Supplementary Materials

Details about primate and rodent data

Primate Data: The primate data we use in this manuscript comes from [1]. These are single unit electrophysiological recordings from monkey V1 as they view 72 drifting sinusoidal stimuli. The entire dataset consisted of 113 neurons and 50 trials per stimulus. Here, we only select neurons with greater than 16000 spikes throughout the entire duration of the recording for all stimuli and trials (at least 4.4 spikes per trial on average). This pruned our dataset to 65 neurons total. The reason we select for high firing rate here is because we want to make sure that there is enough trial-by-trial variability in the neurons to extract meaningful noise latent structure. Additionally, we only use the final 35 trials for our analysis. Because we have to learn an n-dimensional latent structure (n ranging from 1 to 7) per-trial, discarding some trials helped speed up inference of SNP-GPFA.

For cross-validation analysis, we took the 35 trials and randomly divided into 20 train and 15 test trials. Using the co-smoothing procedure described in the manuscript, we learned the noise latents on the held-out trials after withholding two neurons. We then evaluate the log-likelihood on the two held out neuron's 15 held-out trials. We did this over a 5-fold shuffle over held-out trials.

We bin the spikes at 5 ms resolution before performing analysis.

Rodent Data: The rodent data comes from an multi-region two-photon imaging set-up described in [2]. Here, we use data from V1 and AL regions in visual cortex in the 'gratings' stimulus condition described in [3]. These stimuli were 20 repeated trials of 8 4-second flashes of orientated drifting gratings presented at 0.05 cycles per degree and 2 Hz. The rodents were head-fixed and passively viewing stimuli that were identical on each trial. Calcium traces from these data were de-convolved to yield spike-times which were subsequently binned at 100 ms resolution.

The full dataset consisted of 352 V1 and 163 Al neurons, but their firing rates were very low; some neurons only spiked 1 or 2 spikes for the duration of the recording. We pruned the dataset to have at least 70 spikes in the 20 presented trials (at least 3.5 spikes per trial) which yielded 30 V1 and 37 Al neurons. All multi-region analysis was done on these 67 total neurons.

Cross-validation procedure was done as described before, here witholding 10 random trials and 2 neurons, one neuron from V1 and one neuron from AL. Means and standard error was again averaged over 5-fold cross-validation.

Details about multi-region analysis

Simulated data: To validate that our Fourier-BBVI is able to distinguish models with block-diagonal $\mathbf{W_n}$ and full $\mathbf{W_n}$ we first generate data from each model. We simulate 20 trials of 24 Poisson neurons. The signal dimensionality is 2 in each condition. However, for the noise dimensionality, in one condition 2 noise latents each map to all of the neurons, and in another, 2 noise latents maps to half of the neurons, and a separate 2 noise latents map to the other half. This is used to distinguish two brain "regions". We next perform inference on these simulated data using both models. We withhold 10 trials and two neurons (again, one from one region, one from the other), and calculate log-likelihood on the held-out neurons and trials. We plot means and standard error average over five-fold cross validation for each model.

Selecting signal and noise dimensionality for rodent data: Identifying the proper signal and noise dimensionality for multi-region data is presents a challenge as we cannot check all combinations signal and noise dimensionality per-region. To select the dimensionality for this paper, we proceed by first analysing the data as a single region, and then use that information to test the multi-region model. That is, first we identify the optimal signal dimensionality of the V1 data alone and to the optimal signal dimensionality of AL alone, again determined via averaging over five-fold cross validation. We determine 3 signal dimensions are optimal for each of these conditions. On the multi-region analysis, we select a signal dimensionality that is equal to each of these added together: six dimensions total. For the noise, we similarly independently determine the best noise dimensionality on AL and V1 alone. This was determined to be 5 and 4, respectively. We then run inference on the multi-region data with 6 signal dimensions, and block-diagonalized 5 and 4 noise dimensions, and proceed as described in the manuscript.

References

[1] Arnulf BA Graf, Adam Kohn, Mehrdad Jazayeri, and J Anthony Movshon. Decoding the activity of neuronal populations in macaque primary visual cortex. *Nature neuroscience*, 14(2):239, 2011.

[2] Jeffrey N Stirman, Ikuko T Smith, Michael W Kudenov, and Spencer L Smith. Wide field-of-view, multi-region, two-photon imaging of neuronal activity in the mammalian brain. *Nature biotechnology*, 34(8):857, 2016.

[3] Yiyi Yu, Jeffery N Stirman, Christopher R Dorsett, and Spencer LaVere Smith. Mesoscale correlation structure with single cell resolution during visual coding. *bioRxiv*, page 469114, 2018.