## Continuous and discrete dynamic topology

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## Discrete dynamics in topology



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## Structure

## BlueBrain V5 connectome

## Layer structure

- $\quad$ Higher (L1) $=$ inhibition
- Lower (L6) = information processing


## Neuron characteristics

- 31346 in total
- 55 electro-morphological classes


## Other facts

- Diameter is 4
- High dimensional simplices are over-represented
- Reciprocal connections preferentially appear in high-dimensional simplices



## Activity

## Stimulated activity

Reconstruction is stimulated from an "at rest" state.

Transmission is probabilistic, response can not be predicted


200 milliseconds

## Activity extraction

## Extracting features

1. Consider two "active subgraphs" of the full graph for each repetition
2. Consider two "active neighbourhoods" of $N$ vertices in the active subgraph
3. Assign a numerical value to every active neighbourhood


## Parameters



## Used to:

- select $N=50$ neighbourhoods
- assign numerical values to active neighbourhoods

| clustering coefficient | Fagiolo (2007) generalizing Watts-Strogatz (1998) to digraphs | 0.043 |
| :---: | :---: | :---: |
| transitive clustering coefficient | ratio of all 3-cliques at $v$ to all possible 3-cliques at v | 0.051 |
| neighbourhood size | size of closed neighbourhood | 36 |
| number of reciprocal connections | add 1 if $u \rightarrow v$ and $v \rightarrow u$ both exist | 1 |
| adjacency spectral gap | eigenvalues of adjacency matrix | 1 |
| Chung Laplacian spectral gap | of largest strongly connected component | 0.5 |
| transition probability spectral gap | eigenvalues of transition probability matrix | 0.707 |
| Euler characteristic | alternating sum of Betti numbers | 1 |
| normalized Betti coefficient | weighted sum of Betti numbers, weighted by dimension $d$ and number of $d$-simplices | 0.027 |
| density coefficients | ratio of ( $d+1$ )-cliques to $d$-cliques, normalised to be 1 on complete graphs | $\begin{gathered} \{0.028, \\ 0.02,0,0\} \end{gathered}$ |

## Overview: the "pipeline"

## 1. Select neighbourhoods:

Compute graph / topological parameters for all neighbourhoods, select top $N=50$ by parameter $P_{1}$ value
2. Measure active neighbourhoods:

For each selected neighbourhood, compute parameter $P_{2}$ value on each of $B=2$ active subgraphs
3. Classify with measurements as feature vectors

Length of feature vector is $N \cdot B$, number of feature vectors is (8 signals)•(557 repetitions)
Classify with support vector machines (SVM) with 60/40 train/test five different ways
4. Validate with baseline results

Random measurements, random neighbourhood choices, random ambient graph


## Results and extensions



Santander et al, 2023. github.com/danielaegassan/connectome_analysis

Classification accuracy of $\sim 88 \%$ when:

- selecting by a spectral parameter
- featurising by neighbourhood size


## Observations:

- Active neighbourhood size is firing rate
- Euler characteristic is a good classifier
- Density coefficients not useful


## Development:

- github repo for easy parameter measurement
- Double selection for better results


## Continuous dynamics in topology

How can spatial change be quantified as topological change?

## Assumptions:

- Euclidean space
- Linear paths
- Unique locations
- Times with pairwise equal distance are measure zero

Barbara Giunti, TU Graz

David Millman, Montana State University

## Zigzags of simplicial maps

## Movement as algebra

- Fix a radius
- Every pair of points defines a quadratic distance function

Entering a parabola (left): - adds an edge

Exiting a parabola (right): - removes an edge

## Motivation

Recover later homology from earlier homology, without recomputing everything



## The (un)reduced boundary matrix

The matrix $B$ has one row for each simplex, arranged in increasing dimension and increasing entrance time:

$$
B_{i, j}= \begin{cases}1 & \text { simplex of row } i \text { is a face of simplex of column } j \\ 0 & \text { else }\end{cases}
$$






swap edges
$\bullet$ and $\bullet$
swap edges
$\bullet$ and $\bullet$

## The reduction algorithm

Add earlier columns (in modulo 2) to later columns to ensure one pivot per row:


Gives a decomposition $R=B U$

- $\quad B$ is the (unreduced) boundary matrix
- $U$ is an upper triangular matrix recording the column operations
- $\quad R$ is the reduced boundary matrix

Approach: Add / remove columns from $R$, use $U$ to ensure removal keeps $R$ reduced

## Adding a new edge

## Adding a single edge can may have different consequences for:

- number of n-simplices
- number of classes in $H_{n}$
$\left|K_{2}\right|$ increases by $n$
$\left|K_{3}\right|$ increases by $\binom{n}{2}$
$\left|K_{4}\right|$ increases by $\binom{n}{3}$

realized in $\mathbf{R}^{3}$
$\beta_{1}$ increases by 1
$\beta_{2}$ unchanged $\beta_{3}$ unchanged
$\vdots$

realized in $\mathbf{R}^{2}$
$\beta_{1}$ unchanged $\beta_{2}$ increases by $n$ $\beta_{3}$ unchanged

realized in $\mathbf{R}^{n \geqslant 4}$
$\beta_{1}$ unchanged $\beta_{2}$ unchanged $\beta_{3}$ increases by $n$
$n$ copies of

identified at the equator
realized in $\mathbf{R}^{n \geqslant 5}$


## Removing an existing edge

Removing a positive edge

- its column is 0
- pivots in $R$ won't change if this column is removed


## Remove

Case 1:

- Row and column of edge
- Rows and columns of all cofaces


## Clear:

- $\quad R$ after is still reduced

$R$ before

$R$ before


$R$ after



## Removing an existing edge

Removing a negative edge

- its column is not 0
- pivots in $R$ may change if this column is removed

Remove

- Row and column of edge
- Rows and columns of all cofaces

Almost clear:

- $\quad R$ after is still reduced

Carlsson G, de Silva V (2010). Zigzag persistence. Foundations of Computational mathematics. 10, 367-405. doi: https://doi.org/10.1007/s10208-010-9066-0
Cohen-Steiner D, Edelsbrunner H, Morozov D (2006) Vines and vineyards by updating persistence in linear time. SCG 2006: Proceedings of the twenty-second annual symposium on Computational Geometry. doi: https://doi.org/10.1145/1137856.1137877

Edelsbrunner H, Harer J (2010). Computational Topology: An Introduction. American Mathematical Society.
Lütgehetmann D, Govc D, Smith JP, Levi R (2020). Computing Persistent Homology of Directed Flag Complexes. Algorithms. 13(1):19. doi: https://doi.org/10.3390/a13010019

Markram H et al (2015). Reconstruction and Simulation of Neocortical Microcircuitry. Cell. Oct 8;163(2):456-92. doi: 10.1016/j.cell.2015.09.029. PMID: 26451489.
Reimann MW, Nolte M, Scolamiero M, Turner K, Perin R, Chindemi G, Dłotko P, Levi R, Hess K and Markram H (2017) Cliques of Neurons Bound into Cavities Provide a Missing Link between Structure and Function. Front. Comput. Neurosci. 11:48. doi: https://doi.org/10.3389/fncom.2017.00048

Reimann MW, Riihimäki H, Smith JP, Lazovskis J, Pokorny C, et al. (2022) Topology of synaptic connectivity constrains neuronal stimulus representation, predicting two complementary coding strategies. PLOS ONE 17(1): e0261702. https://doi.org/10.1371/journal.pone. 0261702

Riemann MW et al. (2022) Modeling and Simulation of Rat Non-Barrel Somatosensory Cortex. Part I: Modeling Anatomy. bioRxiv 2022.08.11.503144; doi: https://doi.org/10.1101/2022.08.11.503144

Santoro, Matteo (2021) Studying motifs in connectome models. Masters project, Brain-Mind Institute, EPFL.
Pedro Conceição, Dejan Govc, Jānis Lazovskis, Ran Levi, Henri Riihimäki, Jason P. Smith; An application of neighbourhoods in digraphs to the classification of binary dynamics. Network Neuroscience 2022; 6 (2): 528-551. doi: https://doi.org/10.1162/netn a 00228

Santander DE et al (2023). General functions to analyze connectomes. https://github.com/danielaegassan/connectome analysis

