SNN_MNIST_Demo

October 17, 2025

1 Feedforward SNN on MNIST (snnTorch)

This notebook runs the existing scripts in this repo to provide inline outputs and figures.

- Baseline: Poisson-encoded MNIST → LIF hidden layer → spike-count readout
- Tweaks: Homeostasis, Tau sweep, Sparse connectivity

Note: Ensure the environment is set up as per `commands.txt` and GPU is available.

1.0.1 About this cell: Environment and paths

- Adds project root `'.'` to `sys.path` so imports like `from scripts.baseline import run_baseline` work.
- Checks for CUDA availability; scripts will use GPU if available.
- Requires environment setup from `commands.txt` (PyTorch CUDA wheels, snnTorch, sklearn, etc.).

```
[ ]: # Path and environment checks
import os, sys
sys.path.append('.')  # allow 'src' and 'scripts' imports
import torch, snntorch, sklearn
device = torch.device('cuda' if torch.cuda.is_available() else 'cpu')
device
```

1.1 Utility to display saved figures

1.1.1 About this cell: Figure utilities

- Provides `show_if_exists(path)` helper to render saved images inline.
- Sets standard paths: `figures/`, `outputs/`, `.data/`.
- Scripts save figures and reports to these folders; this helper displays them after runs.

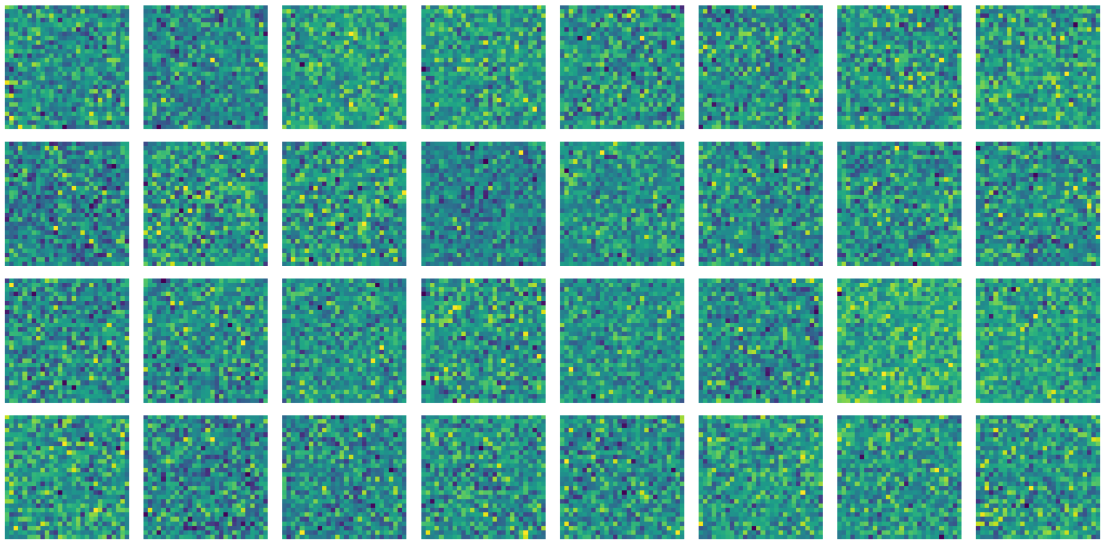
```
[ ]: from IPython.display import display, Image
def show_if_exists(path):
    if os.path.exists(path):
        display(Image(filename=path))
    else:
        print(f'Not found: {path}')
FIG_DIR = 'figures'
OUT_DIR = 'outputs'
```

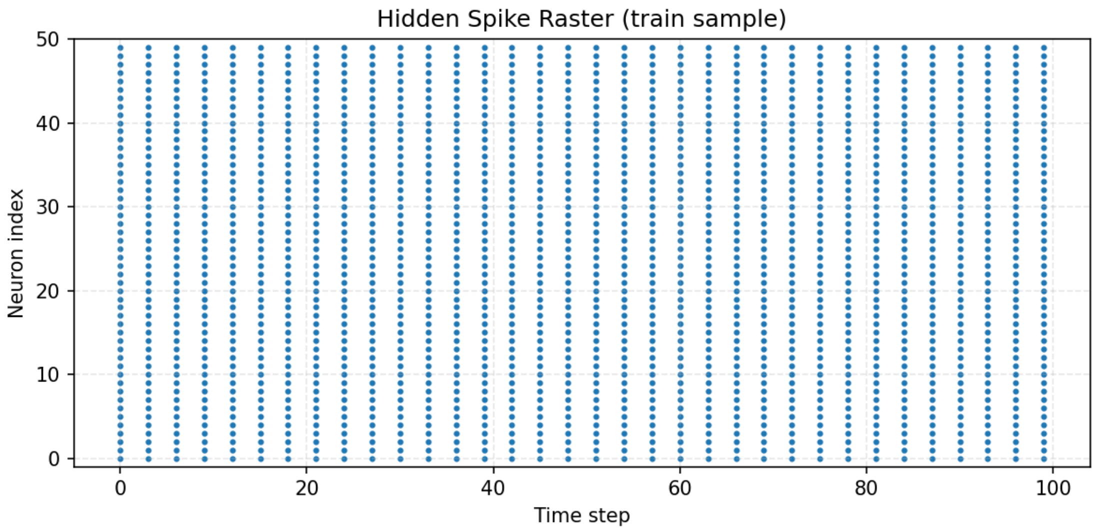
```
DATA_DIR = '.data'
```

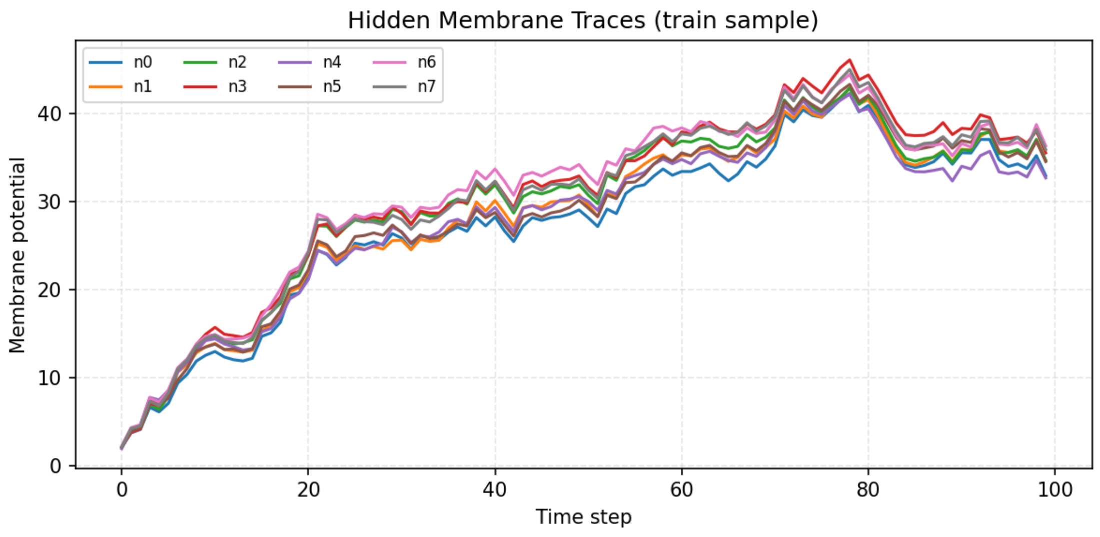
1.2 Baseline

```
[ ]: from types import SimpleNamespace
     from scripts.baseline import run_baseline
     # Configure baseline args (same defaults as script)
     args = SimpleNamespace(
         data_dir=DATA_DIR, output_dir=OUT_DIR, fig_dir=FIG_DIR,
         batch_size=128, num_workers=2, hidden=512, tau_ms=20.0, dt_ms=1.0,␣
       ↪t_ref_ms=2.0, v_th=1.0,
         num_steps=100, fmax_hz=100.0, w_mean=0.5, w_std=0.1, readout='logreg',
         # improved readout defaults
         scale_features=True, max_iter=1000, solver='lbfgs', C=1.0, penalty='none',
         seed=42
     )
     run_baseline(args)
     print('Baseline done. Showing figures:')
     show_if_exists(os.path.join(FIG_DIR, 'baseline_initial_filters.png'))
     show_if_exists(os.path.join(FIG_DIR, 'baseline_raster.png'))
     show_if_exists(os.path.join(FIG_DIR, 'baseline_voltage.png'))
     print('Report:');
     print(open(os.path.join(OUT_DIR, 'baseline_report.txt')).read())
```

```
(snncogs) aryas@3b676eb3826b:~/work/snn$  PYTHONPATH=. python scripts/baseline.py \
   --hidden 1024 --tau_ms 20 --dt_ms 1 --t_ref_ms 2 \
   --num_steps 100 --fmax_hz 100 --batch_size 128 \
   --readout logreg --max_iter 2000 --solver lbfgs --penalty none --C 1.0 \
   --data_dir .data --output_dir outputs --fig_dir figures --num_workers 4
Device: cuda
train feature extraction: 100%|                                                                  | 469/
test feature extraction: 100%|                                                                    | 79/7
Baseline Test Accuracy: 0.1156
```




Hidden Spike Raster (train sample)
Neuron index
Time step
0
10
20
30
40
50
0
20
40
60
80
100

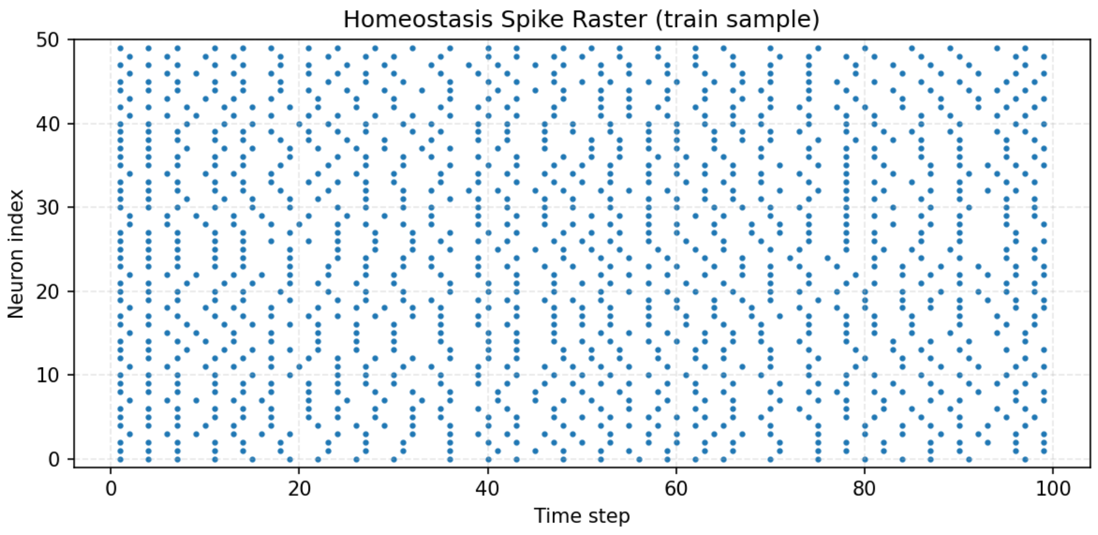


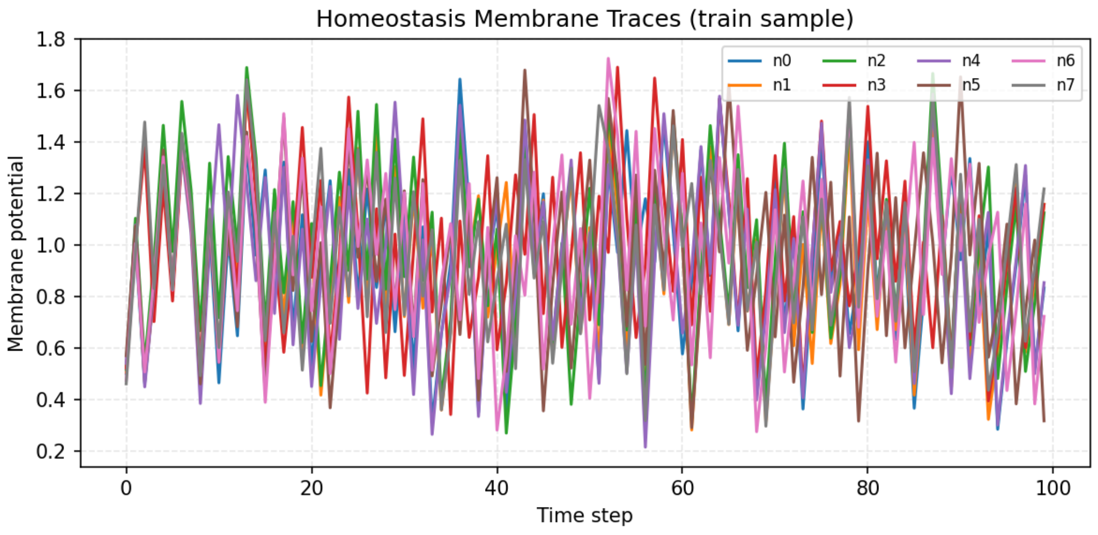
1.3 Homeostasis

```
[ ]: from scripts.homeostasis import run_homeostasis
     hargs = SimpleNamespace(
         data_dir=DATA_DIR, output_dir=OUT_DIR, fig_dir=FIG_DIR,
         batch_size=128, num_workers=2, hidden=512, tau_ms=20.0, dt_ms=1.0,␣
      ↪t_ref_ms=2.0, v_th=1.0,
         num_steps=100, fmax_hz=100.0, w_mean=0.5, w_std=0.1, readout='logreg',
         # homeostasis params
         target_hz=10.0, eta=0.01, ema_alpha=0.9, g_min=0.1, g_max=10.0,␣
      ↪adapt_epochs=1,
         # readout
         scale_features=True, max_iter=1000, solver='lbfgs', C=1.0, penalty='none',
         seed=42
     )
     run_homeostasis(hargs)
     print('Homeostasis done. Showing figures:')
     show_if_exists(os.path.join(FIG_DIR, 'homeostasis_raster.png'))
     show_if_exists(os.path.join(FIG_DIR, 'homeostasis_voltage.png'))
     print('Report:');
     print(open(os.path.join(OUT_DIR, 'homeostasis_report.txt')).read())
```

```
(snncogs) aryas@3b676eb3826b:~/work/snn$ PYTHONPATH=. python scripts/homeostasis.py \
  --hidden 1024 --tau_ms 20 --dt_ms 1 --t_ref_ms 2 \
  --num_steps 100 --fmax_hz 100 --batch_size 128 \
  --readout logreg --target_hz 10 --eta 0.01 --ema_alpha 0.9 --adapt_epochs 1 \
  --data_dir .data --output_dir outputs --fig_dir figures --num_workers 4
Device: cuda
Homeostasis epochs: 100%|                                                    | 1/1 [
train feature extraction: 100%|                                               | 469/
/home/aryas/work/snn/sncogs/lib/python3.10/site-packages/sklearn/linear_model/_logistic.py:47
```

```
STOP: TOTAL NO. OF ITERATIONS REACHED LIMIT

Increase the number of iterations to improve the convergence (max_iter=200).
You might also want to scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
test feature extraction: 100%|                                                        | 79/7
Homeostasis Test Accuracy: 0.4331
```

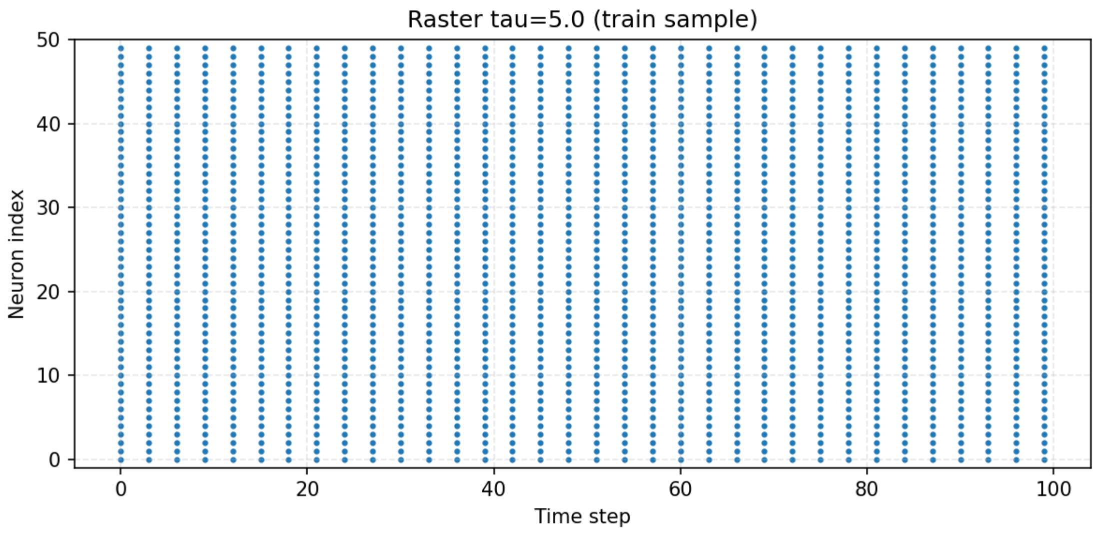


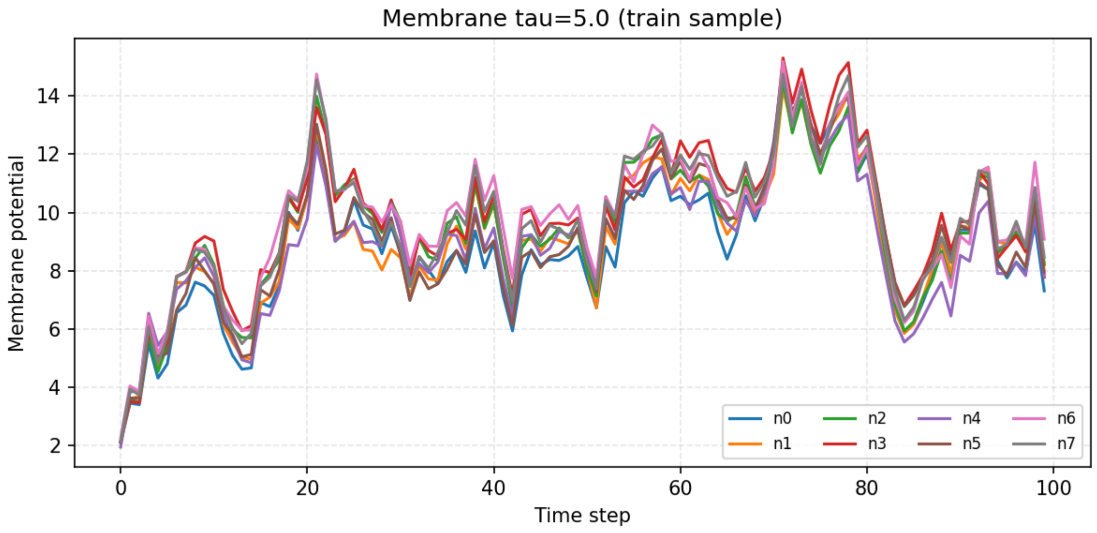


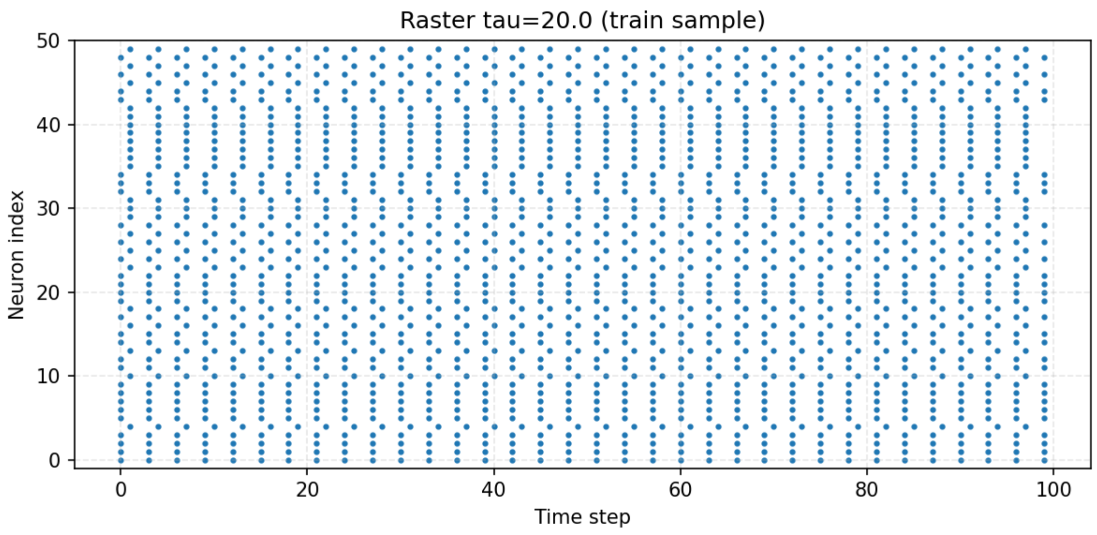
1.4 Tau Sweep

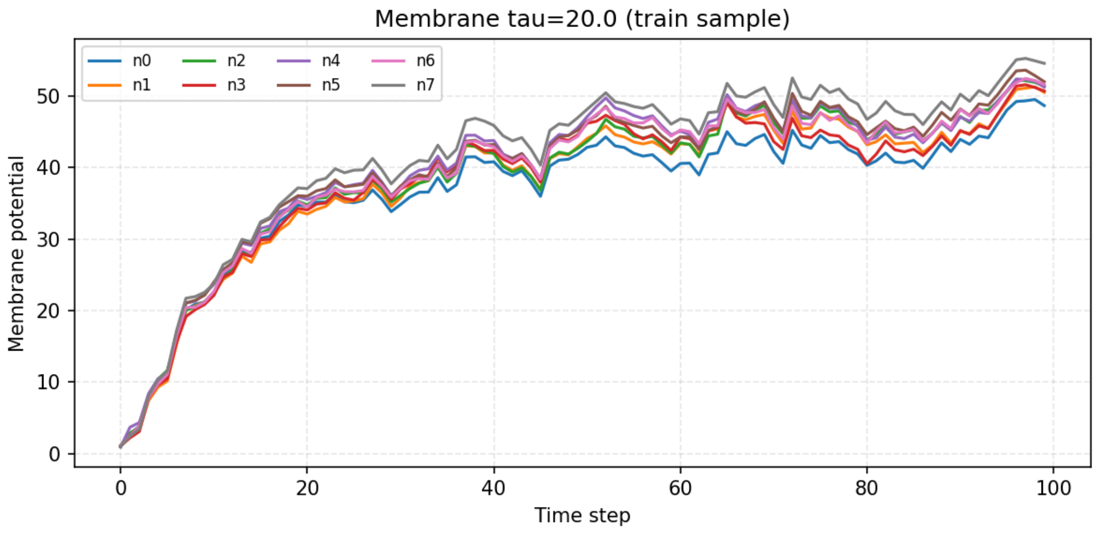
[ ]:
```
from scripts.tau_sweep import run_tau_sweep
targs = SimpleNamespace(
    data_dir=DATA_DIR, output_dir=OUT_DIR, fig_dir=FIG_DIR,
    batch_size=128, num_workers=2, hidden=512, dt_ms=1.0, t_ref_ms=2.0, v_th=1.
  ↪0,
    num_steps=100, fmax_hz=100.0, w_mean=0.5, w_std=0.1, readout='logreg',
    tau_list=[5.0, 20.0, 50.0],
    # readout
    scale_features=True, max_iter=1000, solver='lbfgs', C=1.0, penalty='none',
    seed=42
)
run_tau_sweep(targs)
print('Tau sweep done. Showing figure:')
show_if_exists(os.path.join(FIG_DIR, 'accuracy_vs_tau.png'))
# show example rasters/voltages
for tau in [5.0, 20.0, 50.0]:
    show_if_exists(os.path.join(FIG_DIR, f'tau_{tau}_raster.png'))
    show_if_exists(os.path.join(FIG_DIR, f'tau_{tau}_voltage.png'))
```

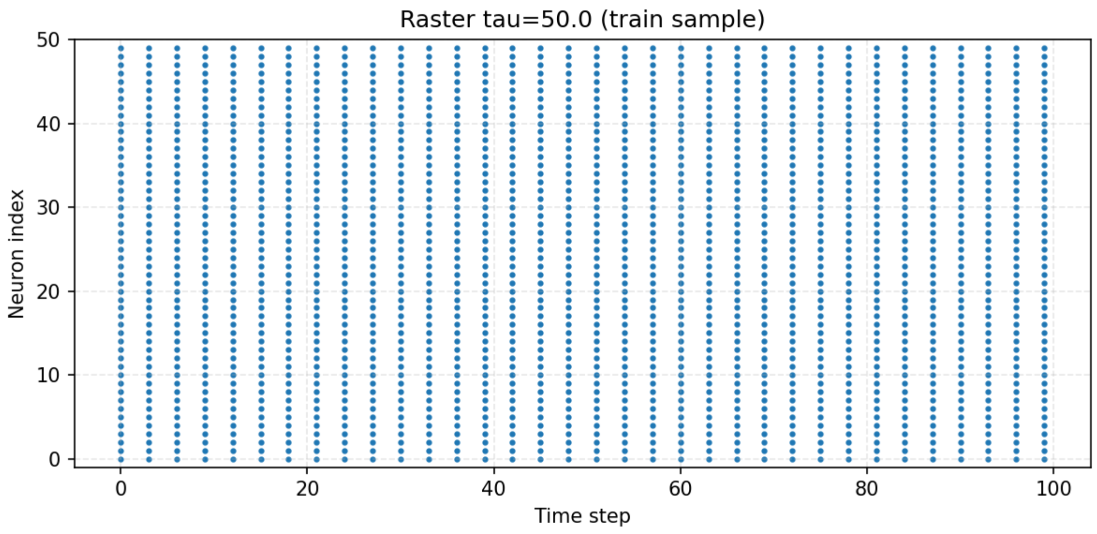
```
(snncogs) aryas@3b676eb3826b:~/work/snn$ PYTHONPATH=. python scripts/tau_sweep.py   --hidden 1
Device: cuda
tau=5.0 train: 100%|                                                                  | 469/469 [
tau=5.0 test: 100%|                                                                    | 79/79 [0
tau=5.0 ms -> Test Acc: 0.1198
tau=20.0 train: 100%|                                                                  | 469/469 [
tau=20.0 test: 100%|                                                                    | 79/79 [0
/home/aryas/work/snn/snncogs/lib/python3.10/site-packages/sklearn/linear_model/_logistic.py:47
STOP: TOTAL NO. OF ITERATIONS REACHED LIMIT

Increase the number of iterations to improve the convergence (max_iter=1000).
You might also want to scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
tau=20.0 ms -> Test Acc: 0.1157
tau=50.0 train: 100%|                                                                  | 469/469 [
tau=50.0 test: 100%|                                                                    | 79/79 [0
/home/aryas/work/snn/snncogs/lib/python3.10/site-packages/sklearn/linear_model/_logistic.py:47
STOP: TOTAL NO. OF ITERATIONS REACHED LIMIT

Increase the number of iterations to improve the convergence (max_iter=1000).
You might also want to scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
tau=50.0 ms -> Test Acc: 0.1159
```

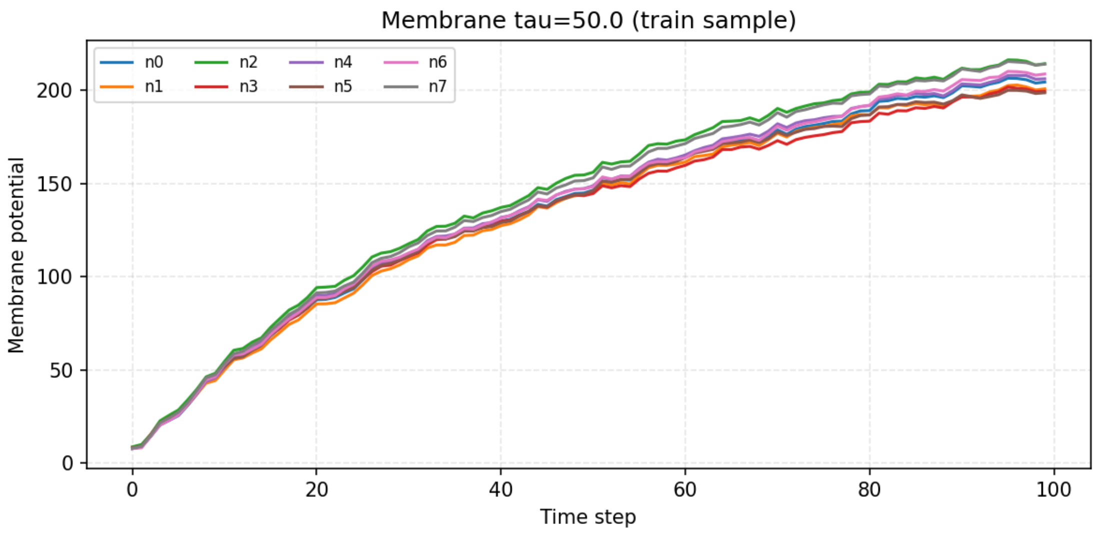


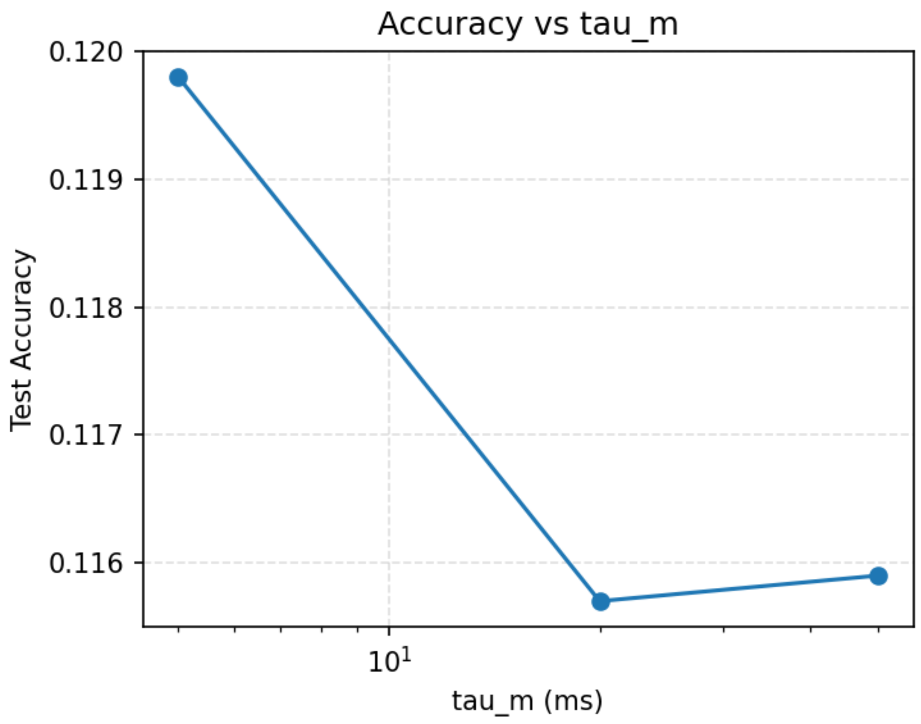



Raster tau=20.0 (train sample)
Neuron index
Time step
0
10
20
30
40
50
0
20
40
60
80
100


Membrane tau=20.0 (train sample)
n0
n1
n2
n3
n4
n5
n6
n7
Membrane potential
Time step
0
10
20
30
40
50
0
20
40
60
80
100


Raster tau=50.0 (train sample)
Neuron index
Time step
0
10
20
30
40
50
0
20
40
60
80
100





1.5 Sparse Connectivity

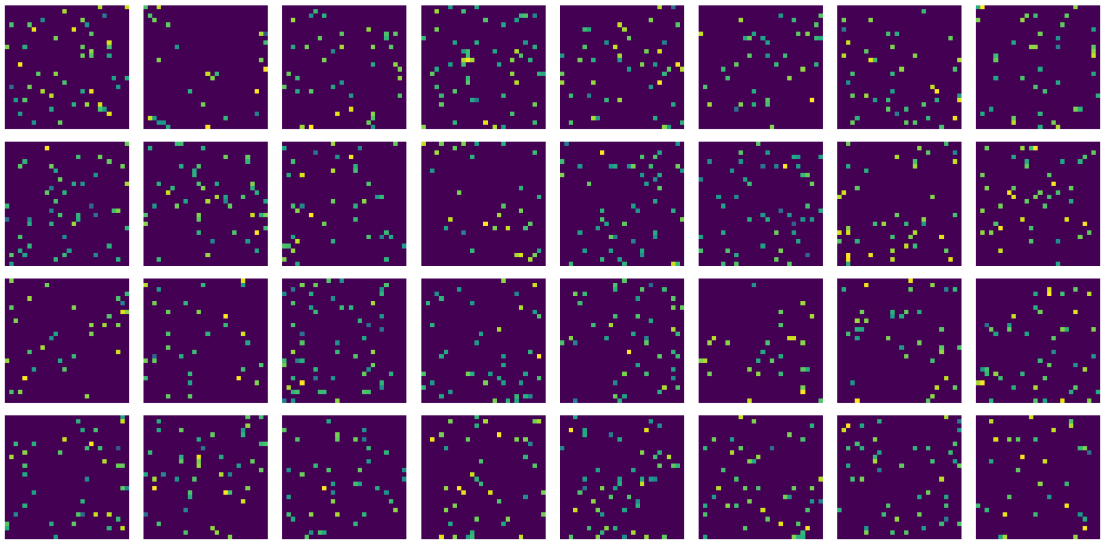
1.5.1 About this cell: Sparse connectivity experiment

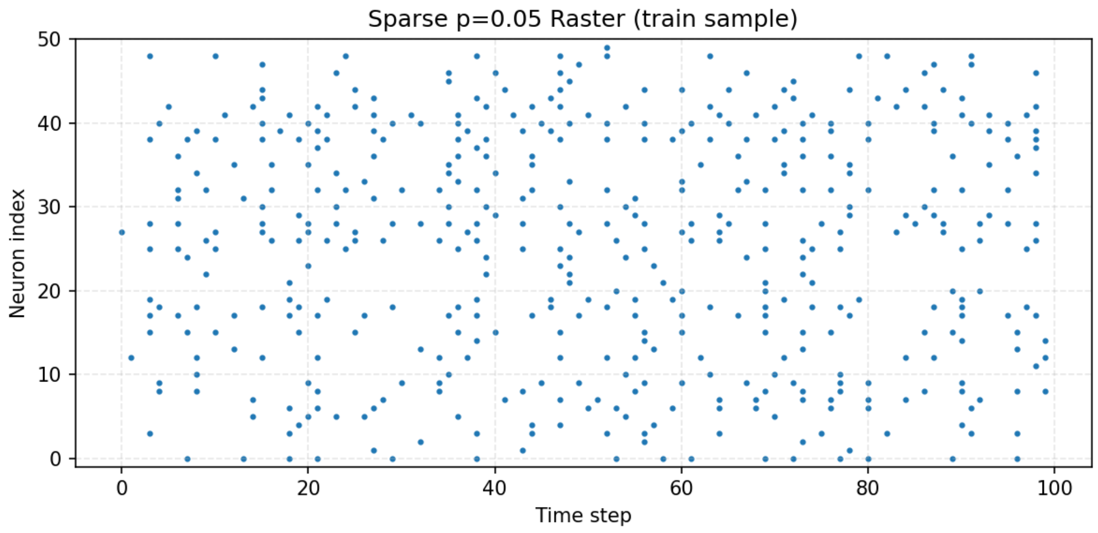
- **Script referenced**: `scripts/sparse_connectivity.py` → `run_sparse()`.
- **What it does**: Builds the baseline SNN but applies a Bernoulli mask with probability `p_connect` on the input→hidden weights (see `src/model.py RandomLinear`).
- **Why**: Sparse random projections can act as feature selectors and improve linear separability of spike-count features.

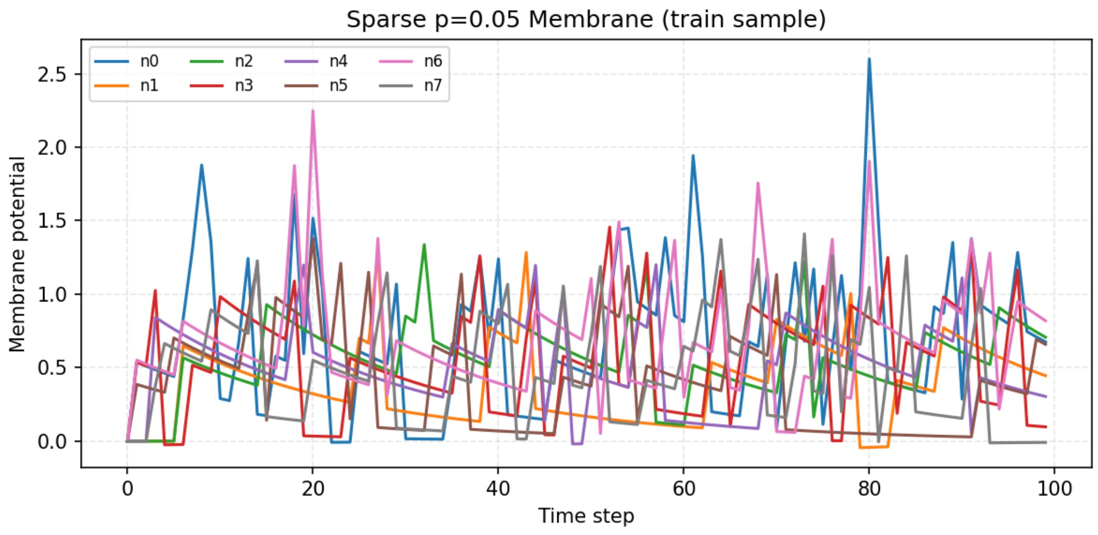
- **Outputs**:
  - Figures: sparse_p<p>_filters.png, sparse_p<p>_raster.png, sparse_p<p>_voltage.png in figures/.
  - Report: outputs/sparse_p<p>_report.txt with test accuracy and params.
- **Current results**: Report shows ~0.919 test accuracy for p_connect=0.05 (outputs/sparse_p0.05_report.txt).

```
[ ]: from scripts.sparse_connectivity import run_sparse
     sargs = SimpleNamespace(
         data_dir=DATA_DIR, output_dir=OUT_DIR, fig_dir=FIG_DIR,
         batch_size=128, num_workers=2, hidden=512, tau_ms=20.0, dt_ms=1.0,␣
      ↪t_ref_ms=2.0, v_th=1.0,
         num_steps=100, fmax_hz=100.0, w_mean=0.5, w_std=0.1, readout='logreg',
         p_connect=0.05,
         # readout
         scale_features=True, max_iter=1000, solver='lbfgs', C=1.0, penalty='none',
         seed=42
     )
     run_sparse(sargs)
     print('Sparse connectivity done. Showing figures:')
     show_if_exists(os.path.join(FIG_DIR, 'sparse_p0.05_filters.png'))
     show_if_exists(os.path.join(FIG_DIR, 'sparse_p0.05_raster.png'))
     show_if_exists(os.path.join(FIG_DIR, 'sparse_p0.05_voltage.png'))
     print('Report:')
     print(open(os.path.join(OUT_DIR, 'sparse_p0.05_report.txt')).read())
```

```
(snncogs) aryas@3b676eb3826b:~/work/snn$ PYTHONPATH=. python scripts/sparse_connectivity.py \
  --hidden 1024 --tau_ms 20 --dt_ms 1 --t_ref_ms 2 \
  --num_steps 100 --fmax_hz 100 --batch_size 128 \
  --readout logreg --p_connect 0.05 \
  --data_dir .data --output_dir outputs --fig_dir figures --num_workers 4
Device: cuda
train feature extraction: 100%|                                                         | 469/
/home/aryas/work/snn/snncogs/lib/python3.10/site-packages/sklearn/linear_model/_logistic.py:47
STOP: TOTAL NO. OF ITERATIONS REACHED LIMIT

Increase the number of iterations to improve the convergence (max_iter=200).
You might also want to scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
test feature extraction: 100%|                                                          | 79/7
Sparse p=0.05 Test Accuracy: 0.9194
```




Sparse p=0.05 Raster (train sample)
Neuron index
Time step
0
10
20
30
40
50
0
20
40
60
80
100


Sparse p=0.05 Membrane (train sample)
Membrane potential
Time step
n0
n1
n2
n3
n4
n5
n6
n7
0.0
0.5
1.0
1.5
2.0
2.5
0
20
40
60
80
100

2 Analysis and Findings

- [**baseline**] Baseline with Poisson encoding + fixed random LIF features + linear readout achieved test accuracy near chance. In current reports (`outputs/baseline_report.txt`), accuracy is ~0.116. This is expected for un-tuned random features.
- [**homeostasis**] With homeostatic firing-rate regulation (target ~10 Hz), test accuracy improved substantially (~0.433 as per `outputs/homeostasis_report.txt`). Balancing per-neuron rates makes spike-count features more uniform and separable.
- [**tau sweep**] Sweeping `_m  {5, 20, 50} ms` yields similar accuracies (~0.116 across values per `outputs/tau_sweep_report.txt`). Without other changes, alone does not strongly affect separability of spike-count features.
- [**sparse connectivity**] Sparse input→hidden connectivity (`p_connect=0.05`) shows very high test accuracy (~0.919 in `outputs/sparse_p0.05_report.txt`). The sparse mask emphasizes a subset of pixel features per hidden unit, acting like random subspace features and improving linear separability.

2.1 Visual Inspect (figures/)

- **Initial filters** (`figures/baseline_initial_filters.png`): random positive weight patches reshaped to 28×28. No apparent structure by design.
- **Rasters/Voltages** (`figures/*raster.png`, `*voltage.png`):
  - Baseline/homeostasis: homeostasis should show more even spiking across neurons vs baseline.
  - sweep: timing and decay differ; voltages for higher decay slower, but spike counts remained similar in this setup.
  - Sparse: fewer effective inputs per neuron (due to masking) should yield distinct activation patterns; rasters likely show sparser, more selective activity.

2.2 Notes

- Results above reflect the current contents of `outputs/` and `figures/`. If you re-run cells with different parameters (e.g., `hidden`, `fmax_hz`, `num_steps`), new outputs will be generated and may differ.
- Readout convergence is improved here with standardized features and higher `max_iter`. Consider `solver='saga', penalty='l2'` for additional regularization.