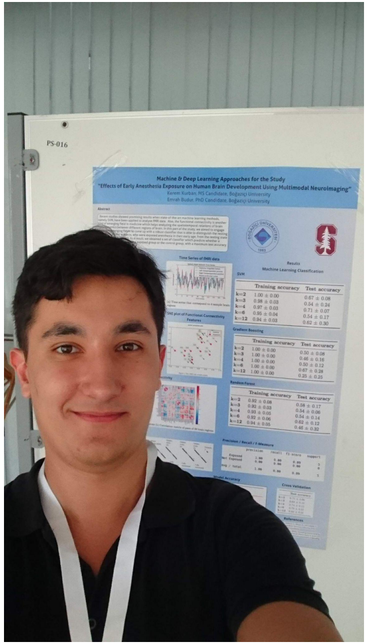
Portfolio

Kerem Kurban

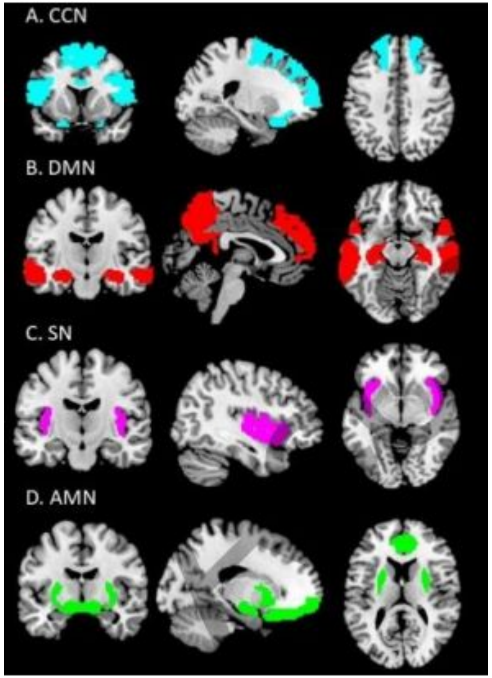
Personal Life



Projects

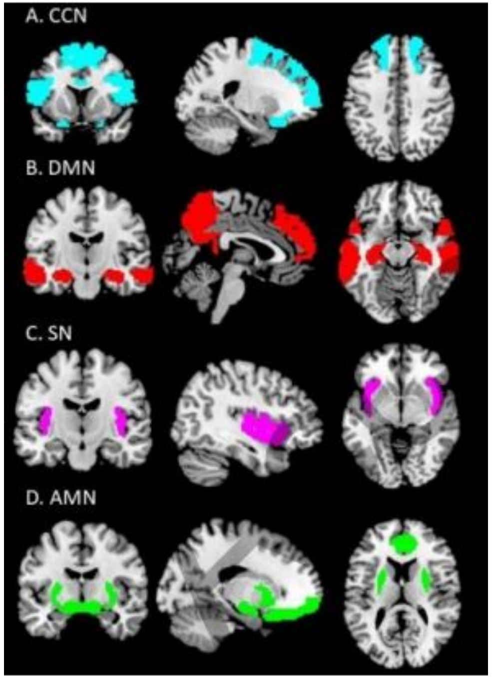
1. **Resting-state network dysconnectivity in ADHD: A system-neuroscience-based meta-analysis** (Sutcubasi et al 2021)
2. **Spiking Neural Network Model of a Computational Animal** (Kurban et al, unpublished)
3. **Simplification of the data-driven hippocampal CA1 microcircuit** (Kurban et al 2021)
4. **Community-based Reconstruction and Simulation of a Full-scale Model of Region CA1 of Rat Hippocampus** (Romani et al 2023)
5. **Topological properties of full scale rat CA1 circuit and their functional implications** (Kurban et al 2022)
6. **A Deep Dive into rat CA1 model : Insights from Network Science** (Kurban et al 2023)
7. **Investigation of different cell types through an analysis of persistent images of axonal trees** (Kurban and Pollina 2023)
8. **Modeling mouse hippocampal formation**

Resting-state network dysconnectivity in ADHD: A system-neuroscience-based meta-analysis



- Consensus brain network dynamics across neuroimaging studies
- Disruption in Major Psychiatric Disorders
    - ADHD
    - Major Depressive Disorder
    - Schizophrenia
    - Bipolar Disease
    - Autism

Resting-state network dysconnectivity in ADHD: A system-neuroscience-based meta-analysis



Functional Networks Important in ADHD

DMN : Default mode network
CCN: Cognitive control network
SN: Salience network
AMN: Affective/motivational network

Resting-state network dysconnectivity in ADHD: A system-neuroscience-based meta-analysis

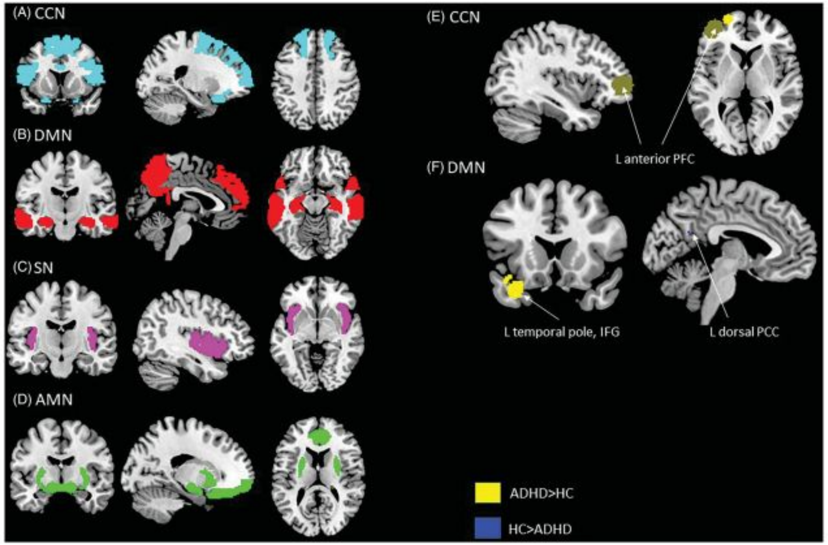


Figure 1. Seeds within a priori networks and results of the meta-analysis. The figure was drawn by authors to show the seeds used in meta-analysis and the abnormal resting-state functional connectivity results of meta-analyses in the whole sample. (a) The left four columns (A, B, C, D) represent the seed regions categorised into a priori networks based on the location of its center-of-mass. (b) The right two columns (E, F) show the significant results of meta-analyses. While the yellow colour on brain images represents elevated connectivity, the blue colour is used for reduced connectivity in ADHD compared to healthy controls. All results are significant at $p < .05$, corrected for family-wise error rate. HC: healthy controls; ADHD: attention-deficit hyperactivity disorder; CCN: cognitive control network; DMN: default mode network; AMN: affective motivational network; SN: salience network; PFC: prefrontal cortex; IFG: inferior frontal gyrus; PCC: posterior cingulate cortex.

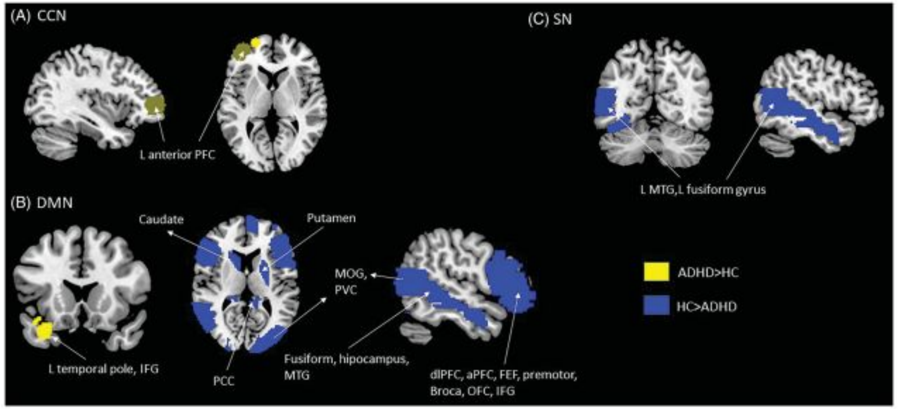
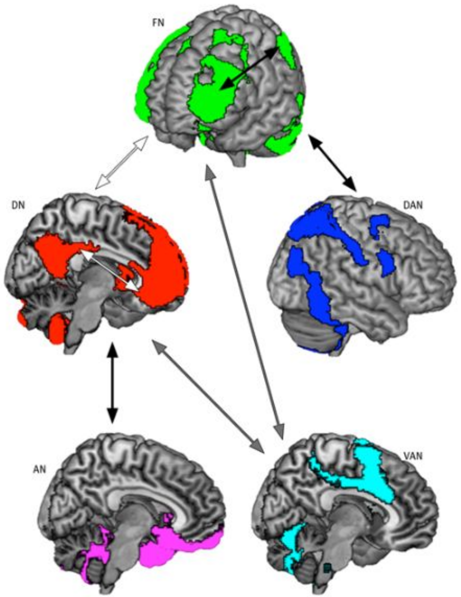


Figure 2. Results of the meta-analysis in children and adolescents. The figure was drawn by authors to show the abnormal resting-state functional connectivity results of meta-analyses in children and adolescents with ADHD. While the yellow colour on brain images represents elevated connectivity, the blue colour is used for reduced connectivity in ADHD compared to healthy controls. All results are significant at $p < .05$, corrected for family-wise error rate. HC: healthy controls; ADHD: attention-deficit hyperactivity disorder; CCN: cognitive control network; DMN: default mode network; SN: salience network; PFC: prefrontal cortex; IFG: inferior frontal gyrus; PCC: posterior cingulate cortex; MOG: middle occipital gyrus; PVC: primary visual cortex; dlPFC: dorsolateral prefrontal cortex; aPFC: anterior prefrontal cortex; FEF: frontal eye field; OFC: orbitofrontal cortex; MTG: middle temporal gyrus.

Altered Network Connectivities in 5 major psychiatric disorders



A Neurocognitive Network Model of Major Depressive Disorder (MDD)
Obtained from Kaiser et al 2015

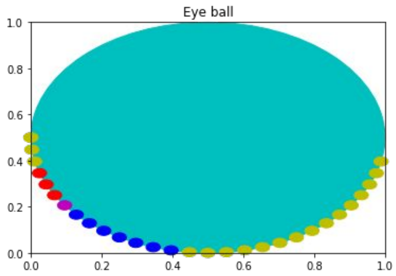
Use Cases:

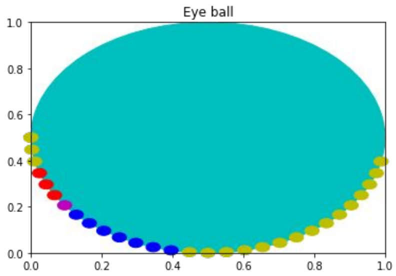
- Consensus targets for stimulation
    - Temporal Interference
    - DBS (only hub-to-hub)

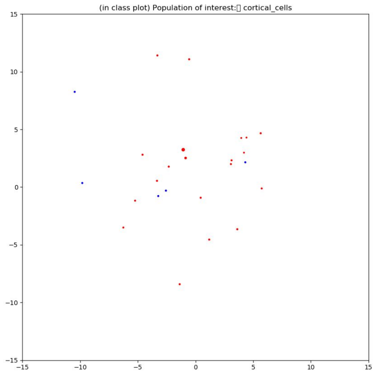
- Measure of cognitive performance
- Progression with Age and Genetic Disposition

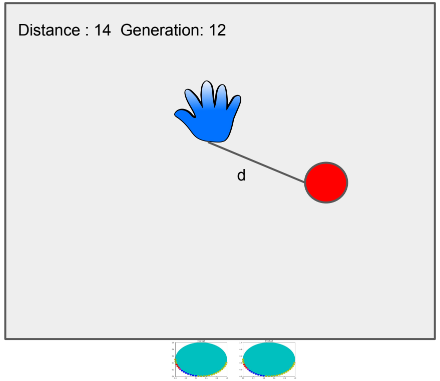
Spiking Neural Network Model of Computational Animal

- The animal has two eyes, each with 180 neurons.
- The task is done in 2 dimensional environment where vision is 1 dimensional
- The cognitive map is desired to turn 1D visual field to 2D plane, so the animal can locate itself in the environment.
- Genetic Algorithm tunes the weights between neurons which initially is ER an graph.









Simplification of the data-driven hippocampal CA1 microcircuit

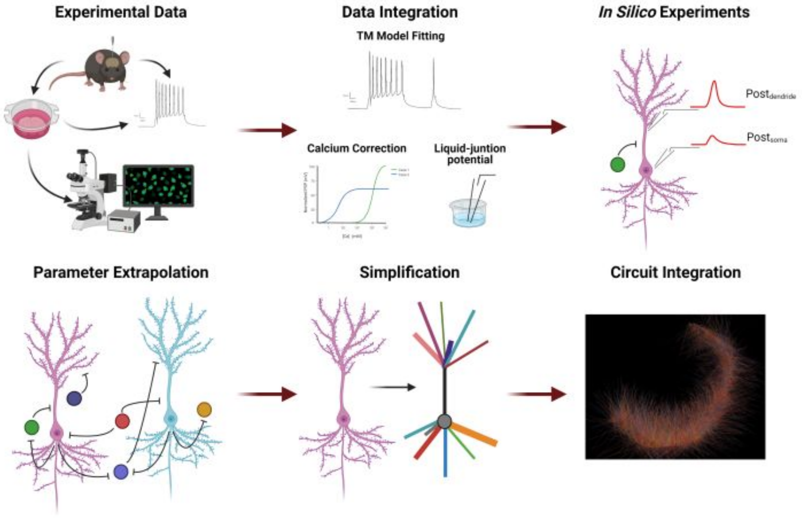
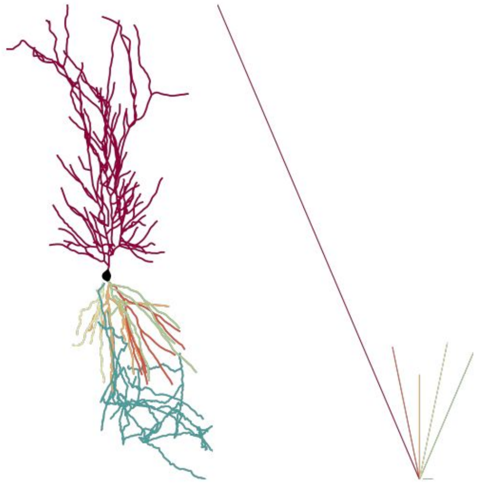


Figure 1.1: The pipeline for the circuit building and the simplification processes.



A CA1 Pyramidal Cell and its simplified version

Simplification of the data-driven hippocampal CA1 microcircuit

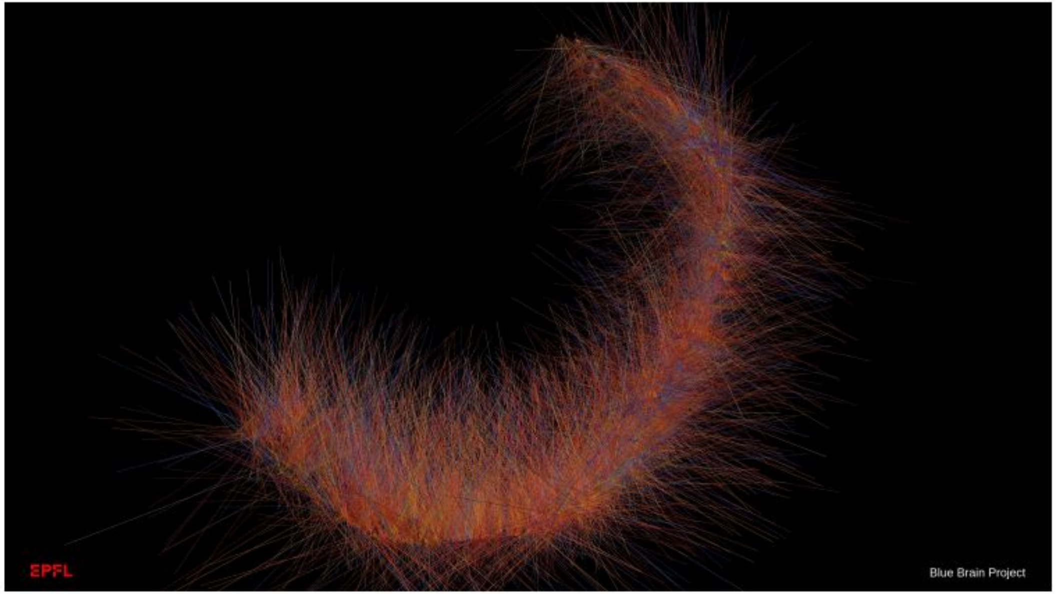


Figure B.4: Visualization of the reduced CA1 Circuit.

Simplification of the data-driven hippocampal CA1 microcircuit

Table 4.4: M-type wise full and reduced cell simulation times, and their respective SPIKE-Synchronization scores with synaptic parameters in Table 4.2

Single Cell Simulations				
M-type	Full(secs)	Reduced(Secs)	Spike_Sync	Ratio
SP_Ivy	67,44	2,9	0,84	23,26
SP_AA	66,63	1,64	0,81	40,63
SP_PVBC	94,42	14,16	0,7	6,67
SP_BS	88,94	6,26	0,9	14,21
SR_SCA	68,88	7,38	0,85	9,33
SO_BP	69,32	3,8	0,83	18,24
SO_Tri	68,59	1,96	0,85	34,99
SP_PC	96,75	3,85	0,79	25,13
SO_OLM	94,95	0,93	0,83	102,1
SO_BS	58,74	3,09	0,8	19,01
SP_CCKBC	62,89	11,08	0,85	5,68
SLM_PPA	56,28	5,99	0,71	9,40

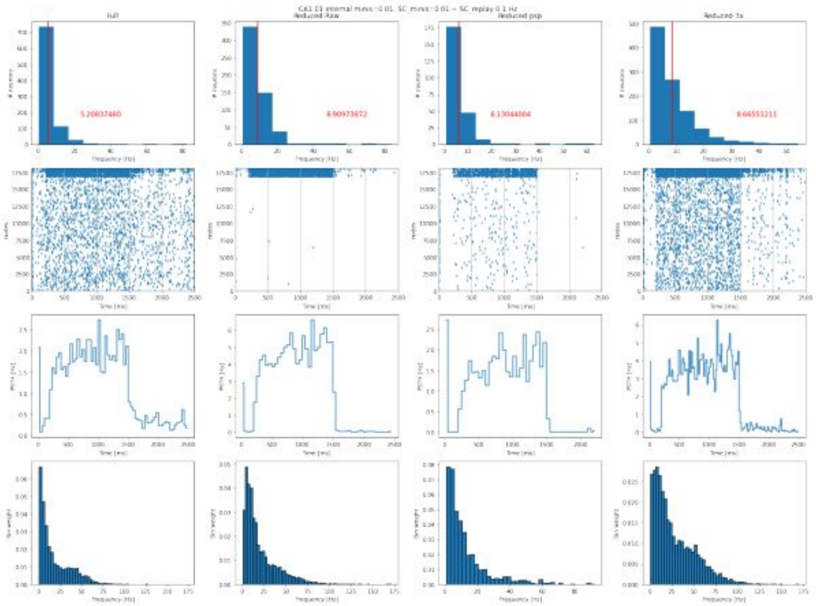
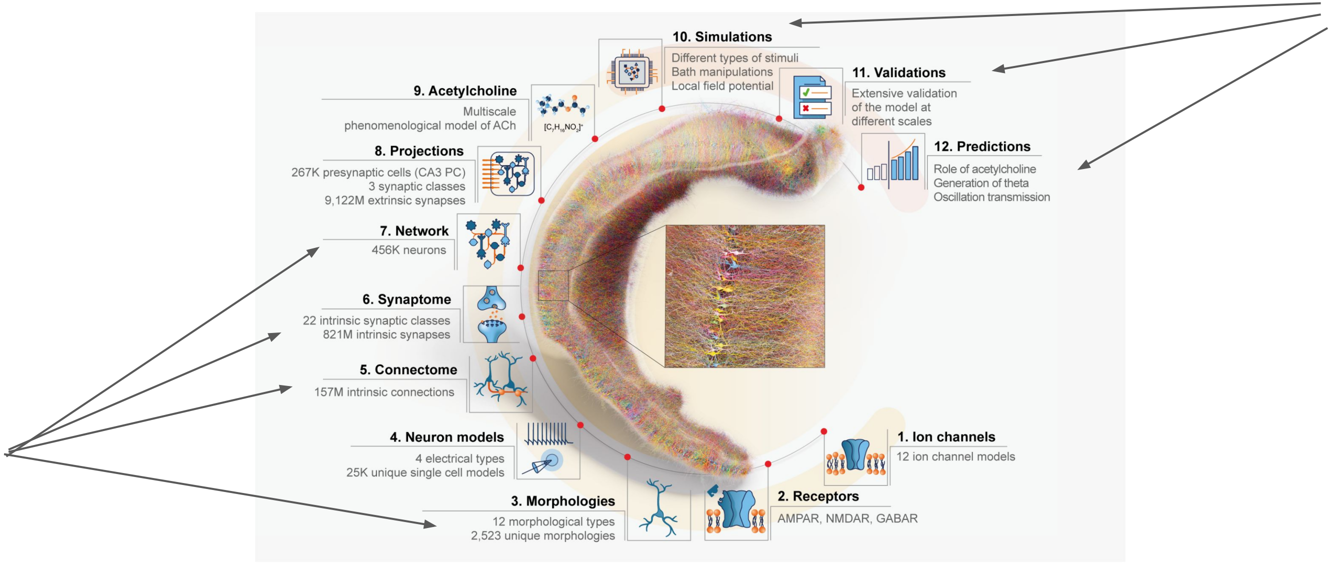


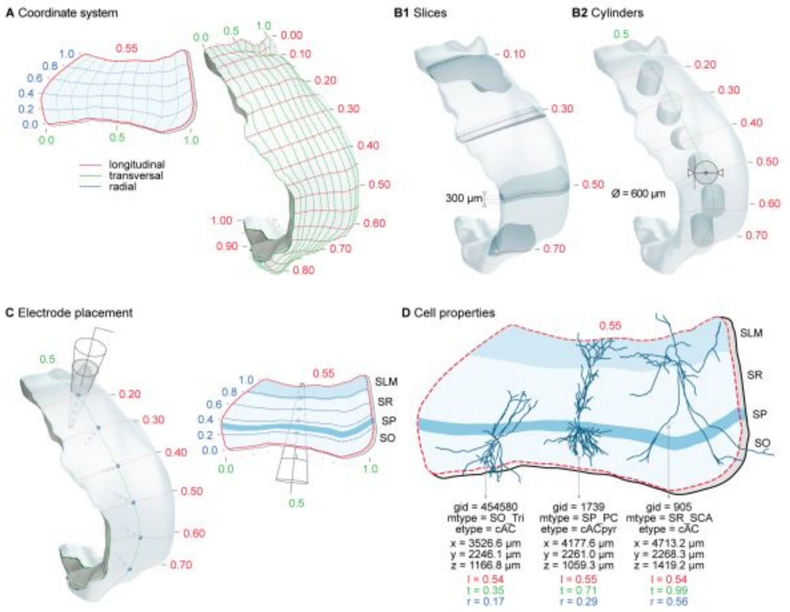
Figure 5.23: Simulation Report Comparisons for full, reduced, psp-validation-corrected and hand-tuned simulations for each m-types per second of CA1 microcircuit simulation.

Community-based Reconstruction and Simulation of a Full-scale Model of Region CA1 of Rat Hippocampus

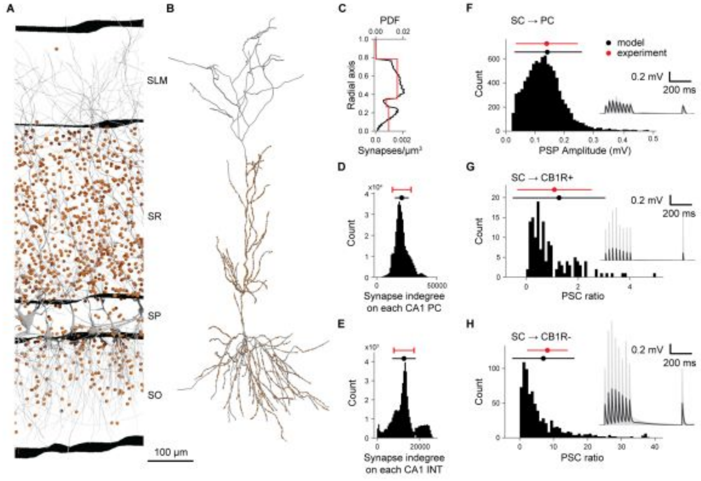


The Circuit Building Pipeline

Community-based Reconstruction and Simulation of a Full-scale Model of Region CA1 of Rat Hippocampus

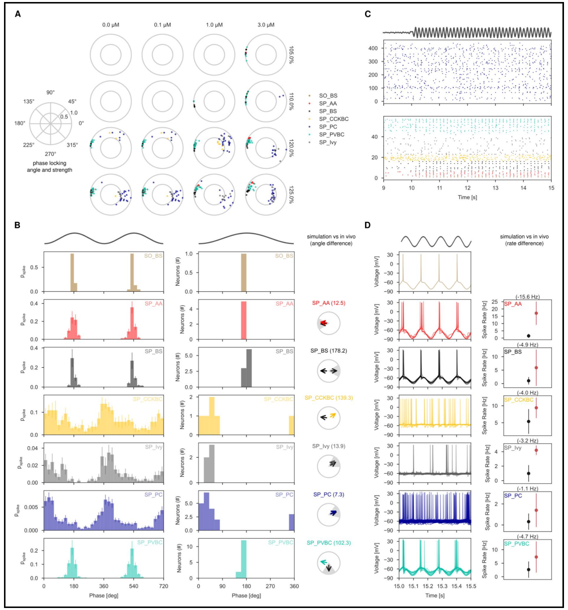


Custom Coordinate System

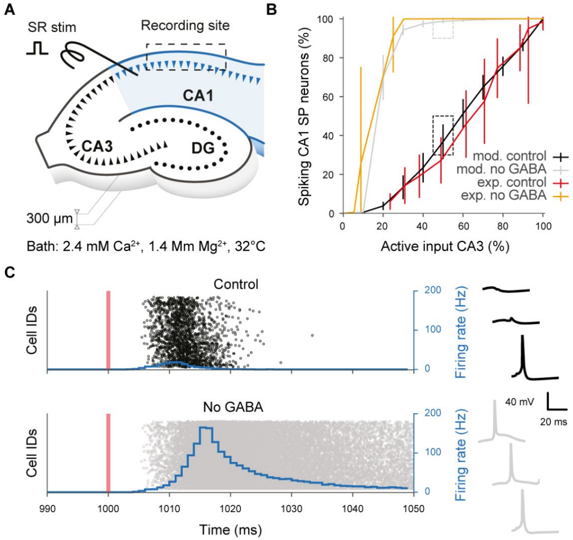


Distribution of Schaffer Collateral Projections

Some emergent properties



Phase Locking



Exc/Inh Balance

A Deep Dive into rat CA1 model : Insights from Network Science

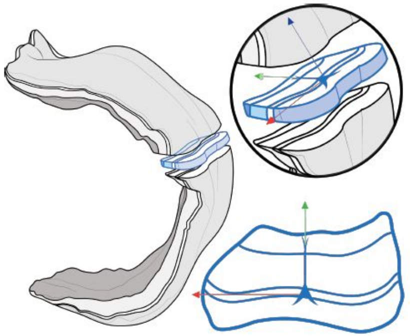


Figure 1: The reconstructed rat CA1 circuit and the slice section used in the experiments and motif calculations.

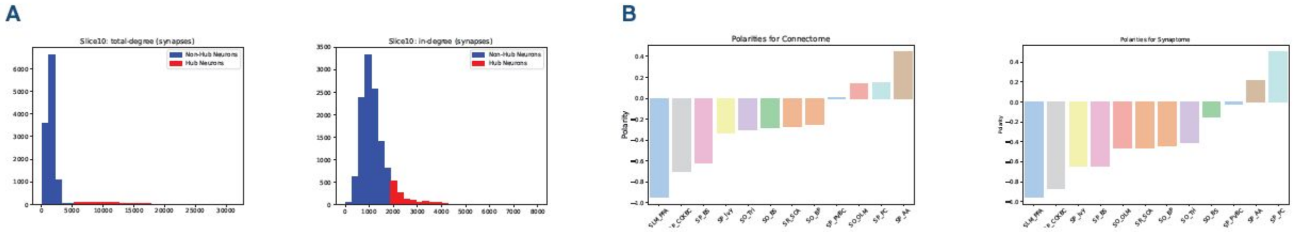


Figure 4: A. Degree distributions for the synaptome for total and indegrees. B. Polarity sorted in ascending order for connectome (binary matrix) and synaptome (weigthed matrix) shows difference in graph structure for cell types.

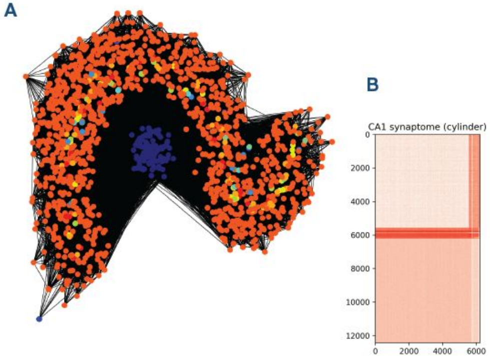


Figure 2: A. 400 um slice from the CA1 network with its CA3 projections (blue nodes) represented as graph with spring layout. Colors indicate the cell types.
B. Adjacency matrix of the slice.

A Deep Dive into rat CA1 model : Insights from Network Science

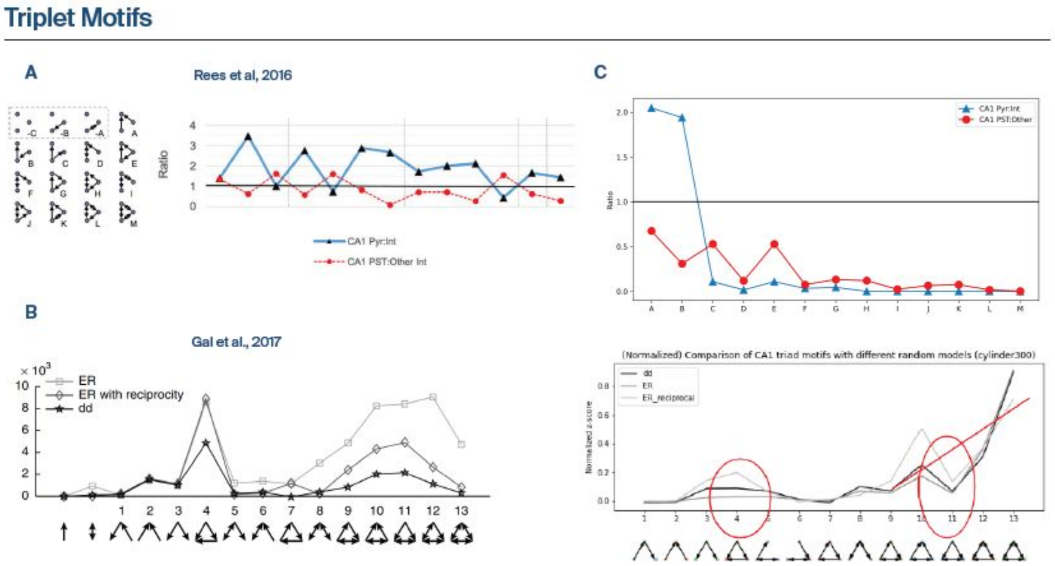
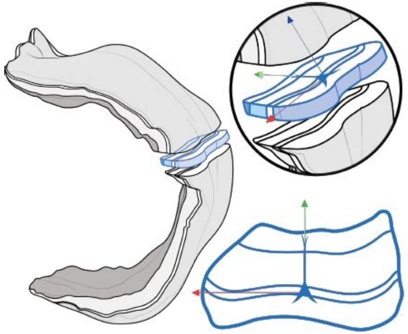


Figure 7: Triplet motif analyses of the CA1 network compared to **A.** neuroinformatic based modeling study [2] and **B.** in-silico neocortex model [4]. Note the different nomenculature for motif naming in both studies. Compared to neocortex models, our CA1 model shows increasing motif patterns from motifs 9-13 with the exception of motif 11 (bidirected version of motif 4).



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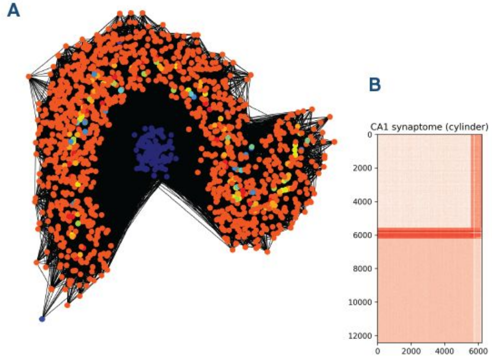


Figure 2: **A.** 400 um slice from the CA1 network with its CA3 projections (blue nodes) represented as graph with spring layout. Colors indicate the cell types.
B. Adjacency matrix of the slice.

A Deep Dive into rat CA1 model : Insights from Network Science

Rich Clubs

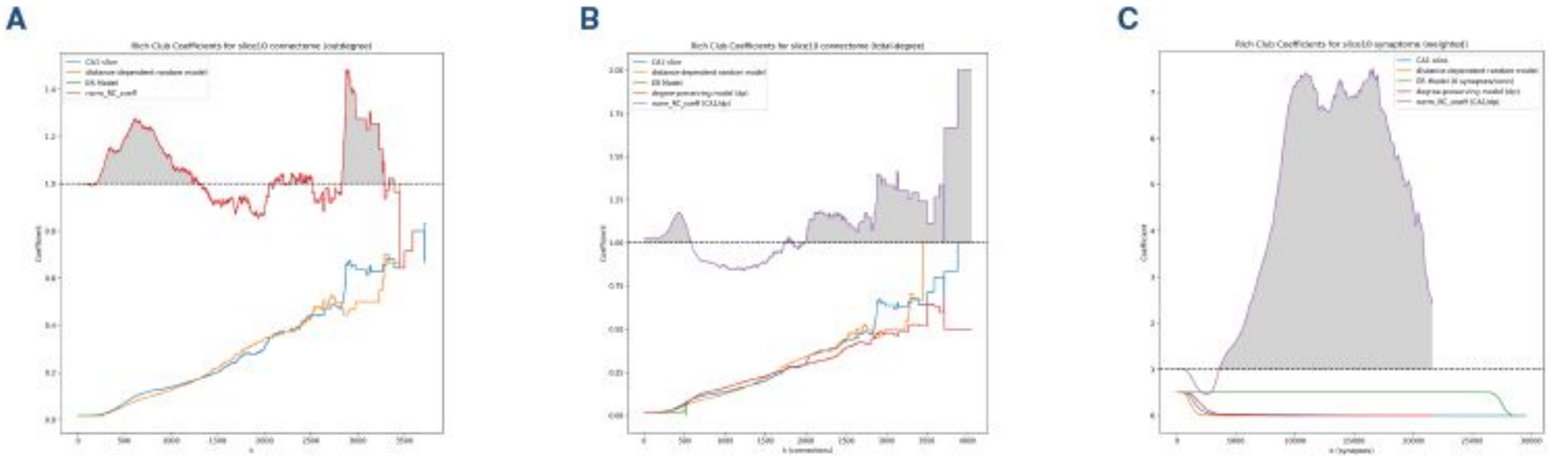
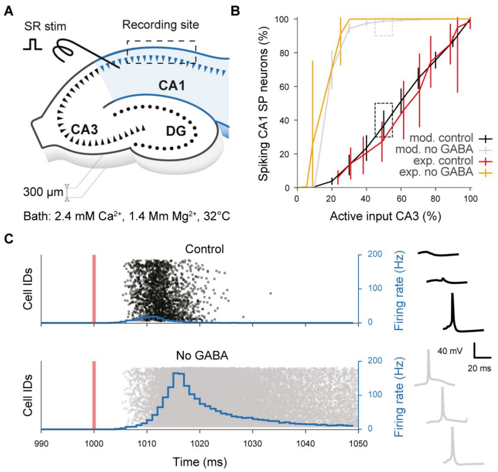


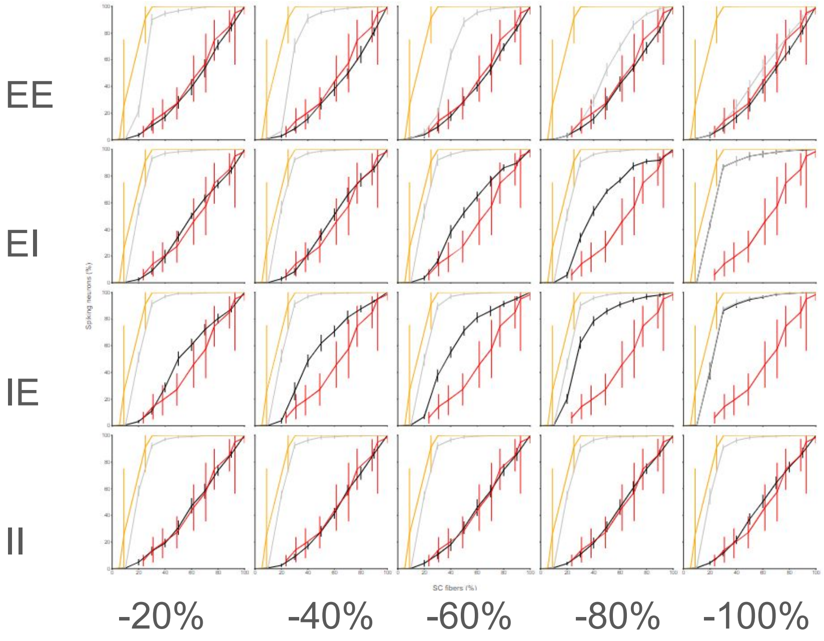
Figure 6: Normalized and non-normalized rich club coefficients (RCCs) for the CA1 connectome and synaptome. RCCs are calculated for directed graphs. **A.** for outdegree (connectome) **B .** total-degree (connectome), and **C .** total-weight (synaptome). For comparisons,Erdos-Renyi graph, distance dependent configurational model, and weight shuffled randomization (for synaptome only) are used as a control with increased complexity.

Topological properties of full scale rat CA1 circuit and their functional implications

In-silico ablation shows that gradual disruption of connections between Exc and Inh neurons result in differential IO dynamics



Original Circuit and Experiment



Disrupted EI balance

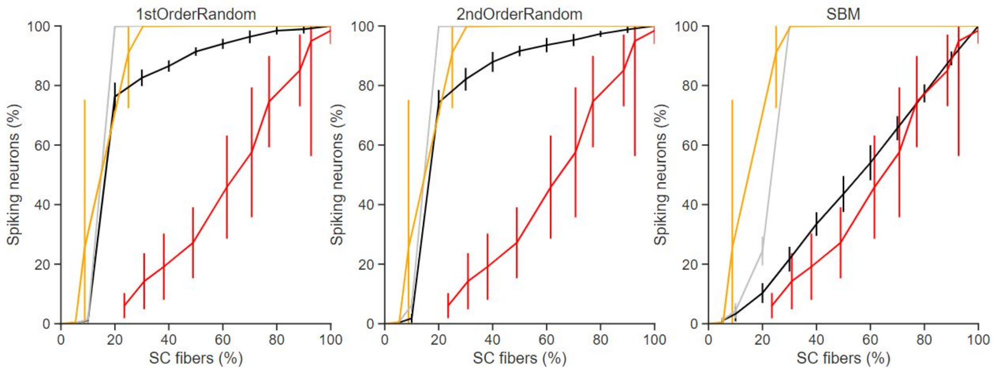
Topological properties of full scale rat CA1 circuit and their functional implications

By generating randomized control models with same node and edge numbers with the original one, we can see where the this property of the model starts to emerge.

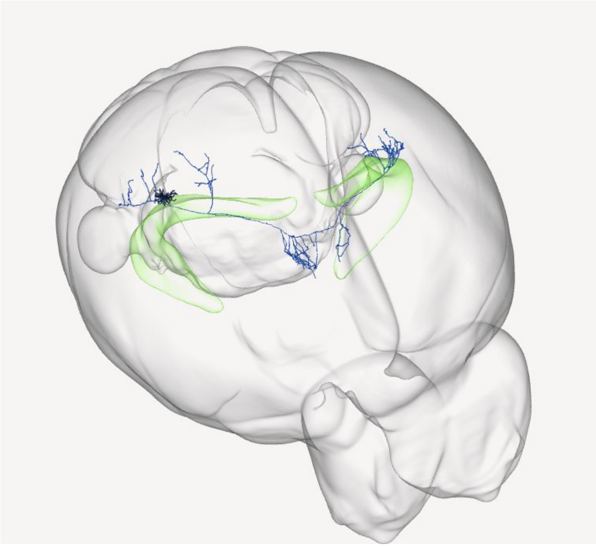
1st order : same number of neurons and connection probability (n,p)

2nd order : Distant-dependent Connection Probability

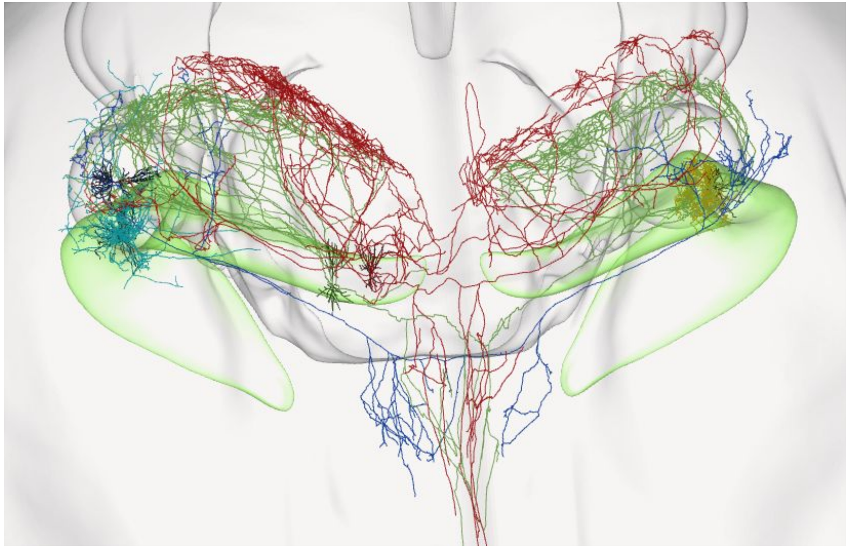
Stochastic Block Model: Combination of 4 1st order models between EE,EI,IE,II



Investigation of projection types (p-types) through an analysis of persistent images of axonal trees

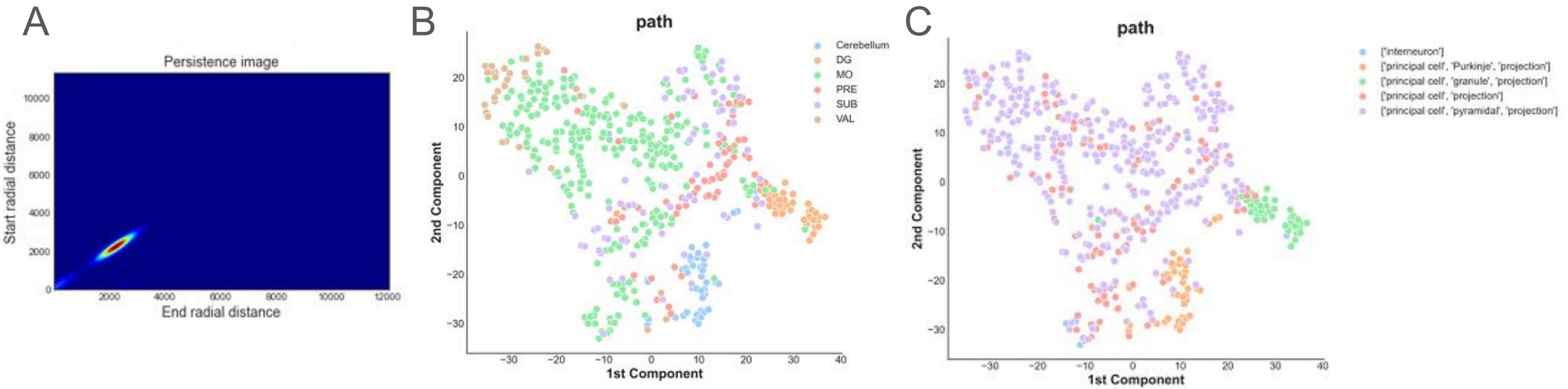


A fully reconstructed CA3 Pyramidal Neuron with complete axon



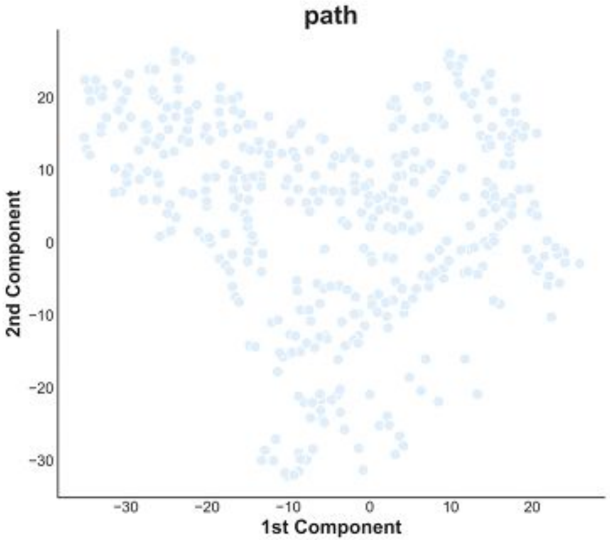
Multiple Reconstructed Morphologies Stress the importance of Axonal Distribution

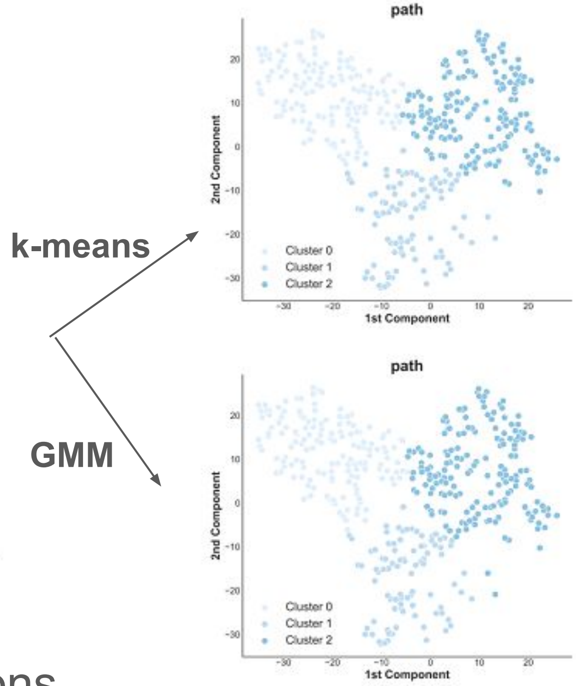
Investigation of projection types (p-types) through an analysis of persistent images of axonal trees

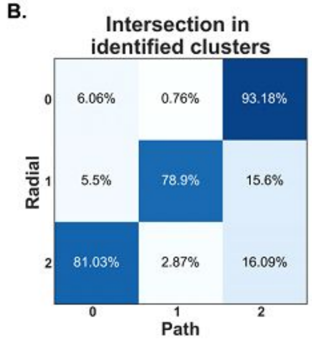


A. Normalized persistent image of an axon. B-C t-SNE mapping of PIs color coded by (B) region or (C) annotated cell type

Investigation of projection types (p-types) through an analysis of persistent images of axonal trees





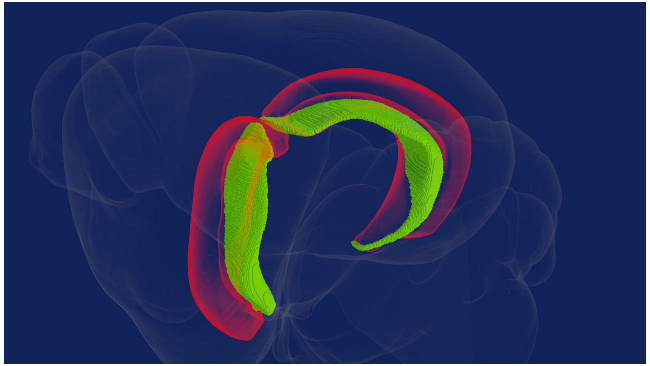


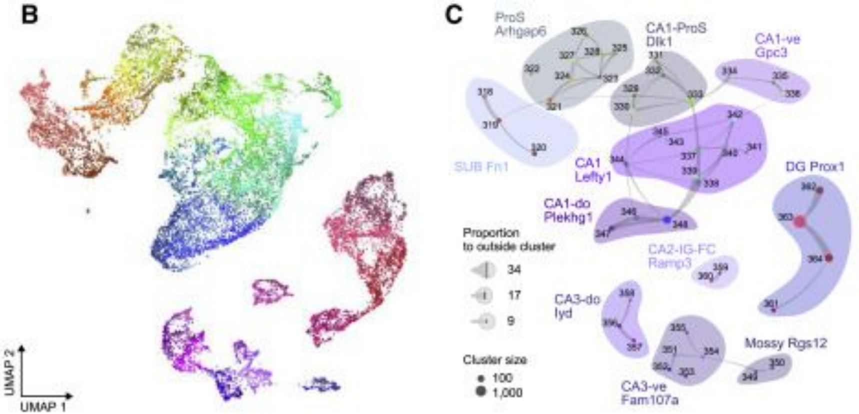
Clustering of Motor Cortex Neurons based on Persistent Axonal Features

Modeling mouse hippocampal formation: From Transcriptomics to Network Dynamics

Challenge in combining transcriptomics (T) into morpho electrical (ME) types

> MET types



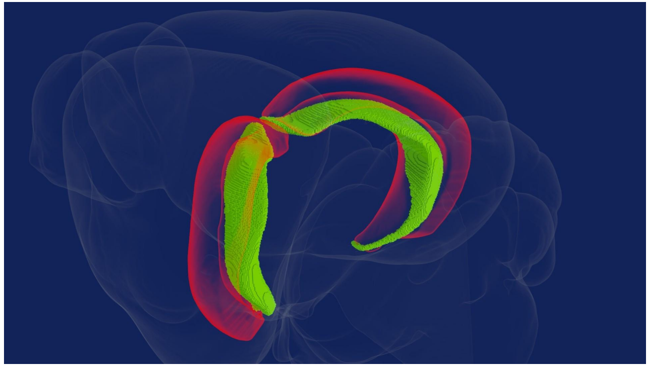


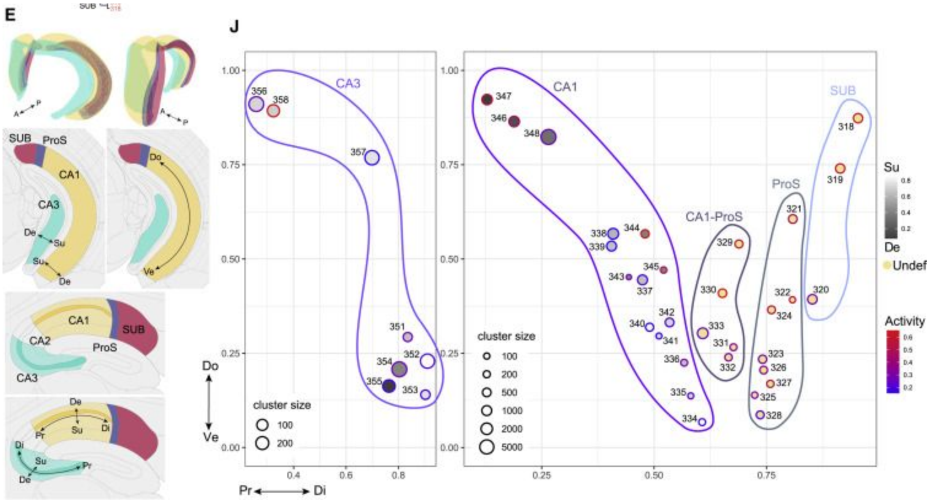
UMAP of hierarchically clustered transcriptomic types (t-types) from whole brain ISH data. Obtained from Yao et al 2020

Modeling mouse hippocampal formation: From Transcriptomics to Network Dynamics

Challenge in combining transcriptomics (T) into morpho electrical (ME) types

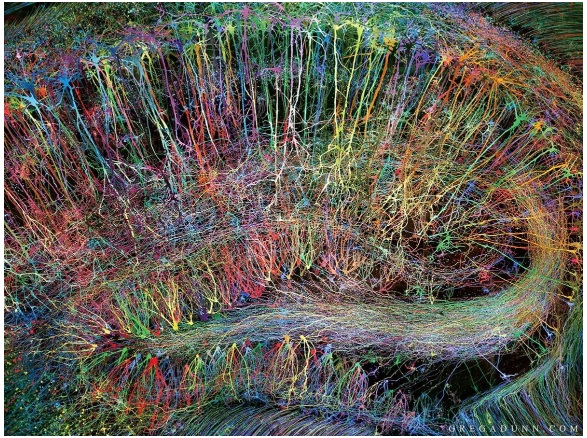
> MET types

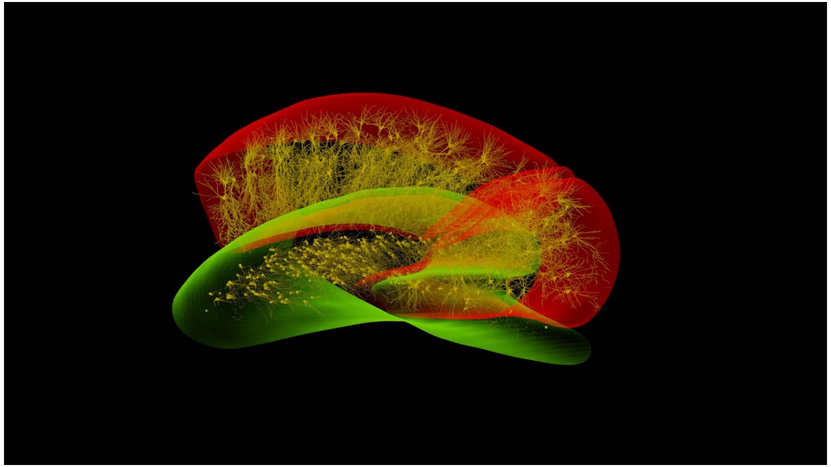




T-types extracted from ISH combined with spatial transcriptomics shows region specific Dorso-Vental / Sup-Deep / Proximo-Distal clusters (Yao et al 2020)

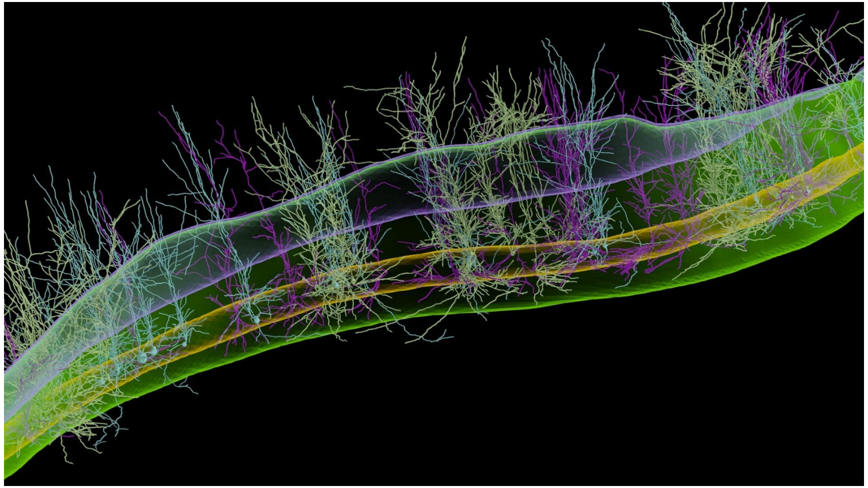
Modeling mouse hippocampal formation

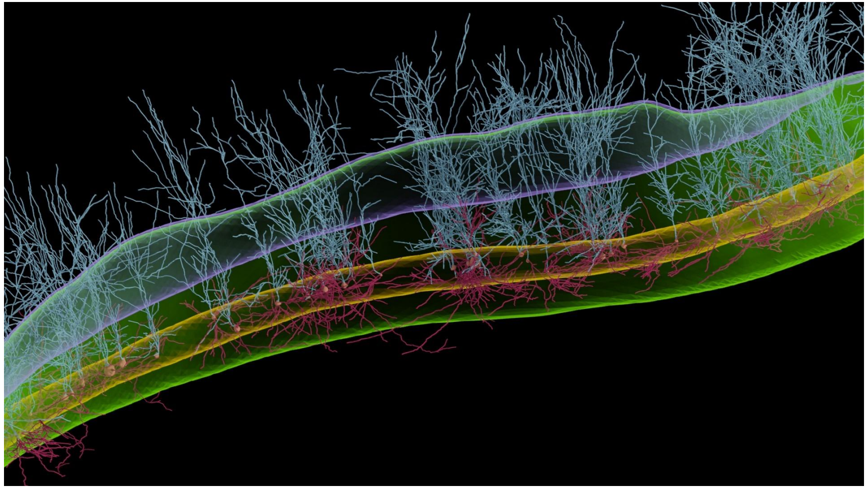




Atlas-abiding synthesis of CA1/2/3 and DG dendrites and axons

Generating Morphologies with same topological structure





Neurons are colored by m-type (left) or neurite type (right)