



Using Topological Data Analysis for Insights into Biological and Artificial Neural Networks

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Outline

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TDA+BNNs: state-of-the-art

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References

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Future: Dissertation, dissertation, dissertation!

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- ▶ A subfield of algebraic topology that has found applications in many disciplines outside math.
- ▶ Based on the idea that data are sampled from an underlying manifold so we can study some algebraic invariants of that space.
- ▶ Important algebraic invariant class are homology groups, which arise from combinatorial representations of the manifold.

Definition. Let $\{a_0, \dots, a_n\}$ be a geometrically independent set in \mathbb{R}^N . The *n-simplex* σ spanned by a_0, \dots, a_n is defined to be the set of all points x of \mathbb{R}^N such that $x = \sum_{i=0}^n t_i a_i$, where $\sum_{i=0}^n t_i = 1$ and $t_i \geq 0$ for all i .

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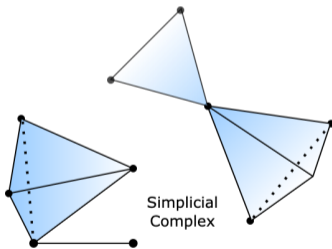
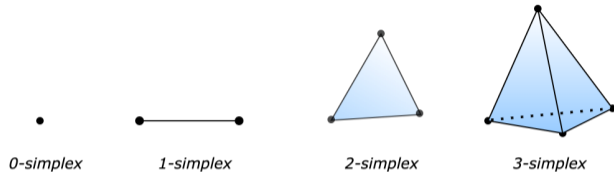
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Definition. A *simplicial complex* K in \mathbb{R}^N is a collection of simplices in \mathbb{R}^N such that (1) every face of a simplex of K is in K , and (2) the intersection of any two simplices of K is a face of each of them.

Examples



Given any topological manifold \mathbb{X} , we can model it using simplices via homology groups.

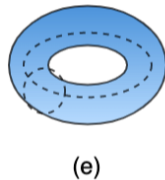
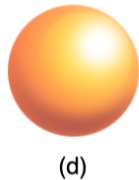
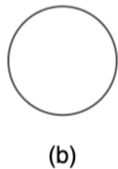
- ▶ The quotient group $H_p(K) := Z_p(K)/B_p(K)$ is the **p -th homology group of K** .

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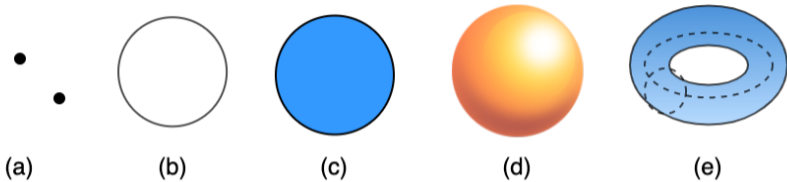
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- ▶ Elements of $H_p(K)$ are p -cycles which do not bound any thing in the middle, and thus describe disconnections, holes, voids and higher-dimensional “absence of stuff” .
- ▶ Homology groups remain invariant under homeomorphisms, i.e. continuous deformations, and thus they encode intrinsic information on the topology of the given manifold \mathbb{X} .

Homology and Betti-Numbers

Betti-number: the dimension of its corresponding homology group, that is $\beta_p := \dim H_p(K)$. For instance β_0 is a count of connected components, β_1 is a count of holes, β_2 is a count of voids, and so on.



Homology and Betti-Numbers



Betti-number	(a)	(b)	(c)	(d)	(e)
β_0	2	1	1	1	1
β_1	0	1	0	0	2
β_2	0	0	0	1	1

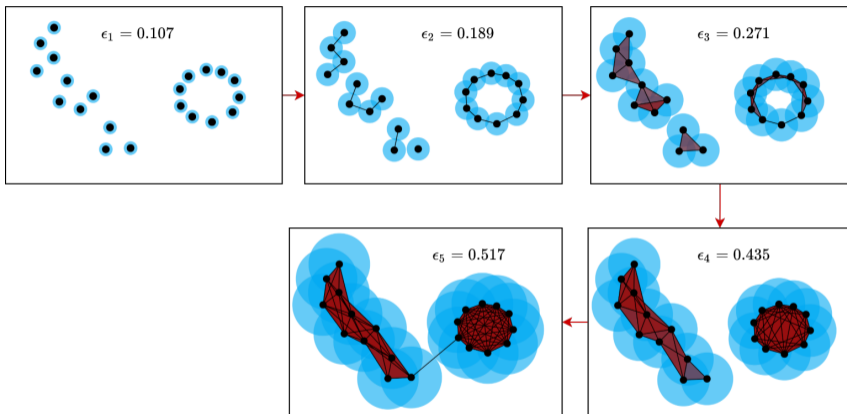
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- ▶ Different topological features occur at different scales, and not clear at what scale these features are born and die.
- ▶ **Persistent Homology** is a tool of TDA used to measure the scale of a topological feature via **filtrations**, sequences of chain complexes along with inclusion maps.
- ▶ We use a *persistence diagram* to store information of the topological features in each filtration.

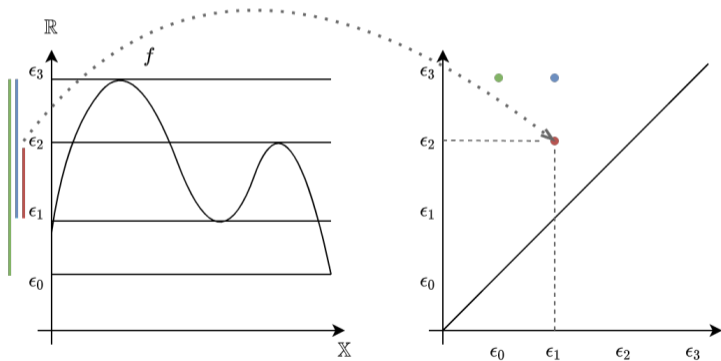
Data and Homology



source: *Henry Adams.*

Sublevel Sets

\mathbb{X} a connected topological space; $f : \mathbb{X} \rightarrow \mathbb{R}$ a continuous function. The *sublevel sets* $\mathbb{X}^\epsilon := f^{-1}(\mathbb{R}_{<\epsilon})$ form a family of nested subspaces for parameters ϵ_i , that is $\mathbb{X}^{\epsilon_0} \subset \mathbb{X}^{\epsilon_1} \subset \mathbb{X}^{\epsilon_2} \subset \dots$. Let $\epsilon_i < \epsilon_j$ we define $\beta(\epsilon_i, \epsilon_j)$ to be the number of components in \mathbb{X}^{ϵ_j} that have a non-empty intersection with \mathbb{X}^{ϵ_i} .



Persistence Diagrams

The persistence diagram encodes the (birth, death) of persistent homology features of a particular rank.

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The space of persistence diagrams can be endowed with a metric induced by Wasserstein distances. We define the distance between two persistence diagrams X and Y as

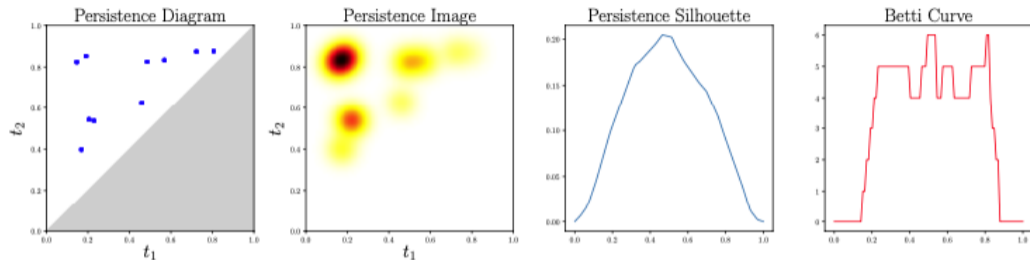
$$W_q(X, Y) := \left[\inf_{\eta: X \rightarrow Y} \sum_{x \in X} \|x - \eta(x)\|_\infty^q \right]^{1/q}.$$

Besides comparing persistence diagrams Wasserstein distances, we can also compute their summary statistics, such as total persistence and the p -norm.

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However, for certain applications, such summaries may lose information and more expressive measurements of the persistent homology features may be desired.

Persistence Diagrams



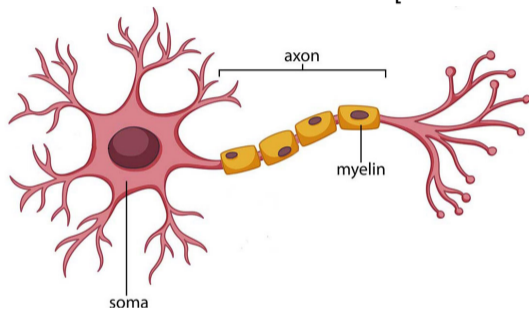
Some common linear representations of persistence diagrams. From left to right: A persistence diagram. Its persistence surface, which is a persistence measure. The corresponding persistence silhouette. The corresponding Betti Curve.

Computations are made using the sklearn-tda library: <https://github.com/MathieuCarriere/sklearntda>.

Image source: Divol and Lacombe [2019]

Biological Neural Networks

The human brain is estimated to have between 10 to 20 billion neurons in the cerebral cortex and 55 to 70 billion neurons in the cerebellum [von Bartheld et al., 2016].



Gray matter is primarily composed of neuron somas, and white matter is mostly made of axons wrapped in myelin *source: Johns Hopkins Medicine*. Not labeled are **dendrites** branching out of the cell body to receive transmissions from other neurons and the **terminal buttons** at the opposite end serve to transmit neuronal signals.

- ▶ Neurons receive electrochemical inputs from other neurons at the dendrites.

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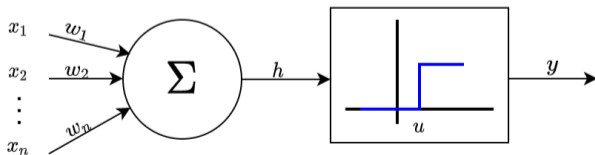
- ▶ Neurons receive electrochemical inputs from other neurons at the dendrites.
- ▶ If the sum of all the inputs is above its activation threshold, the neuron will activate.
- ▶ It will transmit an electrochemical signal along its axon in order to pass that signal on to other neurons through its terminal buttons.
- ▶ Bressler and Menon [2010] argue that large-scale brain networks provide a coherent framework for understanding cognition, allowing for a principled exploration for how cognitive functions emerge from such organization.

Artificial Neural Networks

About 60 years ago, McCulloch and Pitts [1943] proposed a computational model for an artificial neuron. It computes a weighted sum of its n inputs x_j and it outputs a 1 if the sum is above a certain threshold u , and a 0 otherwise. That is,

$$y = \theta \left(\sum_{j=1}^n w_j x_j - u \right),$$

where $\theta(\cdot)$, the activation function, is a unit step function at zero and w_j is the weight associated with the j th input.



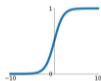
Artificial Neural Networks

Since its introduction, the McCulloch-Pitts neuron has been generalized and different activation functions such as sigmoid (e.g. logistic), Gaussian, and ReLU - rectified linear unit (i.e. the max between 0 and the linear unit) - have been used with the latter being the most popular for training deep networks.

Activation Functions

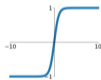
Sigmoid

$$\sigma(x) = \frac{1}{1+e^{-x}}$$



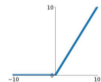
tanh

$$\tanh(x)$$



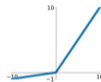
ReLU

$$\max(0, x)$$



Leaky ReLU

$$\max(0.1x, x)$$

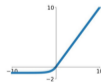


Maxout

$$\max(w_1^T x + b_1, w_2^T x + b_2)$$

ELU

$$\begin{cases} x & x \geq 0 \\ \alpha(e^x - 1) & x < 0 \end{cases}$$



source: medium.com

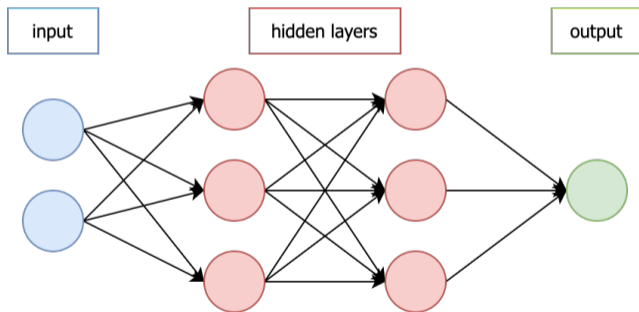
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For example, a *feed-forward neural network*:



For more architectures, here is a [zoo](#) of them.

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- 2 What mechanisms underlie the dynamic engagement and disengagement of brain areas responsible for the formation and dissolution of large-scale functional networks?
- 3 How do different large-scale functional networks cooperate, compete and coordinate their activity during complex cognitive behavior?
- 4 Is knowledge constructed dynamically by large-scale functional networks?

One interesting area of research in neuroscience is concerned with how neuronal signaling generates time-varying functional connectivity (TVFC) throughout multiple brain regions. TVFC, or chronnectomics as introduced by Calhoun et al. [2014], describes a dynamic view of connectivity where different regions of the brain (which all may be evolving spatially in time) are coupled with strength measured as functions of time.

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Calhoun et al. [2014] show through examples that this perspective has been important in assessing the impact of mental illnesses in the brain, while others such as Sagar et al. [2018] applied this perspective to study how the brain dynamically adapts for efficient functioning through multiple tasks.

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My particular interest in this area is how the chronnectome itself changes overtime depending on the age of the individual.

Deep neural networks are powerful learning models for many problems, however one can cause these networks to misclassify their inputs simply by adding a little bit of humanly imperceptible noise to the example, making it an *adversarial example* [Szegedy et al., 2013].

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Using TDA and statistical methods, I plan to investigate the short-comings in the current research related to the detection of adversarial examples in various ANNs architectures.

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For the later situation, Rieck et al. [2018] treat a feed-forward neural network as a stack of bipartite graphs and propose a complexity measure arising from topological features arising in filtrations (using network parameters) of the neural network graph. Using this approach, they were able to distinguish between well trained and badly trained networks.

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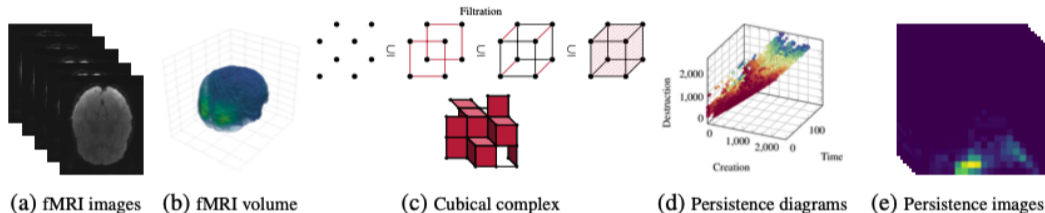
My interest is to use a similar approach for model analysis in various ANNs architectures.

What topological features are revealed from ANNs applied to fMRI data?, and what connections exist between the topological features of the activation network and the ones of the fMRI data itself?

Rieck et al. [2020] analyze time varying fMRI data using *cubical complexes*, which does not require the creation of a correlation graph and uses the 'raw' voxel activations themselves.

TDA+BNNs: state-of-the-art

Rieck et al. [2020] analyze time varying fMRI data using *cubical complexes*, which does not require the creation of a correlation graph and uses the 'raw' voxel activations themselves.



They represent an fMRI stack as a volume from which they create a sequence of cubical complexes. The persistent homology of this sequence results in a set of time-varying persistence diagrams. They calculate summary statistics from the diagrams (not shown), and convert them to vector representations for analysis tasks.

They empirically demonstrate that this representation of fMRI data captures age-related differences between individuals.

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Their approach opens future opportunities for the analysis of the geometry of brain state trajectories and link states back to events, as well as serves as a basis for the investigation of neurological pathologies from a new topological perspective.

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- 3 They build a variational autoencoder architecture that demonstrates how ToFU learns pertinent topology present in the data itself.

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