Uncovering the saliency of local topological features for Alzheimer's disease characterisation

Philip Hartout

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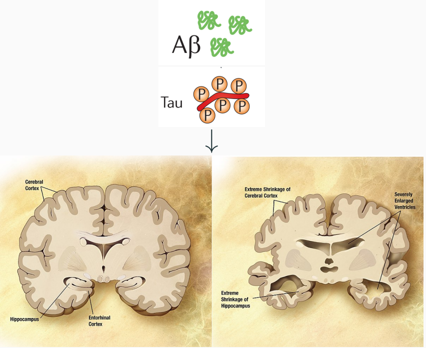

Images adapted from Ittner et al and Wikipedia

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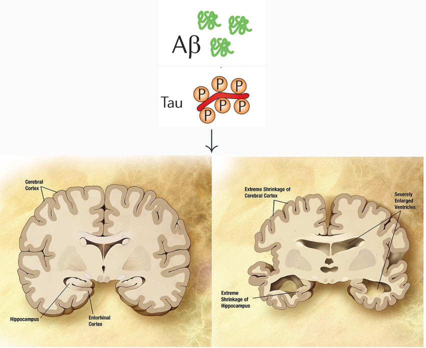

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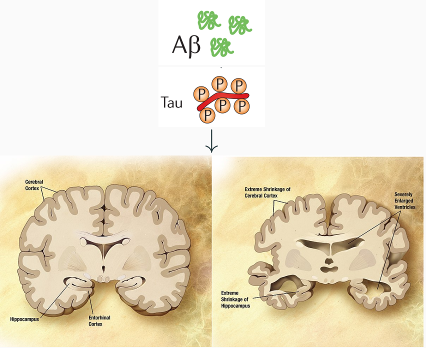

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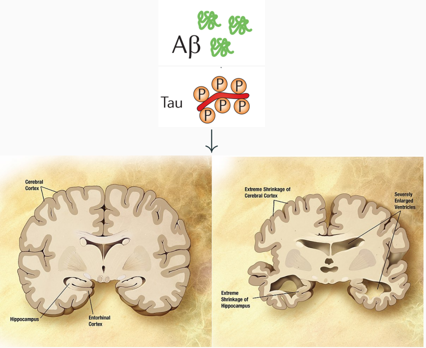

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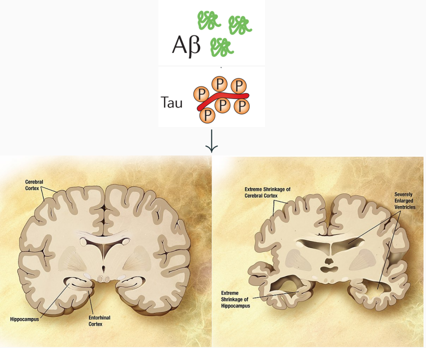

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Topology:

- Concerned with "properties of a geometric object that are preserved under **continuous deformations**, such as [...] crumpling."
- Recently, *persistent homology* has emerged as a way to quantify the shape of data.
- **How can we apply persistent homology to quantify changes in shape due to Alzheimer's disease?**

Topology in AD - Research Avenues

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1. **Classification**

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Topology in AD - Research Avenues

1. **Classification**
2. Subtype identification
3. Progression & forecasting

Determining the patch of interest

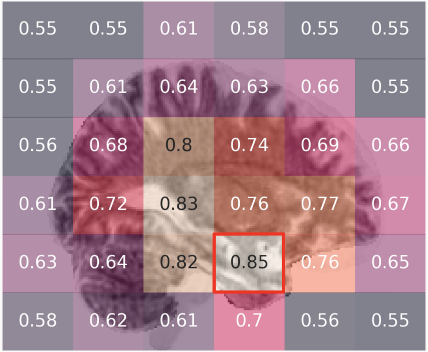

Figure 2: The patch with the highest accuracy was selected. Results from Brüningk, Sarah C *et al* `https://arxiv.org/abs/2011.06531`

Obtaining topological features from sMRI data

- We use the T1-weighting value (fat ≈ 1; water ≈ 0) to compute topological features
- Filtration of point clouds:

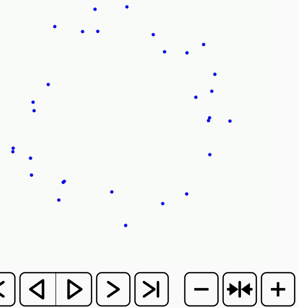

Figure 3: Point cloud filtration. Adapted from `giotto-ai.github.io/gtda-docs/`

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- Filtration of cubical complexes to examine the connected components, cycles, and voids.

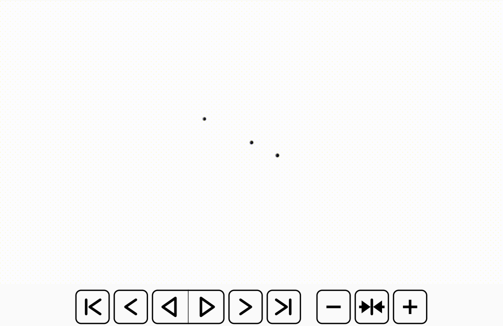
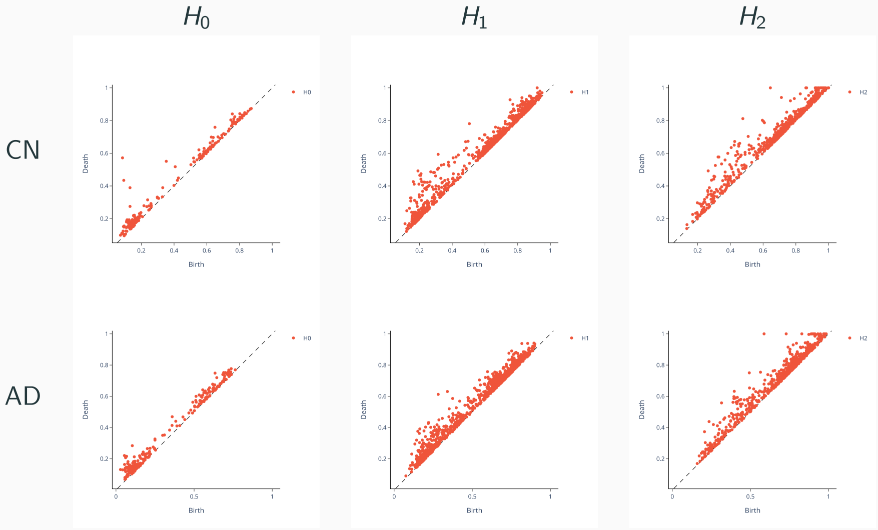
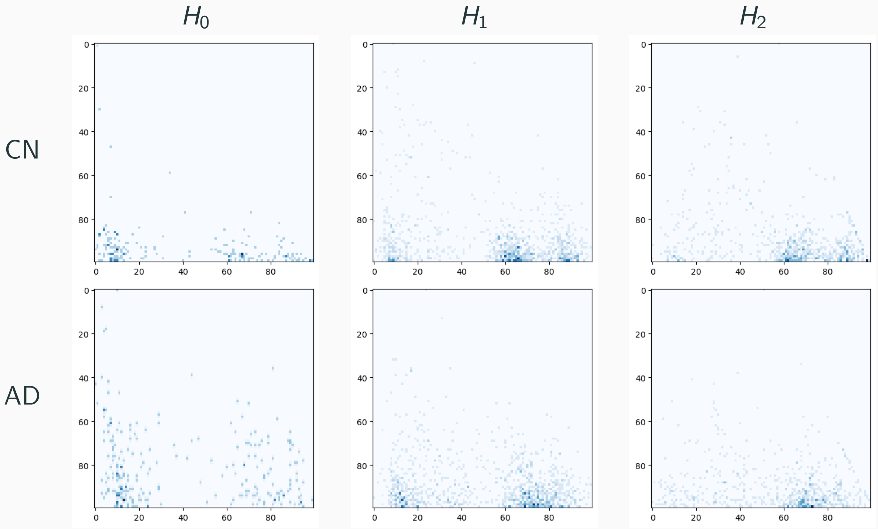


Figure 4: Cubical complex filtration. Adapted from Bastian Rieck `https://youtu.be/4mBcwy1tOJ4`


H_0
H_1
H_2
CN
AD
H0
H1
H2
Death
Birth
0.2
0.4
0.6
0.8
1
0
0.5

I - Classification - Persistence Images



I - Classification - Network architecture

Persistence image (H_0, H_1, H_2)

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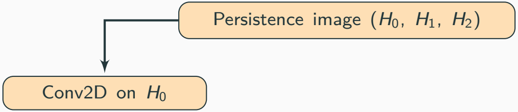

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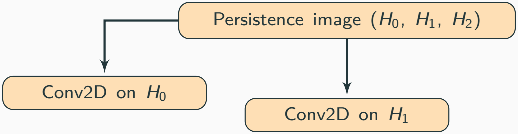

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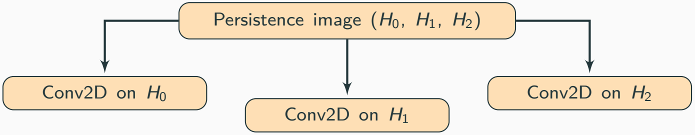

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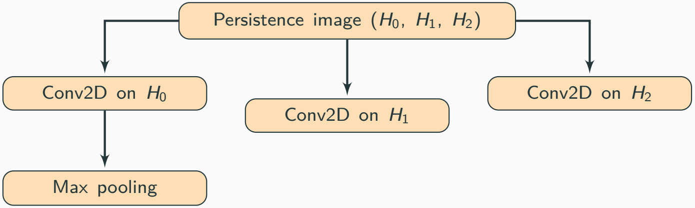

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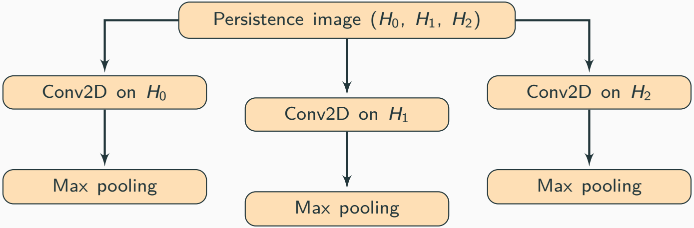

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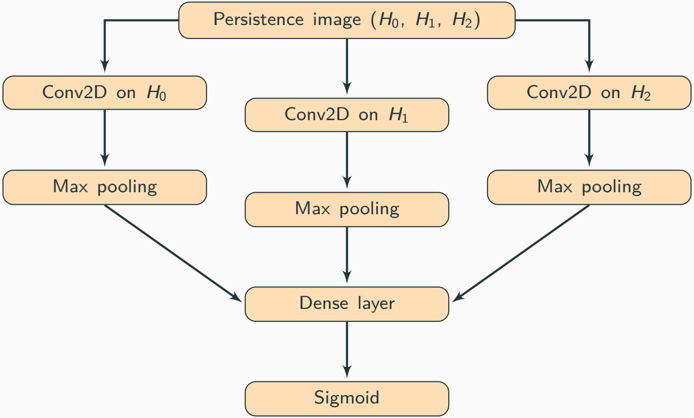

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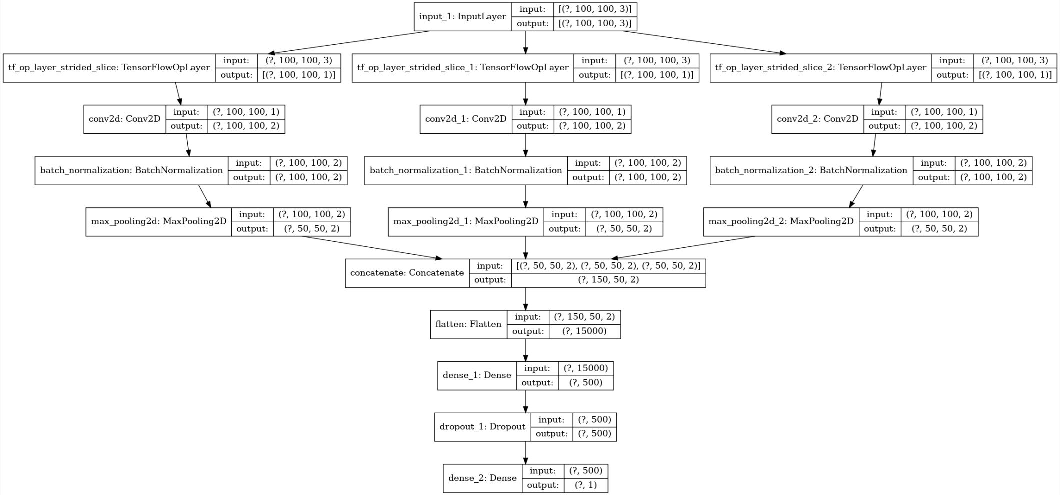

Methodological considerations

- 4 fold CV, 3 inits. Stratified for age, diagnoses and patients spread over folds.
- Same settings as in Brüningk, Sarah C *et al* `https://arxiv.org/abs/2011.06531`

I - Classification - Performance

Local	**PI**	3D Conv	
Global			PI
Validation accuracy	0.79 ± 0.02	0.85 ± 0.06	0.76 ± 0.02
Precision	0.81 ± 0.04	0.87 ± 0.04	0.74 ± 0.02
Recall	0.81 ± 0.02	0.87 ± 0.08	0.88 ± 0.08
AUC	0.85 ± 0.03	0.89 ± 0.05	0.78 ± 0.02

Table 1: Performance metrics of the different models trained on the same data. Metrics from Brüningk, Sarah C *et al* `https://arxiv.org/abs/2011.06531`.

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Persistent homology produces **highly salient compressed** features for AD characterization.

Limitations & Outlook

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Future directions:

- Can persistent homology be used to diagnose **prodromal** forms of AD?

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- Does not take atrophy from **other regions** into account

Future directions:

- Can persistent homology be used to diagnose **prodromal** forms of AD?
- Use a similar approach for **subtype identification**.

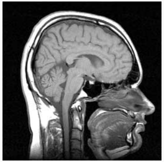
Thanks!

GitHub repository of the project (currently available upon request)

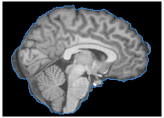
`github.com/pjhartout/TDA_ADNI_MLCB`

With thanks to Bastian Rieck for the supervision and Sarah Brueningk, Felix Hensel, Catherine Jutzeler, Merel Kuijs and Louis Lukas for insightful discussions, code, and data & Karsten Borgwardt for providing the research setting.

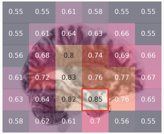
Questions?



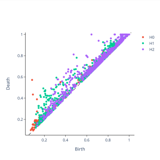
Unprocessed



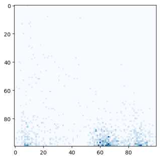
fMRIPrep



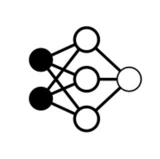
Patch selection



Persistent homology



Persistence Image



Classification

Images adapted from Wikimedia, slicer.org, and Sachin Modgekar