

Uncovering the topology of the temporal region in Alzheimer's disease.

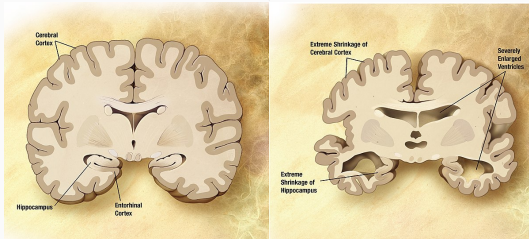
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November 23, 2020

Alzheimer's disease

Alzheimer's disease: 🧠

- Nearly 40 million people live with AD
- Cost in US alone \$ 2 trillion by 2030
- Among leading causes of death in EU



Topology: 🍩 ☕

- Concerned with “properties of a geometric object that are preserved under **continuous deformations**, such as stretching, twisting, crumpling and bending, but not tearing or gluing.”
- Recently, *persistent homology* has emerged to quantify (differences in) the shape of data.
- **How about applying persistent homology to quantify changes in shape due to Alzheimer's disease?**

1. Diagnosis (classification)
2. Subtype identification
3. Progression & forecasting

→ Some findings in these directions will be presented today

Analysis setting

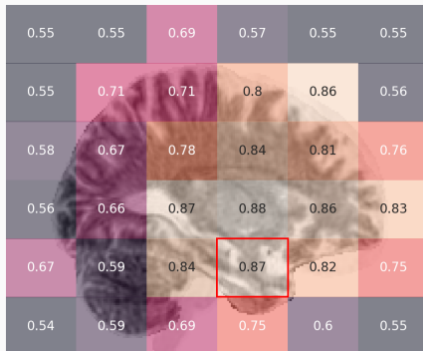


Figure 2: AUCPRC on each patch, achieved using a model described in earlier work. Chosen patch for analyses is boxed in red (patch with highest accuracy).

I - Diagnosis prediction

- Computed the cubical filtration to obtain persistence image for each patch
- Simple CNN to classify AD/CN patients.
- Use same partition as NeurIPS submission, train ANN 3 times on each partition
- Export misclassified samples

I - Persistent homology

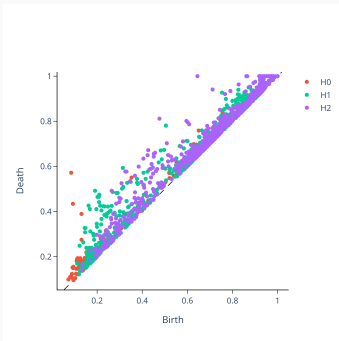


Figure 3: CN

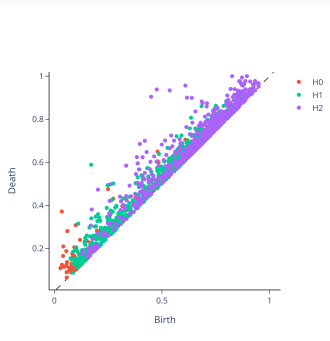


Figure 4: MCI

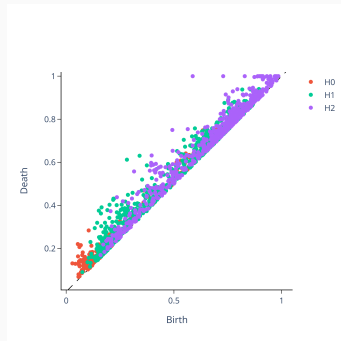


Figure 5: AD

I - Diagnosis prediction - Persistence Images

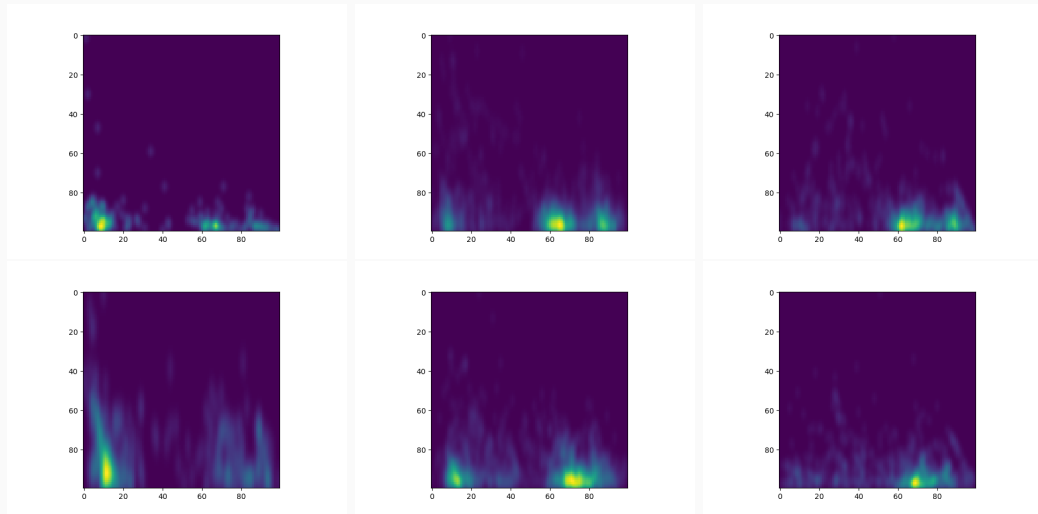
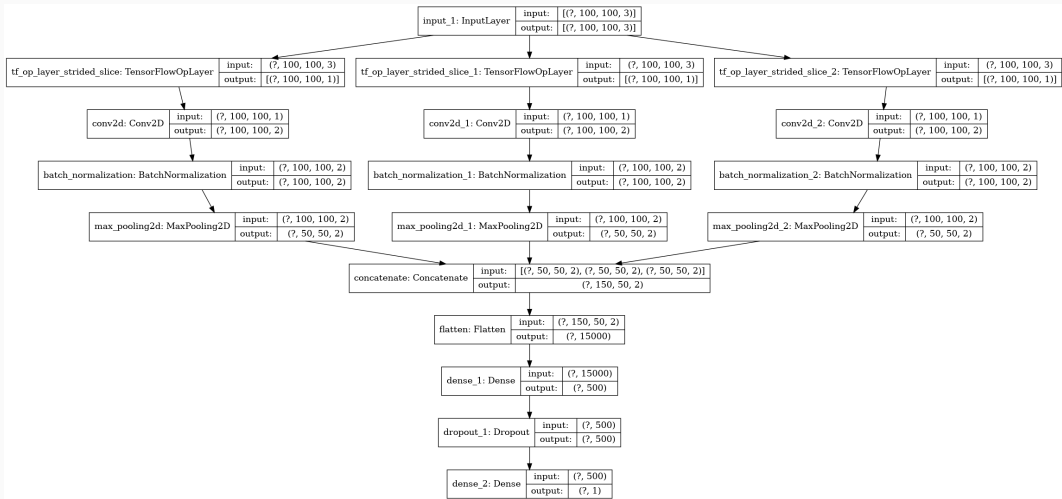


Figure 6: Columns: hom. dimension (0,1,2); Row: Diagnostic category (CN top, AD bottom).

I - Diagnosis prediction - Network architecture



I - Diagnosis prediction - Performance

Performance metric	Model trained on PIs from patches
Training accuracy	0.81 ± 0.01
Validation accuracy	0.78 ± 0.03
Precision	0.81 ± 0.04
Recall	0.77 ± 0.03
AUC	0.85 ± 0.03

Table 1: Performance metrics of the model.

→ using a normal CPU, training takes 1 minute!

II - Distance analysis

Question: How topologically heterogenous is the data?

- Compute a persistence landscape (allows for statistical analysis)
- Compute a median persistence landscape with one layer for each category (CN, MCI, AD)
- Compute L^1 norm from median landscape for each image within category

II - Distance analysis

Average persistence landscape.

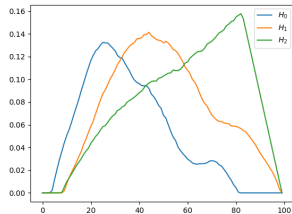


Figure 7: CN

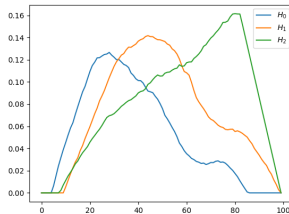


Figure 8: MCI

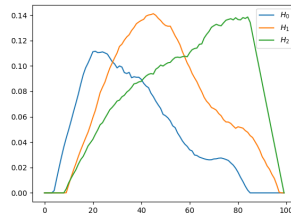


Figure 9: AD

II - Distance analysis

Question: How topologically heterogenous is the data?

	Mean	Median	Standard deviation	Q3	Max	Skewness
CN H_0	2.16	2.00	0.78	2.50	7.41	1.78
CN H_1	2.61	2.27	1.17	2.93	9.47	1.92
CN H_2	2.38	2.23	0.88	2.79	7.19	1.39
MCI H_0	2.24	2.04	0.82	2.55	6.21	1.71
MCI H_1	2.57	2.19	1.29	2.80	11.87	2.57
MCI H_2	2.40	2.27	0.83	2.82	6.55	1.18
AD H_0	2.40	2.18	0.96	2.77	7.77	1.97
AD H_1	2.47	2.13	1.15	2.77	9.28	2.10
AD H_2	2.36	2.20	0.80	2.75	8.39	1.64

Table 2: Summary statistics of the distribution of distances

III - Distance analysis - outline

Question: Among the patients who deteriorate, do we see higher average pairwise distances compared to patients who don't deteriorate?

- The data is a longitudinal dataset (multiple timepoints are available for each patient)
- Some patients deteriorate (transition from CN→MCI or from MCI→AD)
- Compute pairwise distance between patients (L^1 PL distance, Wasserstein distance and bottleneck distance), and average for each patient.

III - Distance analysis - examples

Example of L^1 norm between PLs of a deteriorating patient.

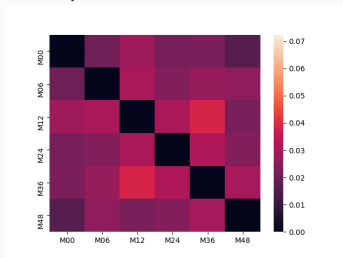


Figure 10: H_0

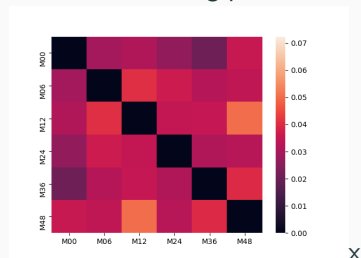


Figure 11: H_1

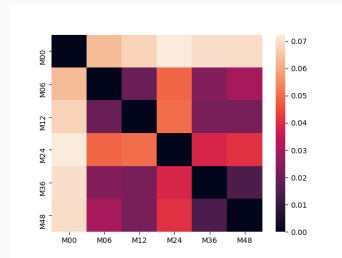


Figure 12: H_2

III - Distance analysis - further examples

Example of L^1 norm between PLs of a subject who does *not* deteriorate.

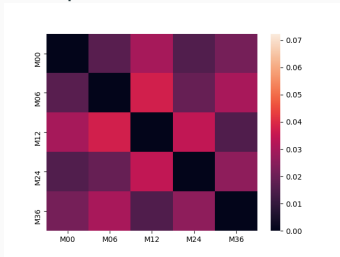


Figure 13: H_0

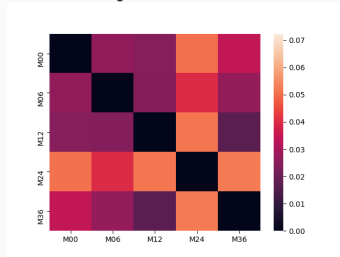


Figure 14: H_1

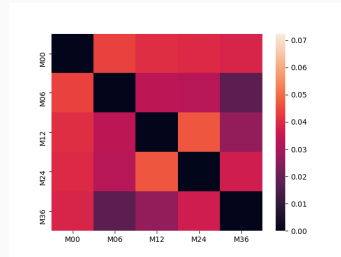


Figure 15: H_2

III - Distance analysis - population-level results

Persistence landscape L^1 norm

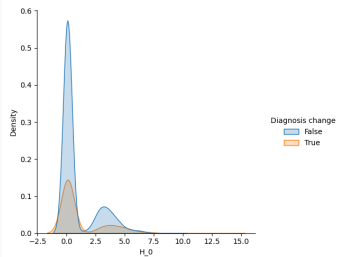


Figure 16: H_0

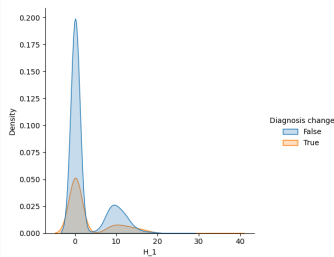


Figure 17: H_1

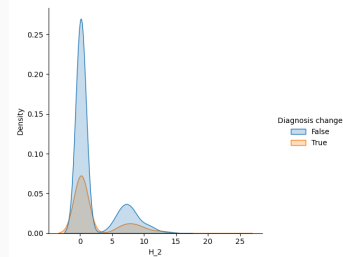


Figure 18: H_2

III - Distance analysis - population-level results

Bottleneck L^1 norm

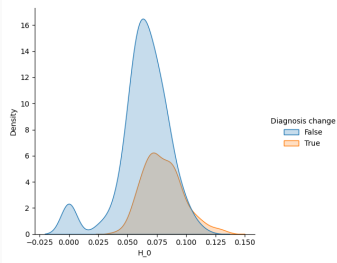


Figure 19: H_0

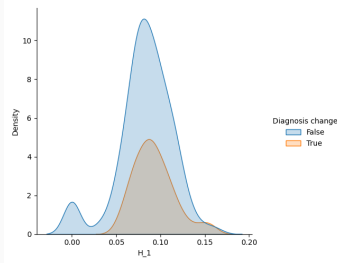


Figure 20: H_1

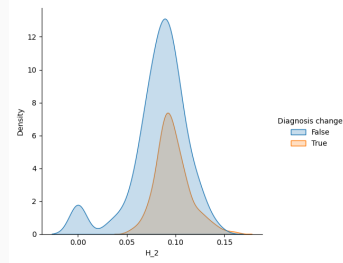


Figure 21: H_2

III - Distance analysis - population-level results

Wasserstein distance

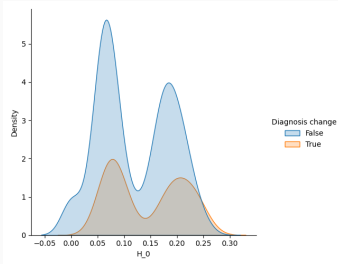


Figure 22: H_0

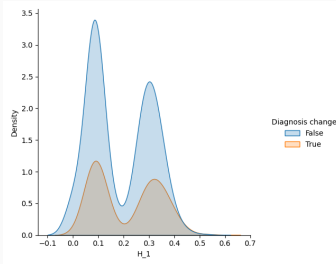


Figure 23: H_1

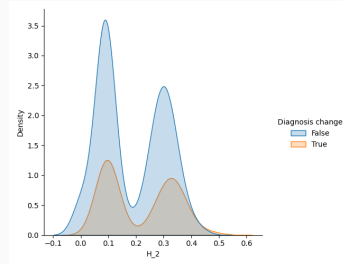


Figure 24: H_2

Limitations & Outlook

1. Diagnosis

- Performance can be enhanced by taking local features from other patches and passing them through convolutions. Especially useful when dealing with subtypes of Alzheimer's which show atrophy in other, larger brain regions.
- Neural architecture could be made a little deeper with additional convolutions, but was not the sole aim of the lab rotation
- Problem could also be made more useful (and challenging) by looking at diagnosing prodromal forms of AD.

2. Distances

- In general, very *coarse* analysis (does not pick out subtypes or use individual features to differentiate between images), sensitive to noise.
- Deep image clustering could be applied for subtype identification & better heterogeneity investigation.
- Could learn better (topology-based) embeddings to better distinguish between people who progress versus those who do not.