Title: Does structure in neural correlations during spontaneous behaviour match anatomical structure?

300-word Summary

Information in the brain is carried in correlated network activity. Decades of research has established that these correlations play a crucial role in representing sensory information[1]. Recent findings show that spontaneous behaviours can explain correlations in parts of the brain not usually related to motor control[2]. In order to understand the brain, we must understand networks of correlated neurons. The question arises, are correlated networks restricted to anatomical brain regions?

Because of limitations in recording technology almost all research has explored correlations between neurons within a given brain region. Relatively little is known about correlations between neurons in different brain regions. However, the recent development of 'Neuropixels' probes[3] has allowed extracellular voltage measurements to be collected from multiple brain regions simultaneously routinely, and in much larger numbers than traditional methods. In this project we used a publicly available Neuropixels dataset to analyse correlations between different brain regions.

Using eight probes each in three mice, readings from 2296, 2668, and 1462 cells respectively in nine different brain regions were extracted during approximately 1 hour of continuous activity. Each mouse was behaving spontaneously and could use their front paws to turna wheel[2]. Using these data, we examined pairwise spike count correlations between neurons within the same region, and between neurons in different regions. We found that cells from the same region tend to be more strongly correlated than cells from different regions. We also found that this difference in strength reduces when a longer time bin is used to bin spike counts.

We used a cutting edge community detection method[4] to detect communities in the network induced by pairwise correlations. We found that these communities generally exist across multiple brain regions. However, at shorter time-scales we found that communities dominated by cells from a single region were more prevelant.

Additional Detail

The three mice from which the data were collected had some potentially important differences. The first mouse was a 73 day old female wild type. The second mouse was a 113 day old male mutant (TetO-GCaMP6s, Camk2a-tTa). The third mouse was a 99 day old male mutant (Ai32, Pvalb-Cre).

Before we measured the spike count correlations between cells, we had to decide what length of time bin would be suitable for binning the spike counts. Taking a similar approach to the authors of [5], we evaluated the average correlations from many cell pairs using different values for the time bin width. We found that correlations increased logarithmically with the size of the bin width. This result was consistent across all three mice. We used a bin width of 2s in order to capture the magnitude of the correlations, without completely averaging out short-term dynamics. However, we still performed our analyses at time bin widths ranging from 50ms to 3s in order to assess the effect of the bin width. The same dataset was used in [2], they used 1.2s time bins for their analyses.

In order to assess the significance of our correlation measures, we also measured the shuffled correlation between each pair. We found that the mean correlation was usually an order of magnitude greater than the mean shuffled correlation.

Due to the large number of cells, and the even larger number of cell pairs, in order to make these measurements in a reasonable amount of time, a local supercomputer was used to perform the calculations using parallelisation to speed up the process.

In order to compare *within-region* mean correlations to *between-region* mean correlations, we created correlation matrices, with within-region correlations on the main diagonal, and between-region correlations everywhere else. There appeared to be no consistency in correlation patterns across the three mice.

Notes

- Mouse make-up, they were all different. inconsistencies may be down to mutations?

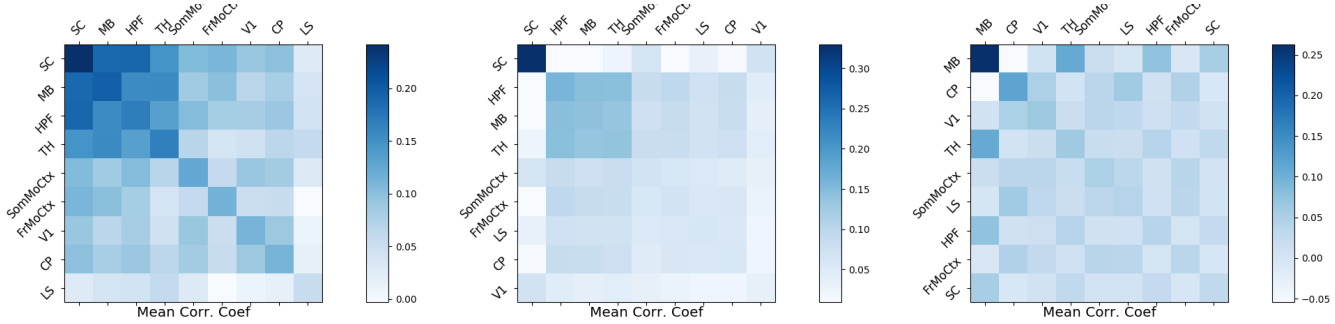

Figure 1: Matrices showing the mean spike count correlation taken across pairs of neurons from various brain regions. One matrix for each mouse. Entries on the main diagonal correspond to pairs where each cell is from the same region. All other entries have pairs of cells from different regions.

- Repeat idea?
- picking suitable time bins
- correlation histogram results largely agree with previous findings, cite cohen and kohn.
- regional correlation matrices, not consistent
- within vs between for Krebs only (only two figures maybe)
- regional communities

Used a super computer. Details about network noise rejection, and community detection, including consensus clustering.

Could reflect dispersion of correlations across regions over time.

References

[1] Marlene R Cohen, John H R Maunsell, *Attention improves performance primarily by reducing interneuronal correlations*, Nature Neuroscience 12, 1594–1600, (2009)

[2] Carsen Stringer, Marius Pachitariu, Nicholas Steinmetz, Charu Bai Reddy, Matteo Carandini, Kenneth D. Harris, *Spontaneous behaviors drive multidimensional, brainwide activity*, Science 364, (2019)

[3] James J. Jun, Nicholas A. Steinmetz, Timothy D. Harris, *Fully integrated silicon probes for high-density recording of neural activity*, Nature 551, 232–236, (2017)

[4] Mark D. Humphries, Javier A. Caballero, Mat Evans, Silvia Maggi, Abhinav Singh, *Spectral rejection for testing hypotheses of structure in networks*, arXiv:1901.04747, (2019)

[5] Marlene R Cohen, Adam Kohn, *Measuring and interpreting neuronal correlations*, Nature Neuroscience 14, 811-819, (2011)