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

Philip Hartout

November 26, 2020

Alzheimer's disease

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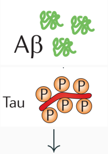

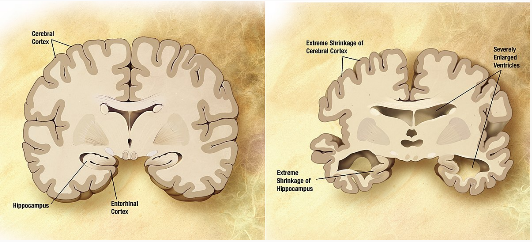

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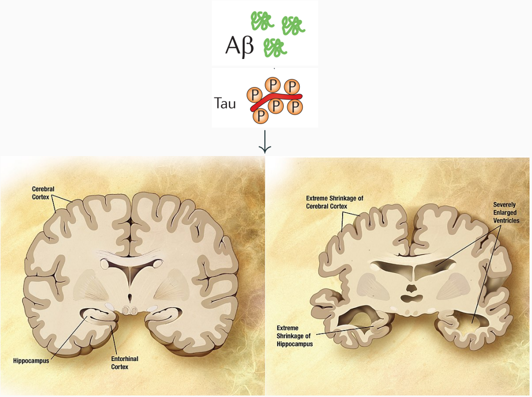

Topology: 🍩 ☕

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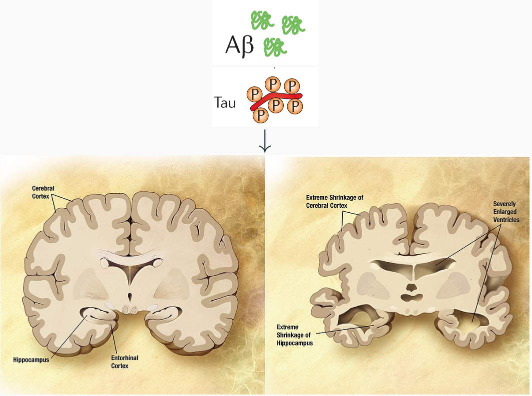

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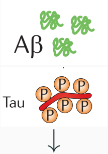

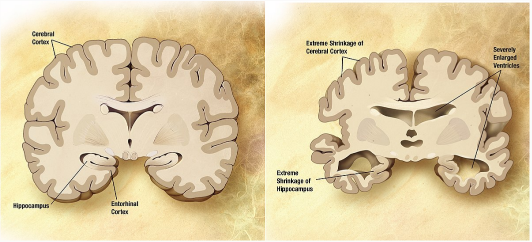

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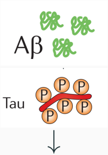

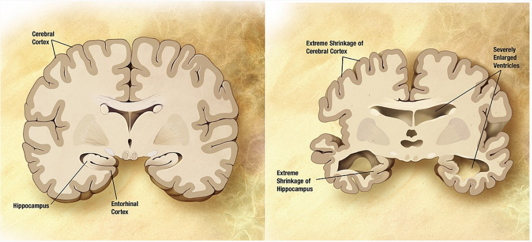

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- Recently, *persistent homology* has emerged to quantify (differences in) the shape of data.
- **How can we apply persistent homology to quantify changes in shape due to Alzheimer's disease?**

Topology in AD - Research Avenues 🧭

1. **Classification**

Topology in AD - Research Avenues

1. **Classification**
2. Subtype identification

Topology in AD - Research Avenues

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

Analysis setting

Unprocessed

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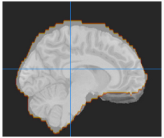

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Analysis setting

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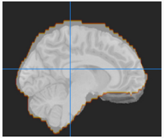

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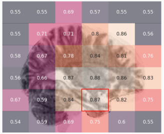

Patch selection

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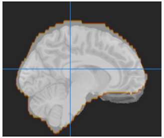

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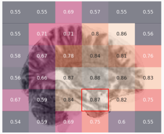

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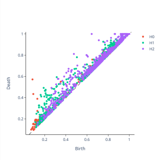

Persistence homology

Analysis setting

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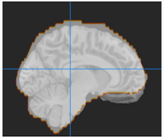

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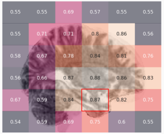

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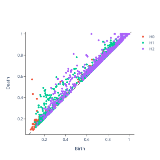

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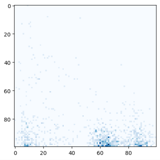
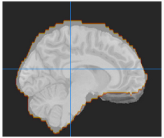


Persistence Image

Analysis setting

Unprocessed



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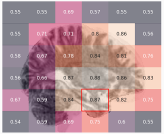

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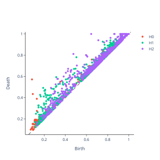

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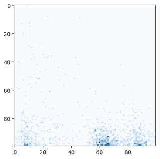

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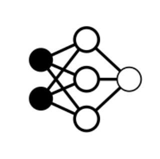

Classification

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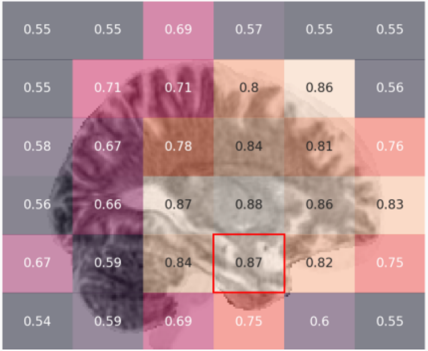


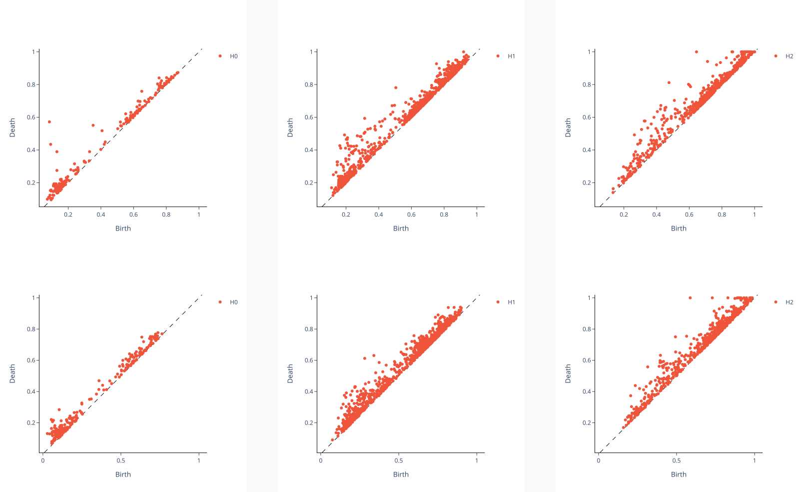
Figure 2: AUPRC on each patch, achieved using a model described in earlier work. Chosen patch for analyses is boxed in red (patch with highest accuracy).

I - Persistent homology

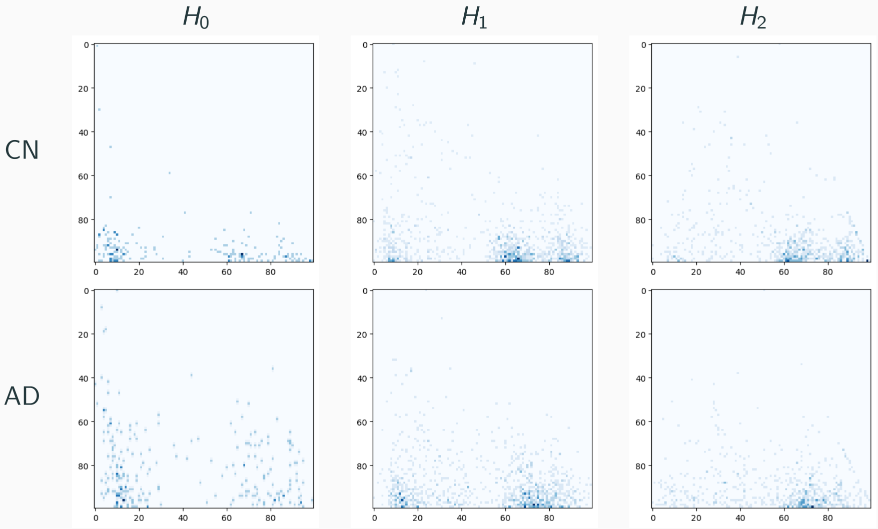
H_0 H_1 H_2

CN

AD



I - Classification - Persistence Images



I - Classification - Network architecture

Persistence image (H_0, H_1, H_2)

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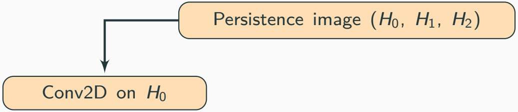

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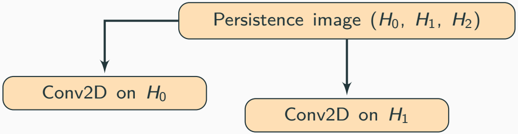

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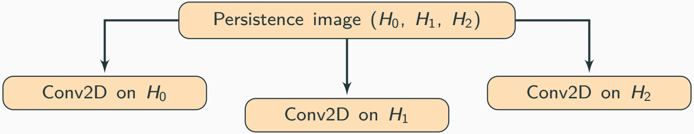

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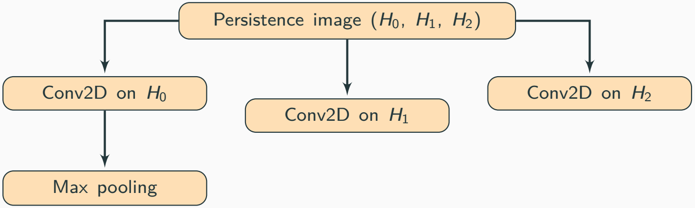

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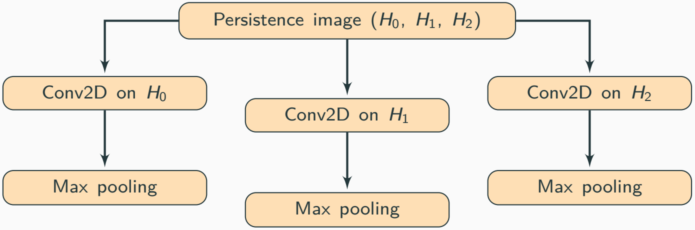

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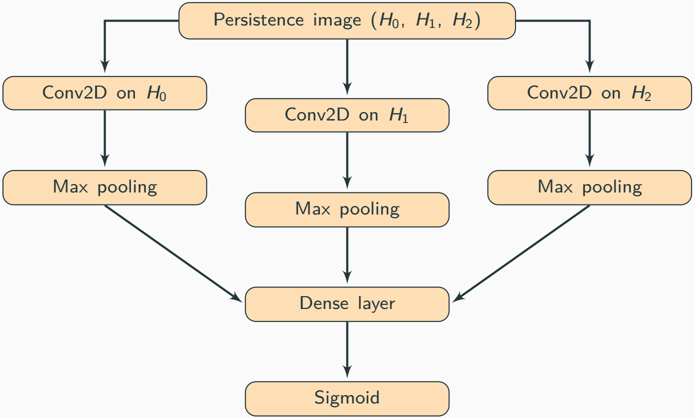

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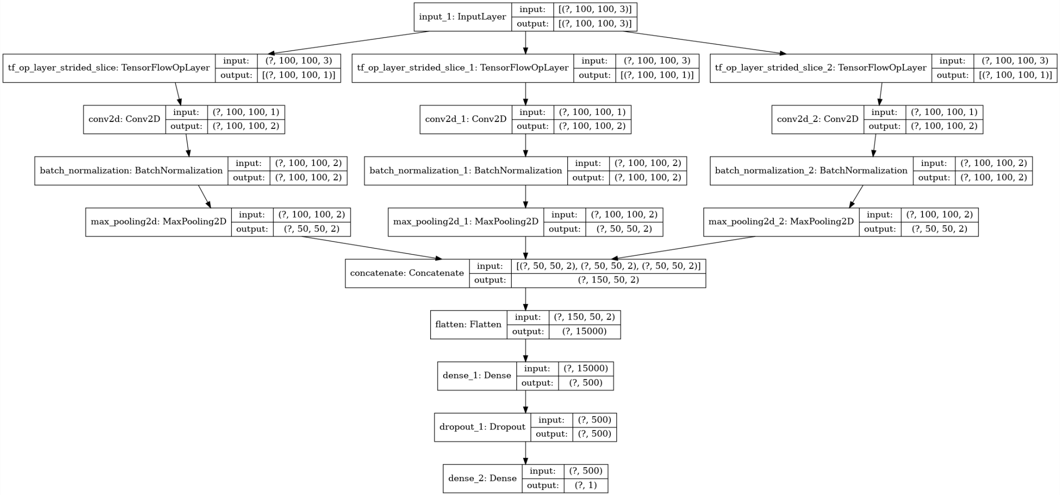

Methodological considerations

- 4 fold CV, 3 inits. Stratified for age, diagnoses and no patients are spread over folds.
- Same experimental settings as from 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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Future directions:

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

Thanks!

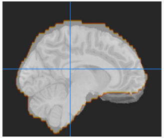
GitHub repository of the project

`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?

Unprocessed



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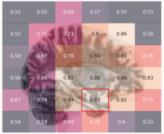

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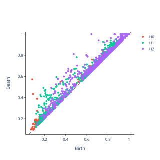
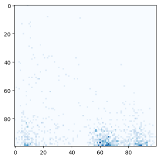
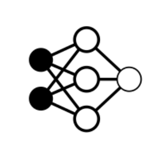


Persistence homology



Persistence Image



Classification

Backup slides

II - Distance analysis among patients in CN, MCI & AD

Median persistence landscape.

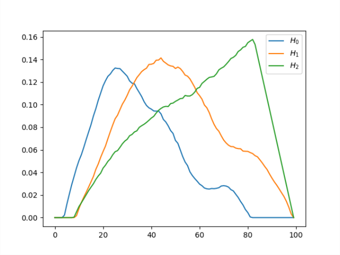


Figure 3: CN

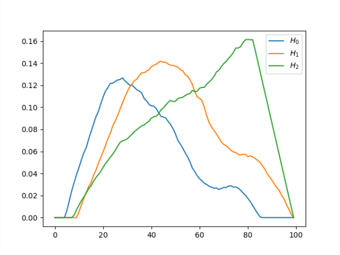


Figure 4: MCI

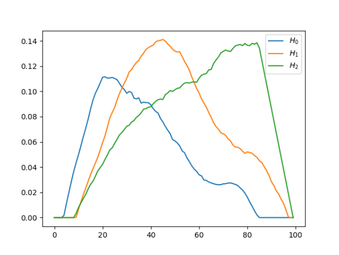


Figure 5: AD

II - Distance analysis among patients in CN, MCI & AD

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 among patients who deteriorate vs. those who don't

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

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- 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 among patients who deteriorate vs. those who don't

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

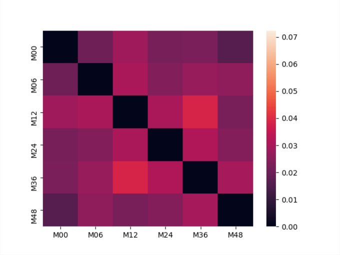

Figure 6: H_0

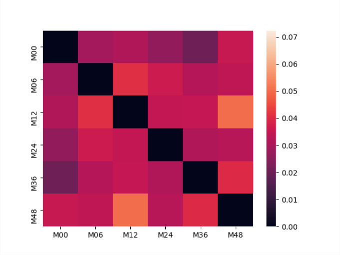

Figure 7: H_1

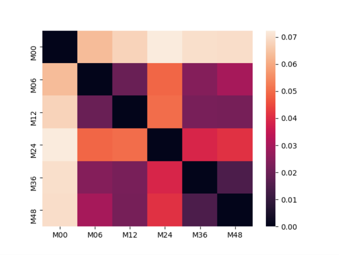

Figure 8: H_2

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

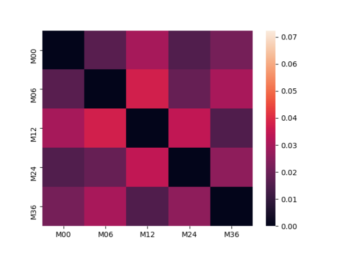

Figure 9: H_0

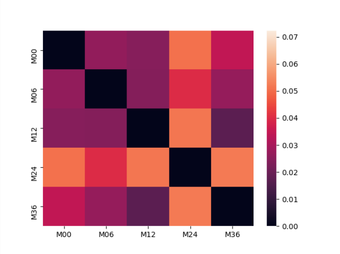

Figure 10: H_1

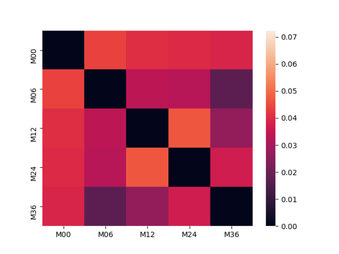

Figure 11: H_2

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

Persistence landscape L^1 norm

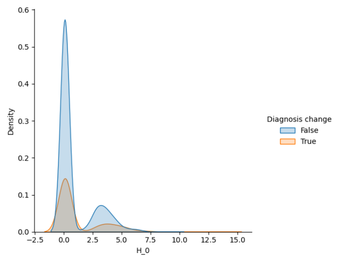

Figure 12: H_0

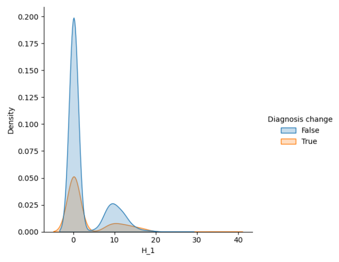

Figure 13: H_1

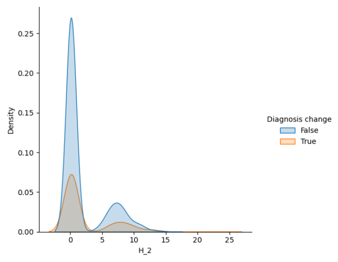

Figure 14: H_2

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

Bottleneck L^1 norm

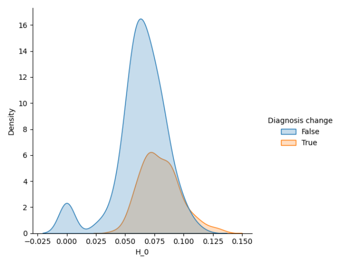

Figure 15: H_0

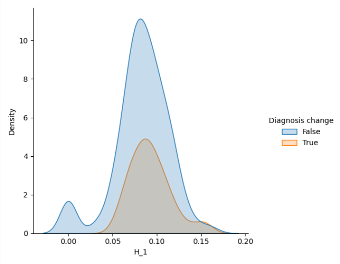

Figure 16: H_1

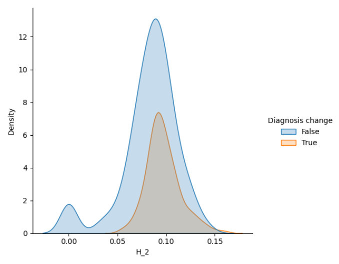

Figure 17: H_2

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

Wasserstein distance

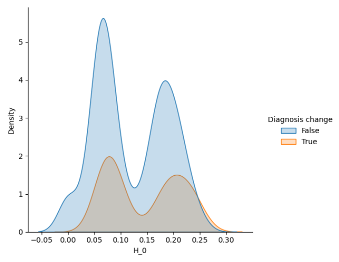

Figure 18: H_0

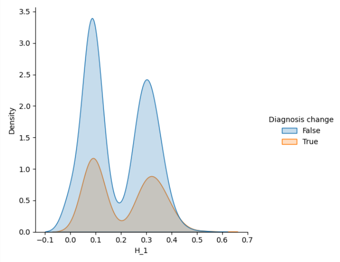

Figure 19: H_1

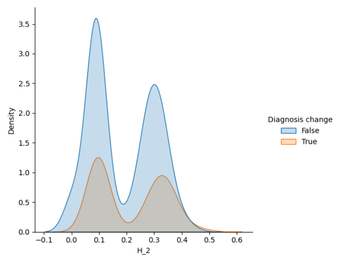

Figure 20: H_2