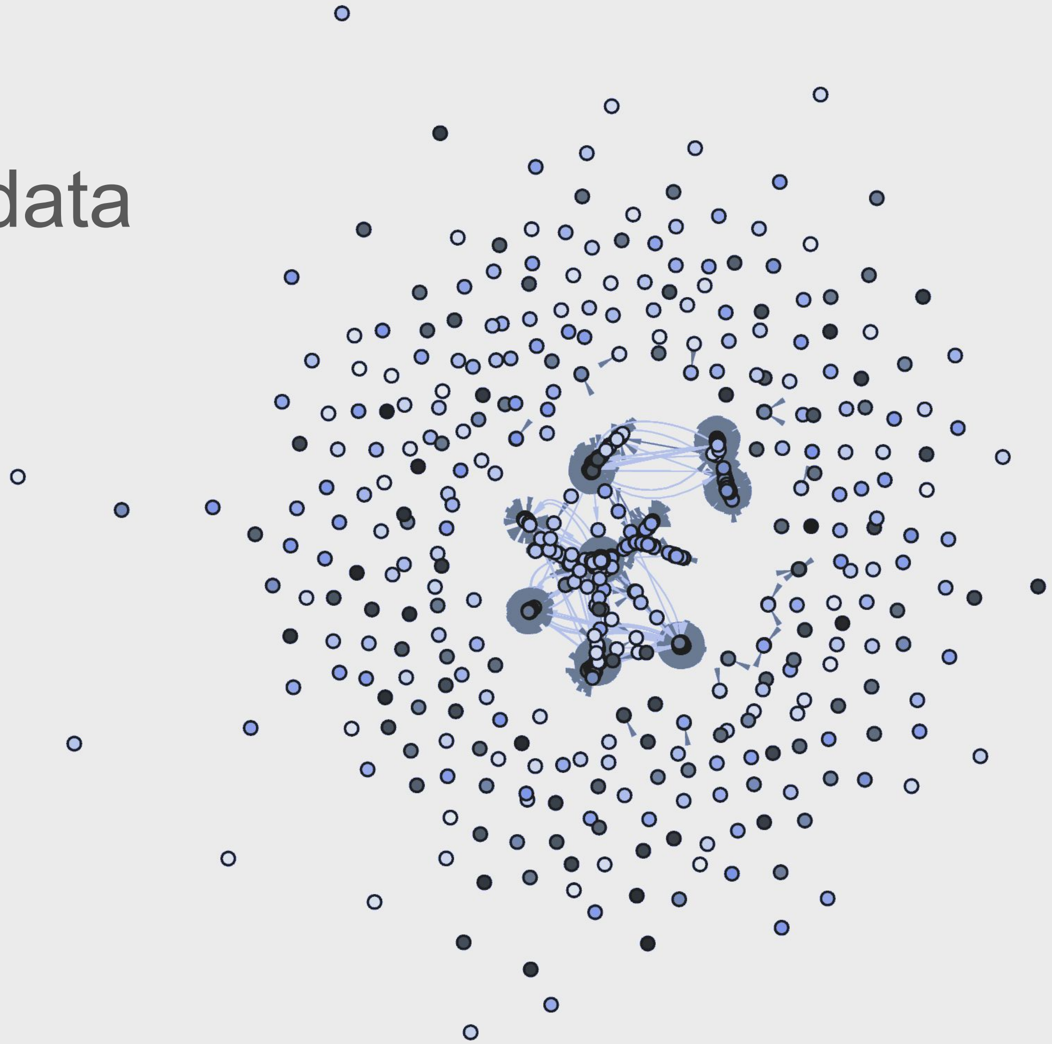
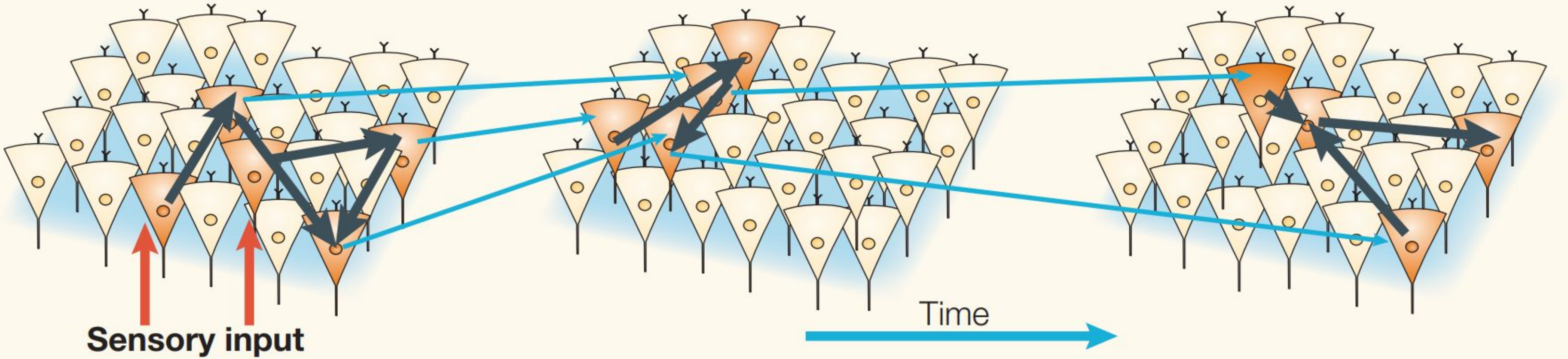
Community detection from large spike-train data



team funci

Juliana, Baruc, Luis, Sara

Question: Groups of coordinated neurons



Harris KD. Neural signatures of cell assembly organization.
Nature reviews neuroscience. 2005

Question: Groups of coordinated neurons

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- How do these groups overlap with brain areas?
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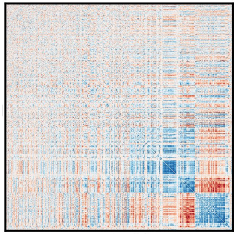
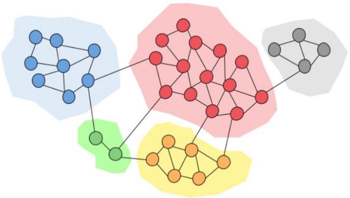
Pipeline

Spike trains

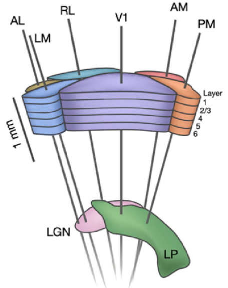
Functional connectivity



Detected communities



Community correlates



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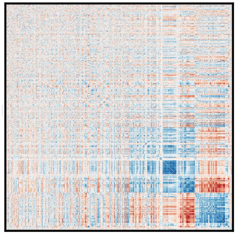
Spike trains

x-corr

(GLM)

Functional connectivity



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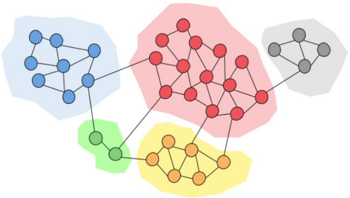

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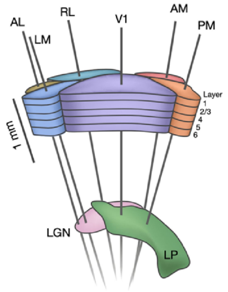
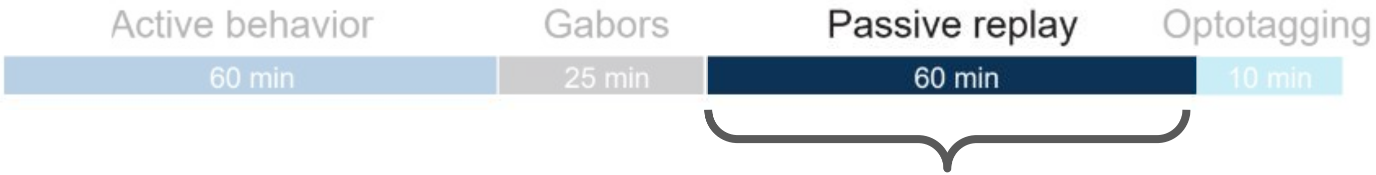
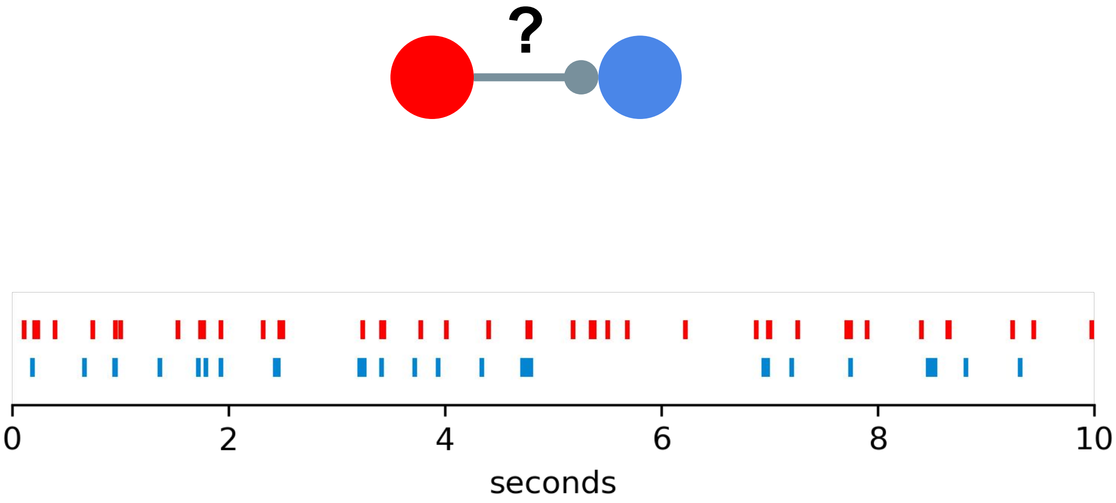


Data

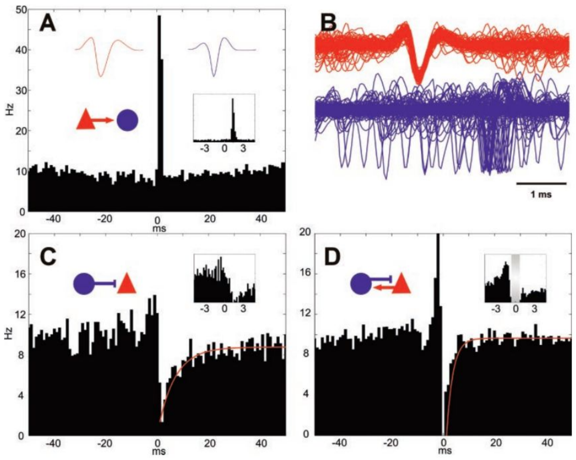
- 1 session, 60 min, passive replay
- Multi-area
- 1,158 good units
- 34,397,026 spikes
- **668,746 pairs**



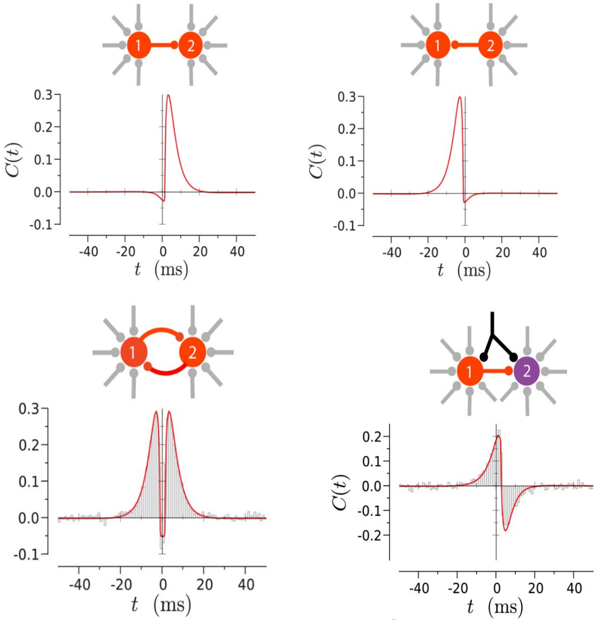
Cross-correlograms



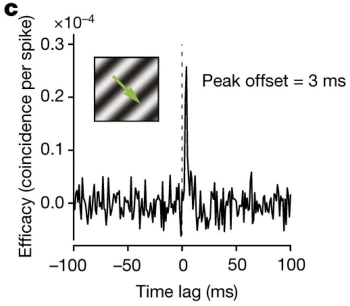
History



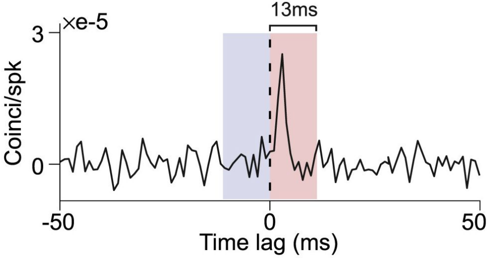
Bartho 2004, JN



Ostojic 2009, JN

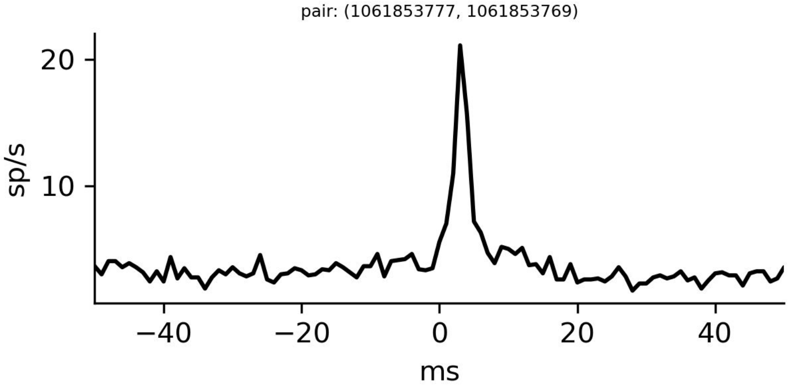


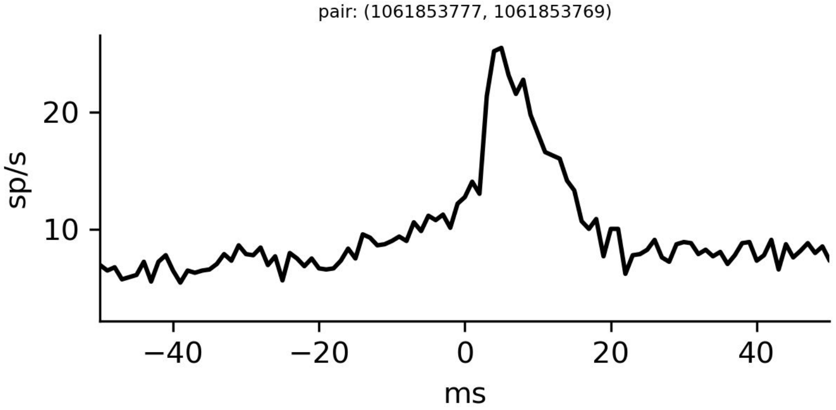
Siegle 2021 Nature

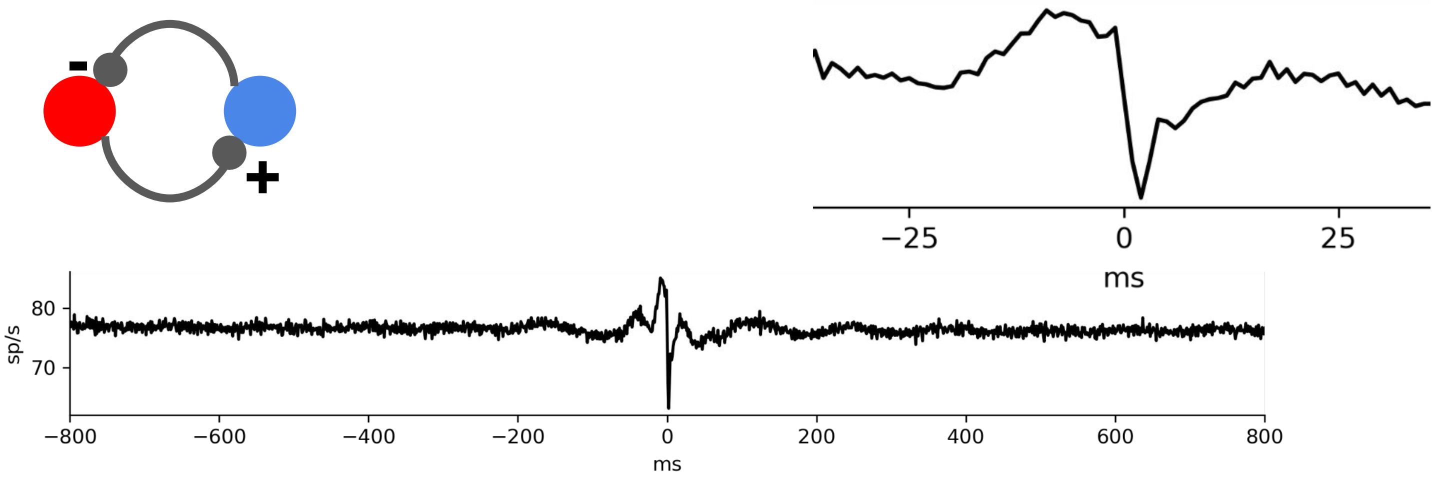


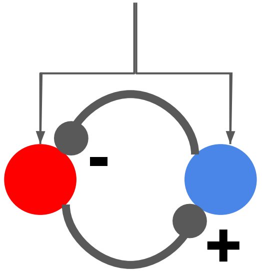
Jia 2022, Neuron

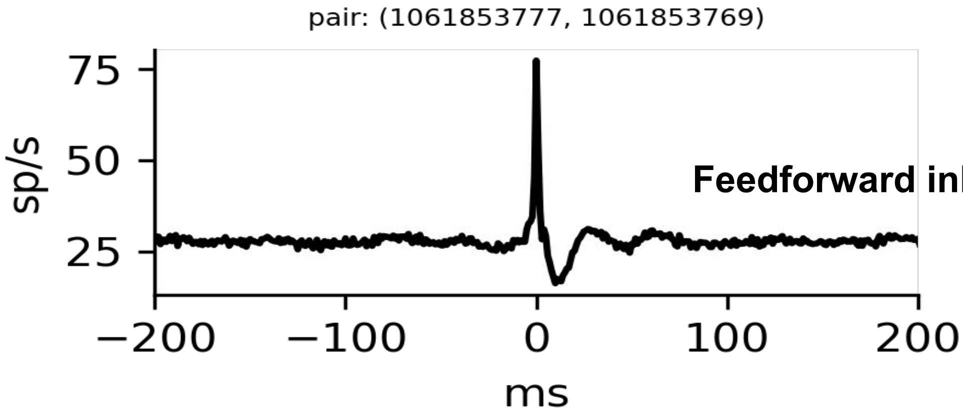
Examples of cross-correlograms from our data





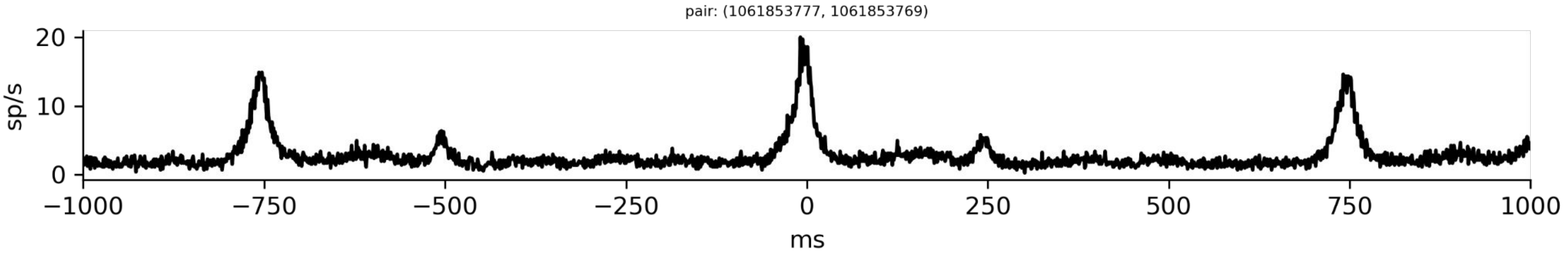




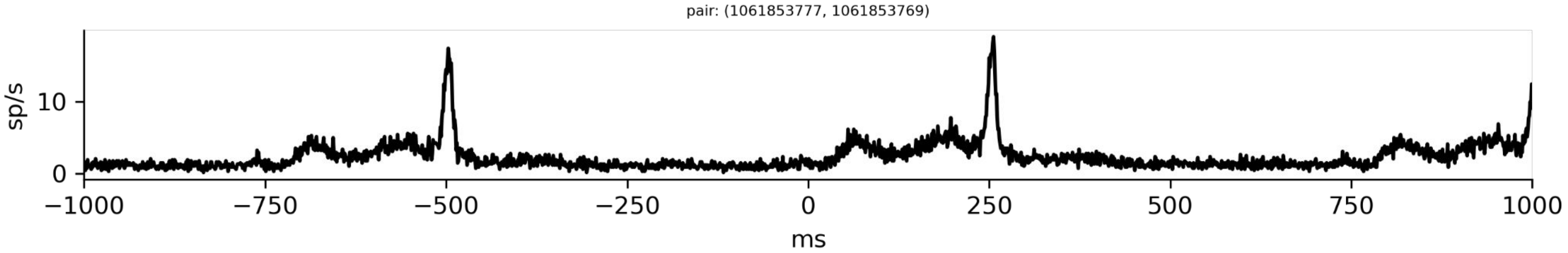


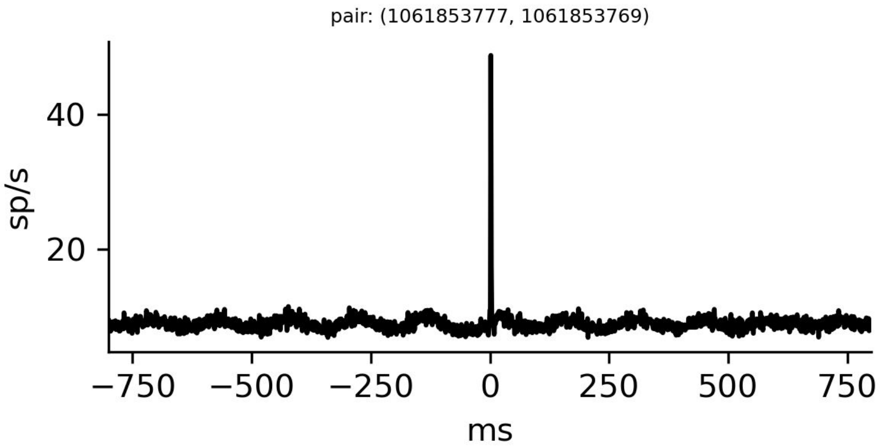
Feedforward inhibition

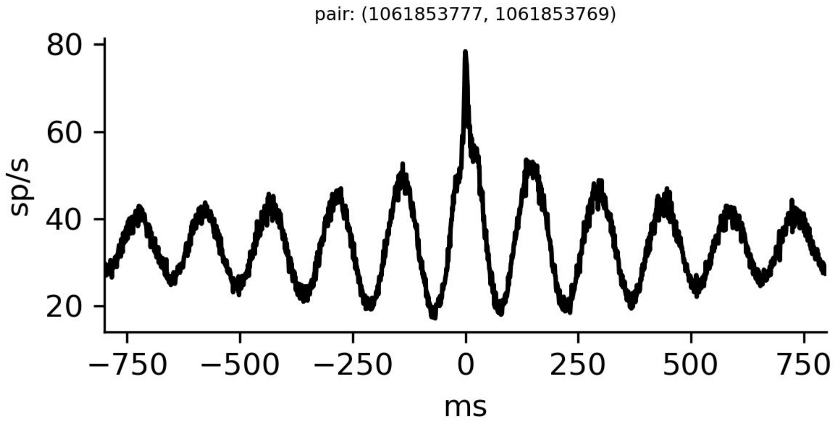
Pair a & b both locked to the stimulus



Pair a & b where a is locked to the start of the stimulus and b is locked to the stop




pair: (1061853777, 1061853769)
40
20
sp/s
−750
−500
−250
0
250
500
750
ms

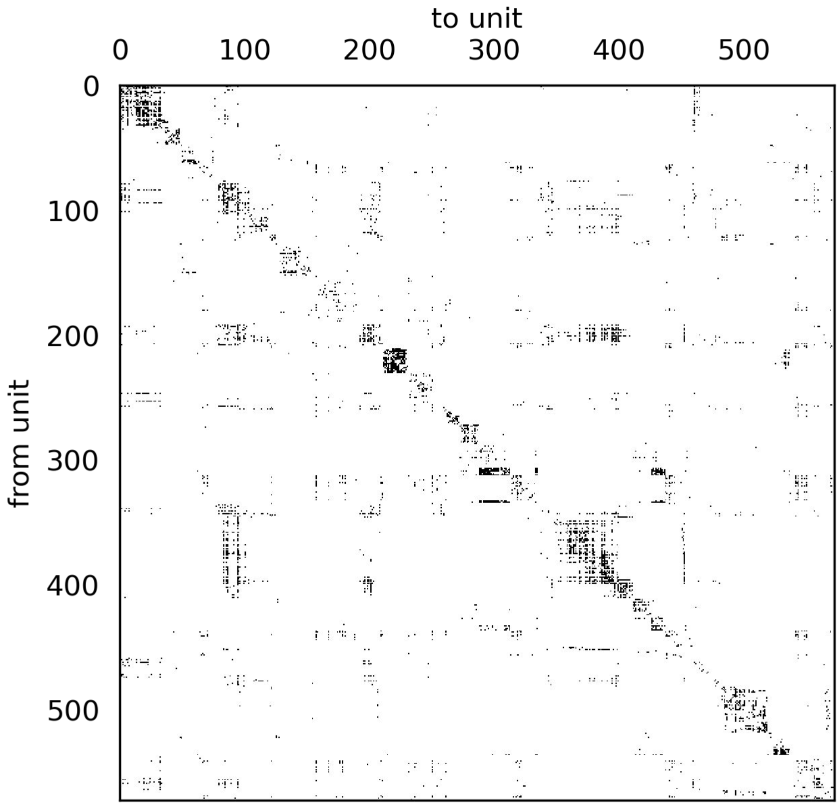

pair: (1061853777, 1061853769)
80
60
40
20
sp/s
−750
−500
−250
0
250
500
750
ms

The connectivity matrix

Metric of connectivity

- Cross correlograms with 1ms resolution
- Disregard zero lag peaks
- For now: not looking at inhibition(negative peaks)
- For each pair:
  Cij = z-scored peak in [0, +200] ms

  Cji = z-scored peak in [-200, 0] ms



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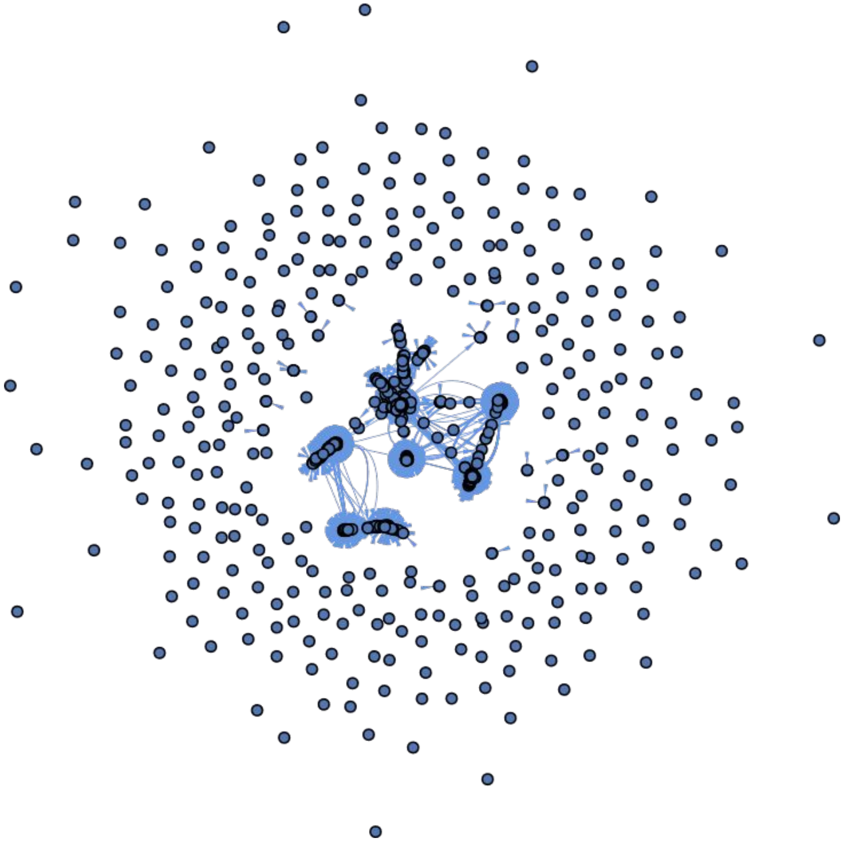

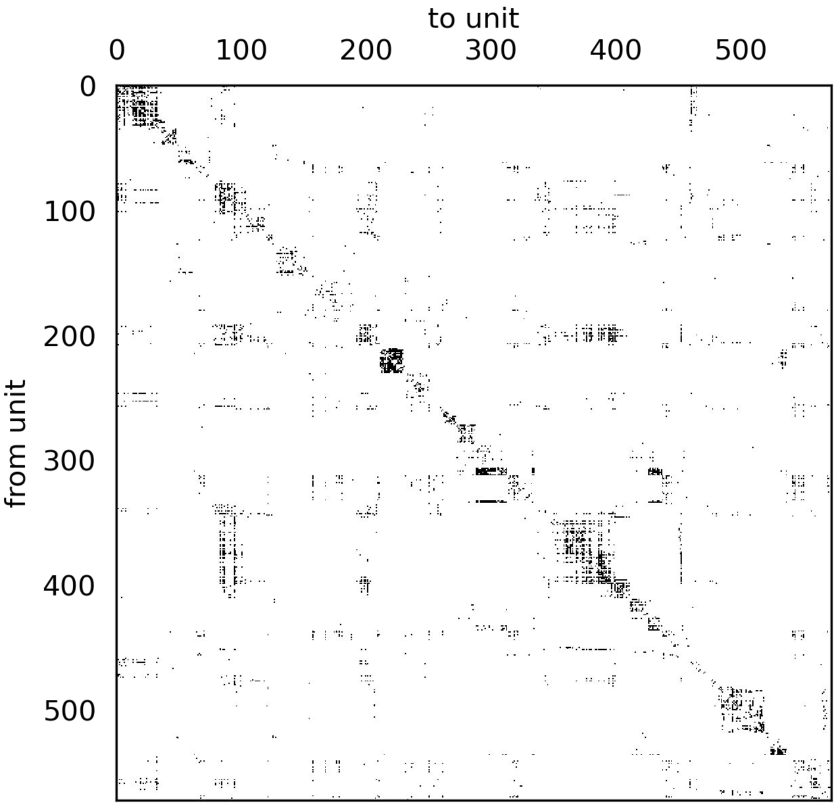

Community detection

- Groups of densely connected neurons, with sparser connections between groups (groups of highly correlated neurons during passive replay).
- Measure **modularity**

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$$Q = \text{fraction of edges within communities} - \text{expected fraction of such edges}$$

$$Q = \frac{1}{m} \sum_{ij} \left[A_{ij} - \frac{k_i^{\text{in}} k_j^{\text{out}}}{m} \right] \delta_{c_i, c_j}$$

$$m = \text{total edges in graph}$$

$$A = \text{adjacency matrix}$$

$$k_i^{\text{in}} = \text{in-degree of node } i$$

$$k_j^{\text{out}} = \text{out-degree of node } j$$

$$\delta_{c_i, c_j} = \begin{cases} 1 & \text{if } c_i = c_j \\ 0 & \text{if } c_i \neq c_j \end{cases}$$

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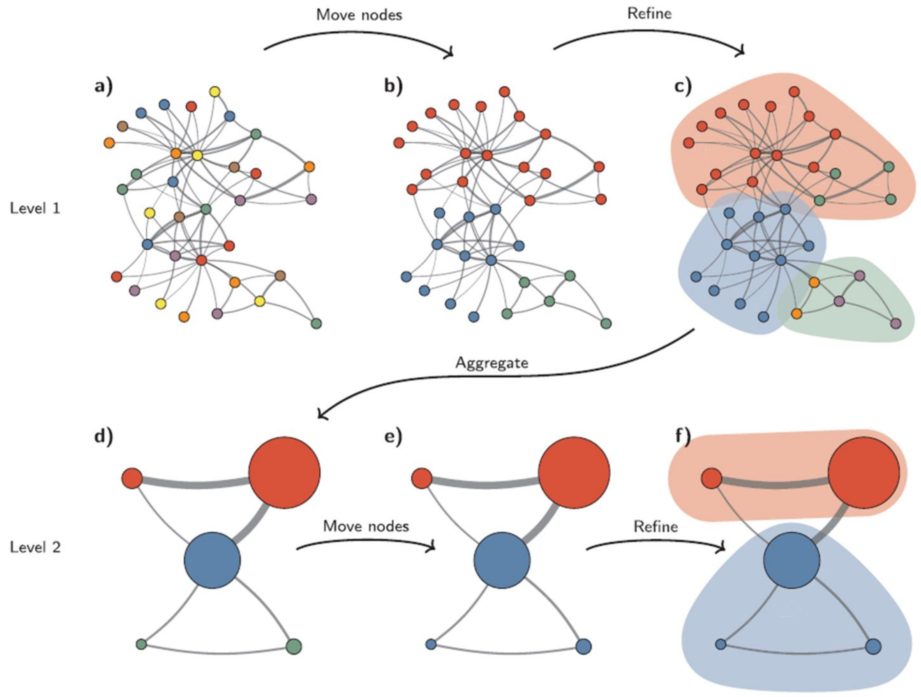
$Q_1 < Q_2$

Leiden algorithm

Greedy modularity optimization algorithm for directed, weighted graphs.



Start with singletons partition

Move nodes: visit all nodes (random order but in a smart way). Determine best community for each (increase in Q).

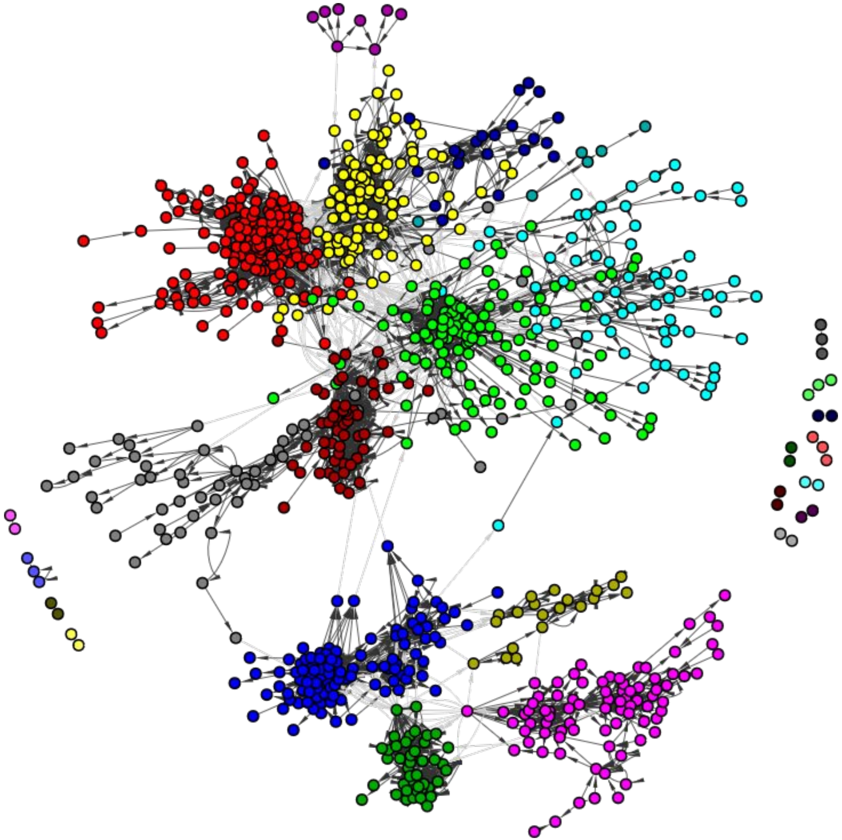
Refine: avoids having disconnected components

Aggregate: nodes are refined partition and edges are summed across communities

Start over on this new graph.

Traag, V.A., Waltman, L. & van Eck, N.J. From Louvain to Leiden: guaranteeing well-connected communities. *Sci Rep* 9, 5233 (2019).

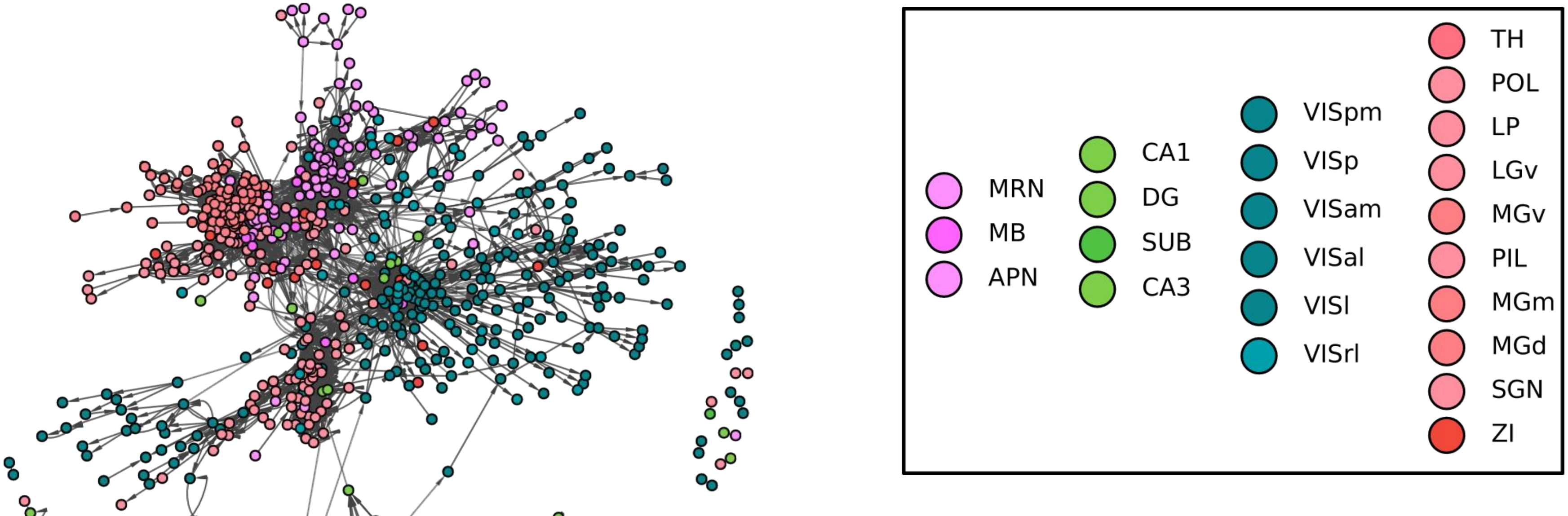
Results: communities

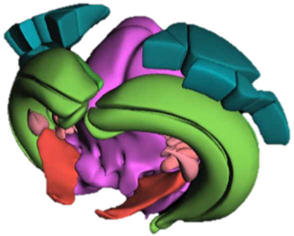


Community ID	Number of members (n)
0	151
1	120
2	103
3	98
4	82
5	68
6	55
7	55
8	45
9	22
10	20
11	8
12	6

Community ID	Number of members (n)
15	3
16	3
13	3
14	3
17	2
18	2
19	2
20	2
21	2
22	2
23	2
24	2
25	2

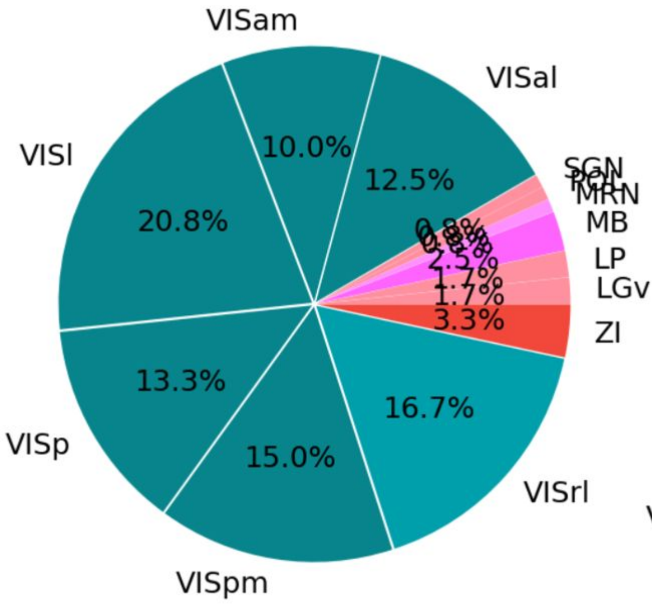
Structure


MRN
MB
APN
CA1
DG
SUB
CA3
VISpm
VISp
VISam
VISal
VISl
VISrl
TH
POL
LP
LGv
MGv
PIL
MGm
MGd
SGN
ZI

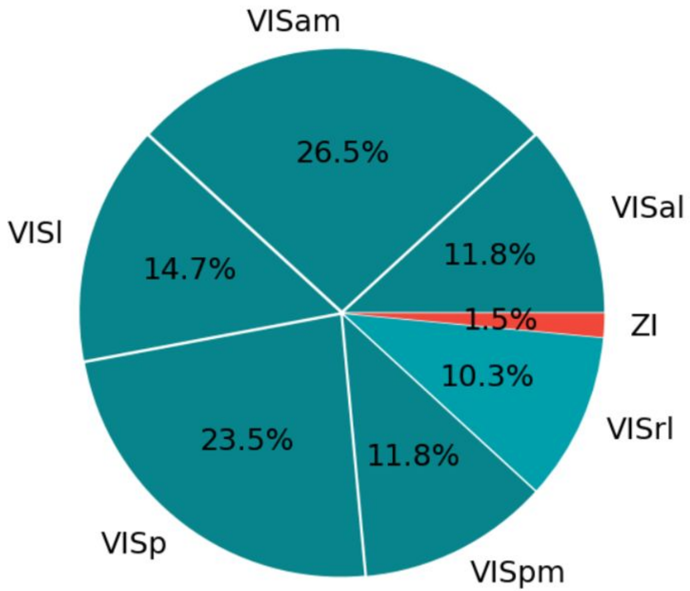


Visual areas

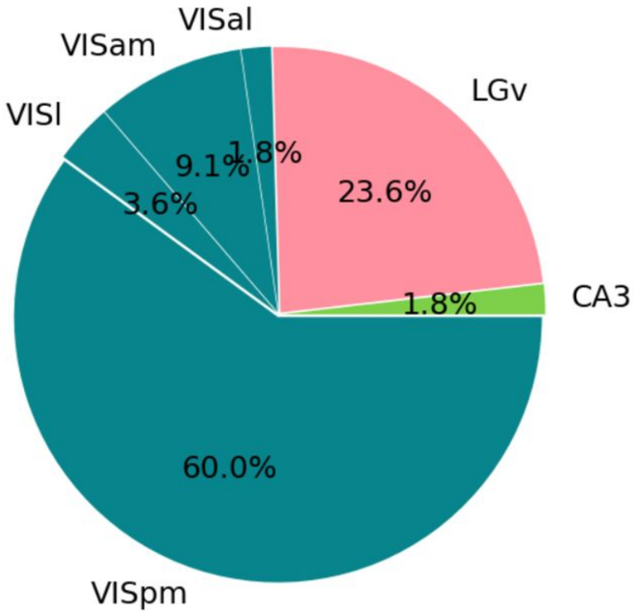
'Community 1' n = 120

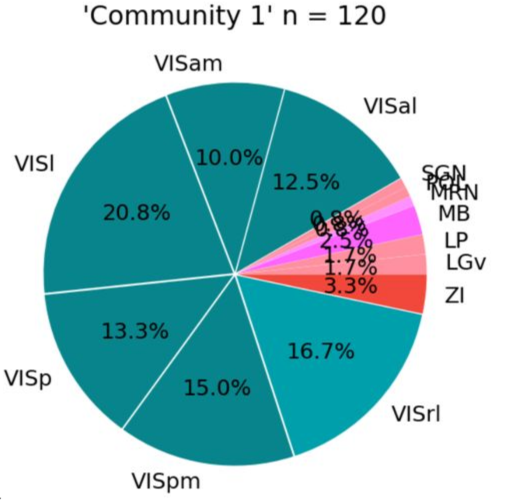


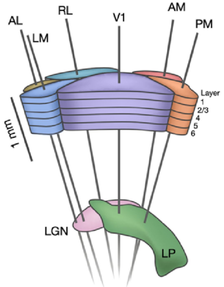
'Community 5' n = 68

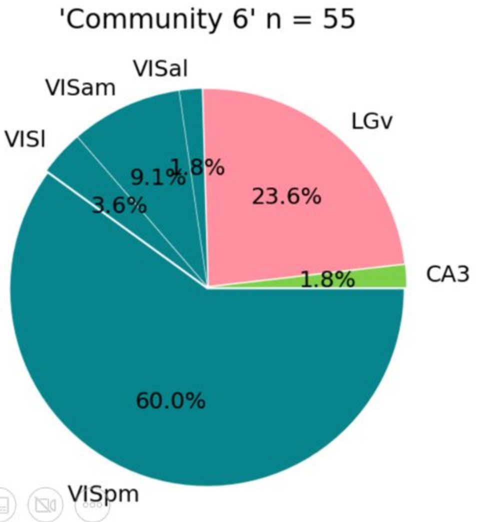


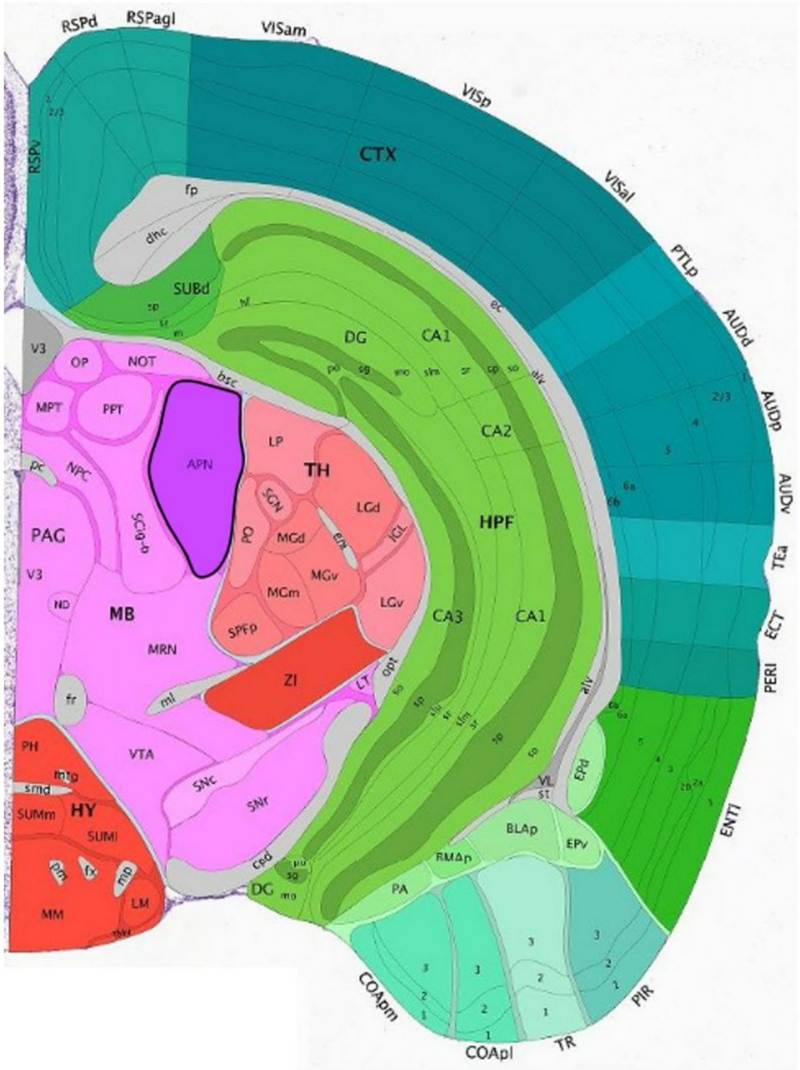
'Community 6' n = 55



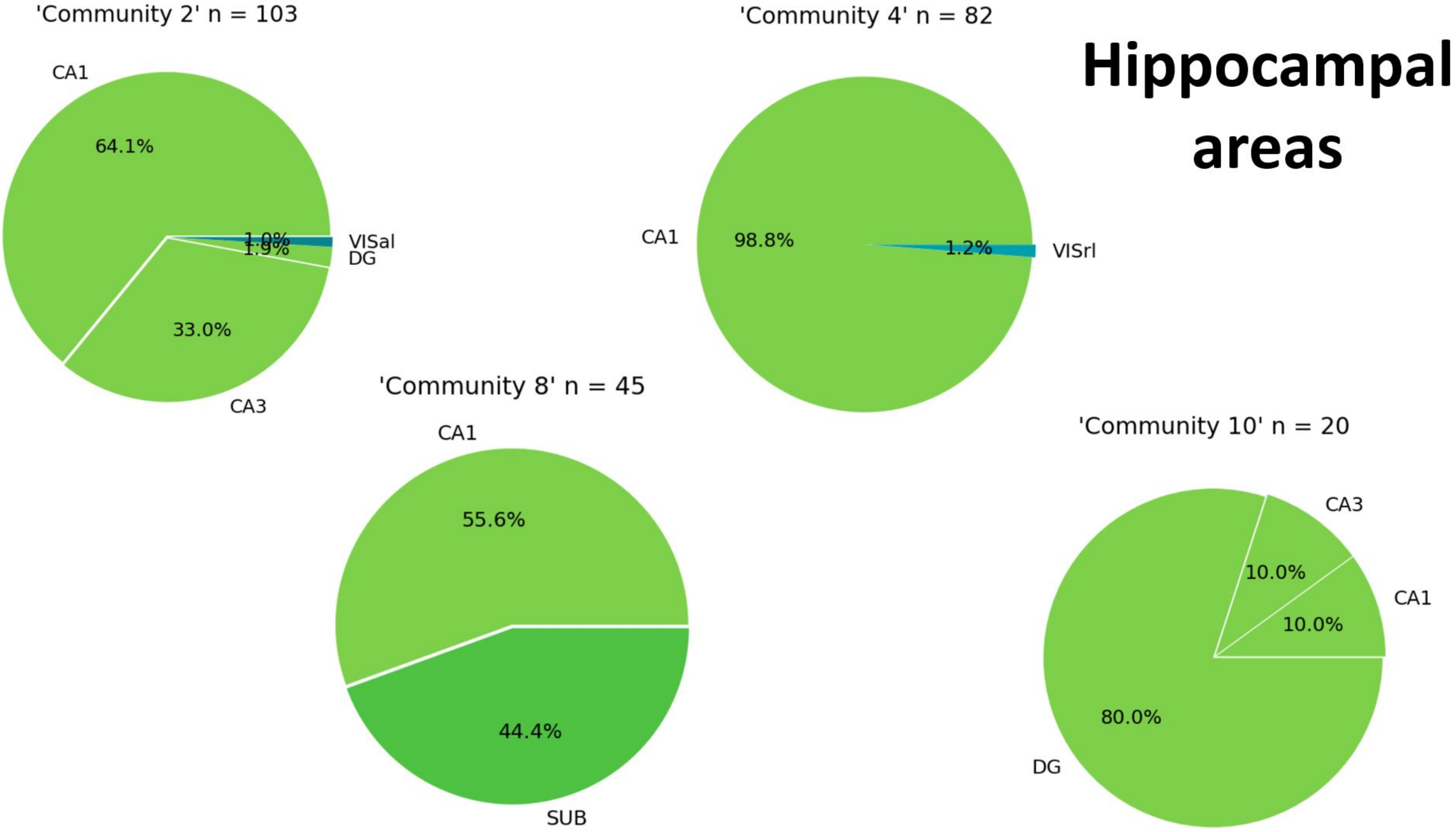






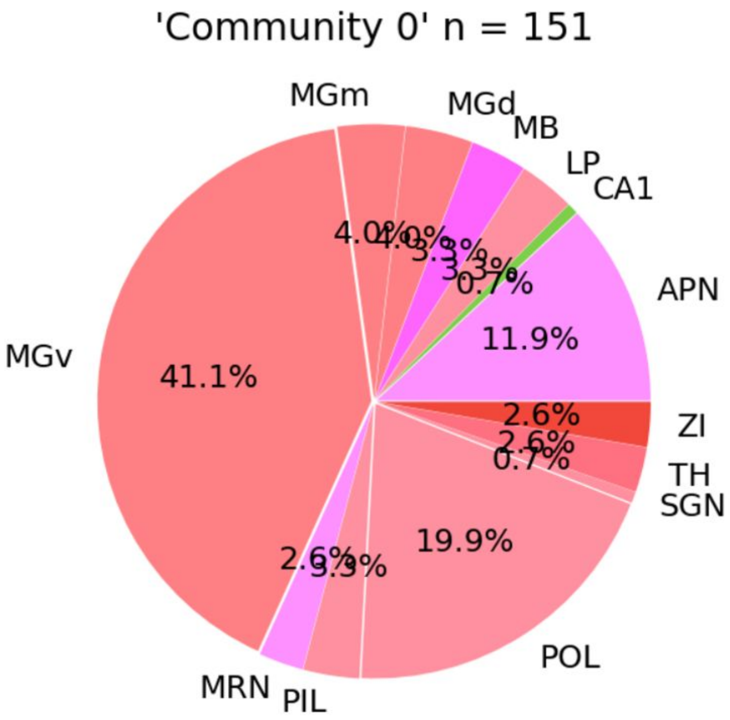


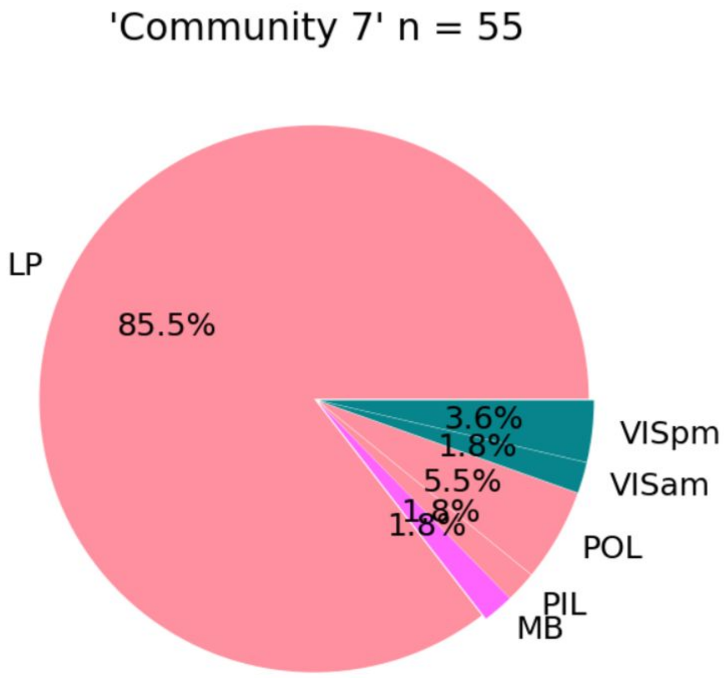
APN
CA1
CA3
DG
LGv
LP
MB
MGd
MGm
MGv
MRN
PIL
POL
SUB
TH
VISal
VISam
VISl
VISp
VISpm
VISrl
ZI



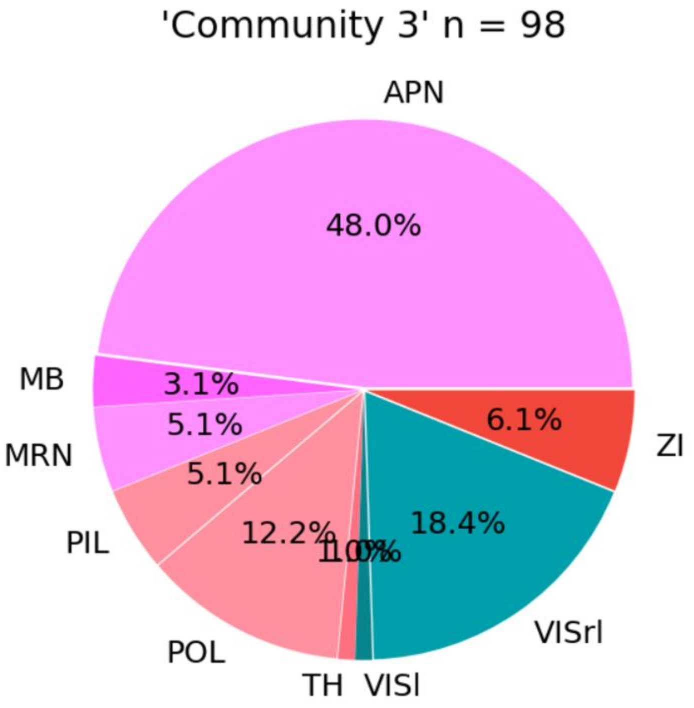
Hippocampal areas
'Community 2' n = 103
CA1
64.1%
1.0%
1.9%
VISal
DG
33.0%
CA3
'Community 4' n = 82
CA1
98.8%
1.2%
VISrl
'Community 8' n = 45
CA1
55.6%
44.4%
SUB
'Community 10' n = 20
CA3
10.0%
CA1
10.0%
80.0%
DG

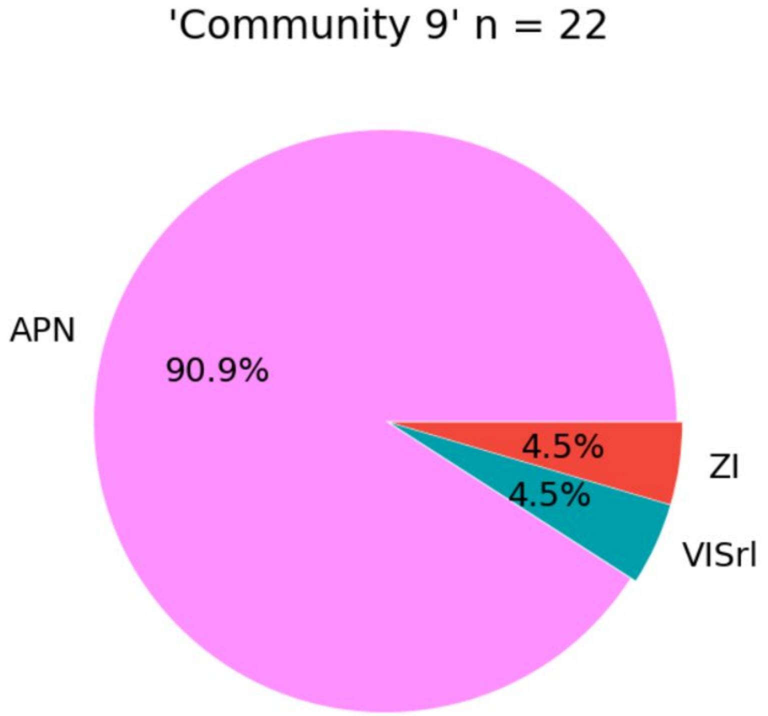
Thalamic areas





Midbrain areas





Conclusions

We were able to extract short time-scale pairwise interactions using cross correlograms.

Leiden algorithm proves to be efficient at handling large networks, and succeeds at revealing structure in functional brain networks.

We successfully identified and quantified communities of cells functionally connected in different areas of the brain.

Identifying functional connectivity could shed some light in deciphering the neural circuits involved in a specific behavioral outcome.

Thank you!

Questions?