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

Philip Hartout

November 24, 2020

Alzheimer’s disease

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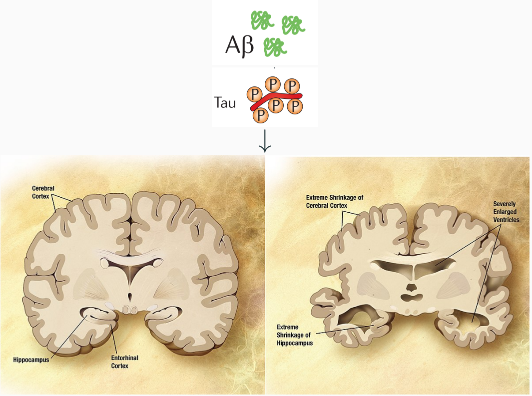

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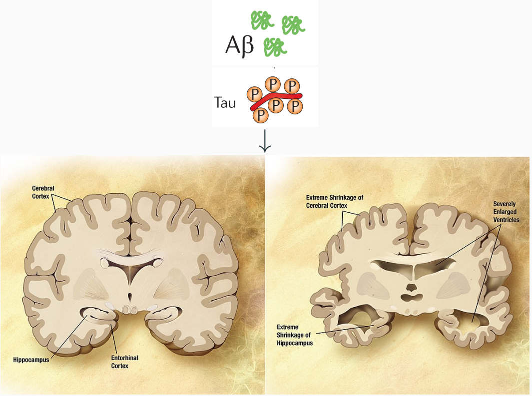

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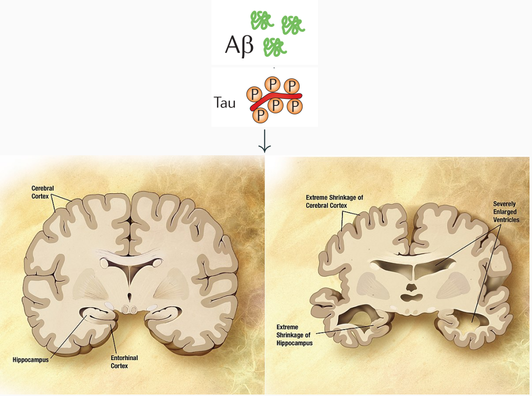

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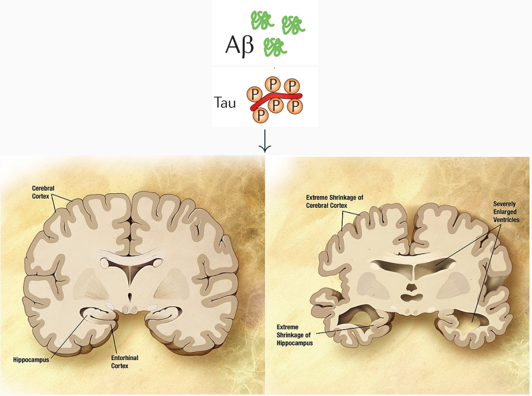

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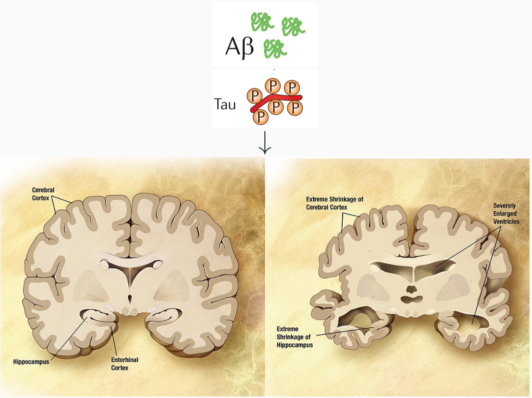

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- Recently, *persistent homology* has emerged to quantify (differences in) the shape of data.
- **How can we apply persistent homology to quantify changes in shape due to Alzheimer's disease?**

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$\rightarrow$ Some findings in these directions will be presented today

Analysis setting

Raw T1-weighted sMRI

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Raw T1-weighted sMRI → *fMRIprep*

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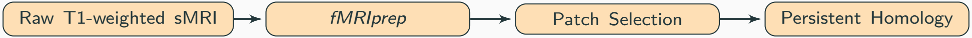
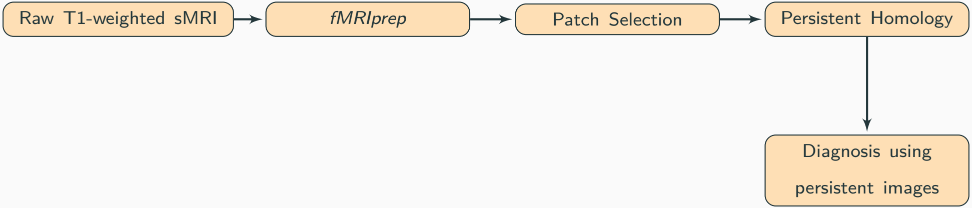
Raw T1-weighted sMRI → *fMRIprep* → Patch Selection

Analysis setting



Analysis setting



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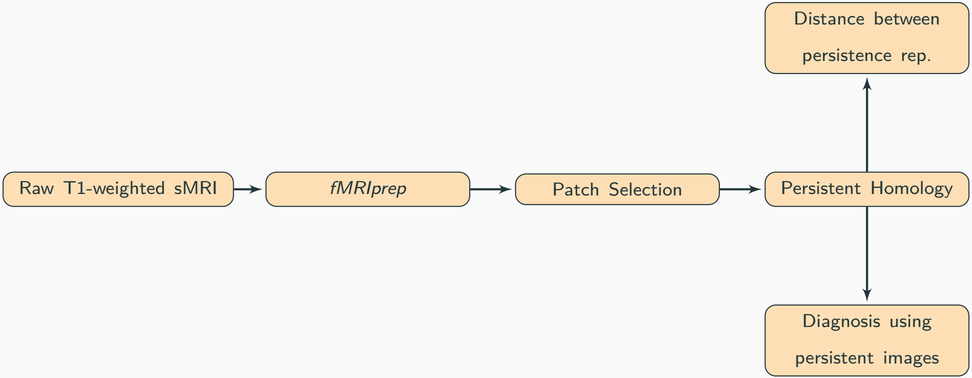

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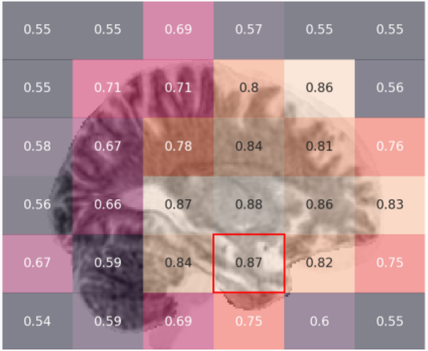

Figure 2: AUCPRC on each patch, achieved using a model described in earlier work. Chosen patch for analyses is boxed in red (patch with highest accuracy).

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- Use same partition as NeurIPS submission, train ANN 3 times on each partition

I - Persistent homology

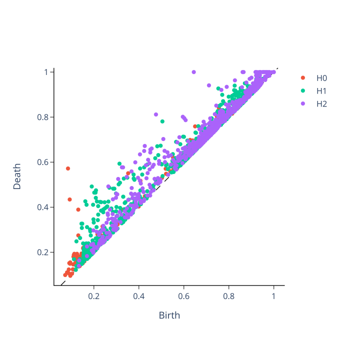


Figure 3: CN

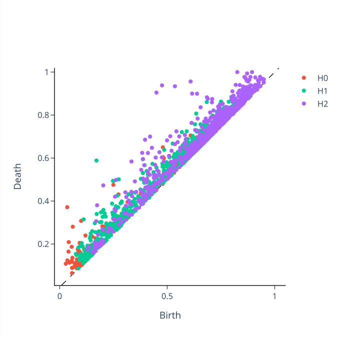


Figure 4: MCI

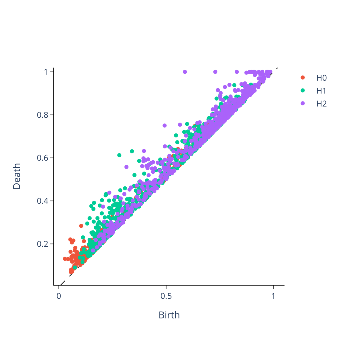
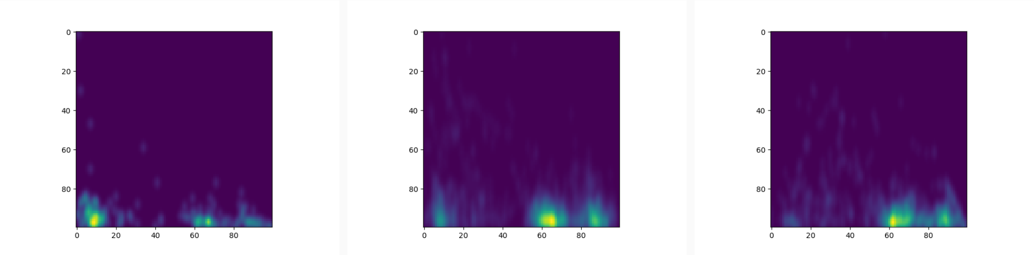


Figure 5: AD

I - Diagnosis prediction - Persistence Images



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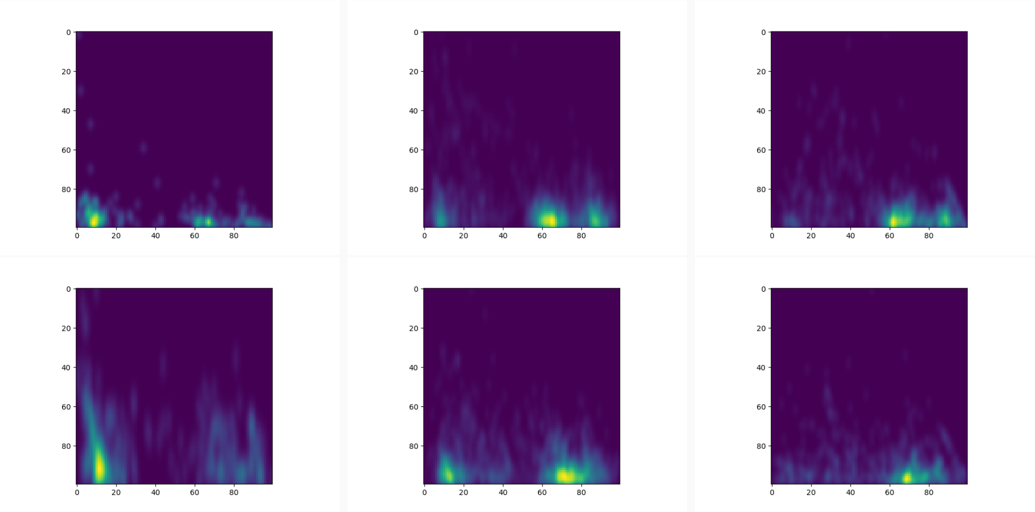
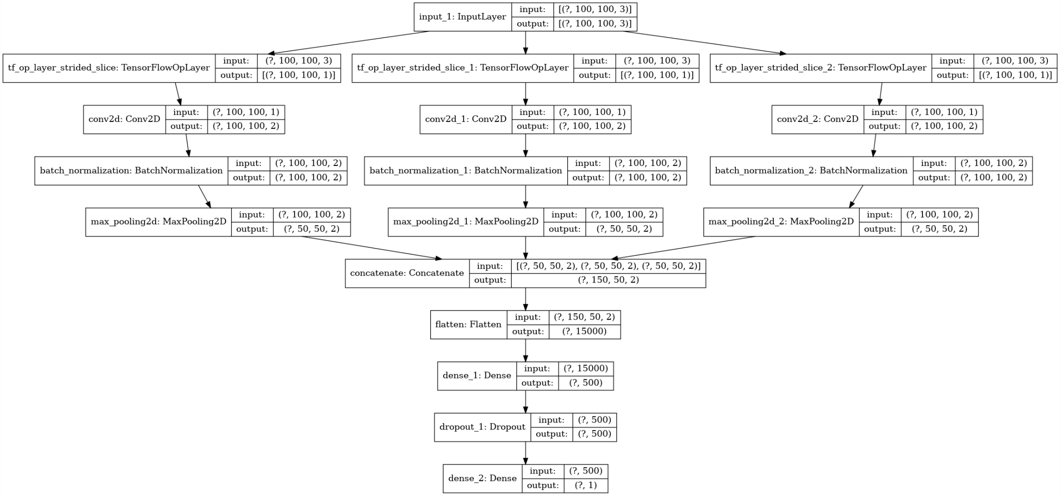


Figure 6: Columns: hom. dimension (0,1,2); Row: Diagnostic category (CN top, AD bottom).

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

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$\rightarrow$ using a normal CPU, training takes 1 minute!

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- 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

Median persistence landscape.

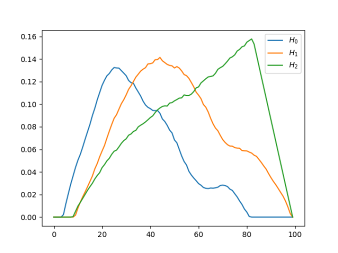

Figure 7: CN

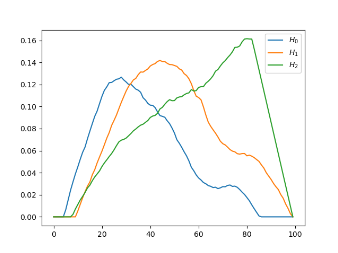

Figure 8: MCI

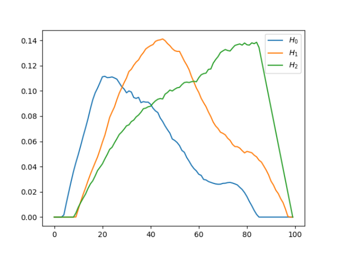

Figure 9: AD

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	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

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

III - Distance analysis among patients who deteriorate vs. those who don't

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

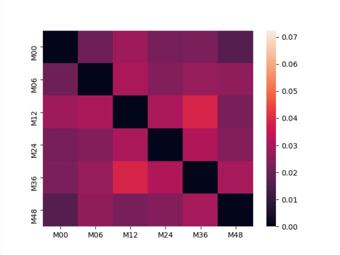

Figure 10: H_0

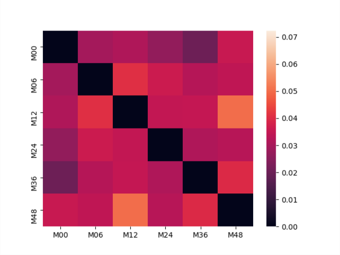

Figure 11: H_1

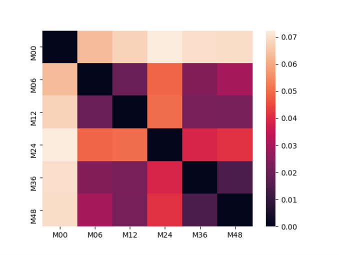

Figure 12: H_2

III - Distance analysis among patients who deteriorate vs. those who don't

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

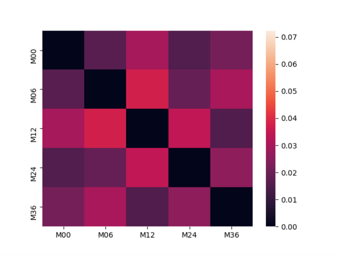

Figure 13: H_0

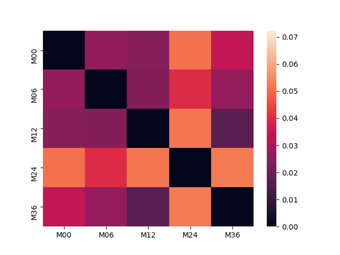

Figure 14: H_1

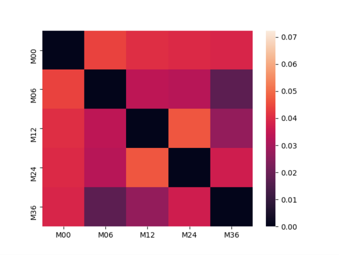

Figure 15: H_2

III - Distance analysis among patients who deteriorate vs. those who don't

Persistence landscape L^1 norm

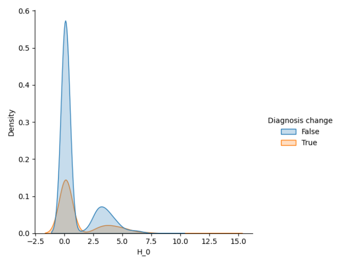

Figure 16: H_0

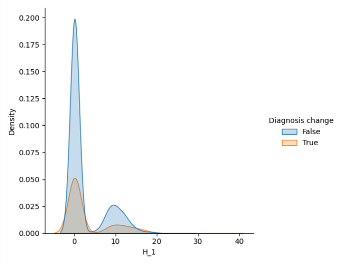

Figure 17: H_1

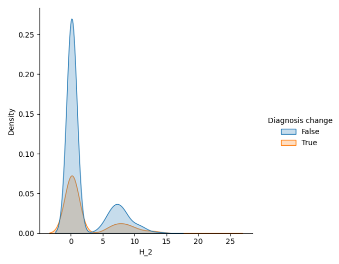

Figure 18: H_2

III - Distance analysis among patients who deteriorate vs. those who don't

Bottleneck L^1 norm

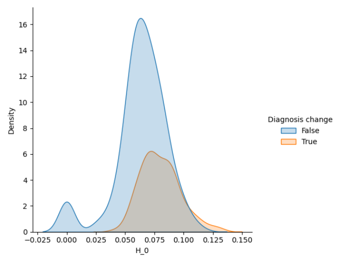

Figure 19: H_0

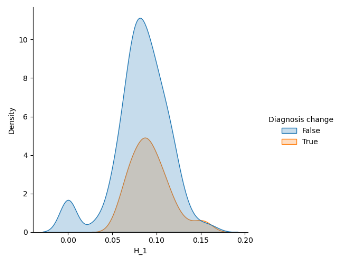

Figure 20: H_1

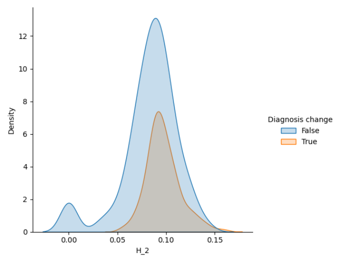

Figure 21: H_2

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Wasserstein distance

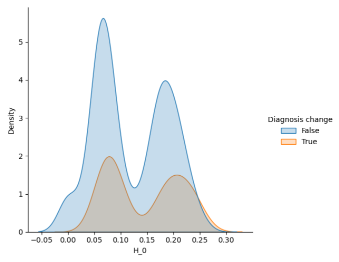

Figure 22: H_0

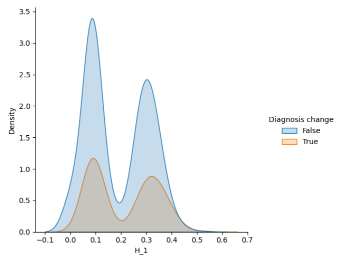

Figure 23: H_1

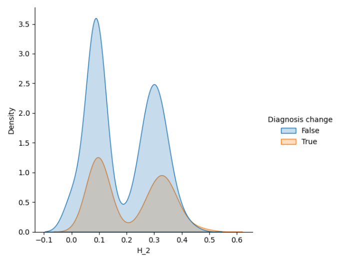

Figure 24: H_2

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2. Distances
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   - Could learn better (topology-based) embeddings to better distinguish between people who progress versus those who do not and more finegrained subtype identification resilient noise.

Summary

GitHub repository of the project

`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.

Questions?