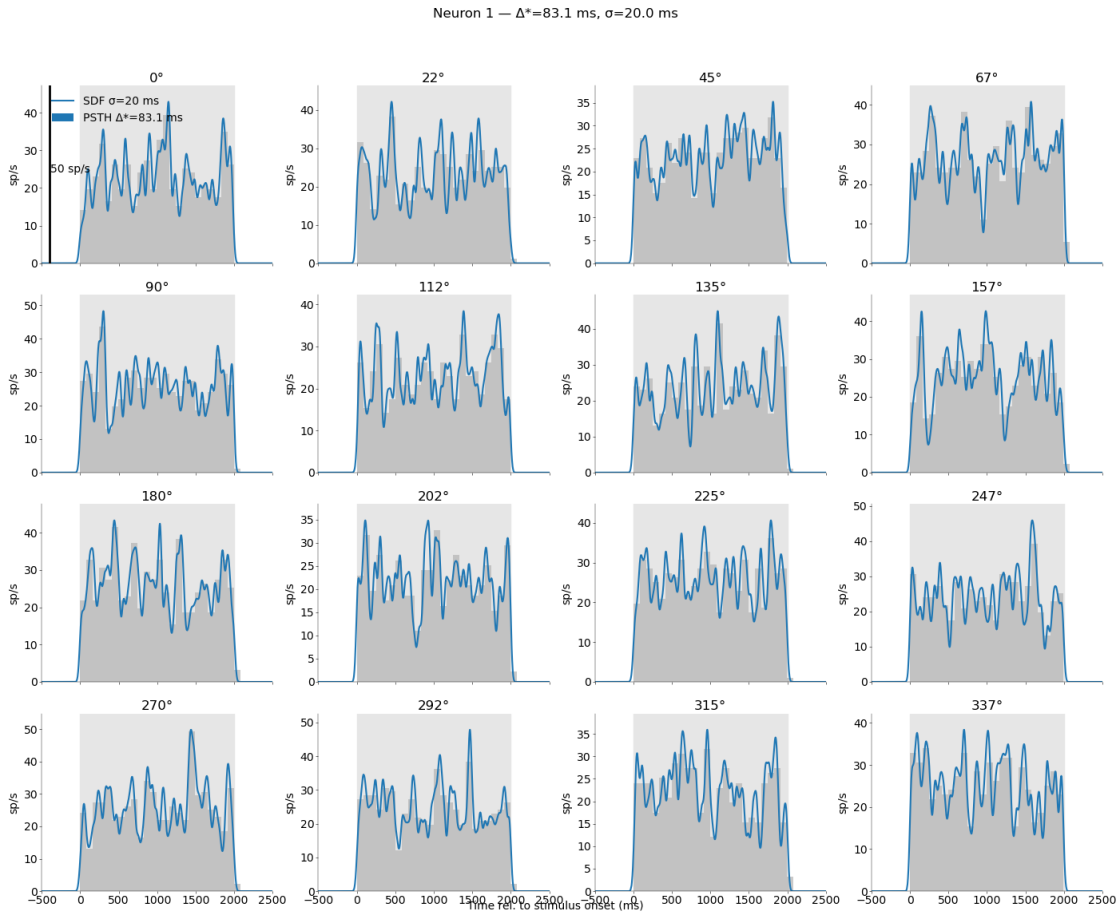
```
            st = sub[sub.Trial == t].relTime.values
            cnts, _ = np.histogram(st, bins=psth_edges)
            trial_counts.append(cnts)
        rate_hist = np.mean(trial_counts, axis=0) / (Δ / 1000.0)

        # SDF → all-trial hist → sp/s → smooth
        hist1, _ = np.histogram(sub.relTime.values, bins=np.append(tvec,␣
↪tvec[-1] + 1))
        rate1 = hist1 / n_trials * 1000.0
        sdf = np.convolve(rate1, gauss, mode="same")

        # plot
        ax.axvspan(0, stimDur, color="0.9", zorder=-1)
        ax.bar(
            psth_centers, rate_hist, width=Δ, color="0.7", edgecolor="none",␣
↪alpha=0.7
        )
        ax.plot(tvec, sdf, color="C0", lw=1.5)

        # format
        ax.set_xlim(-bg, stimDur + ag)
        ax.set_ylim(0, max(rate_hist.max(), sdf.max()) * 1.1)
        ax.set_title(f"{int(d)}°")
        ax.set_ylabel("sp/s")

    # turn off any unused axes
    for ax in axes[len(dirs) :]:
        ax.axis("off")

    # shared legend & scale bar
    axes[0].bar([], [], color="0.7", alpha=0.7, label=f"PSTH Δ*={Δ:.1f} ms")
    axes[0].plot([], [], color="C0", lw=1.5, label="SDF  =20 ms")
    axes[0].legend(loc="upper left")
    axes[0].plot([-400, -400], [0, 50], "k", lw=2)
    axes[0].text(-390, 25, "50 sp/s", va="center")

    # global labels & title
    fig.text(0.5, 0.04, "Time rel. to stimulus onset (ms)", ha="center")
    fig.suptitle(f"Neuron {neuron} - Δ*={Δ:.1f} ms,  ={sigma:.1f} ms", y=0.98)

    plt.tight_layout(rect=[0, 0.03, 1, 0.95])
    plt.show()
```

Plot the same 3 examples you selected in Task 1

[12]:
```
for neuron in [dir_sel[1], ori_sel[3], non_sel[0]]:
    plotPSTH(spikes, neuron)
```


Neuron 13 — Δ*=97.7 ms, σ=20.0 ms
0°
22°
45°
67°
90°
112°
135°
157°
180°
202°
225°
247°
270°
292°
315°
337°
SDF σ=20 ms
PSTH Δ*=97.7 ms
sp/s
Time rel. to stimulus onset (ms)


Neuron 16 — Δ*=93.3 ms, σ=20.0 ms
50 sp/s
0°
22°
45°
67°
90°
112°
135°
157°
180°
202°
225°
247°
270°
292°
315°
337°
SDF σ=20 ms
PSTH Δ*=93.3 ms
sp/s
Time rel. to stimulus onset (ms)



1.4 Task 3: Fit and plot tuning functions

The goal is to visualize the activity of each neuron as a function of stimulus direction. First, compute the spike counts of each neuron for each direction of motion and trial. The result should be a matrix `x`, where x_{jk} represents the spike count of the j-th response to the k-th direction of motion (i.e. each column contains the spike counts for all trials with one direction of motion). If you used dataframes above, the `groupby()` function allows to implement this very compactly. Make sure you don't loose trials with zero spikes though. Again, other implementations are completely fine.

Fit the tuning curve, i.e. the average spike count per direction, using a von Mises model. To capture the non-linearity and direction selectivity of the neurons, we will fit a modified von Mises function:

$$f(\theta) = \exp(\alpha + \kappa(\cos(2 * (\theta - \phi)) - 1) + \nu(\cos(\theta - \phi) - 1))$$

Here, θ is the stimulus direction. Implement the von Mises function in `vonMises()` and plot it to understand how to interpret its parameters ϕ, κ, ν, α. Perform a non-linear least squares fit using a package/function of your choice. Implement the fitting in `tuningCurve()`.

Plot the average number of spikes per direction, the spike counts from individual trials as well as your optimal fit.

Select two cells that show nice tuning to test your code.

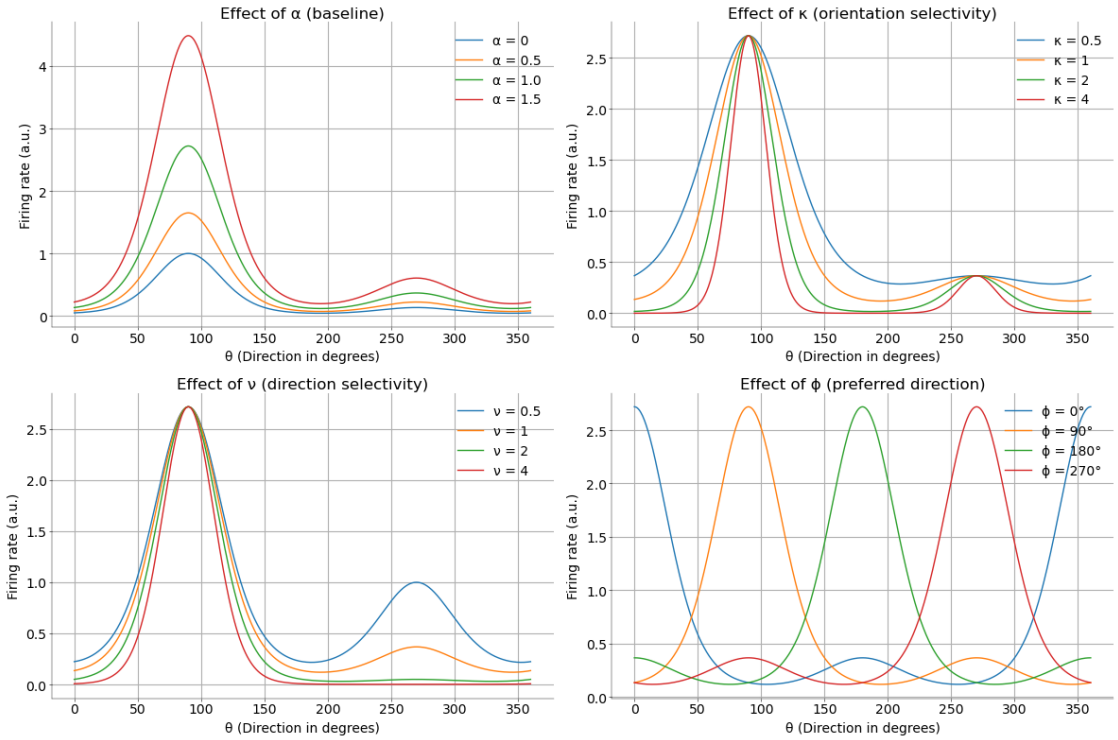
Grading: 5 pts

[13]:
```
def vonMises( : np.ndarray,  : float,  : float,  : float,  : float) -> np.ndarray:
    """Evaluate the parametric von Mises tuning curve
        with parameters p at locations theta.

    Parameters
    ----------

     : np.array, shape=(N, )
        Locations. The input unit is degree.

     ,  ,  ,   : float
        Function parameters

    Return
    ------
    f: np.array, shape=(N, )
        Tuning curve.
    """

    # ------------------------------------
    # Implement the Mises model (0.5 pts)
    # ------------------------------------
    return np.exp(  +   * (np.cos(2 * (  -  )) - 1) +   * (np.cos(  -  ) - 1))
```

Plot the von Mises function while varying the parameters systematically.

[14]:
```
# ------------------------------------------------------------------------------
# plot von Mises curves with varying parameters and explain what they do (2 pts)
# ------------------------------------------------------------------------------
import numpy as np
import matplotlib.pyplot as plt


def plot_vonMises_param_effects():
      = np.linspace(0, 360, 500)

    # Baseline parameters
      = 1.0
      = 1.0
      = 1.0
      = 90.0
```

```
    theta_rad = np.deg2rad( )  # convert degrees to radians
    phi_rad = np.deg2rad( )  # convert degrees to radians

    fig, axs = plt.subplots(2, 2, figsize=(12, 8))
    axs = axs.ravel()

    # Vary   (baseline)
    for a in [0, 0.5, 1.0, 1.5]:
        f = vonMises(theta_rad,  =a,  = ,  = ,  =phi_rad)
        axs[0].plot( , f, label=f"  = {a}")
    axs[0].set_title("Effect of   (baseline)")
    axs[0].legend()

    # Vary   (orientation tuning sharpness)
    for k in [0.5, 1, 2, 4]:
        f = vonMises(theta_rad,  = ,  =k,  = ,  =phi_rad)
        axs[1].plot( , f, label=f"  = {k}")
    axs[1].set_title("Effect of   (orientation selectivity)")
    axs[1].legend()

    # Vary   (direction tuning sharpness)
    for n in [0.5, 1, 2, 4]:
        f = vonMises(theta_rad,  = ,  = ,  =n,  =phi_rad)
        axs[2].plot( , f, label=f"  = {n}")
    axs[2].set_title("Effect of   (direction selectivity)")
    axs[2].legend()

    # Vary   (preferred direction)
    for phi in [0, 90, 180, 270]:
         _rad = np.deg2rad(phi)
        f = vonMises(theta_rad,  = ,  = ,  = ,  = _rad)
        axs[3].plot( , f, label=f"  = {phi}°")
    axs[3].set_title("Effect of   (preferred direction)")
    axs[3].legend()

    for ax in axs:
        ax.set_xlabel("  (Direction in degrees)")
        ax.set_ylabel("Firing rate (a.u.)")
        ax.grid(True)

    plt.tight_layout()
    plt.show()


plot_vonMises_param_effects()
```



Plot the von Mises function while varying the parameters systematically and explain what they do. The von Mises function used for fitting tuning curves is:

$$f(\theta) = \exp(\alpha + \kappa(\cos(2(\theta - \phi)) - 1) + \nu(\cos(\theta - \phi) - 1))$$

The parameters each distinctly describe the shape of the distribution:

α **- Baseline/Amplitude:** This is related to the neuron's baseline firing rate or the overall responsiveness. A larger alpha generally means the neuron fires more across all tested directions, or has a higher peak response. We see in the plot that going from a range of $\alpha = 0$ to $\alpha = 1.5$ all peaks show respective increase.

κ **- Orientation Selectivity / Bimodal Component Strength** This term creates a response pattern that is 180° periodic (i.e., it has two peaks in a 360° range). kappa controls the strength and sharpness of this bimodal component.

ν **- Direction Selectivity** Controls the strength and sharpness of this unimodal component. We see that $\nu = 4$ has a flat bimodal peak.

ϕ **- Preferred Direction/Orientation -** ϕ **is the neuron's preferred direction (if** ν is dominant) or preferred orientation axis (if κ is dominant). It shifts the entire tuning curve horizontally along the direction axis. We note the shift in peak as we vary the ϕ above.

[15]:
```python
def compute_spike_count_matrix(counts: np.ndarray, dirs: np.ndarray) -> np.
↪ndarray:
    """Compute the spike count matrix from the counts and dirs.

    Parameters
    ----------
    counts: np.ndarray
        The spike counts for each trial.

    dirs: np.ndarray
        The stimulus directions for each trial.

    Returns
    -------
    spike_count_matrix: np.ndarray
        The computed spike count matrix.
    """
    unique_stim_directions_deg = np.unique(dirs)
    num_unique_directions = len(unique_stim_directions_deg)
    logger.debug(f"Unique stimulus directions: {unique_stim_directions_deg}")
    logger.debug(f"Number of unique stimulus directions:␣
↪{num_unique_directions}")

    unique_stim_directions_deg = np.unique(dirs)
    num_unique_directions = len(unique_stim_directions_deg)

    spike_count_matrix_x = np.zeros((nTrials, num_unique_directions))

    for k_idx, direction_value in enumerate(unique_stim_directions_deg):

        counts_for_this_direction = counts[dirs == direction_value]
        if len(counts_for_this_direction) == nTrials:
            spike_count_matrix_x[:, k_idx] = counts_for_this_direction
        else:
            actual_trials_found = len(counts_for_this_direction)
            if actual_trials_found >= nTrials:
                spike_count_matrix_x[:, k_idx] = counts_for_this_direction[:
↪nTrials]
            else:  # actual_trials_found < nTrials
                spike_count_matrix_x[:actual_trials_found, k_idx] = (
                    counts_for_this_direction
                )
    return spike_count_matrix_x
```

[16]:
```python
def inital_von_mises_params(
    mean_counts_to_fit: np.ndarray, unique_dirs_rad: np.ndarray
) -> tuple:
```

```
    """Initial guess for the von Mises parameters based on mean counts.
    Parameters
    ----------
    mean_counts_to_fit: np.ndarray
        The mean counts for each direction.
    unique_dirs_rad: np.ndarray
        The unique directions in radians.
    Returns
    -------
    tuple: (alpha_guess, kappa_guess, nu_guess, phi_guess_rad)
        Initial guesses for the parameters of the von Mises function.
    """
    if not np.any(mean_counts_to_fit > 1e-9):
        alpha_guess = np.log(1e-6)
        phi_guess_rad = 0.0
    else:
        # For alpha, use log of mean of positive counts, or log of max if all␣
↪else fails
        positive_mean_counts = mean_counts_to_fit[mean_counts_to_fit > 1e-9]
        if len(positive_mean_counts) > 0:
            alpha_guess = np.log(np.maximum(1e-6, np.
↪mean(positive_mean_counts)))
        else:
            alpha_guess = np.log(np.maximum(1e-6, np.max(mean_counts_to_fit)))

        phi_guess_rad = unique_dirs_rad[np.argmax(mean_counts_to_fit)]

    kappa_guess = 1.0
    nu_guess = 1.0
    return alpha_guess, kappa_guess, nu_guess, phi_guess_rad
```

[17]:
```
def plot_tuning_curve_fit(
    neuron_id: int,
    counts: np.ndarray,
    dirs: np.ndarray,
    mean_counts_to_fit: np.ndarray,
    p_opt: np.ndarray,
    r_squared: float = None,
) -> None:
    """Plot the tuning curve fit for a single neuron.
    Parameters
    ----------
    neuron_id: int
        The ID of the neuron being plotted.
    counts: np.ndarray
        The spike counts for each trial.
    dirs: np.ndarray
```

```
        The stimulus directions for each trial.
    mean_counts_to_fit: np.ndarray
        The mean counts for each direction.
    p_opt: np.ndarray
        The optimized parameters from the von Mises fit.
    r_squared: float, optional
        The R-squared value of the fit, if available.
    """
    plt.figure(figsize=(10, 7))
    # 1. Plot individual trial spike counts (scatter plot)
    # Add some jitter to x-values for better visibility if many trials per␣
↪direction
    unique_stim_directions_deg = np.unique(dirs)
    unique_dir_vals_plot = np.unique(dirs)
    dir_spacing = (
        np.min(np.diff(unique_dir_vals_plot)) if len(unique_dir_vals_plot) > 1␣
↪else 22.5
    )
    jitter_strength = dir_spacing * 0.05  # Small jitter

    jittered_dirs = np.copy(dirs).astype(float)
    for ud in unique_dir_vals_plot:
        trials_for_dir_mask = dirs == ud
        num_trials_this_dir = np.sum(trials_for_dir_mask)
        if num_trials_this_dir > 1:
            jittered_dirs[trials_for_dir_mask] += np.random.uniform(
                -jitter_strength, jitter_strength, num_trials_this_dir
            )

    plt.scatter(
        jittered_dirs,
        counts,
        alpha=0.3,
        s=25,
        color="darkgray",
        label="Individual Trial Counts",
        zorder=1,
    )

    # 2. Plot average spike counts per direction
    # Calculate standard error of the mean (SEM) for error bars if desired
    # sem_counts = np.std(spike_count_matrix_x, axis=0) / np.
↪sqrt(spike_count_matrix_x.shape[0])
    # plt.errorbar(unique_stim_directions_deg, mean_counts_to_fit,␣
↪yerr=sem_counts,
    #              fmt='o', color='dodgerblue', markersize=8, capsize=5,
    #              label='Mean Counts (±SEM)', zorder=2)
```

```
    # Or simpler, just plot mean points:
    plt.plot(
        unique_stim_directions_deg,
        mean_counts_to_fit,
        "o",
        color="dodgerblue",
        markersize=8,
        label="Mean Spike Count",
        zorder=2,
    )

    # 3. Plot the fitted von Mises curve (if fit was successful)
    if p_opt is not None:
        theta_plot_deg = np.linspace(0, 360, 361)  # Smooth range of angles in␣
↪degrees
        theta_plot_rad = np.deg2rad(
            theta_plot_deg
        )  # Convert to radians for vonMises function

        fitted_values = vonMises(theta_plot_rad, *p_opt)

        plt.plot(
            theta_plot_deg,
            fitted_values,
            "-",
            color="red",
            linewidth=2.5,
            label=(
                f"Von Mises Fit (R²={r_squared:.2f})"
                if r_squared is not None
                else "Von Mises Fit"
            ),
            zorder=3,
        )
    else:
        logger.info(f"Neuron {neuron_id if neuron_id else 'Unknown'}: No fit to␣
↪plot.")

    plt.xlabel("Direction of motion (degrees)")
    plt.ylabel("Spike count")
    title_parts = ["Tuning Curve"]
    if neuron_id is not None:
        title_parts.append(f"Neuron {neuron_id}")
    if p_opt is None:
        title_parts.append("(Fit Failed)")

    plt.title(" - ".join(title_parts))
```

```
    plt.xticks(np.arange(0, 361, 45))
    plt.xlim(-10, 370)  # Give a bit of space around 0 and 360

    # Adjust y-limits dynamically
    min_y_val = 0
    if len(counts) > 0:
        min_y_val = min(0, np.min(counts) - 1)
        max_y_val = np.max(counts) + max(
            1, np.std(counts) * 0.5
        )  # Ensure some space above max count
        if p_opt is not None:  # Also consider fitted curve for ymax
            max_y_val = max(max_y_val, np.max(fitted_values) * 1.1)
        plt.ylim(bottom=min_y_val, top=max_y_val)
    else:
        plt.ylim(bottom=0, top=1)  # Default if no counts

    plt.legend(loc="upper right")
    plt.grid(True, linestyle="--", alpha=0.6)
    plt.tight_layout()
    plt.show()
```

[18]:
```
def tuningCurve(
    counts: np.ndarray, dirs: np.ndarray, show: bool = True, neuron_id=None
) -> np.ndarray:
    """Fit a von Mises tuning curve to the spike counts in count with
    direction dir using a **least-squares fit**.

    Parameters
    ----------

    counts: np.array, shape=(total_n_trials, )
        the spike count during the stimulation period

    dirs: np.array, shape=(total_n_trials, )
        the stimulus direction in degrees

    show: bool, default=True
        Plot or not.
    neuron_id: int, optional
        The ID of the neuron being fitted. Used for logging and plotting.
        If None, will be set to 'Unknown' in logs and plots.

    Return
    ------
    p: np.array or list, (4,)
        parameter vector of tuning curve function
    """
```

```
    # ----------------------------------------
    # Compute the spike count matrix (0.5 pts)
    # ----------------------------------------
    logger.info("Fitting tuning curve...")
    logger.info(f"Counts: {counts.shape}")
    logger.info(f"Dirs: {dirs.shape}")

    spike_count_matrix_x = compute_spike_count_matrix(counts, dirs)

    logger.info(f"Spike count matrix shape: {spike_count_matrix_x.shape}")
    logger.info(f"Spike count matrix: {spike_count_matrix_x}")

    # ------------------------------------------------------------
    # fit the von Mises tuning curve to the spike counts (0.5 pts)
    # ------------------------------------------------------------

    # 1. Calculate mean spike counts per direction
    mean_counts_to_fit = np.mean(spike_count_matrix_x, axis=0)
    logger.info(f"Mean counts to fit: {mean_counts_to_fit}")

    # 2. Get unique directions (degrees) and convert to radians
    # 'dirs' is the original 1D array of directions for all trials passed to␣
↪tuningCurve
    unique_stim_directions_deg = np.unique(dirs)
    unique_dirs_rad = np.deg2rad(unique_stim_directions_deg)
    logger.info(f"Unique directions (radians) for fitting: {unique_dirs_rad}")

    # Check if there's enough data to fit (at least as many points as␣
↪parameters)
    if len(unique_dirs_rad) < 4:  # vonMises has 4 parameters
        logger.warning(
            f"Not enough unique directions ({len(unique_dirs_rad)}) to fit the␣
↪von Mises model. Need at least 4. Skipping fit."
        )
        p_opt = None  # Indicate fit failed
    else:
        alpha_guess, kappa_guess, nu_guess, phi_guess_rad =␣
↪inital_von_mises_params(
            mean_counts_to_fit, unique_dirs_rad
        )
        p0 = [alpha_guess, kappa_guess, nu_guess, phi_guess_rad]
        logger.info(f"Initial parameter guesses (p0): {p0}")
        # Bounds: alpha, kappa>=0, nu>=0, phi in [0, 2*pi]
        bounds = ([-np.inf, 0, 0, 0], [np.inf, np.inf, np.inf, 2 * np.pi])
        # Fit the von Mises function to the mean counts
        # 4. Perform the non-linear least squares fit
        r_squared = None
```

```
        try:
            p_opt, p_cov = opt.curve_fit(
                f=vonMises,  # Your vonMises function (make sure it's defined␣
↪and accessible)
                xdata=unique_dirs_rad,
                ydata=mean_counts_to_fit,
                p0=p0,
                bounds=bounds,
                maxfev=5000,  # Maximum number of function evaluations
            )
            residuals = mean_counts_to_fit - vonMises(unique_dirs_rad, *p_opt)
            ss_res = np.sum(residuals**2)
            ss_tot = np.sum((mean_counts_to_fit - np.mean(mean_counts_to_fit))␣
↪** 2)
            if ss_tot == 0:  # Avoid division by zero if all mean_counts are␣
↪the same
                r_squared = 1.0 if ss_res < 1e-9 else 0.0
            else:
                r_squared = 1 - (ss_res / ss_tot)
            logger.info(
                f"Neuron {neuron_id if neuron_id else 'Unknown'}: R-squared =␣
↪{r_squared:.3f}"
            )
            logger.info(f"Optimized parameters (p_opt): {p_opt}")
        except RuntimeError:
            logger.warning(
                "RuntimeError: Optimal parameters not found during curve_fit.␣
↪Fit failed."
            )
            p_opt = (
                None  # Or assign np.full(4, np.nan) if you prefer NaNs for␣
↪failed fits
            )
        except ValueError as e:
            logger.warning(f"ValueError during curve_fit: {e}. Fit failed.")
            p_opt = None

        if show:
            # -----------------------------------------
            # plot the data and fitted tuning curve (1 pt)
            # -----------------------------------------
            plot_tuning_curve_fit(
                neuron_id=neuron_id,
                counts=counts,  # spike_count_matrix_x.flatten(),
                dirs=dirs,
                mean_counts_to_fit=mean_counts_to_fit,
```

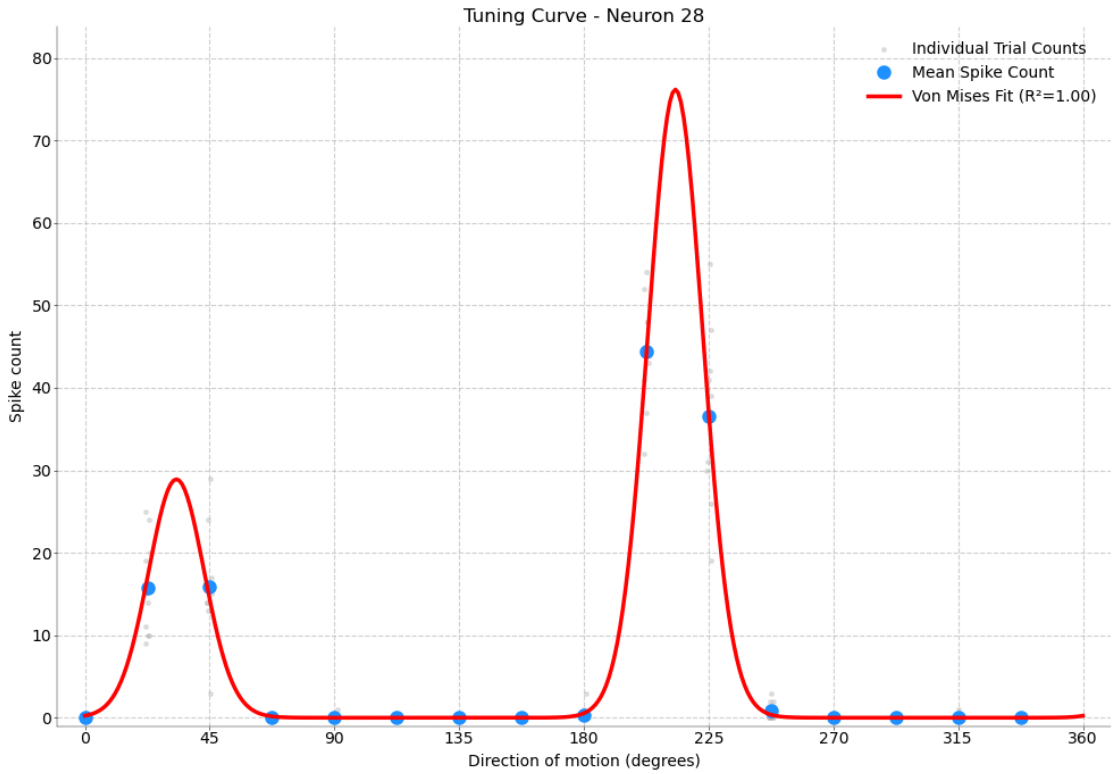
```
                p_opt=p_opt,
                r_squared=r_squared,  # Replace with actual R-squared value if␣
↪available
                # r_squared=1 - (np.sum((mean_counts_to_fit -␣
↪vonMises(unique_dirs_rad, *p_opt))**2) / np.sum((mean_counts_to_fit - np.
↪mean(mean_counts_to_fit))**2))
            )
        return p_opt
```

Plot tuning curve and fit for different neurons. Good candidates to check are 28, 29 or 37.

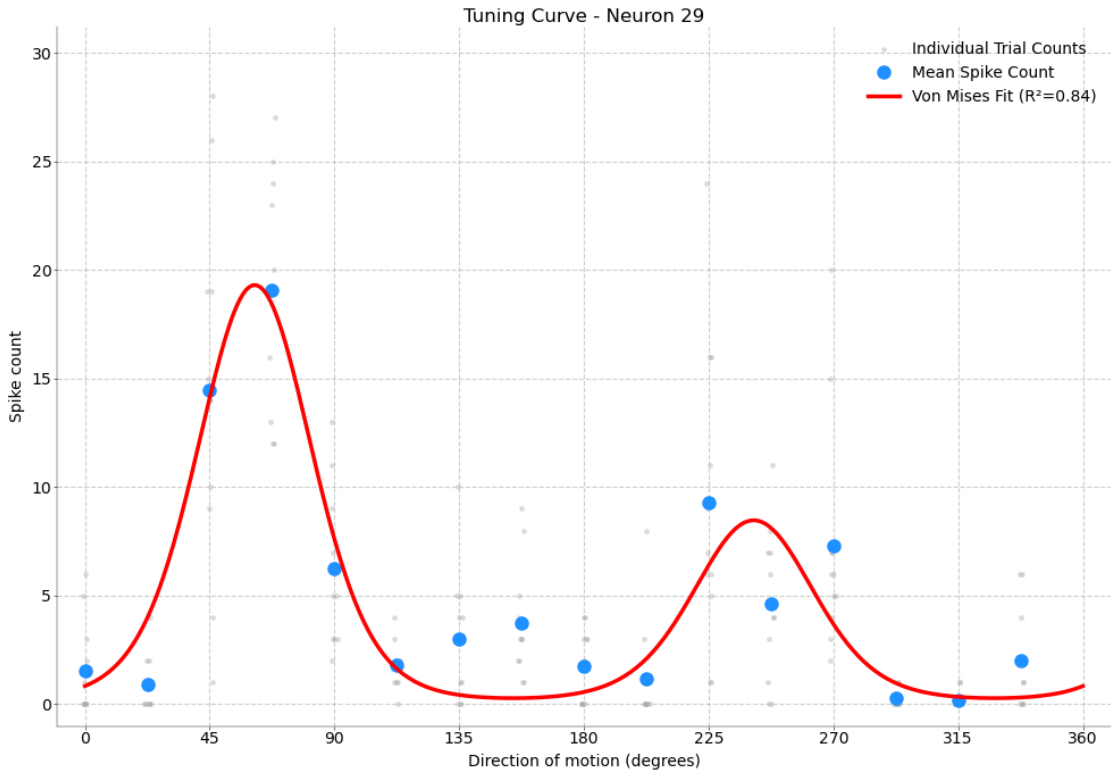
[19]:
```
def get_data(spikes, neuron):
    spk_by_dir = (
        spikes[spikes["Neuron"] == neuron]
        .groupby(["Dir", "Trial"])["stimPeriod"]
        .sum()
        .astype(int)
        .reset_index()
    )

    dirs = spk_by_dir["Dir"].values
    counts = spk_by_dir["stimPeriod"].values

    # because we count spikes only when they are present, some zero entries in␣
↪the count vector are missing
    for i, Dir in enumerate(np.unique(spikes["Dir"])):
        m = nTrials - np.sum(dirs == Dir)
        if m > 0:
            dirs = np.concatenate((dirs, np.ones(m) * Dir))
            counts = np.concatenate((counts, np.zeros(m)))

    idx = np.argsort(dirs)
    dirs_sorted = dirs[idx]  # sorted dirs
    counts_sorted = counts[idx]

    return dirs_sorted, counts_sorted
```

[20]:
```
# ------------------------------------------------------------
# plot the average number of spikes per direction, the spike
# counts from individual trials as well as your optimal fit
# for different neurons (0.5 pts)
# ------------------------------------------------------------
neurons_to_plot = [28, 29, 37]
for neuron in neurons_to_plot:
    dirs_sorted, counts_sorted = get_data(spikes, neuron)
    result = tuningCurve(counts_sorted, dirs_sorted, show=True,␣
↪neuron_id=neuron)
```

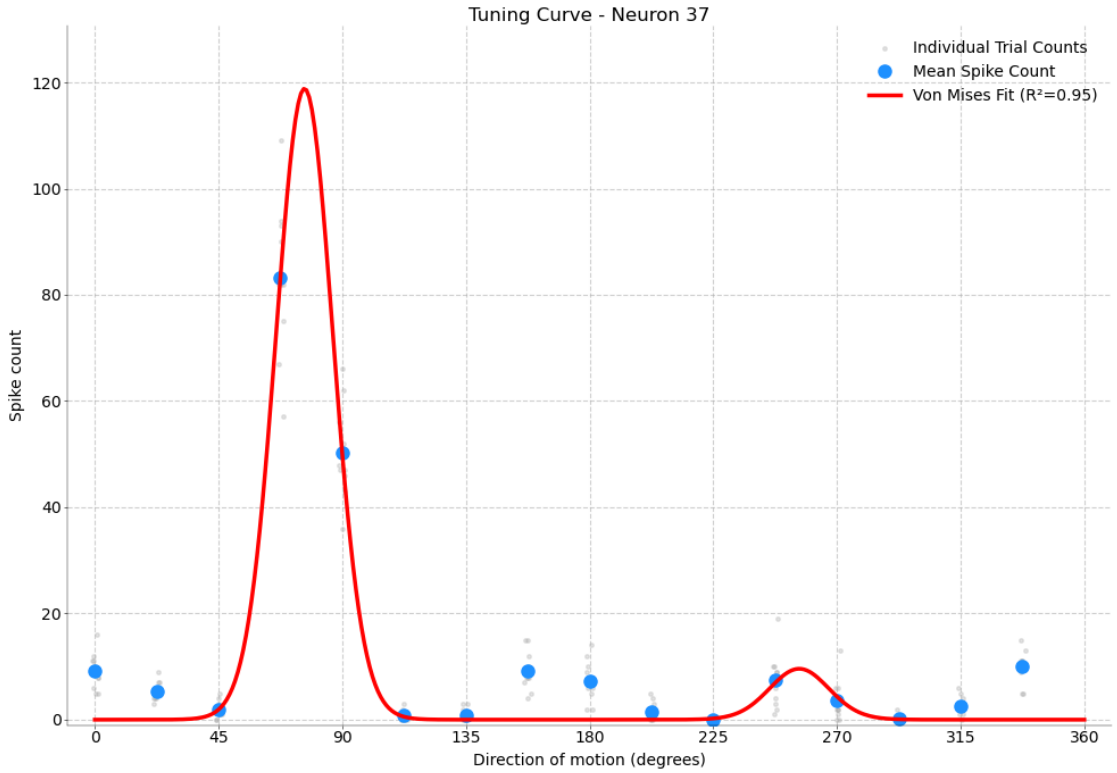
```
    if result is not None:
        print(
            f"Neuron {neuron}: dirs_sorted.shape = {dirs_sorted.shape},␣
↪counts_sorted.shape = {counts_sorted.shape}"
        )
    else:
        print(f"Neuron {neuron}: No result from tuningCurve()")
```




```
Neuron 28: dirs_sorted.shape = (176,), counts_sorted.shape = (176,)
```




```
Neuron 29: dirs_sorted.shape = (176,), counts_sorted.shape = (176,)
```

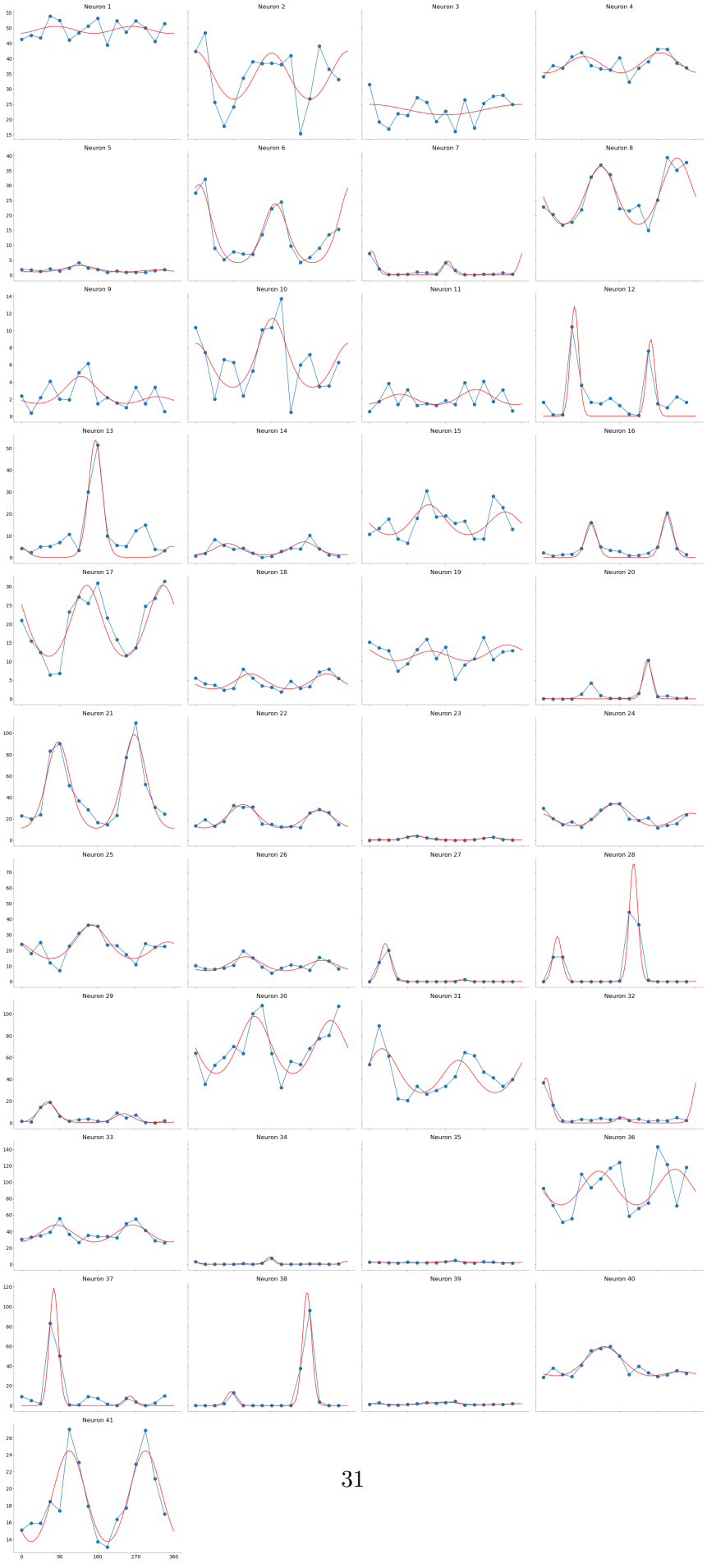



```
Neuron 37: dirs_sorted.shape = (176,), counts_sorted.shape = (176,)
```

1.4.1 Tuning Curves for neurons visualized

[21]:
```
all_neuron_ids = spikes["Neuron"].unique()
num_neurons = len(all_neuron_ids)
ncols = 4
nrows = int(np.ceil(num_neurons / ncols))

fig, axes = plt.subplots(
    nrows, ncols, figsize=(ncols * 5, nrows * 4), sharex=True, sharey="row"
)
axes = axes.flatten()


for i, neuron_id in enumerate(all_neuron_ids):
    if i >= len(axes):
        break
    ax = axes[i]
    dirs_sorted, counts_sorted = get_data(spikes, neuron_id)

    p_opt = None
```

```
    r_sq = None
    try:
        p_opt = tuningCurve(counts_sorted, dirs_sorted, neuron_id=neuron_id,␣
↪show=False)
    except Exception as e:
        logger.warning(f"Error fitting tuning curve for neuron {neuron_id}:␣
↪{e}")
        p_opt = None
    # You'd also need mean_counts_to_fit and unique_stim_directions_deg here
    spike_count_matrix_x = compute_spike_count_matrix(counts_sorted,␣
↪dirs_sorted)
    mean_counts_to_fit = np.mean(spike_count_matrix_x, axis=0)
    unique_stim_directions_deg = np.unique(dirs_sorted)

    ax.plot(unique_stim_directions_deg, mean_counts_to_fit, "o-")
    if p_opt is not None:
        theta_plot_deg = np.linspace(0, 360, 100)
        fitted_values = vonMises(np.deg2rad(theta_plot_deg), *p_opt)
        ax.plot(theta_plot_deg, fitted_values, "r-")
    ax.set_title(f"Neuron {neuron_id}")
    ax.set_xticks(np.arange(0, 361, 90))

for j in range(i + 1, nrows * ncols):
    if j < len(axes):  # Check if axes[j] exists
        fig.delaxes(axes[j])

plt.tight_layout()
plt.show()
```


Neuron 1
Neuron 2
Neuron 3
Neuron 4
Neuron 5
Neuron 6
Neuron 7
Neuron 8
Neuron 9
Neuron 10
Neuron 11
Neuron 12
Neuron 13
Neuron 14
Neuron 15
Neuron 16
Neuron 17
Neuron 18
Neuron 19
Neuron 20
Neuron 21
Neuron 22
Neuron 23
Neuron 24
Neuron 25
Neuron 26
Neuron 27
Neuron 28
Neuron 29
Neuron 30
Neuron 31
Neuron 32
Neuron 33
Neuron 34
Neuron 35
Neuron 36
Neuron 37
Neuron 38
Neuron 39
Neuron 40
Neuron 41
0
90
180
270
360

1.5 Task 4: Permutation test for direction tuning

Implement a permutation test to quantitatively assess whether a neuron is direction/orientation selective. To do so, project the vector of average spike counts, $m_k = \frac{1}{N}\sum_j x_{jk}$ on a complex exponential with two cycles, $v_k = \exp(\psi i \theta_k)$, where θ_k is the k-th direction of motion in radians and $\psi \in 1, 2$ is the fourier component to test (1: direction, 2: orientation). Denote the projection by $q = m^T v$. The magnitude $|q|$ tells you how much power there is in the ψ-th fourier component.

Estimate the distribution of |q| under the null hypothesis that the neuron fires randomly across directions by running 1000 iterations where you repeat the same calculation as above but on a random permutation of the trials (that is, randomly shuffle the entries in the spike count matrix x). The fraction of iterations for which you obtain a value more extreme than what you observed in the data is your p-value. Implement this procedure in the function `testTuning()`.

Illustrate the test procedure for one of the cells from above. Plot the sampling distribution of |q| and indicate the value observed in the real data in your plot.

How many cells are tuned at $p < 0.01$?

Grading: 3 pts

[22]:
```python
def compute_null_distribution(
    counts: np.ndarray,
    dirs: np.ndarray,
    v_k: np.ndarray,
    niters: int,
    rng: np.random.Generator,
) -> np.ndarray:
    """Compute the null distribution of |q| under the null hypothesis.

    Parameters
    ----------
    counts: np.ndarray
        The spike counts for each trial.

    dirs: np.ndarray
        The stimulus directions for each trial.

    v_k: np.ndarray
        The complex exponential vector for the specified psi.

    niters: int
        Number of iterations for the permutation test.

    rng: np.random.Generator
        Random number generator for reproducibility.
    Returns
```

```
    -------
    q_distribution_null: np.ndarray
        The computed null distribution of |q|.

    """
    # Initialize an array to store the |q| values from each permutation
    q_distribution_null = np.zeros(niters)
    logger.info(f"Starting permutation test with {niters} iterations...")

    for i in range(niters):
        shuffled_trial_counts = rng.permutation(counts)
        permuted_spike_matrix =␣
↪compute_spike_count_matrix(shuffled_trial_counts, dirs)
        m_k_permuted = np.mean(permuted_spike_matrix, axis=0)

        q_complex_permuted = np.dot(m_k_permuted, v_k)
        q_magnitude_permuted = np.abs(q_complex_permuted)

        q_distribution_null[i] = q_magnitude_permuted
    logger.info("Permutation test finished.")
    return q_distribution_null
```

[23]:
```
def plot_null_distribution(
    q_distribution_null: np.ndarray,
    q_observed_magnitude: float,
    niters: int,
    title: str = "Null Distribution of |q|",
):
    """Plot the null distribution of |q| and the observed |q|.

    Parameters
    ----------
    q_distribution_null: np.ndarray
        The computed null distribution of |q|.

    q_observed_magnitude: float
        The observed magnitude of |q| from the original data.

    niters: int
        Number of iterations for the permutation test.
    """
    plt.figure(figsize=(8, 6))

    # Plot the histogram of the null distribution
    plt.hist(
        q_distribution_null,
        bins=50,
```

```
        density=True,
        alpha=0.7,
        color="skyblue",
        label=f"Null Distribution of |q|\n({niters} permutations)",
    )

    # Add a vertical line for the observed |q|
    plt.axvline(
        x=q_observed_magnitude,
        color="red",
        linestyle="--",
        linewidth=2,
        label=f"Observed |q| = {q_observed_magnitude:.4f}",
    )

    plt.title(title)
    plt.xlabel("|q|")
    plt.ylabel("Density")
    plt.legend()
    plt.grid()
    plt.show()
```

[24]:
```
def testTuning(
    counts: np.ndarray,
    dirs: np.ndarray,
    psi: int = 1,
    niters: int = 1000,
    show: bool = False,
    random_seed: int = 2046,
    neuron: int = None,
) -> Tuple[float, float, np.ndarray]:
    """Plot the data if show is True, otherwise just return the fit.

    Parameters
    ----------

    counts: np.array, shape=(total_n_trials, )
        the spike count during the stimulation period

    dirs: np.array, shape=(total_n_trials, )
        the stimulus direction in degrees

    psi: int
        fourier component to test (1 = direction, 2 = orientation)

    niters: int
        Number of iterations / permutation
```

```
    show: bool
        Plot or not.

    random_seed: int
        Random seed for reproducibility.

    Returns
    -------
    p: float
        p-value
    q: float
        magnitude of second Fourier component

    qdistr: np.array
        sampling distribution of |q| under the null hypothesis

    """
    # --------------------------------
    # Calculate m, nu and q (0.5 pts)
    # --------------------------------
    # m - This is the vector of average spike counts for each unique stimulus direction.
    spike_count_matrix = compute_spike_count_matrix(counts, dirs)
    m_k = np.mean(spike_count_matrix, axis=0)

    # Get unique directions and convert to radians for v_k
    unique_stim_directions_deg = np.unique(dirs)
    theta_k_rad = np.deg2rad(unique_stim_directions_deg)

    # v_k - This is the complex exponential vector for the specified psi.
    # It should be based on the unique radian directions theta_k_rad.
    v_k = np.exp(1j * psi * theta_k_rad)

    # q - This is the projection of m_k onto v_k.
    q_complex_observed = np.dot(m_k, v_k)
    q_observed_magnitude = np.abs(q_complex_observed)

    logger.debug(f"Observed q magnitude: {q_observed_magnitude}")
    logger.debug(f"Observed q complex: {q_complex_observed}")
    logger.debug(f"Observed m_k: {m_k}")
    logger.debug(f"Observed v_k: {v_k}")

    # ------------------------------------------------------------------------
    # Estimate the distribution of q under the H0 and obtain the p value (1 pt)
    # ------------------------------------------------------------------------
    # Ensure reproducibility using a random number generator
```

```
    # Hint: Access random functions of this generator
    rng = np.random.default_rng(random_seed)

    q_distribution_null = compute_null_distribution(
        counts=counts, dirs=dirs, v_k=v_k, niters=niters, rng=rng
    )

    # Calculate the p-value.
    #    This is the proportion of permuted |q| values that are as extreme as,
    #    or more extreme than, the |q| observed from the original data.
    # We use smoothing to avoid p-values of 0 or 1.
    p_value = (np.sum(q_distribution_null >= q_observed_magnitude) + 1) /␣
↪(niters + 1)
    # p_value = np.sum(q_distribution_null >= q_observed_magnitude) / niters

    logger.info(
        f"Observed |q|: {q_observed_magnitude:.4f}, Calculated p-value:␣
↪{p_value:.35f}"
    )

    if show:
        neuron_title_str = "" if neuron is None else f"Neuron: {neuron}"
        title = f"Null Distribution {neuron_title_str} $\Psi$ : {psi}  P Value:␣
↪{p_value:.05f}"
        plot_null_distribution(
            q_distribution_null, q_observed_magnitude, niters, title=title
        )
    qdistr = q_distribution_null
    return p_value, q_observed_magnitude, qdistr
```

[25]:
```
def test_neuron_tuning(all_neuron_ids, spikes, niters=1000):
    """Test the tuning of a neuron for direction and orientation."""
    tuning_results = []

    for i, neuron_id in enumerate(all_neuron_ids):
        logger.info(f"Processing neuron {i+1}/{len(all_neuron_ids)}: ID␣
↪{neuron_id}...")

        # Get data for the current neuron
        dirs_sorted, counts_sorted = get_data(spikes, neuron_id)

        # Test for direction tuning (psi=1)
        p_direction, q_direction, _ = testTuning(
            counts_sorted,
            dirs_sorted,
            psi=1,
            niters=niters,
```

```
            show=False,
            neuron=neuron_id,
        )

        # Test for orientation tuning (psi=2)
        p_orientation, q_orientation, _ = testTuning(
            counts_sorted,
            dirs_sorted,
            psi=2,
            niters=niters,
            show=False,
            neuron=neuron_id,
        )

        tuning_results.append(
            {
                "neuron_id": neuron_id,
                "p_direction": p_direction,
                "q_direction": q_direction,
                "p_orientation": p_orientation,
                "q_orientation": q_orientation,
            }
        )

    return pd.DataFrame(tuning_results)
```

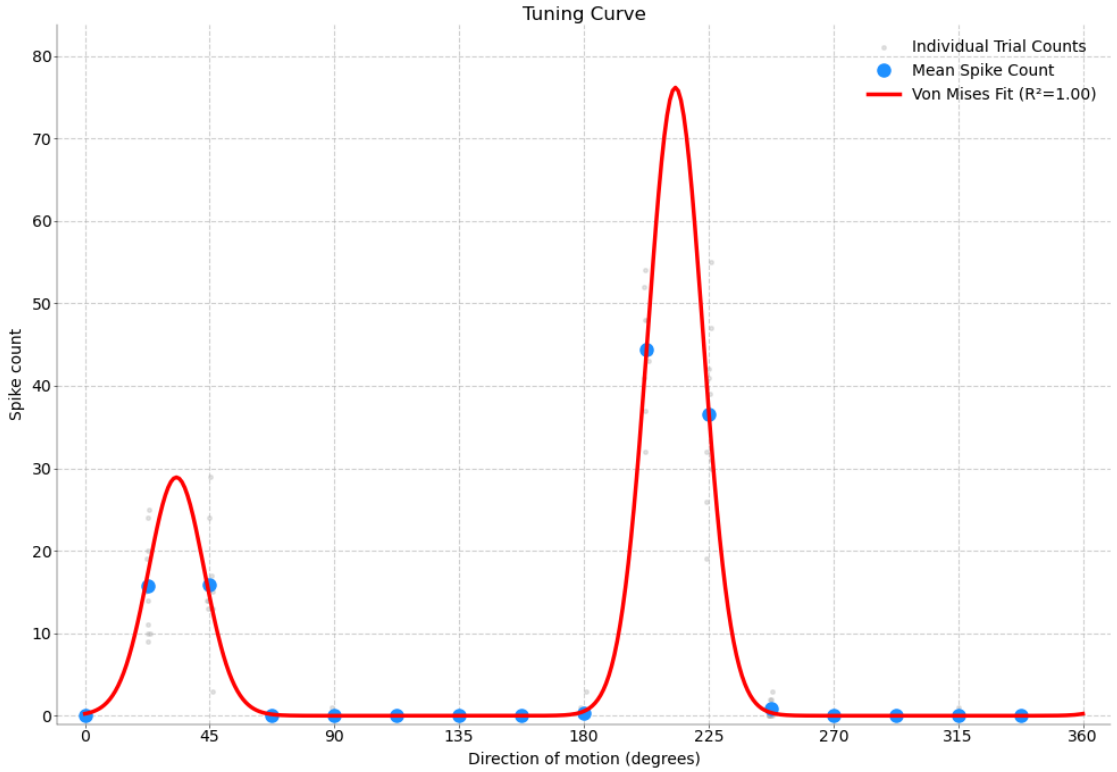
[26]:
```
def filter_tuning_results(tuning_results_df, alpha_threshold=0.01):
    """Filter the tuning results based on the significance level."""
    logging.debug(f"\n--- Tuning Selectivity Results (p < {alpha_threshold})␣
↪---")

    direction_selective_neurons = tuning_results_df[
        tuning_results_df["p_direction"] < alpha_threshold
    ]
    orientation_selective_neurons = tuning_results_df[
        tuning_results_df["p_orientation"] < alpha_threshold
    ]

    logging.debug(f"\nDirection Selective Neurons (psi=1, p <␣
↪{alpha_threshold}):")
    if not direction_selective_neurons.empty:
        logging.debug(
            direction_selective_neurons[["neuron_id", "p_direction",␣
↪"q_direction"]]
        )
    else:
        logging.debug(
```

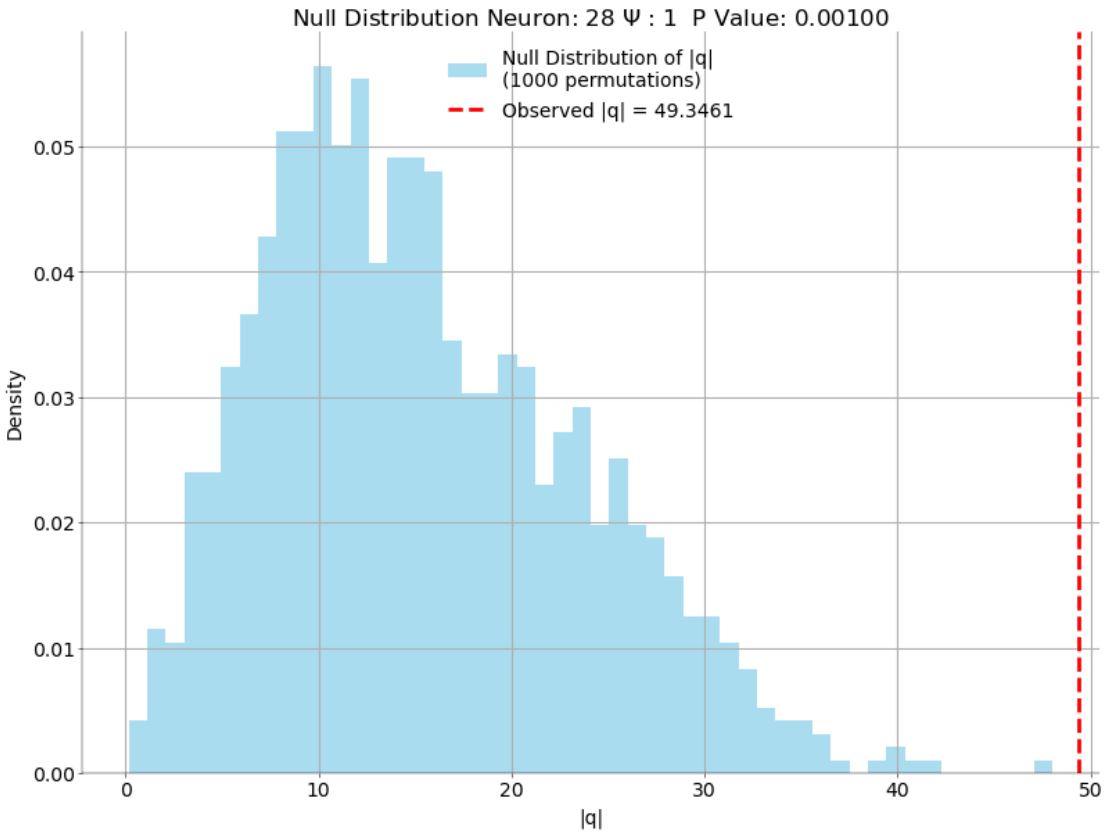
```
            "No neurons found to be significantly direction selective at this␣
↪threshold."
        )

    logging.debug(f"\nOrientation Selective Neurons (psi=2, p <␣
↪{alpha_threshold}):")
    if not orientation_selective_neurons.empty:
        logging.debug(
            orientation_selective_neurons[
                ["neuron_id", "p_orientation", "q_orientation"]
            ]
        )
    else:
        logging.debug(
            "No neurons found to be significantly orientation selective at this␣
↪threshold."
        )

    both_selective = tuning_results_df[
        (tuning_results_df["p_direction"] < alpha_threshold)
        & (tuning_results_df["p_orientation"] < alpha_threshold)
    ]
    logging.debug(
        f"\nNeurons Selective for BOTH Direction and Orientation (p <␣
↪{alpha_threshold}):"
    )
    if not both_selective.empty:
        logging.debug(both_selective[["neuron_id", "p_direction",␣
↪"p_orientation"]])
    else:
        logging.debug(
            "No neurons found to be significantly selective for both at this␣
↪threshold."
        )

    strictly_direction_selective = tuning_results_df[
        (tuning_results_df["p_direction"] < alpha_threshold)
        & (tuning_results_df["p_orientation"] >= alpha_threshold)
    ]
    logging.debug(
        f"\nNeurons Strictly Direction Selective (p_dir < {alpha_threshold},␣
↪p_ori >= {alpha_threshold}):"
    )
    if not strictly_direction_selective.empty:
        logging.debug(
```

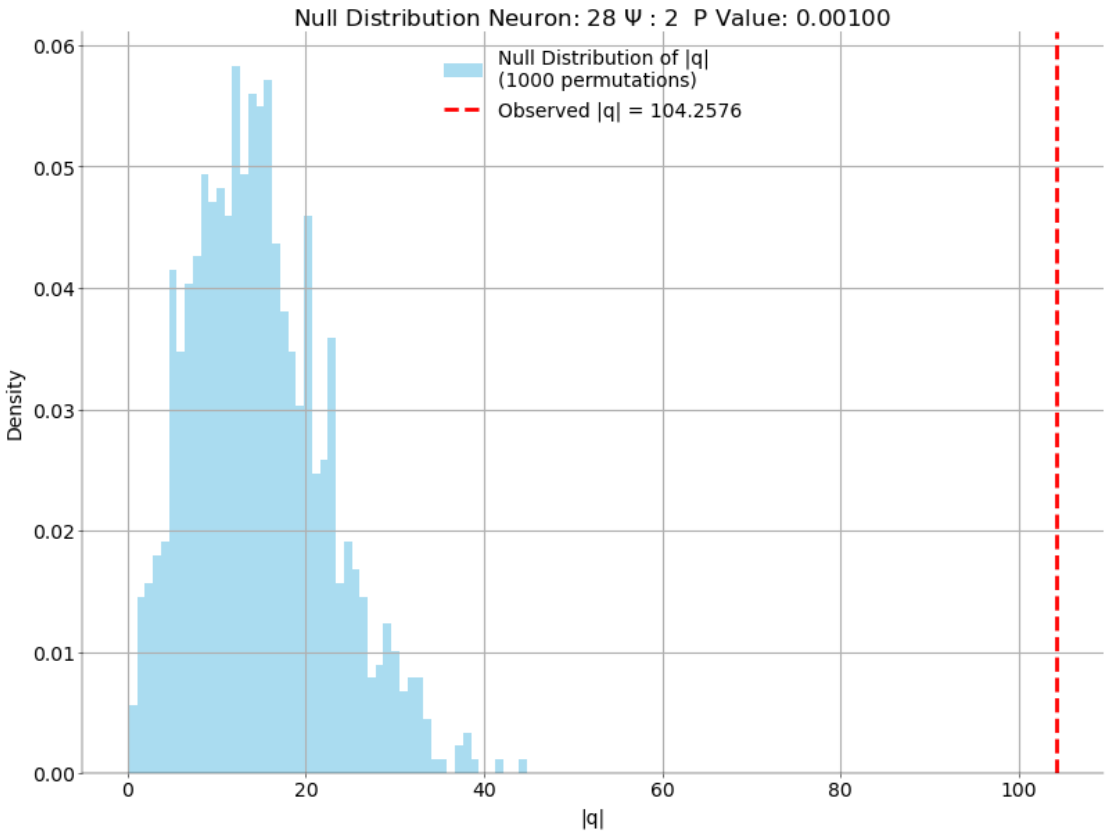
```
            strictly_direction_selective[["neuron_id", "p_direction",␣
↪"p_orientation"]]
        )
    else:
        logging.debug(
            "No neurons found to be strictly direction selective at this␣
↪threshold."
        )
    return (
        direction_selective_neurons,
        orientation_selective_neurons,
        both_selective,
        strictly_direction_selective,
    )
```

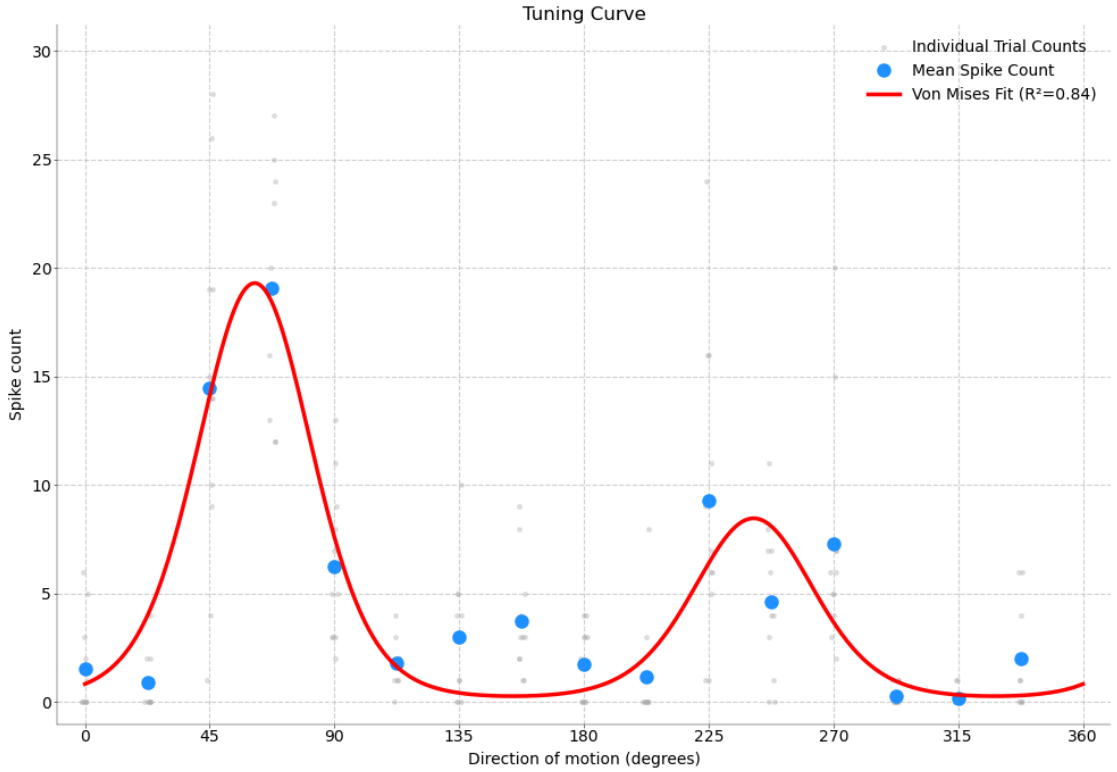
Show null distribution for the example cell:

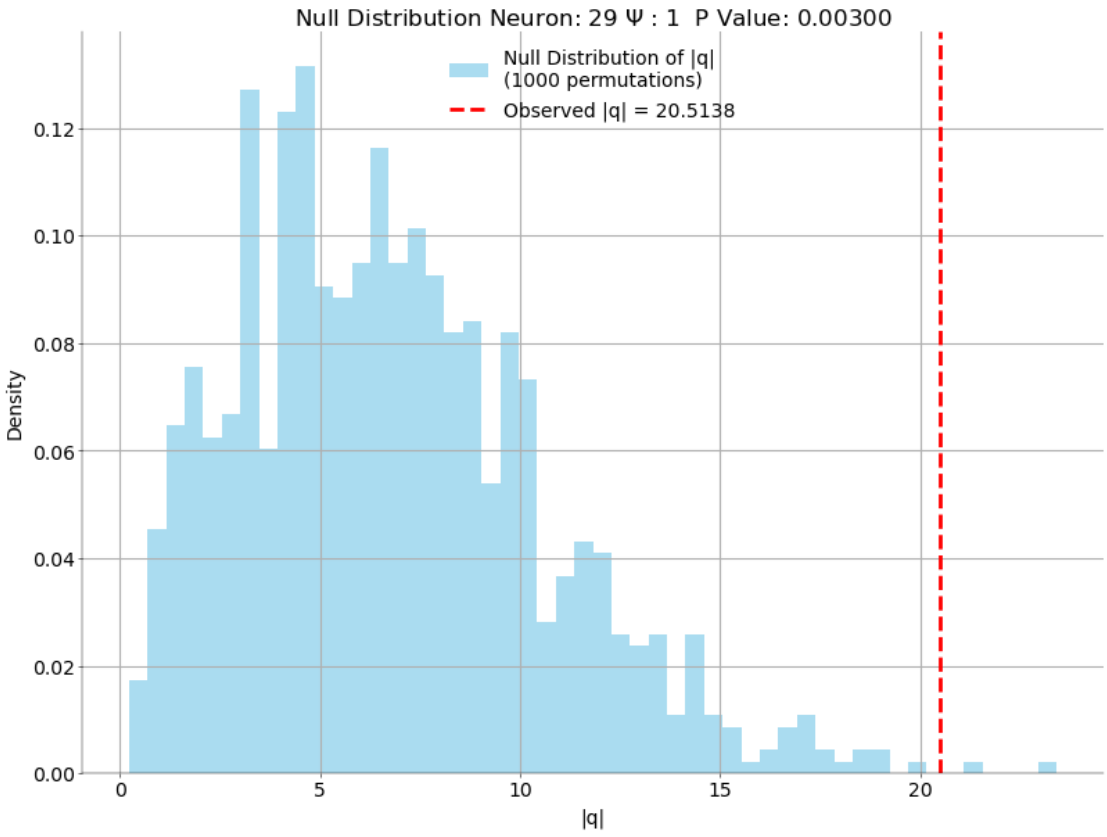
[27]:
```
# ------------------------------------------------------------
# Plot null distributions for example cells 28 & 29. (1 pt)
# ------------------------------------------------------------
neurons_to_plot = [28, 29]
for neuron in neurons_to_plot:
    dirs_sorted, counts_sorted = get_data(spikes, neuron)
    result = tuningCurve(counts_sorted, dirs_sorted, show=True)
    for psi in [1, 2]:
        p_value, q_observed_magnitude, qdistr = testTuning(
            counts_sorted, dirs_sorted, psi=psi, show=True, niters=1000,␣
↪neuron=neuron
        )
        logger.info(
            f"Neuron:{neuron} psi == {psi} ->  p-value: {p_value},␣
↪q_observed_magnitude: {q_observed_magnitude}"
        )
```

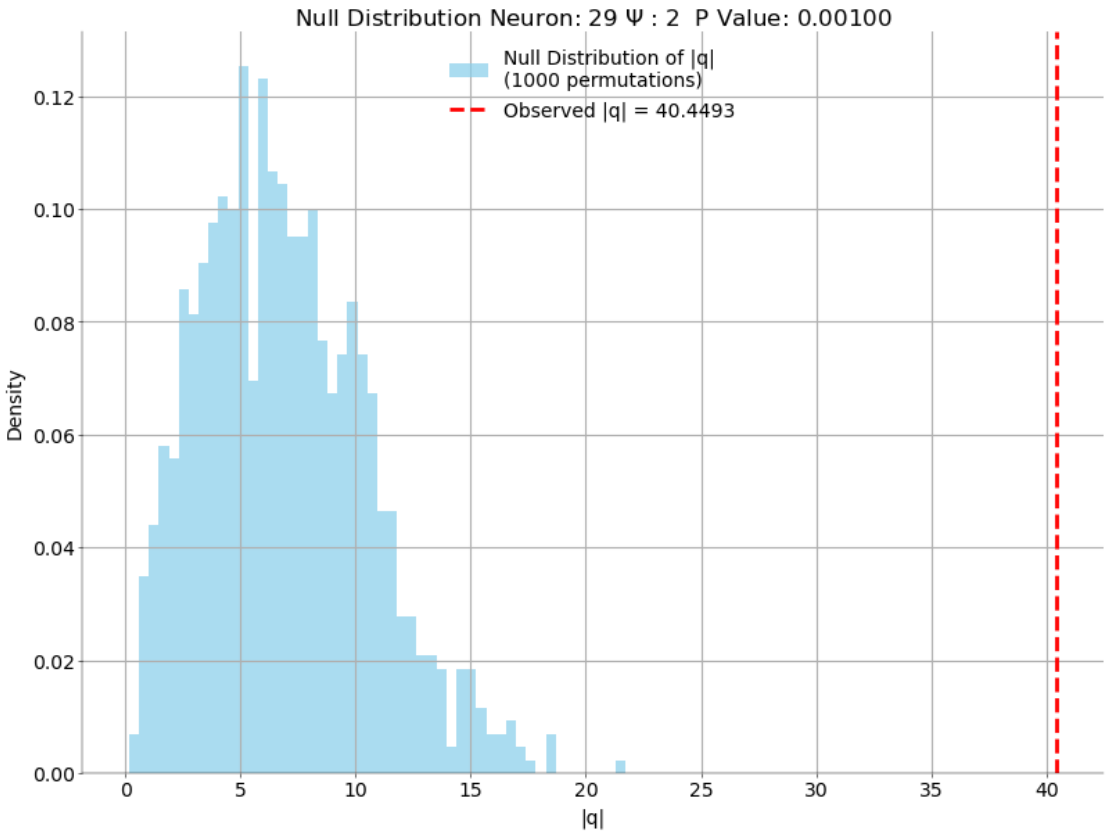

Tuning Curve
Individual Trial Counts
Mean Spike Count
Von Mises Fit (R²=1.00)
Spike count
Direction of motion (degrees)
0
10
20
30
40
50
60
70
80
0
45
90
135
180
225
270
315
360


Null Distribution Neuron: 28 Ψ : 1 P Value: 0.00100
Null Distribution of |q|
(1000 permutations)
Observed |q| = 49.3461
Density
0.00
0.01
0.02
0.03
0.04
0.05
0
10
20
30
40
50
|q|


Null Distribution Neuron: 28 Ψ : 2 P Value: 0.00100
Null Distribution of |q|
(1000 permutations)
Observed |q| = 104.2576
Density
|q|
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0
20
40
60
80
100


Tuning Curve
Individual Trial Counts
Mean Spike Count
Von Mises Fit (R²=0.84)
Spike count
Direction of motion (degrees)
0
5
10
15
20
25
30
0
45
90
135
180
225
270
315
360


Null Distribution Neuron: 29 Ψ : 1 P Value: 0.00300
Null Distribution of |q|
(1000 permutations)
Observed |q| = 20.5138
Density
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0
5
10
15
20
|q|



Test all cells for orientation and direction tuning

[28]:
```
# ------------------------------------------------
# Test all cells for orientation / direction tuning.
# Which ones are selective? (0.5 pts)
# ------------------------------------------------
# %%
neuron_tuning_results_df = test_neuron_tuning(
    np.unique(spikes["Neuron"]), spikes, niters=1000
)
# %% Filter the results based on the significance level
(
    direction_selective_neurons,
    orientation_selective_neurons,
    both_selective,
    strictly_direction_selective,
) = filter_tuning_results(neuron_tuning_results_df, alpha_threshold=0.01)
```

[29]:
```
num_direction_tuned = len(direction_selective_neurons)
num_orientation_tuned = len(orientation_selective_neurons)
num_both_tuned = len(both_selective)
```

```
total_unique_tuned_cells = num_direction_tuned + num_orientation_tuned -␣
 ↪num_both_tuned

print(
    f"Total number of unique neurons showing any tuning (direction or␣
 ↪orientation, p < 0.01): {total_unique_tuned_cells}"
)
```

```
Total number of unique neurons showing any tuning (direction or orientation, p <
0.01): 34
```

Number of direction tuned neurons:

[30]:
```
print(f"Number of direction selective neurons:␣
 ↪{len(direction_selective_neurons)}")
```

```
Number of direction selective neurons: 12
```

Number of orientation tuned neurons:

[31]:
```
print(f"Number of orientation selective neurons:␣
 ↪{len(orientation_selective_neurons)}")
```

```
Number of orientation selective neurons: 34
```

[32]:
```
print(f"Number of neurons selective for both: {len(both_selective)}")
print(
    f"Number of strictly direction selective neurons:␣
 ↪{len(strictly_direction_selective)}"
)
```

```
Number of neurons selective for both: 12
Number of strictly direction selective neurons: 0
```

[33]:
```
print("List direction sensitive Neurons:")
print(direction_selective_neurons)
print("---")
print("List orientation sensitive Neurons:---")
print(orientation_selective_neurons)
print("---")
```

```
List direction sensitive Neurons:
    neuron_id  p_direction  q_direction  p_orientation  q_orientation
12         13     0.000999    77.950288       0.000999      48.359041
19         20     0.000999     9.297844       0.000999      12.687638
23         24     0.001998    31.400913       0.000999      61.437416
24         25     0.003996    35.699993       0.000999      64.973538
26         27     0.000999    31.640129       0.000999      32.030661
27         28     0.000999    49.346055       0.000999     104.257627
28         29     0.002997    20.513794       0.000999      40.449320
```

```
30          31      0.000999    89.125639       0.000999     126.462049
31          32      0.000999    43.971208       0.000999      47.458766
36          37      0.000999   124.294759       0.000999      98.977689
37          38      0.000999   119.906485       0.000999     142.278675
39          40      0.000999    90.873419       0.002997      57.588171
---
List orientation sensitive Neurons:---
    neuron_id  p_direction  q_direction  p_orientation  q_orientation
1           2     0.476523    13.188314       0.000999      69.584958
2           3     0.063936    16.616565       0.001998      27.711406
5           6     0.122877    19.423996       0.000999      79.765526
6           7     0.277722     3.554301       0.000999      12.721692
7           8     0.608392    12.447186       0.000999      81.147705
9          10     0.339660     8.790470       0.002997      20.855551
11         12     0.206793     5.174151       0.000999      14.809007
12         13     0.000999    77.950288       0.000999      48.359041
13         14     0.767233     2.969608       0.000999      24.945998
14         15     0.239760    16.927466       0.000999      43.273723
15         16     0.859141     3.880623       0.000999      42.754483
16         17     0.025974    24.372216       0.000999      79.649865
17         18     0.116883     7.239444       0.000999      14.349402
19         20     0.000999     9.297844       0.000999      12.687638
20         21     0.955045     9.478136       0.000999     285.435722
21         22     0.070929    20.760966       0.000999      70.947070
22         23     0.044955     4.684794       0.000999      11.984867
23         24     0.001998    31.400913       0.000999      61.437416
24         25     0.003996    35.699993       0.000999      64.973538
25         26     0.582418     6.110360       0.000999      27.314082
26         27     0.000999    31.640129       0.000999      32.030661
27         28     0.000999    49.346055       0.000999     104.257627
28         29     0.002997    20.513794       0.000999      40.449320
29         30     0.881119    10.492633       0.000999     194.989028
30         31     0.000999    89.125639       0.000999     126.462049
31         32     0.000999    43.971208       0.000999      47.458766
32         33     0.399600    15.009117       0.000999      76.786618
33         34     0.010989     5.643544       0.000999       9.966181
35         36     0.024975    79.275292       0.000999     191.295301
36         37     0.000999   124.294759       0.000999      98.977689
37         38     0.000999   119.906485       0.000999     142.278675
38         39     0.043956     5.267488       0.001998       7.868793
39         40     0.000999    90.873419       0.002997      57.588171
40         41     0.900100     2.887781       0.000999      41.503439
---
```