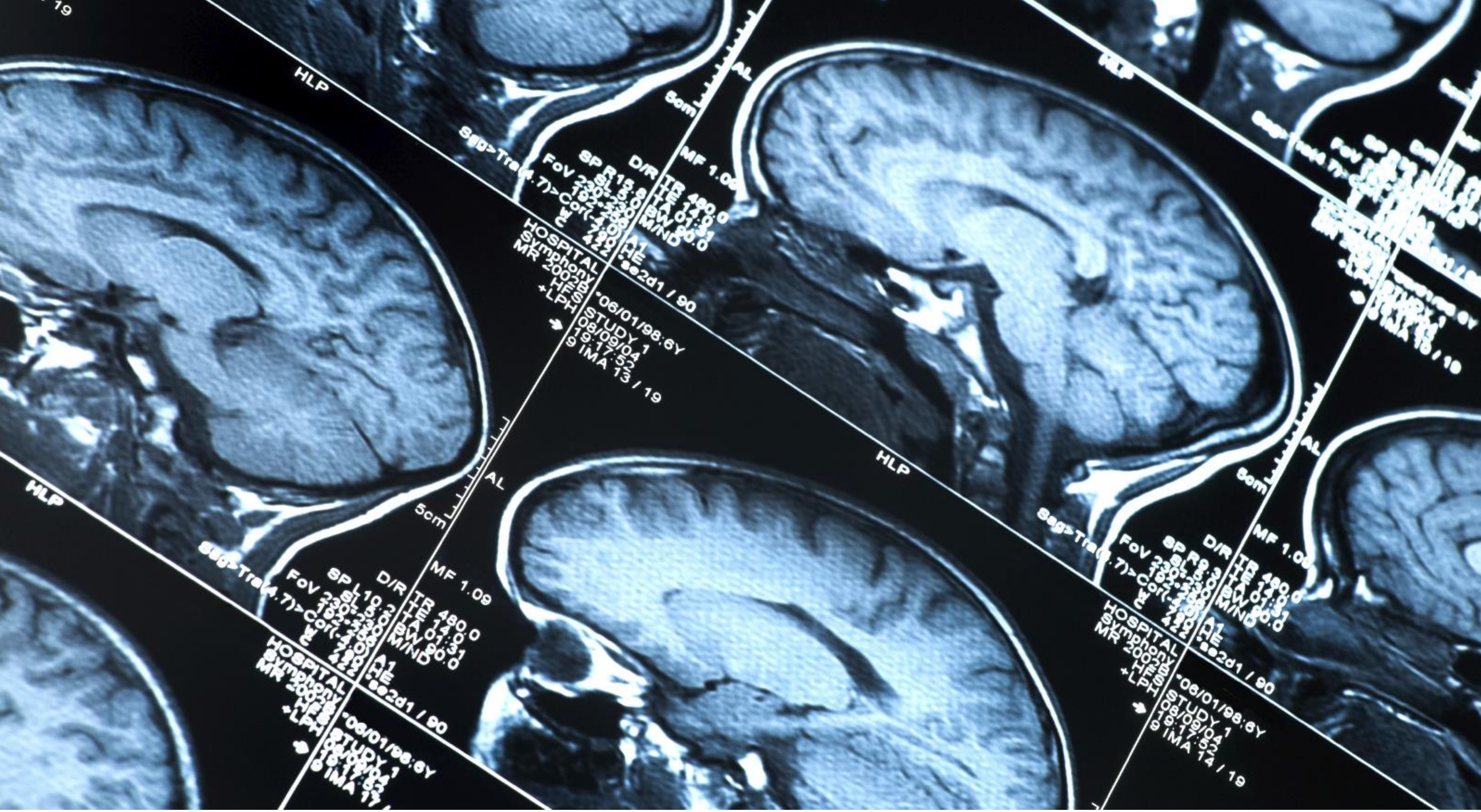


End-Term Presentation

Supervisors: Susanne Dandl, Florian Pfisterer, Giuseppe Casalicchio
Referees: Jana Gauss, Leo Schaabner, Kai Becker, Jonas Klingele, Katharina Brenner

Munich, 17. Mar 2022

TEAM Connectome
Innolab 2021

Agenda

1. Introduction

10,935,444

people are estimated to have dementia in Europe [1]

~£25 billion a year

cost of dementia to the economy in UK [2]

1 in 2

People in the UK know someone with dementia [3]

6x

more research expenses in UK on cancer than dementia research [3]

Source: [1] Alzheimer Europe.org, [2] Wittenberg et al (2019), [3] AlzheimerresearchUK.org

Use and potential benefits of our final product

With connectome, millions of elderly people could delay the progress of alzheimer disease

10.9
MILLION

Alzheimer Patients

There are estimated to be more than 10.9 million alzheimer disease patients in Europe [1].

Every
3
SEC

New Cases

A new person develops symptoms of alzheimer disease worldwide [2], thereby, alzheimer is the most widespread form of dementia.

$175
THOUSAND

High costs

Total annual costs per Alzheimer disease patient can be up to $175,000 per year (2010)!

Source: [1] Alzheimer Europe.org, [2] https://www.alzint.org/about/dementia-facts-figures/, [3] Costs of Alzheimer's to Medicare and Medicaid

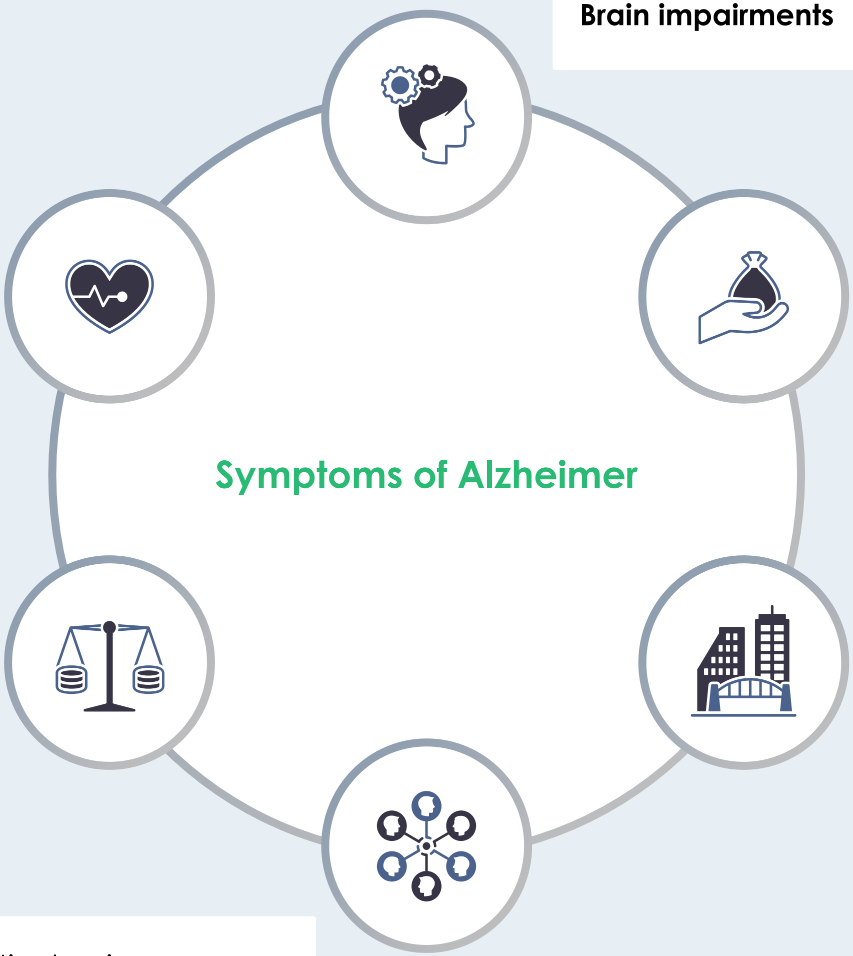
Alzheimer Patients suffer severe brain impairments

Alzheimer's disease is the most common cause of dementia — a continuous decline in thinking, behavioural and social skills that affects a person's ability to function independently

Severe Memory Losses & **Brain impairments**

Changes in personality and behavior: Depression, social withdrawel, irritability and aggressiveness

Decline in the ability to make **reasonable decisions** and judgments



Risk factors: Age, Alcohol, poor sleeping habits, genetics, lifelong learning and social engagement, lifestyle and more

Once-routine activities that require sequential steps, such as planning and cooking a meal, become a struggle

Difficulties having a conversation (due to **memory and language loss**)

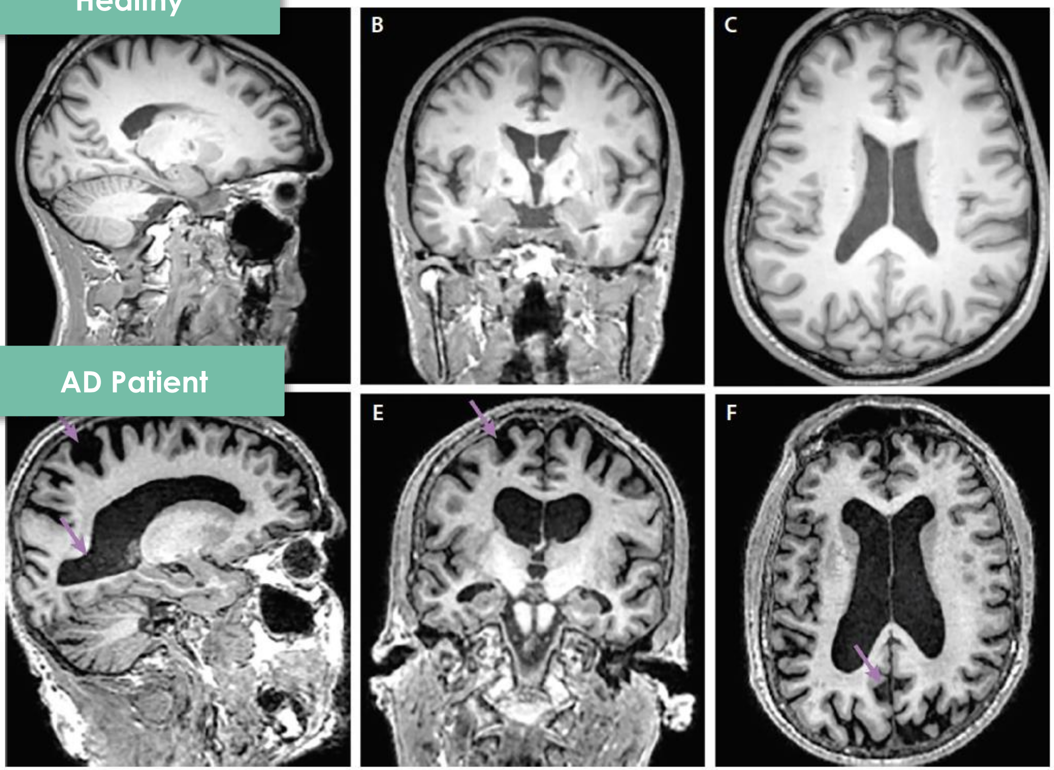
Source: Mayoclinic.org, Alzheimer Europe.org

Alzheimer Disease causes atrophy and neural connectivity loss

Alzheimer's disease is a progressive neurologic disorder that causes the brain to shrink (atrophy) and brain cells to die

Healthy

AD Patient



Typical cortical volume of healthy individual (top row) compared with advanced Alzheimer's disease (AD)

Alzheimer Disease

Atrophy

Progressive degeneration or shrinkage of muscle or nerve tissue

Loss in Connectivity

Loss of synaptical relations between brain areas (Regions of interest, ROIs)

Presentation of our project partner – Dr. Boris Rauchmann

LMU LUDWIG-MAXIMILIANS-UNIVERSITÄT MÜNCHEN

LMU KLINIKUM DER UNIVERSITÄT MÜNCHEN

Boris-Stephan **Rauchmann**
LMU Munich
Verified email at med.uni-muenchen.de
Cited by 620

Education

Ludwig-Maximilians-Universität München
Staatsexamen, Medizin
2016

Harvard University
Medicine
2013

Previous research

Focus of research on Imaging biomarkers in psychiatric disorders

2022 Paper

MRI connectivity-based spread of microglial activation in early Alzheimer's disease

Source: Rauchmann et al (2022), Picture: https://www.linkedin.com/in/dr-boris-rauchmann-9869b5b5/?originalSubdomain=de

Identifying Alzheimer early is key to improve the disease progress

Identify the Alzheimer status of a patient with the results of Connectome!

Source: https://www.northampton.ac.uk/news/older-people-asked-to-get-physical-for-research-to-help-people-after-a-fall/

2. Goal & Results

Goal & Results

Delcode data

Goal	• Prediction & explanation of Alzheimer Diagnosis based on connectivity matrices

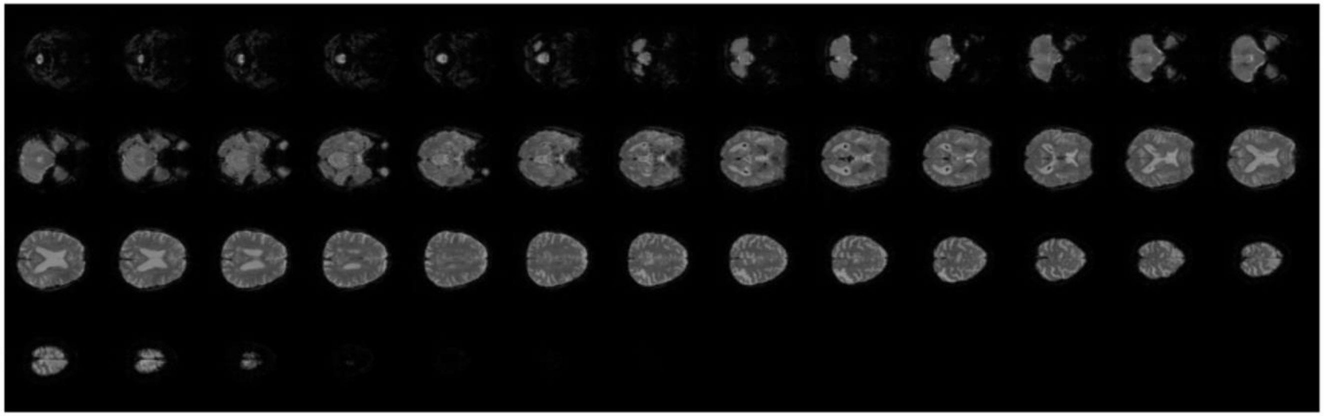
Results	• Pipeline:
	  • automation of training, evaluation and interpretation
	  • for several models
	  • for several dataset options, e.g. aggregation

3. Database

Base Data

fMRI Scans

Raw data for each subject coming from fMRI scans in compressed NIFTI format (time series of slices of the brain)



Excel sheet

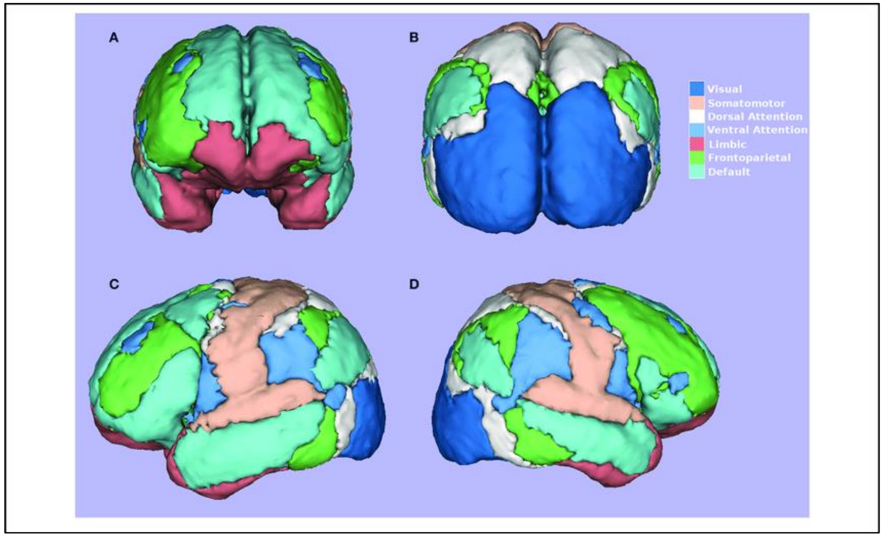
Excel sheet with additional information about the subjects

	A	B	C	D	E	F	G	H	I	J
1	ConnID	Repseudonym	siteid	age	visdat	sex	prmdiag	edyears	MEM_scor	Apoe
2	1	0a8d02f2b	11	66	17.08.2016	0	2	17	0,054016	0
3	2	0a71a953d	17	72	30.03.2015	0	1	20	-0,468749	1
4	3	0a61339db	11	72	13.05.2015	1	1	16	-0,093521	0
5	4	0b28aed58	17	76	18.01.2016	0	1	20	0,466027	0
6	5	0c1c5ae77	8	64	12.03.2015	1	1	13	1,452099	0
7	6	0c8ca3f3b	2	65	06.03.2017	0	4	20	1,054216	0
8	7	0cc2d1099	11	74	10.06.2015	1	1	12	0,774303	0
9	8	0df733308	2	75	27.11.2014	1	2	12	-1,815235	0
10	9	0e3cd430b	5	73	24.09.2015	1	1	15	0,691397	0
11	10	0e27a6de5	10	71	19.11.2014	1	1	14	0,659272	0
12	11	0f1b4b7ac	11	68	26.10.2017	1	2	13	-0,583224	1

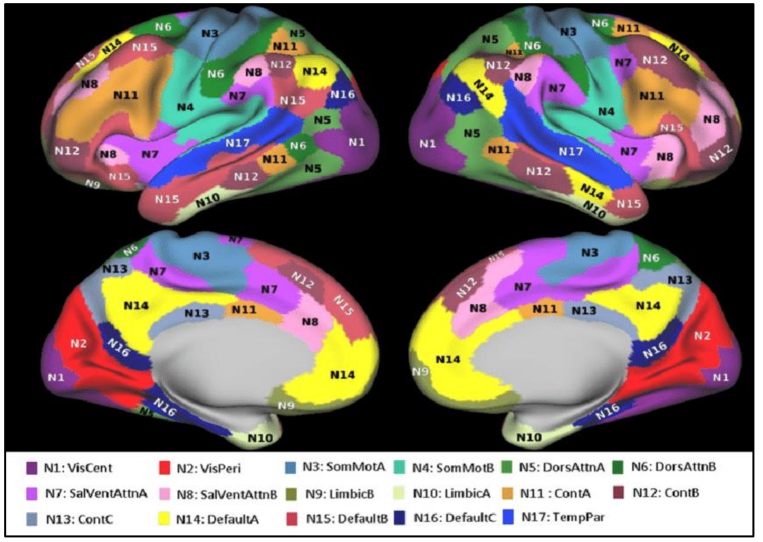
Necessary knowledge

Connectivity	Connectivity describes the relationship between two points of the brain. If one region of the brain is highly active and it correlates to another region also being highly active, the connectivity score is high.
Brain atlas	A brain atlas (for us: Brainnetome) organizes the assignment of subregions of the brain on a scan. The connectivity matrix is based on those subregions.
Network	A network combines several subregions into regions of interest (ROI). We used the Yeo7 network creating 7 well defined ROIs plus 1 out of the remaining subregions and also implemented the Yeo17 network.

Yeo7 Network



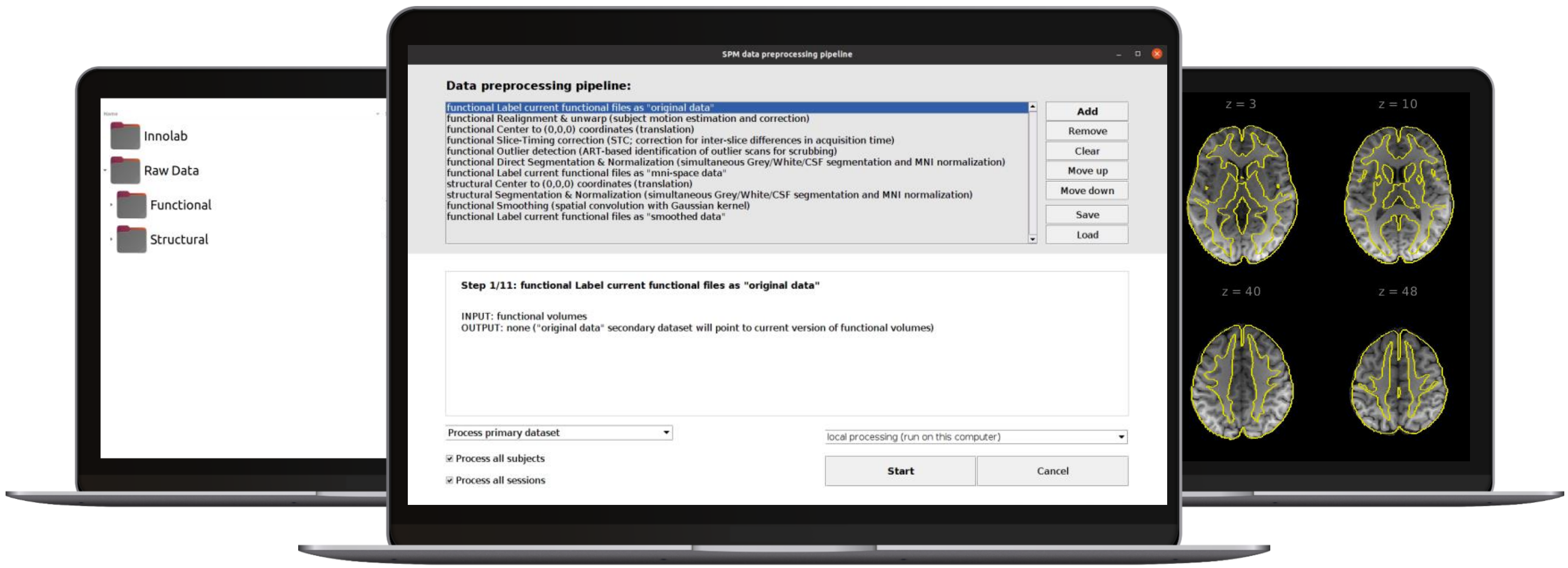
Yeo17 Network



Sources: https://www.researchgate.net/figure/Network-parcellation-of-Yeos-17-networks-The-17-networks-include-the-following-regions_fig1_352966687
https://www.researchgate.net/figure/Seven-Yeo-Networks-Yeo-et-al-2011-A-Frontal-B-Posterior-C-Left-D-Right_fig2_324361441

Data Preparation Conn

Input and data preprocessing pipeline in Conn



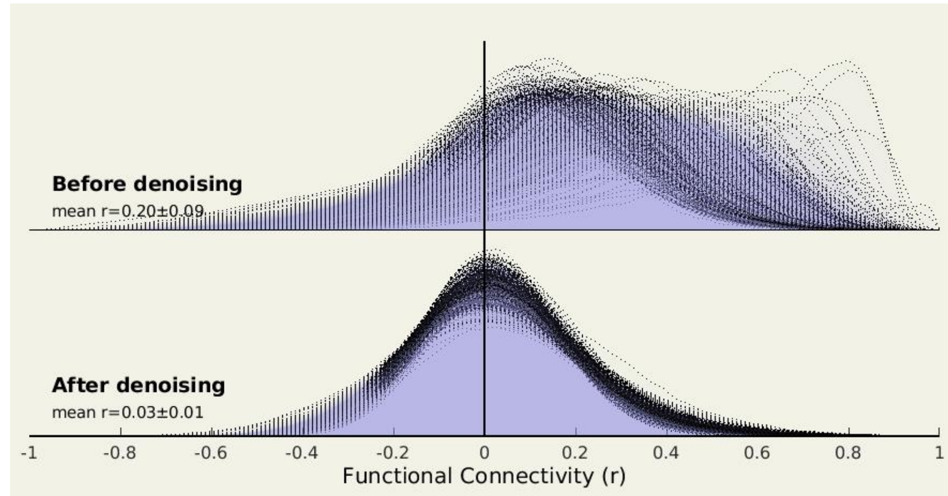
File System
Original fMRI Scans

Conn Preprocessing Pipeline

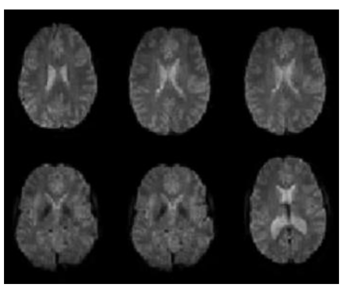
Resulting processed fMRI Scans

Data Preparation Conn

Input	Raw fMRI Scans divided in structural and functional data
Conn preprocessing	• Realignment and unwarping of scans • Slice Timing Correction • Centering and Normalization • Labeling
Conn denoising	Removal of • Physiological artifacts • Residual subject movement effects • Remaining global effects
Output	Processed fMRI Scans and subject connectivity matrizes

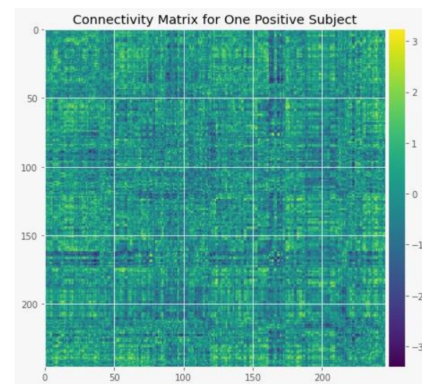


Comparison of connectivity distrubution for individual subjects before and after denoising



fMRI data

Atlas based parcellation



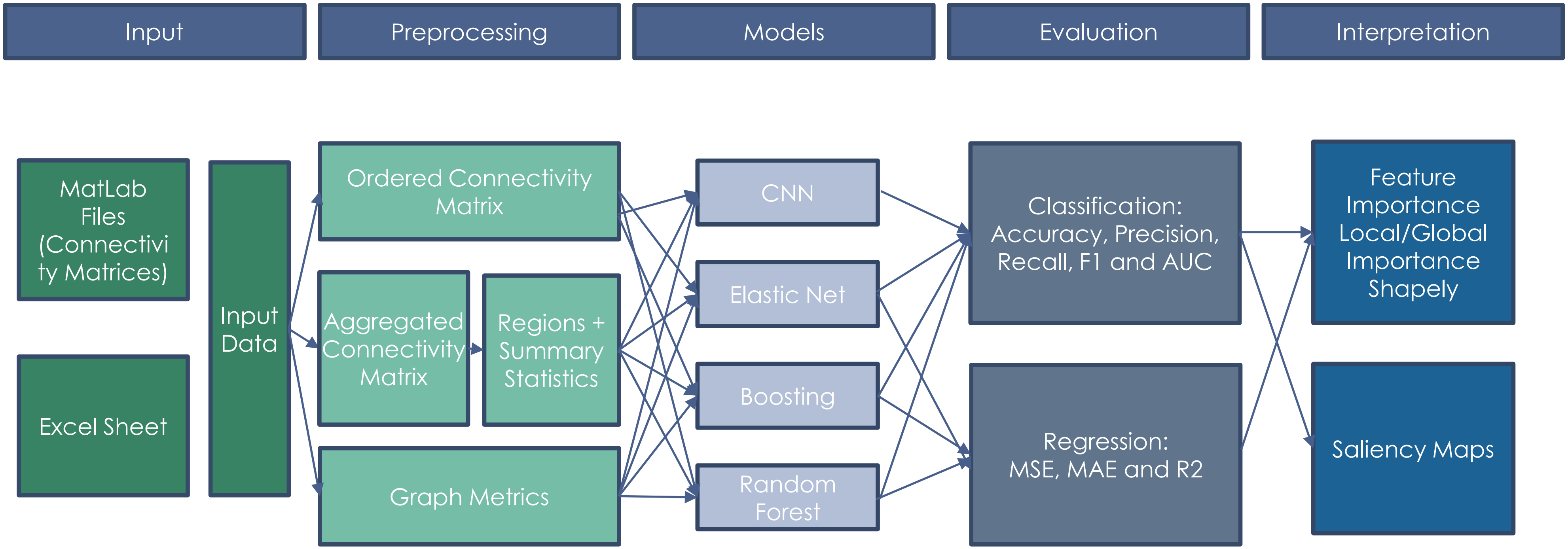
Connectivity matrix

Source parcellation image: Fan L et al. (2016). Cerebral Cortex. 26(8). 3508–3526.

4. Pipeline

Pipeline

Easy to use modular pipeline for the analysis of connectivity matrices.



5. Presentation of individual steps in the Pipeline

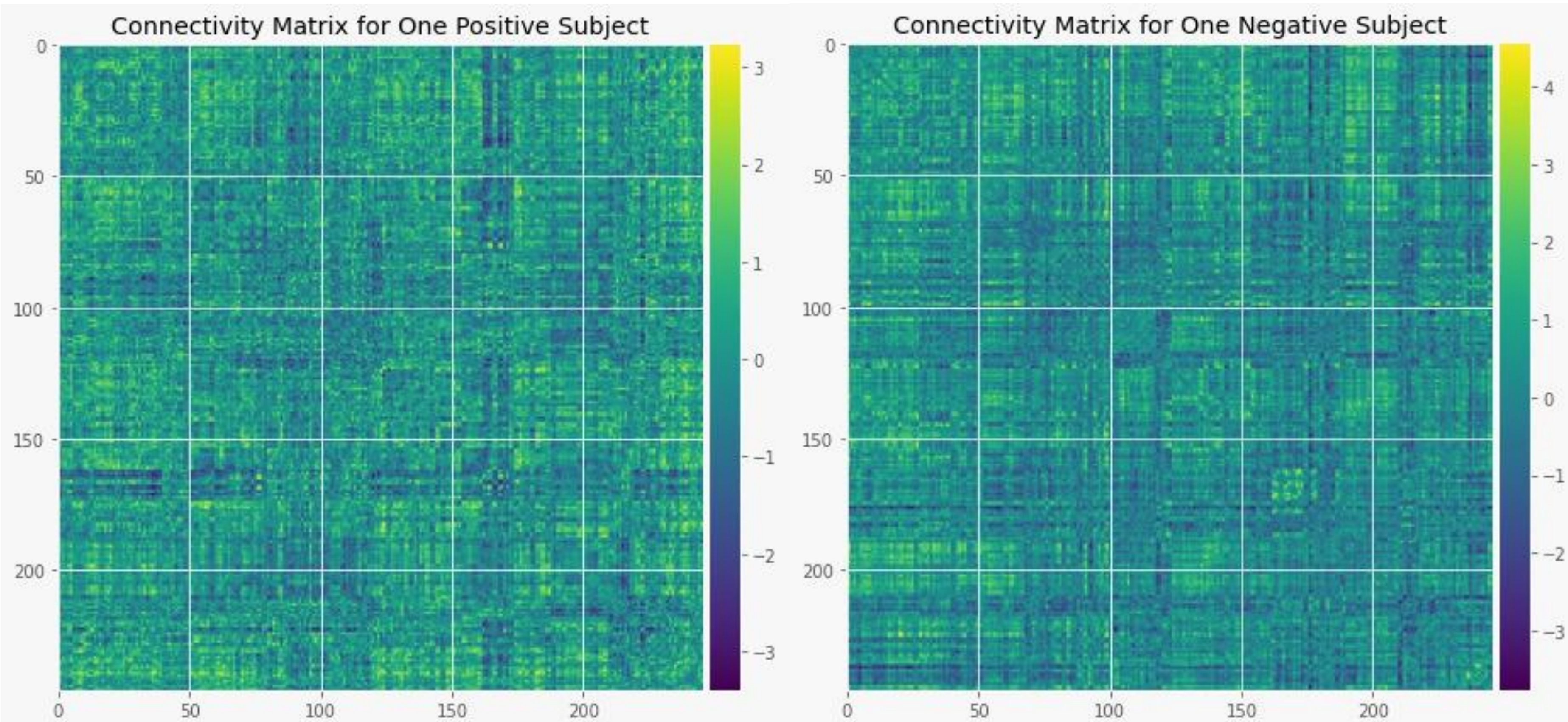
Presentation of individual steps - Input

	ConnID	Repseudonym	siteid	age	visdat	sex	prmdiag	edyears	MEM_score	Apoe	IDs	1_2	1_3	1_4	1_5	1_6
0	241	40ea07c4b	17	70	20.04.2017	0	2	13	-0.704825	1.0	241.0	1.296958	0.769522	0.619436	0.761443	0.599535
1	447	9017e3b68	13	69	22.04.2015	0	1	18	-0.070936	0.0	447.0	0.999838	0.265437	0.064838	0.273070	0.127590
2	335	196ee7b2f	18	71	01.08.2017	1	4	14	0.402379	1.0	335.0	0.895672	0.651591	0.448917	0.544044	0.334888
3	294	76e76ffd1	10	64	19.05.2015	0	4	13	0.694175	1.0	294.0	0.712479	0.144807	-0.023512	0.332856	0.361201
4	630	c9d453efd	16	78	10.07.2018	0	0	16	0.127429	1.0	630.0	0.418850	0.053622	-0.132746	0.220394	0.035202
5	80	3e330542a	11	80	14.09.2016	0	2	14	-0.393099	0.0	80.0	0.941932	0.542740	0.163409	0.396125	0.288348
6	149	6fb1f7b34	17	73	02.06.2016	0	2	19	-0.772829	0.0	149.0	1.101941	0.742916	0.739465	0.389852	0.088832
7	561	ae818e1d7	2	62	15.08.2016	1	2	12	-1.418144	1.0	561.0	0.856906	0.731896	0.516456	0.463045	0.448376

8 rows × 30146 columns

Input | Preprocessing | Models | Evaluation | Interpretation

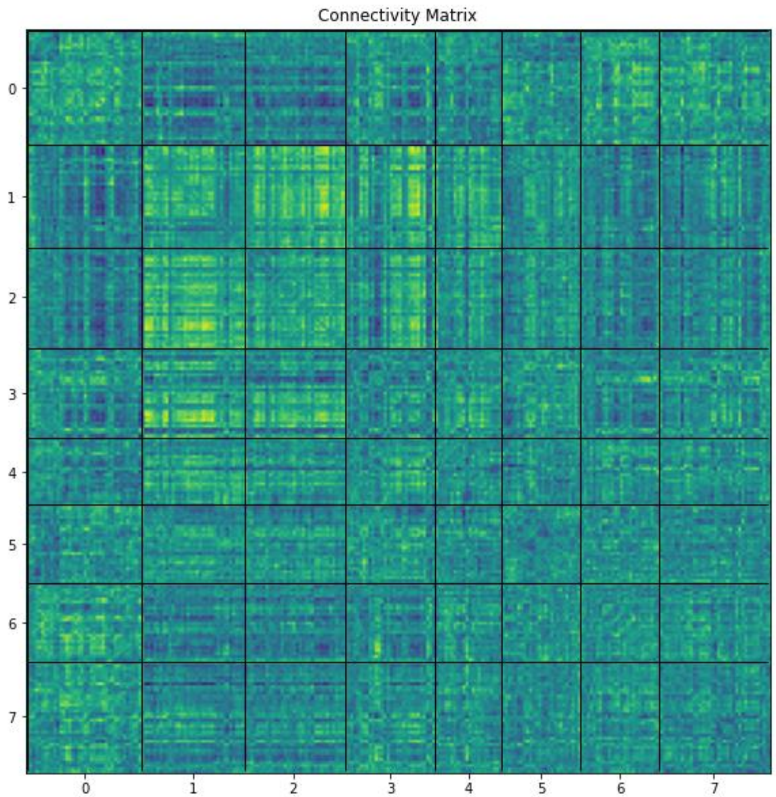
Insights | Example Pictures of Matrices after preprocessing



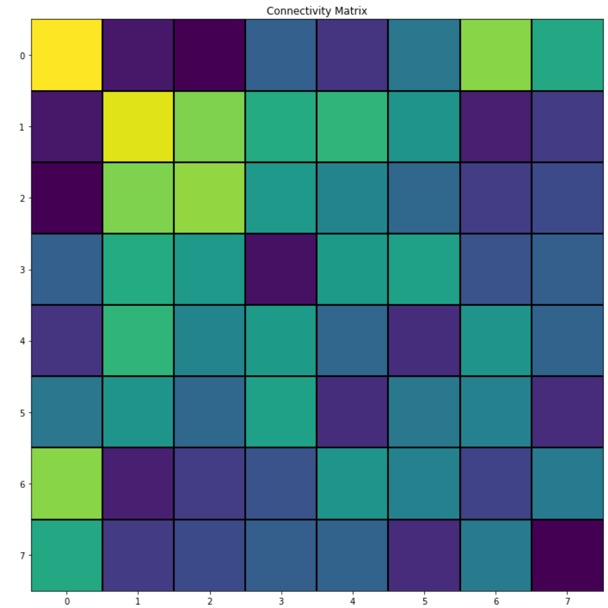
Input | Preprocessing | Models | Evaluation | Interpretation

Preprocessing – Region aggregation

Idea: Condense the information of the connectivity Matrix



Computed Summary Statistics:
- Mean
- Max
- Greater threshold c



Networks:
- Yeo7
- Yeo17

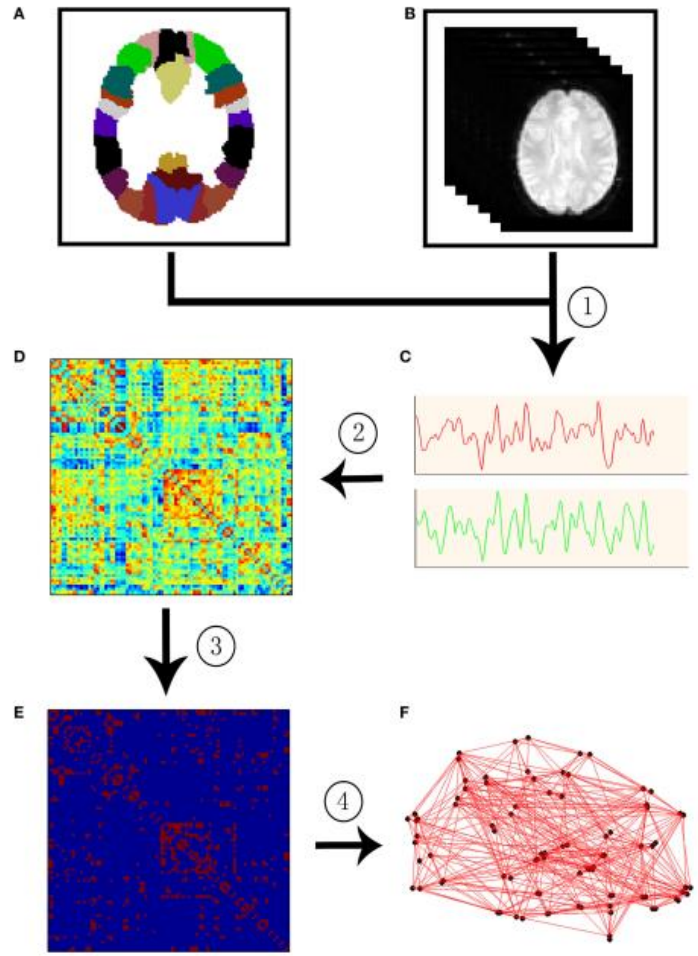
Input | Preprocessing | Models | Evaluation | Interpretation

Preprocessing – Graph Metrics

Idea: Use measures and methods from Graph Theory to analyse brain connectivity data

Procedure

1. Obtain connectivity data as described before
2. Transform connectivity matrix (D) into adjacency matrix (E) based on a threshold
3. Compute graph theoretical measures and analyse networks



Input | Preprocessing | Models | Evaluation | Interpretation

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Source: Wang et al.(2010)

Graph Metrics

Graph theory based approaches applied to human brain connectivity data

Graph Theoretical Approaches	• Natural framework for exact mathematical representations of complex networks • Networks represented as a graph by **G(N, K)** – with **N** nodes and **K** edges o **node**: brain region, **edge**: connectivity between two regions
Advantages	• Allows us to quantitatively characterise the relation and organisation of different brain regions • Possible to detect subnetworks • Valuable features for further modelling
Our Approach & Used Software	• Python library: bctpy • **Approach**: compute graph theoretical measures and use those in the further modelling procedure • Used measures: degree, modularity, community structure, clustering coefficient, characteristic path length • More infos about Graph Metrics: Wang et al. (2010), Hallquist and Hillary (2018)

Sources: Wang et al, Hallquist et al.

Graph Metrics – Selected Measures / Metrics

Degree	• Number of nodes connected to the respective node → Sum over the row/column of the respective adjacency matrix
Density	• Ratio of the number of observed connections to the number of possible connections • Tells us how connected the brain regions for the respective observation are
Modularity	• Every node is assigned to a subnetwork of the graph • Optimal community structure or clusters are determined

Input | **Preprocessing** | Models | Evaluation | Interpretation

Used Machine Learning Methods

The relative efficacy of different machine learning regression algorithms for different types of neuroimaging data are not known in literature[1].

Elastic Net	• For different alpha values: 0 (Ridge), 0.1, …, 1 (Lasso) • Advantage: interpretation of coefficients
Random Forest	• Interpretation by feature importance (impurity decrease) • Just for baseline reference • In principle, the Random Forest is useful for this application, but only for less features.
Gradient Boosting	• Interpretation by feature importance (impurity decrease) • (Theoretically) possibility to automatically account for interactions
Neural Network	• 2D convolutional NN • Only method that uses spatial information of matrices • Requries special convolutional filters for brain data

Source: Jollans, L., Boyle, R., Artiges, E., Banaschewski, T., Desrivières, S., Grigis, A., … & Whelan, R. (2019). Quantifying performance of machine learning

Models: Elastic Net

Elastic Net	• LM/logistic regression with elastic net penalty: mix of L1 (Lasso) and L2 (Ridge) • Tuning parameter: regularization strength, L1-ratio -> determines ratio of L1 and L2 penalization, for 0, 0.1, 0.2, ..., 1
Pros & Cons	• Pro: Interpretation of coefficients • Con: less flexible than other models, e.g. no interactions or non-linear effects -> we included further options for modelling
Options	• All two-way interactions • Quadratic functions • Squared or absolute values
Used Software	• R: glmnet for both regression and classification, evaluation on validation data set • Python: (3- or 5-fold) CV using LogisticRegressionCV and ElasticNetCV

Models: Gradient Boosting

Gradient Boosting	• Sequential fitting of weak base-learners (e.g. decision trees or linear models) • One of the most-used ML algorithm for tabular data
Pros & Cons	• **Pro**: o very efficient implementations (Python: lightgbm & xgboost) o usually showing good performance on tabular learning tasks o Often work well right out of the box • **Con**: o Interpretability - per default not possible to explain predictions easily
Options	• Have a large number of hyperparameters depending on used base-learner • Applicable to binary/multiclass classification, regression or ranking
Used Software	• Python library: lightgbm (Microsoft) • LGBMRegressor and LGBMClassifier • Tuning: Bayesian Optimisation (bayesian-optimization)

Models: Explainable Boosting Machine

EBM

- Compared to GB: features are modelled separately using **p** trees
- Usually 5 or 10k iterations/trees are modelled sequentially per feature
- Residuals passed on from one feature to next
- Estimated complex functions are simply combined in a sum + intercept added

Pros & Cons

- **Pro**: simple and intuitive explanation of the predictions
- **Con**: computationally very costly
  - infeasible when using all connectivity features
  - Feature selection has to be performed beforehand

Options

- Usually work well with default parameters –
  complexity can be adjusted with the main parameter (iterations/trees)
- Interactions are also considered – selects and fits the **n** most important two-way interactions
- Tuning rather hard/infeasible very high computational cost of fitting just one model

Used Software

- Python library: interpret (Microsoft research)
- ExplainableBoostingRegressor and ExplainableBoostingClassifier

Neural Networks – Design Ideas/Constraints

Spatial Structure

- Incorporate the spatial structure of the connectivity matrix
- Normal CNN Filters have the property of Equivariance to translation

→ Use specially designed filters for connectivity matrices

Overfitting

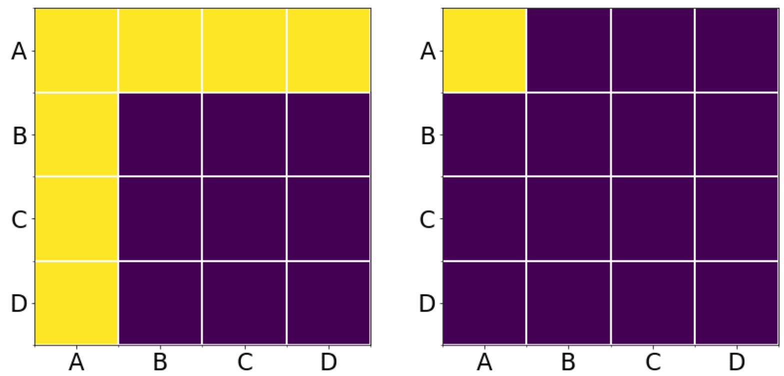
- Not many training examples

→ Shallow and Simple Networks
→ Heavy Regularization
→ Data Augmentation

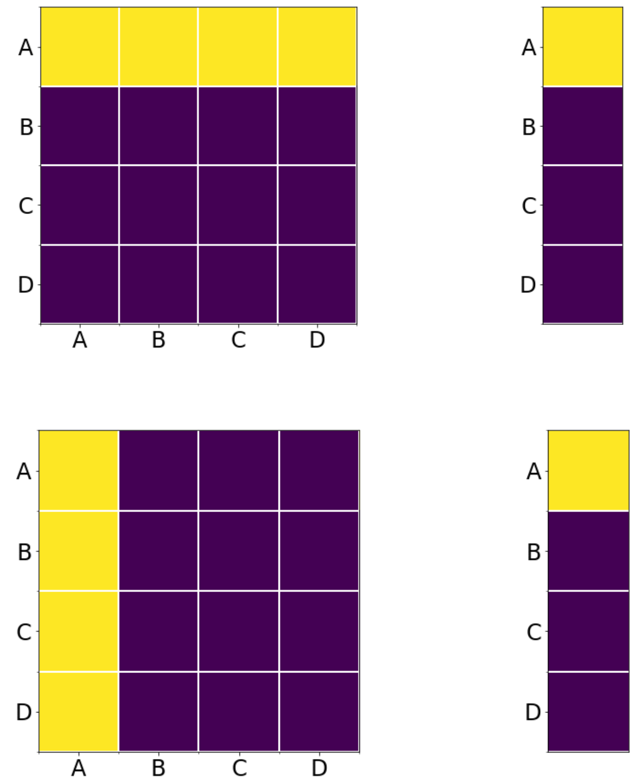
Neural Networks – Special Filters

Edge-to-Edge

- **Combine the signal at a point with the signal from the direct neighbours**

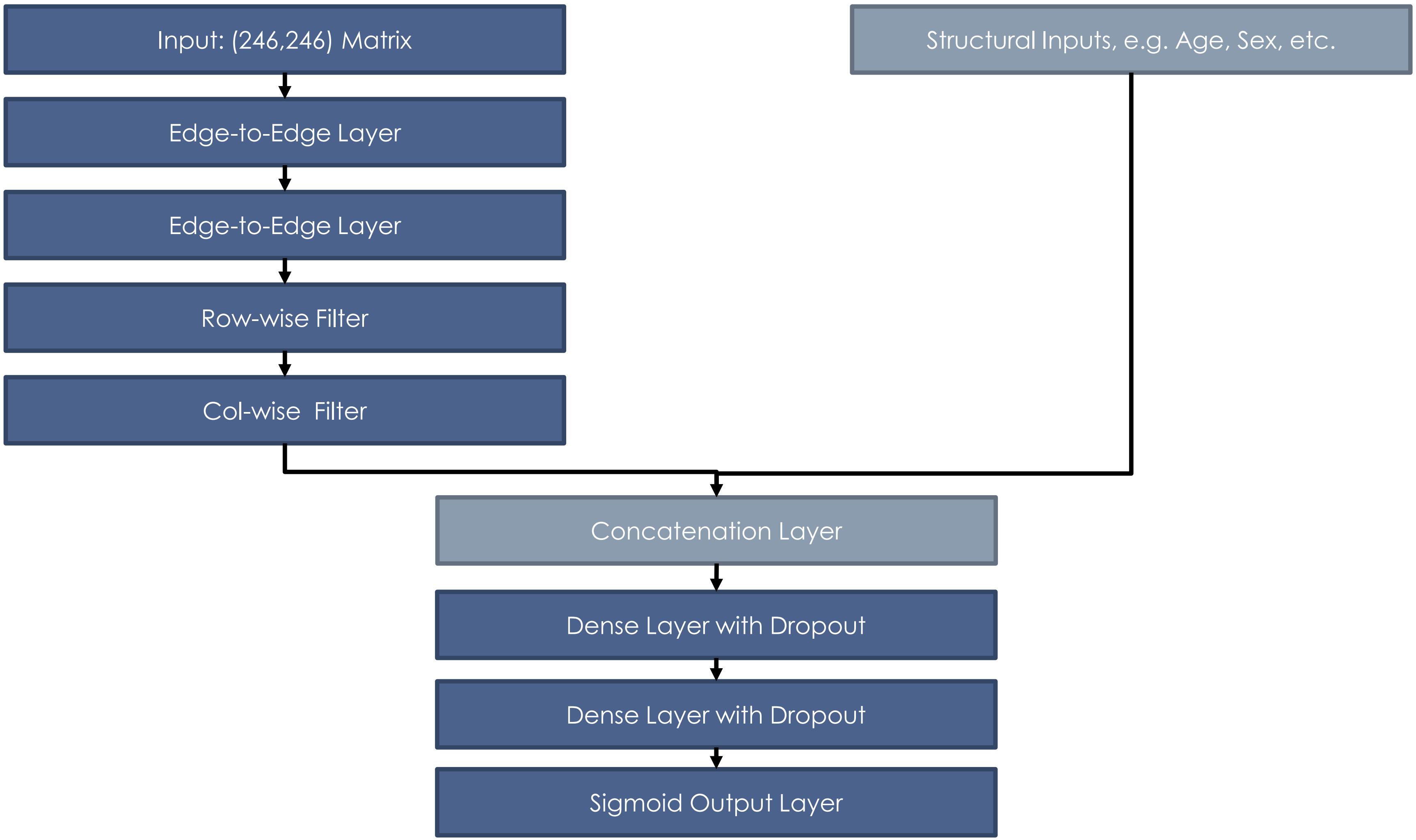


Row/Column Filters



Kawahara, J., Brown, C. J., Miller, … (2017). BrainNetCNN: Convolutional neural networks for brain networks NeuroImage, 146, 1038-1049.

Neural Networks – Architecture



Source: Kawahara, J., Brown, C. J., Miller, … (2017). BrainNetCNN: Convolutional neural networks for brain networks NeuroImage, 146, 1038-1049.

Evaluation: Comparison of performance

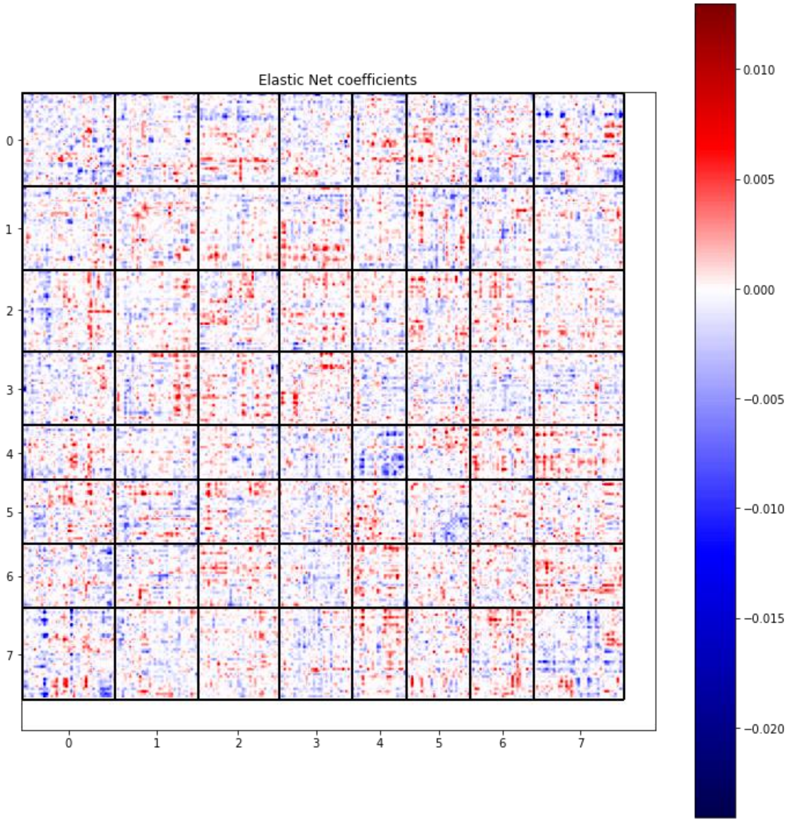
Model	Accuracy	AUC	Precision	Recall	F1
Baseline/ Intercept	0.59				
Elastic Net – Conn data	**0.80**	**0.86**	**0.88**	0.76	**0.82**
Elastic Net – Regions aggregated	max: 0.71 mean: 0.74 zero: 0.76	max: 0.76 mean: **0.84** zero: 0.81	max: 0.80 mean: 0.82 zero: 0.82	max: 0.67 mean: 0.73 zero: 0.75	max: 0.73 mean: 0.77 zero: 0.78
GB (default/dart)	Conn: 0.72 / 0.70 Conn + GMs: 0.71/ 0.77 Zero: 0.72 / 0.69 Zero + GMs: 0.76 / 0.73	Conn: 0.73 / 0.72 Conn + GMs: 0.72 / 0.79 Zero: 0.73 / 0.69 Zero + GMs: 0.76 / 0.74	Conn: 0.82 / 0.85 Conn + GMs: 0.82 / **0.90** Zero: 0.82 / 0.76 Zero + GMs: 0.83 / 0.81	Conn: 0.67 / 0.60 Conn + GMs: 0.65 / 0.67 Zero: 0.67 / 0.69 Zero + GMs: 0.73 / 0.71	Conn: 0.74 / 0.70 Conn + GMs: 0.73 / 0.77 Zero: 0.74 / 0.72 Zero + GMs: 0.78 / 0.76
EBM	Conn: 0.77 Conn + GMs: **0.79** Zero: 0.74 Zero + GMs: 0.74	Conn: 0.77 Conn + GMs: 0.80 Zero: 0.75 Zero + GMs: 0.76	Conn: 0.85 Conn + GMs: 0.87 Zero: 0.83 Zero + GMs: 0.84	Conn: 0.73 Conn + GMs: 0.75 Zero: 0.71 Zero + GMs: 0.69	Conn: 0.78 Conn + GMs: **0.80** Zero: 0.76 Zero + GMs: 0.76
NN – Conn Matrices	0.72	0.78	0.77	**0.76**	0.76
NN – Regions Greater Zero	0.68	0.70	0.67	**0.80**	0.73

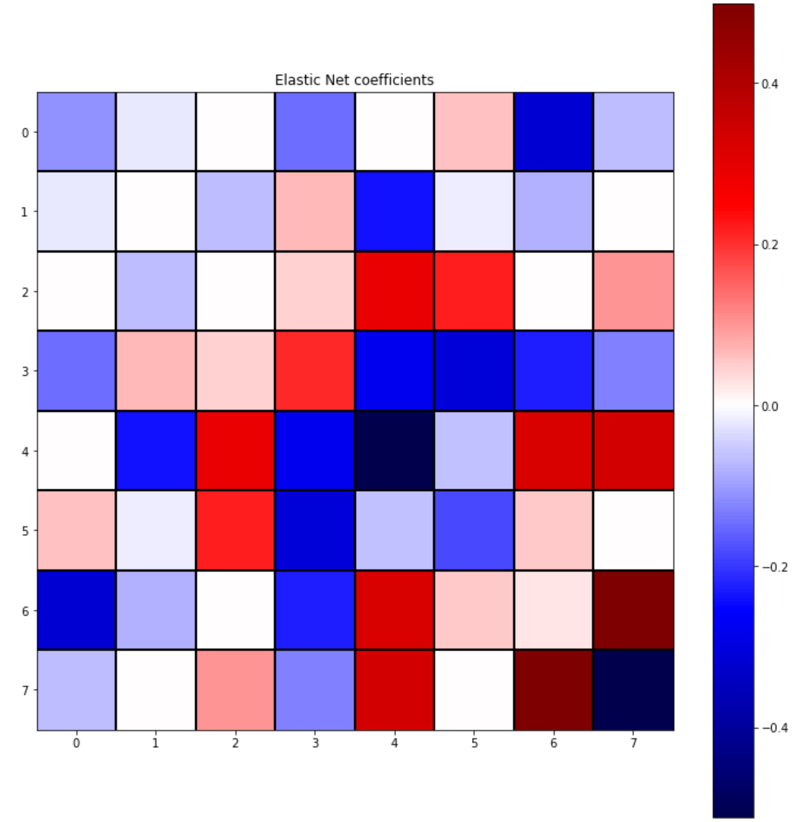
Input | Preprocessing | Models | Evaluation | Interpretation

Interpretation & Visualization: Elastic Net

Interpretation & Visualization

- Only model that gives coefficients of features
- Visualization as matrix (for connectivity data)





Left: coefficients of elastic net on connecitivity data
Right: coefficients of model on aggregated data (percentage > 0)

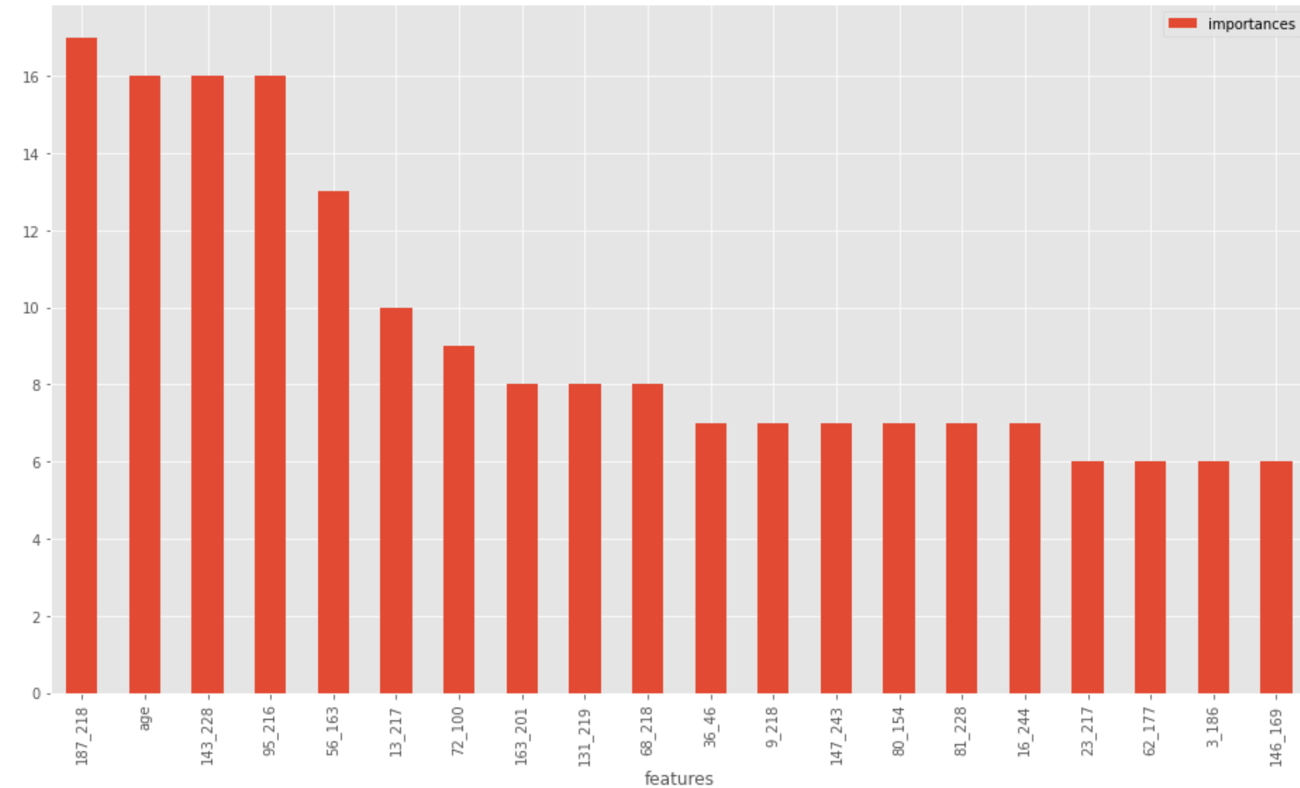
Yeo7 network:
4 = ventral attention
7 = default
0 = no network

Input | Preprocessing | Models | Evaluation | **Interpretation**

Interpretation & Visualization: Gradient Boosting

Interpretation & Visualization

- One default possibility: Feature Importance
- Drawback: no interactions considered



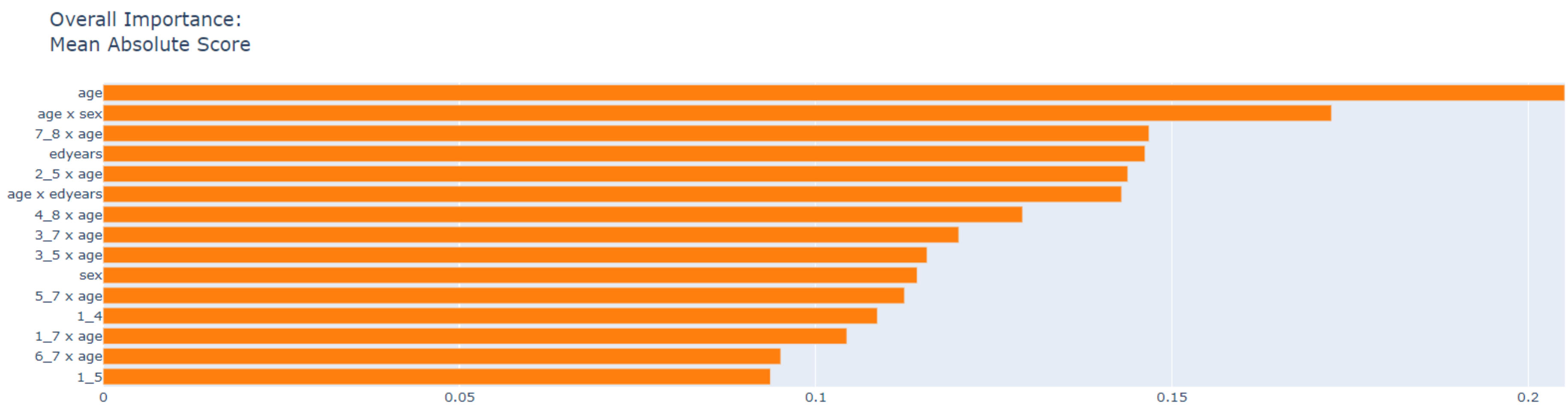
Input | Preprocessing | Models | Evaluation | **Interpretation**

Interpretation & Visualization: EBM

Interpretation & Visualization

Global:
- Plots / curves of the marginal effects of one feature
- Effect-maps of two-way interactions

Local:
- Contributions of features to a given prediction / example



Input | Preprocessing | Models | Evaluation | **Interpretation**

Interpretation & Visualization: EBM

Interpretation & Visualization

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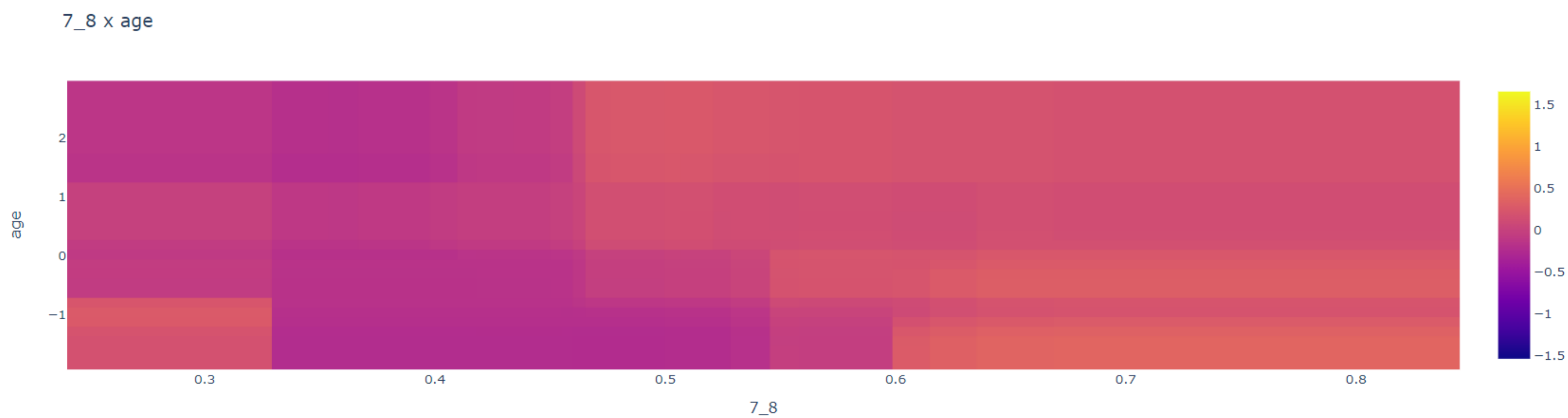

Input | Preprocessing | Models | Evaluation | Interpretation

Interpretation & Visualization: EBM

Interpretation & Visualization

Global:
- Plots / curves of the marginal effects of one feature
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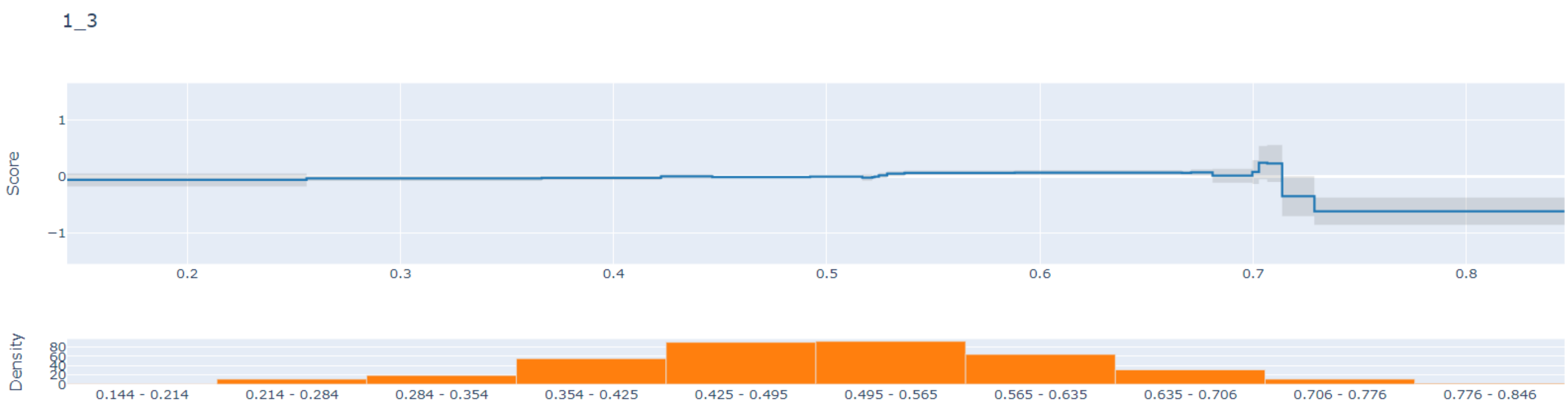

Interpretation & Visualization: EBM

Interpretation & Visualization

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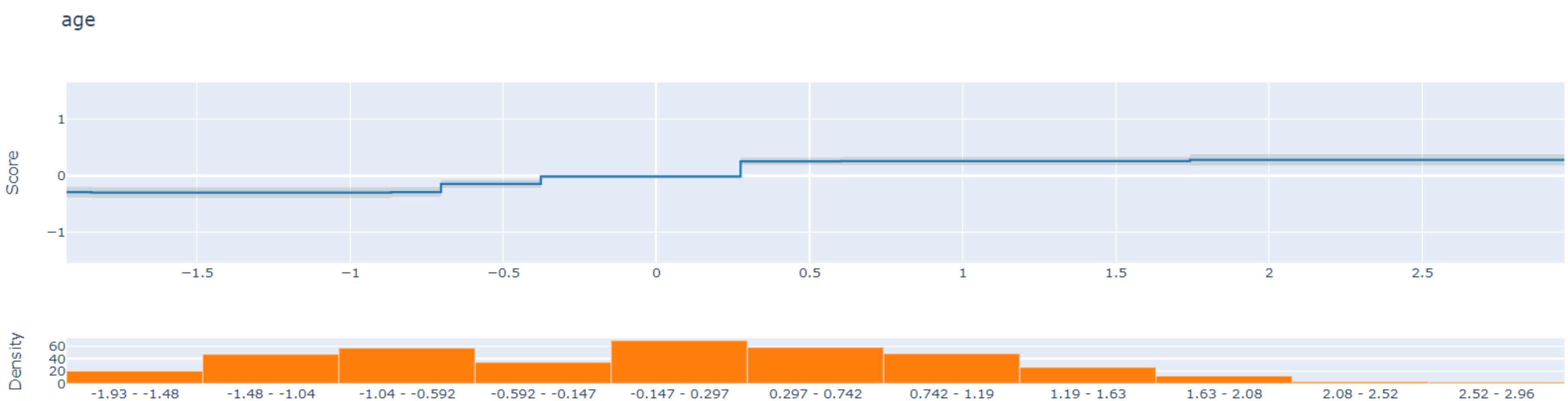


Input | Preprocessing | Models | Evaluation | **Interpretation**

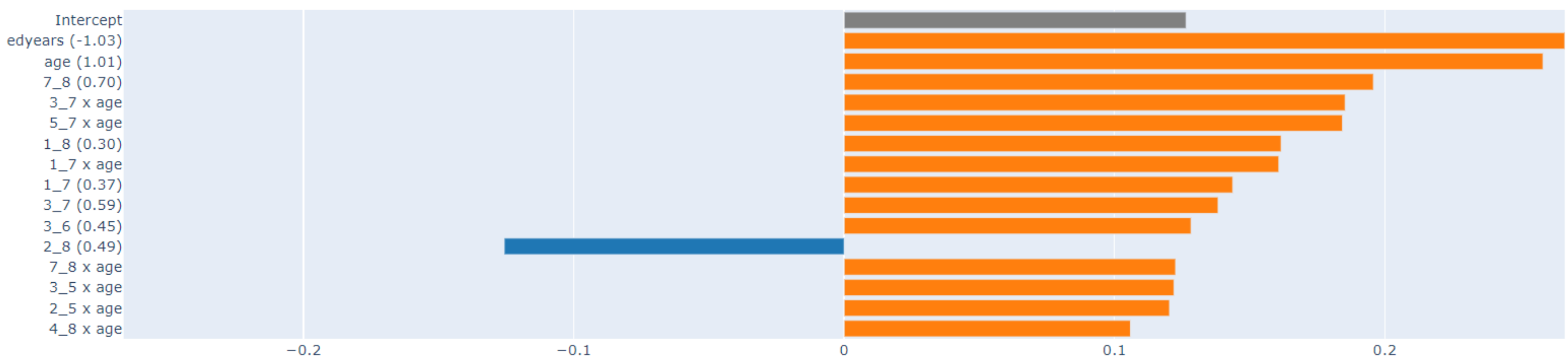
Interpretation & Visualization: EBM

Interpretation & Visualization

Global:
- Plots / curves of the marginal effects of one feature
- Effect-maps of two-way interactions

Local:
- Contributions of features to a given prediction / example

Predicted (1.0): 0.942 | Actual (1.0): 0.942



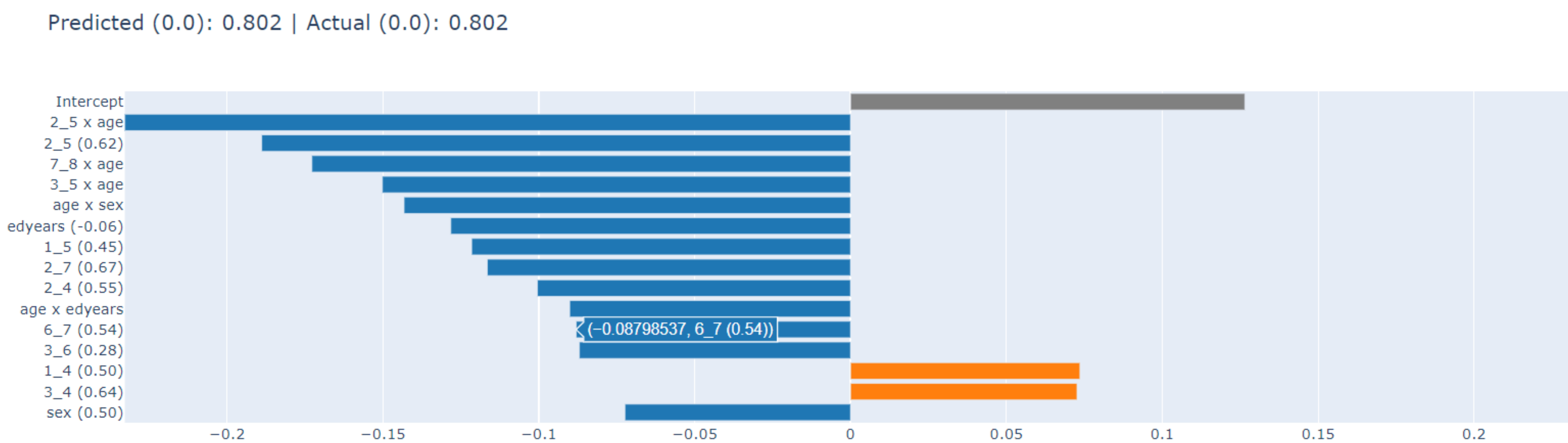
Input | Preprocessing | Models | Evaluation | **Interpretation**

Interpretation & Visualization: EBM

Interpretation & Visualization

Global:
- Plots / curves of the marginal effects of one feature
- Effect-maps of two-way interactions

Local:
- Contributions of features to a given prediction / example



Input | Preprocessing | Models | Evaluation | Interpretation

Interpretation & Visualization: Grouped (Permutation) Feature Importance

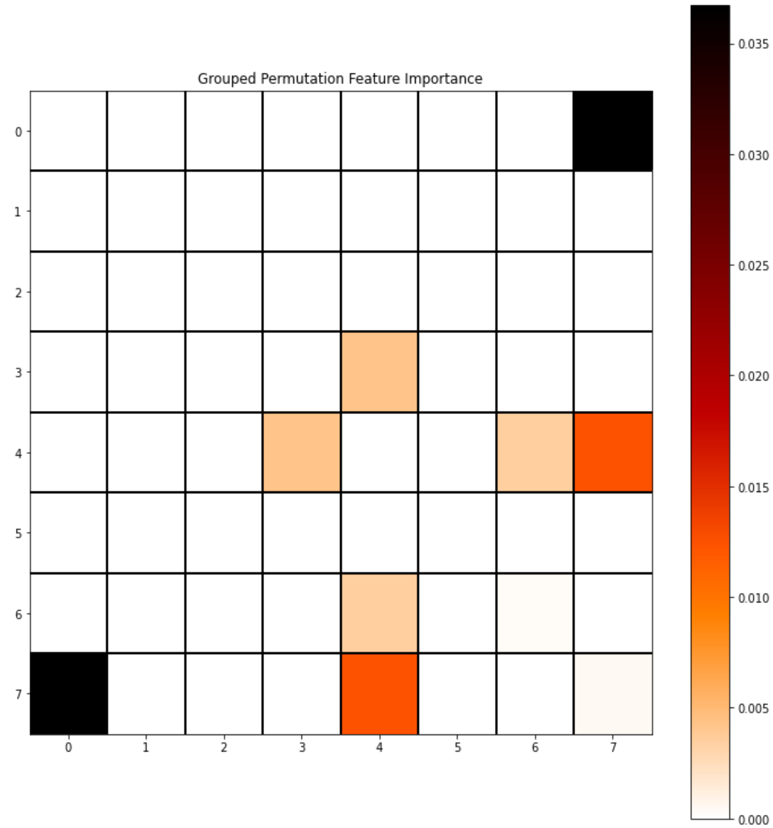
Idea	• Measure importance of a group of features, here: yeo7 Network • Similar to permutation FI: permute values of one feature, measure decrease in performance • Grouped FI: permute feature values of one group *jointly* -> doesn't destroy dependency within one group
Procedure	• For every group G, repeat m times: - jointly permute feature values of G - measure decrease in performance (decrease in accuracy/increase in RMSE) • Calculate average decrease over m repetitons
Group Only Permutation FI	• Alternative to Grouped Permutation FI • Compare performance after permuting *all* features jointly with performance after permuting all features *except* group G
Alternative: Refitting methods	• Disadvantage of Permutation FI: might fail due to extrapolation in regions without observations • But: refitting methods are computationally more expensive • Leave One Group Out Importance: compare full model to model without group G • Leave One Group In Importance: compare null model to model with only group G

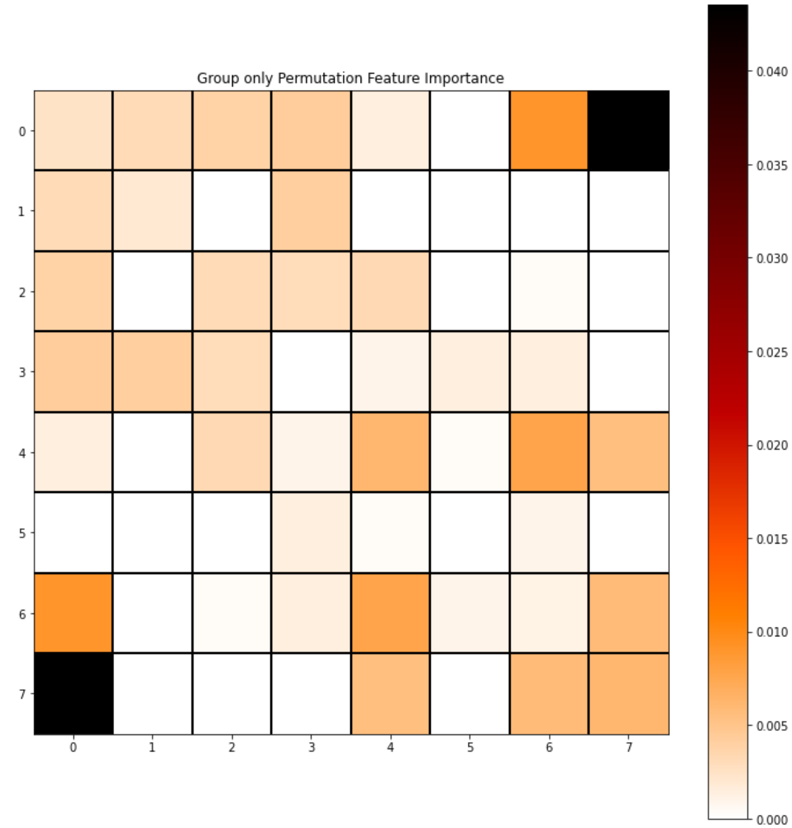
Source: Au, Quay et al. "Grouped Feature Importance and Combined Features Effect Plot."

Interpretation & Visualization: Grouped (Permutation) Feature Importance

Interpretation & Visualization

- The higher the decrease in performance, the more important is a group
- Visualization of values as matrix





Grouped Feature Importance: model on aggregated data (percentage > 0)
Left: grouped permutation FI
Right: group only permutation FI

Yeo7 network:
4 = ventral attention
7 = default
0 = no network

Input | Preprocessing | Models | Evaluation | Interpretation

Interpretation & Visualization: Shapley Values

Idea

- **Model-agnostic** method to obtain the contributions of the features to a given prediction relative to the overall average prediction
- Background in Game Theory: interpreting features as "players" and prediction as "payout"
- **Calculate**: Average marginal contribution of a feature value across all possible coalitions/combinations

Procedure

For one of **M** iterations for a given instance **x** and a feature-(index) **j**:

1. Draw random instance **z** from data **X**
2. randomly permute the order of **z** and **x**
3. Construct two new instances $\mathbf{x}_{+j}$ and $\mathbf{x}_{-j}$ with all feature values of **x** after the **j**-th feature (**j+**) or including the **j**-th feature replaced by the feature values of **z**
4. Compute the marginal contribution: $\mathbf{c}_{j,xm} = \mathbf{f}(\mathbf{x}_{+j}) - \mathbf{f}(\mathbf{x}_{-j})$

To estimate the average marginal contribution of feature **j** we average over all **M** iterations

Interpretation: Contribution of a feature value to the difference between the actual prediction and the mean prediction

Pros & Cons

Pro:

- Relatively simple to calculate
- Distributes effects „fairly", i.e. delivers a full explanation of the prediction

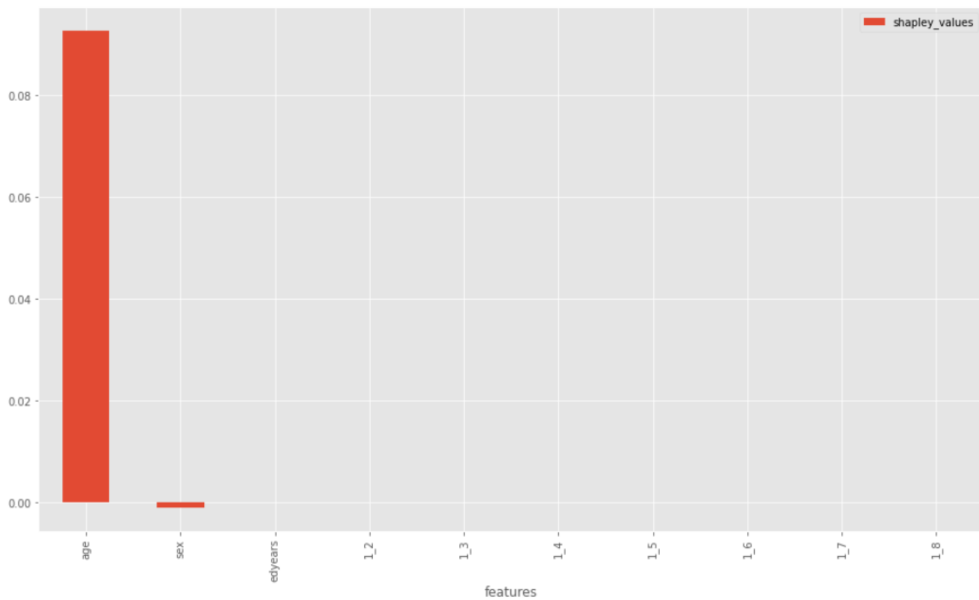
Con:

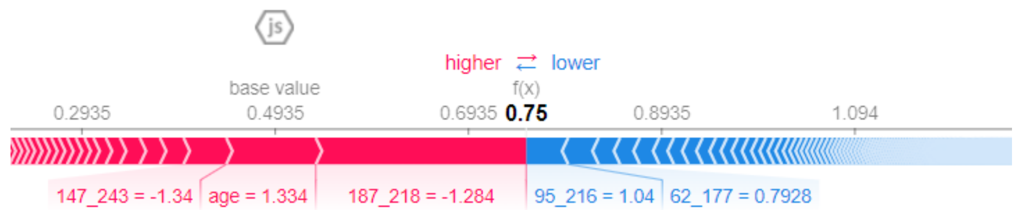
- for **k** features 2^k possible coalitions → scales exponentially with the number of features
- Shapley values have to be estimated
- Returns a simple value per feature → no statement about estimated function („if x changes by … y changes by …")

Input | Preprocessing | Models | Evaluation | **Interpretation**

Interpretation & Visualization: Shapley Values

Used Software	• Python library: shap • More info about shapley values
Interpretation & Visualization	• Local explanation of a prediction • **Dependence plots**: SHAP values based on the values of a given feature • Most important features based on average absolute SHAP/shapley values





Input | Preprocessing | Models | Evaluation | **Interpretation**

Interpretation & Visualization: Shapley Values

Used Software	• Python library: shap • More info about shapley values
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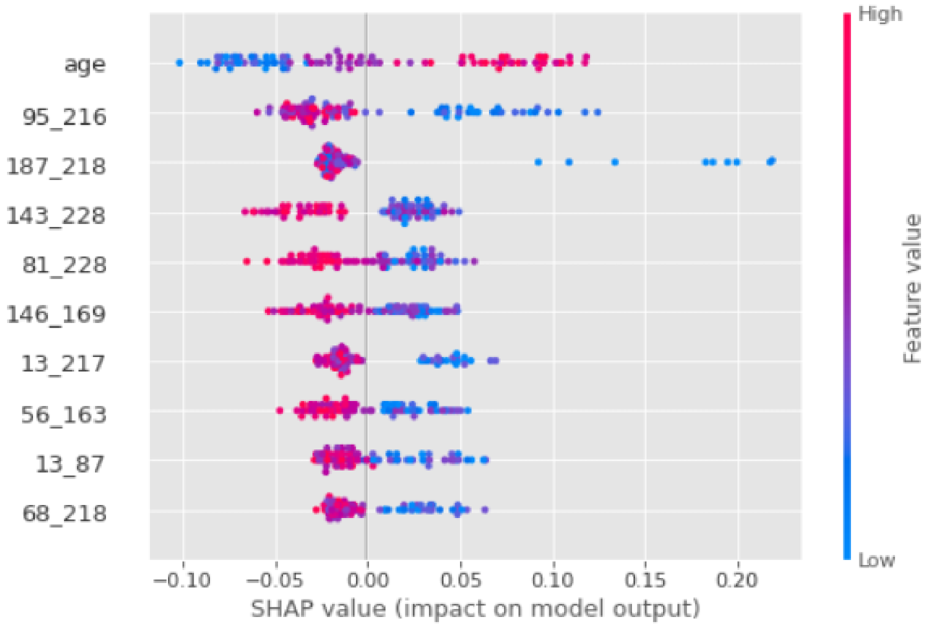

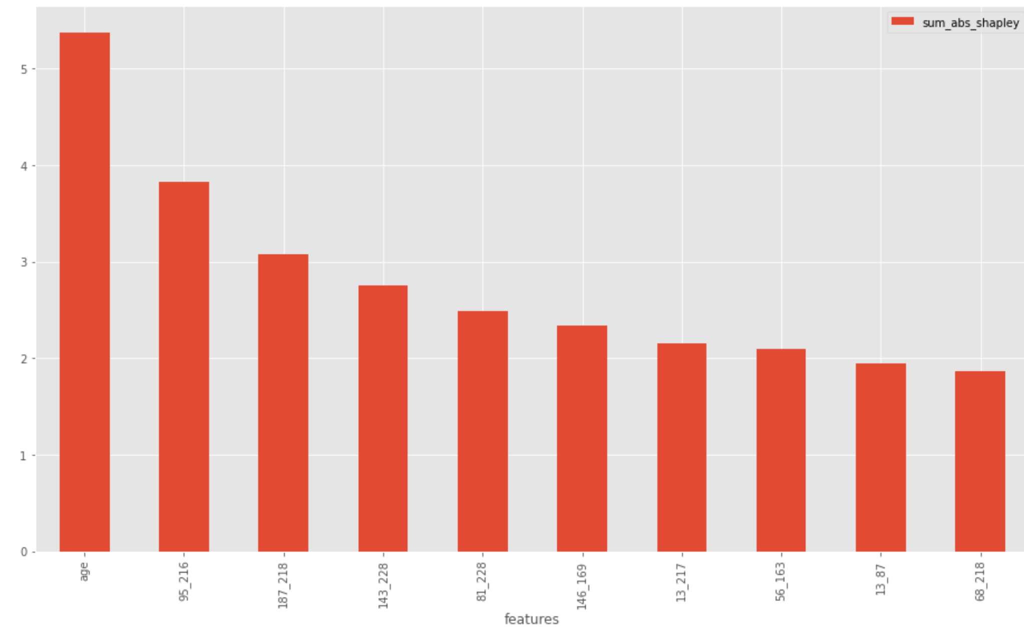

Input | Preprocessing | Models | Evaluation | **Interpretation**

Interpretation & Visualization: Shapley Values

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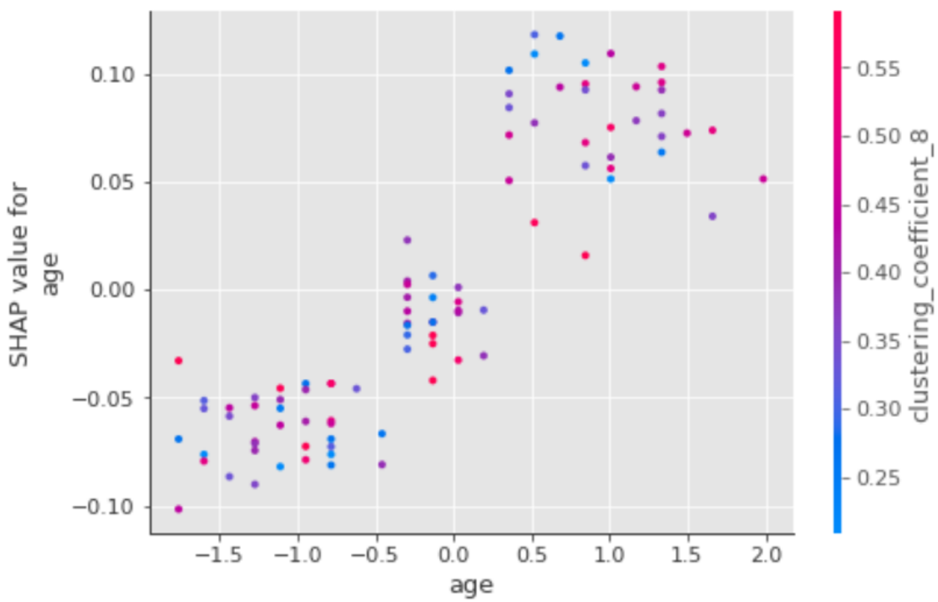
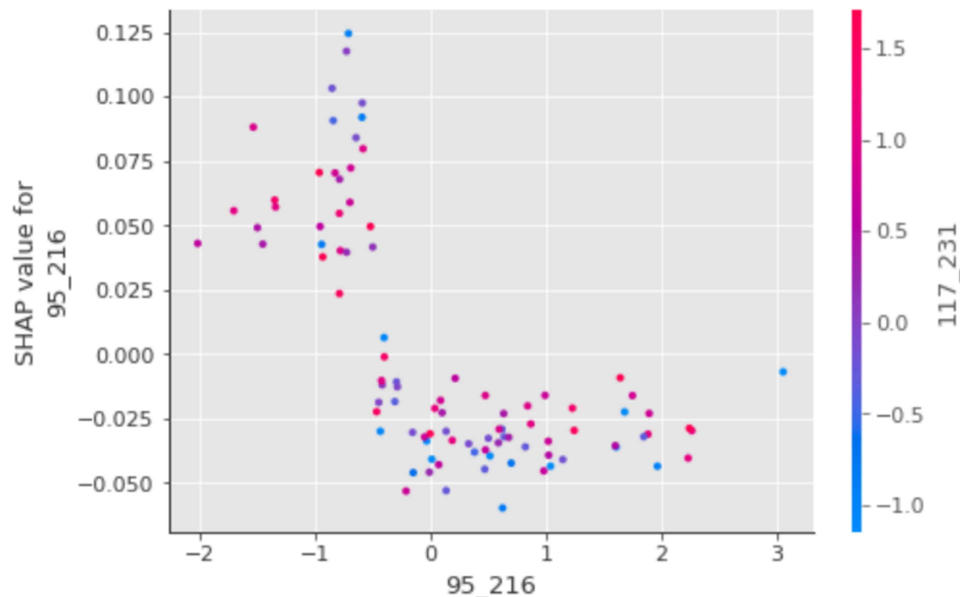




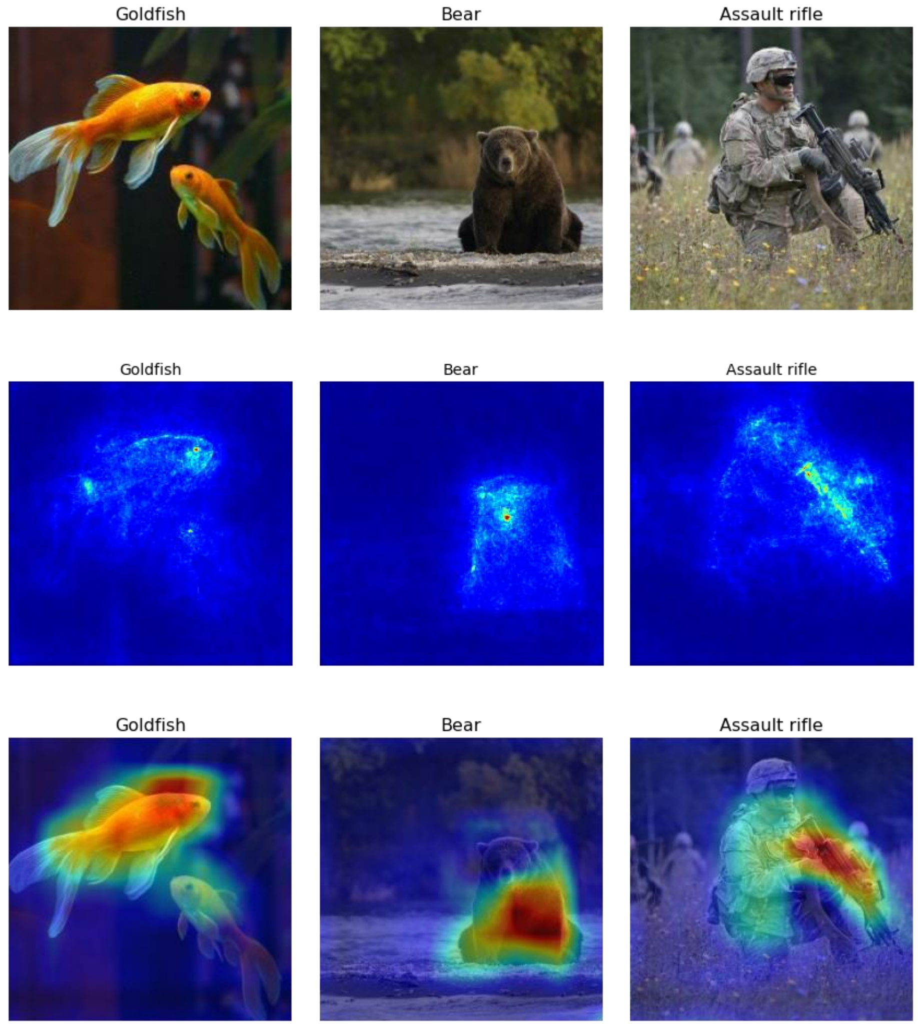
Input | Preprocessing | Models | Evaluation | **Interpretation**

Neural Network – Feature Attribution

Original Image

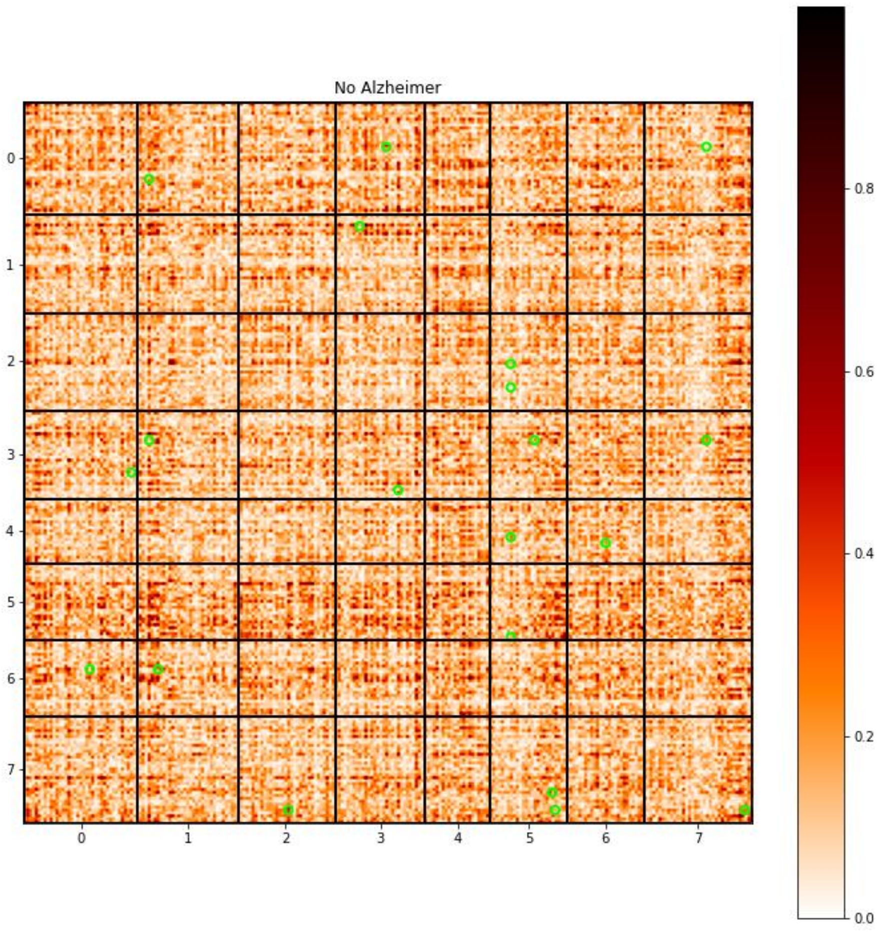
Saliency Maps

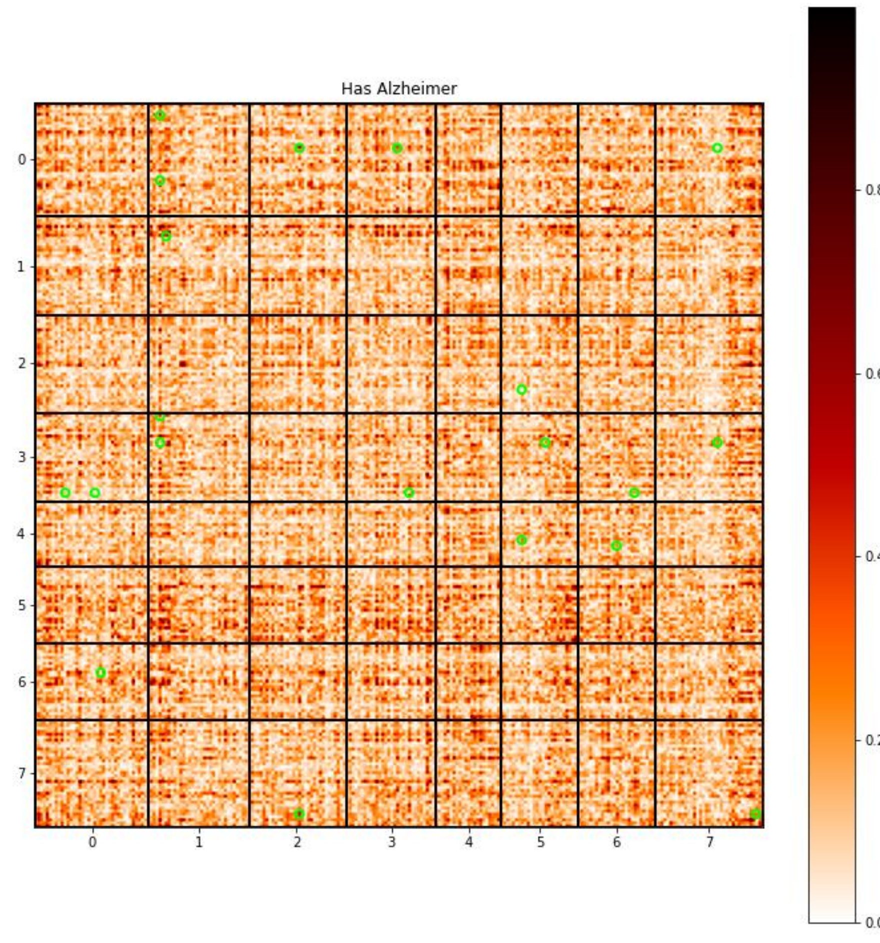
Grad CAM



Source: keisen.github.io/tf-keras-vis-docs/examples/attentions.html

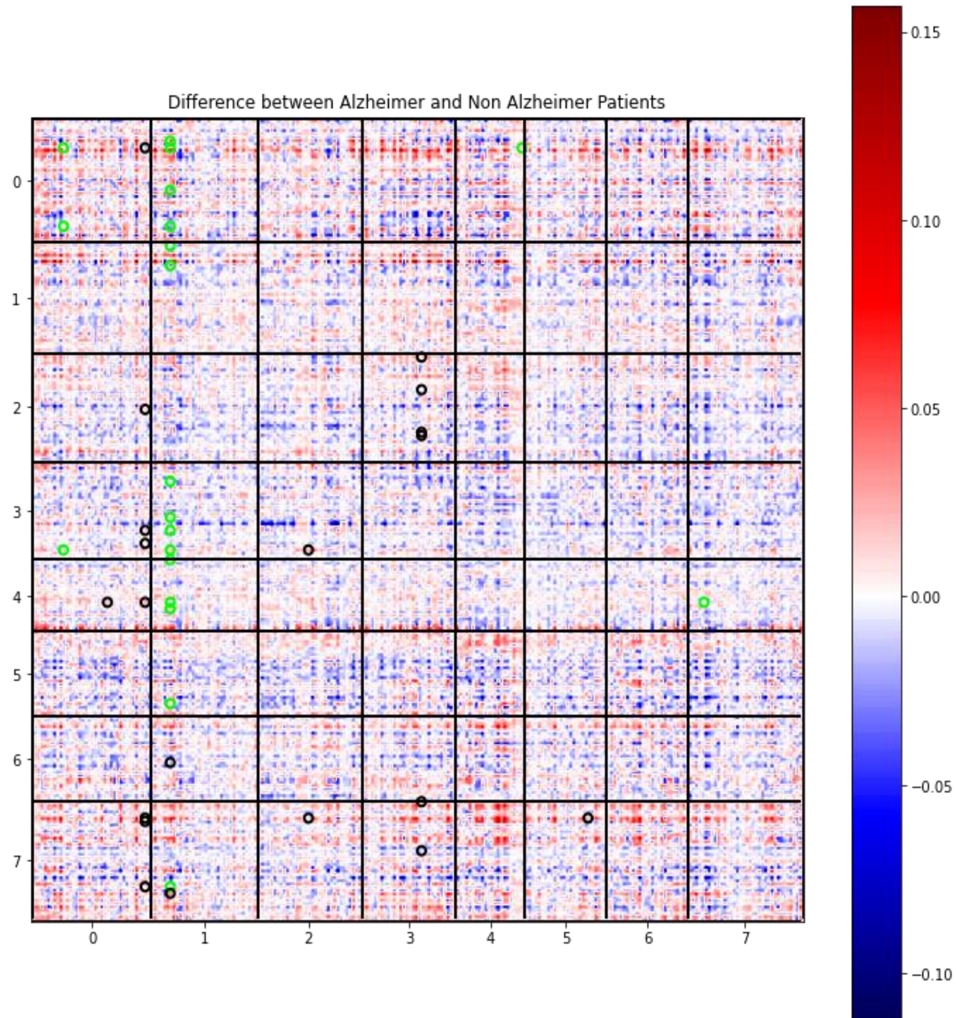
Neural Networks – Feature Attribution Results





Input | Preprocessing | Models | Evaluation | **Interpretation**

Neural Networks – Feature Attribution Results



Biggest 20 values

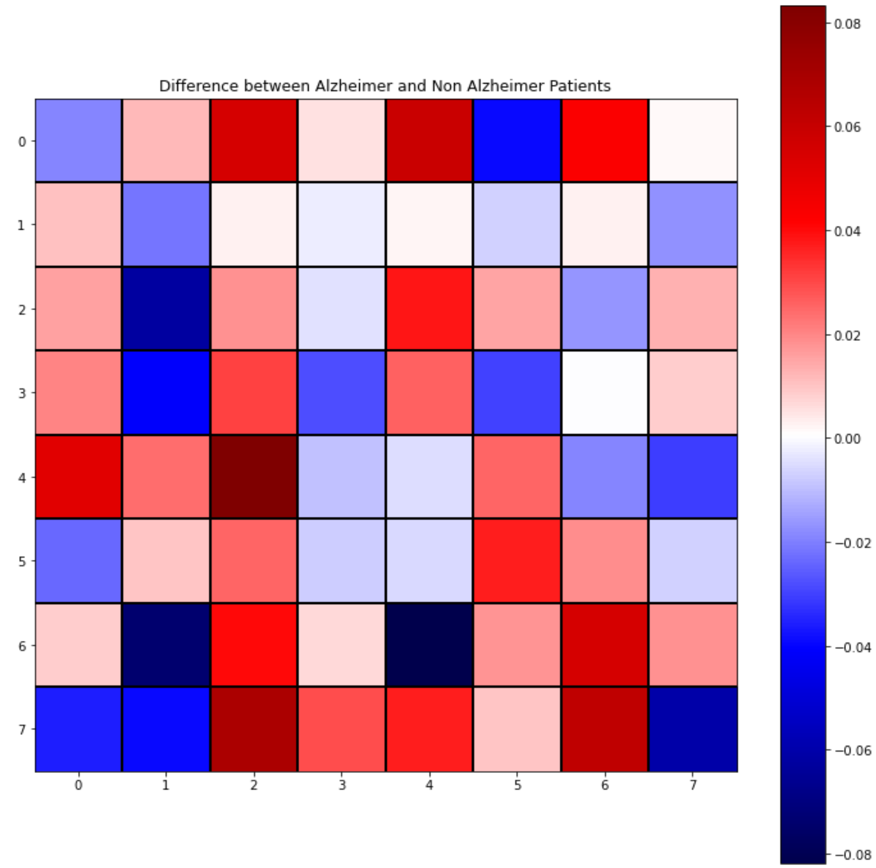
Important Regions for Alzheimer predictions:
- Posterior parahippocampal gyrus
- Caudal Hippocampus

Smallest 20 values

Important Regions for Non-Alzheimer predictions:
- Caudal Temporal Thalamus
- Rostral Area 7

Input | Preprocessing | Models | Evaluation | Interpretation

Neural Networks – Aggregated Regions

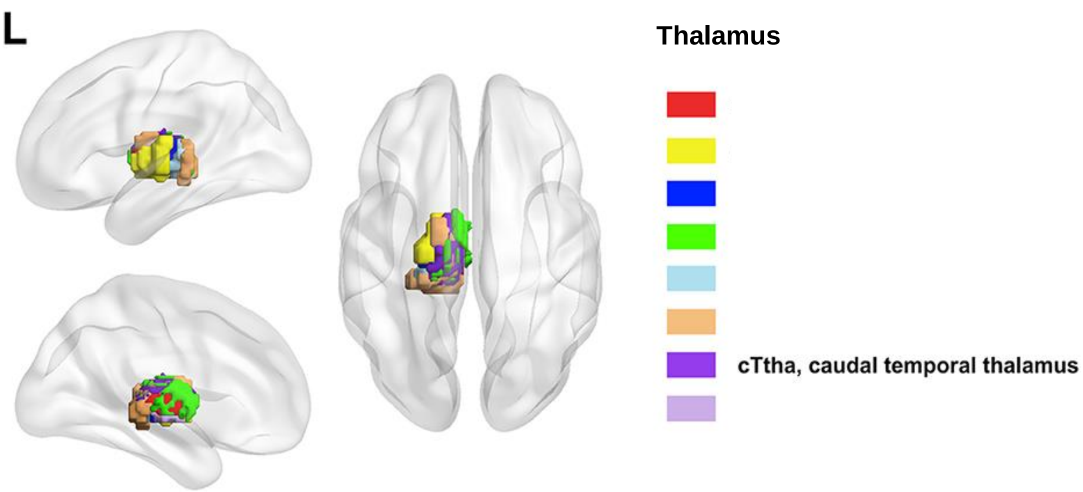


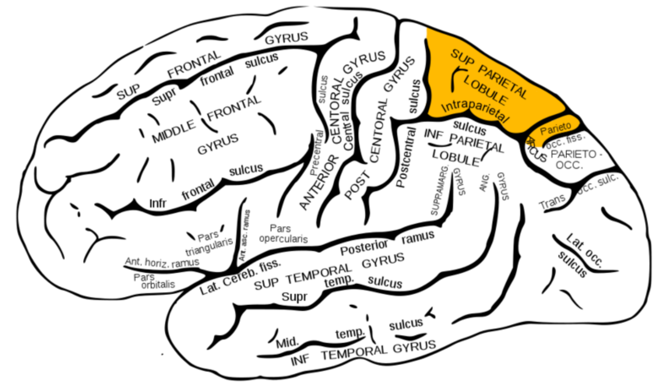
Weaknesses of this technique:

- Resulting plots no longer symmetric
- Model treats inputs with same input meaning differently

Explanation of Identified Brain subregions with key importance for Alzheimer

Identified Brain Areas: Caudal Temporal Thalamus and Rostral area 7





Caudal Temporal Thalamus

- Part of the Thalamus
- Function: roles as a sensory relay in visual, auditory, somatosensory, motor activity, emotion, memory, arousal, and other sensorimotor association functions.

Rostral Area 7

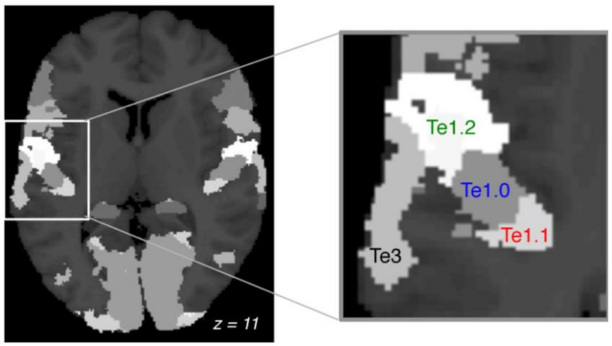
- Part of the Superior parietal lobule
- Function: The superior parietal lobule has close links with the occipital lobe and is involved in attention and visuospatial perception, including the representation and manipulation of objects.

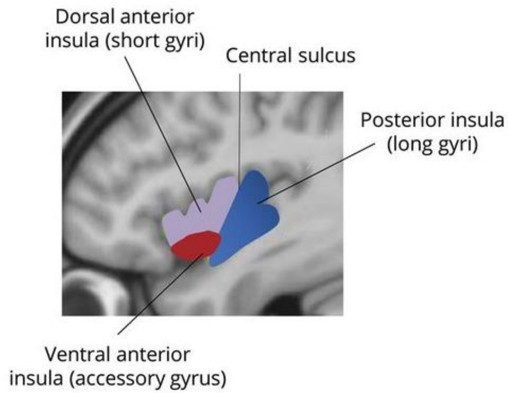
Input | Preprocessing | Models | Evaluation | **Interpretation**

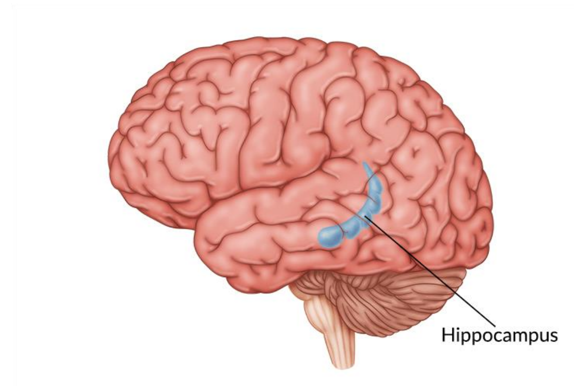
Source: *Spiegel et al (1955), Caudal Temporal Thalamus ; Boecker et al (1998), Rostral Area 7*

Identified Brain subregions with key importance for Alzheimer

Identified Brain Areas: ***TE1.0 and TE1.2, Dorsal Agranular Insular and Caudal Hippocampus***







TE1.0 and TE1.2

- Part of the subregions of the primary auditory cortex & Heschl´s Gyrus
- Function: This area is not only important for language comprehension, but more importantly, it has a crucial role in speech production, phonologic retrieval, and semantic processing

Dorsal Agranular Insular

- Part of the Insular Cortex
- Function: The Insular Cortex processes of external and bodily sensory information, bodily- and self-awareness, feelings and complex social-affective functions like empathy, social interactions and learning and memory

Caudal Hippocampus

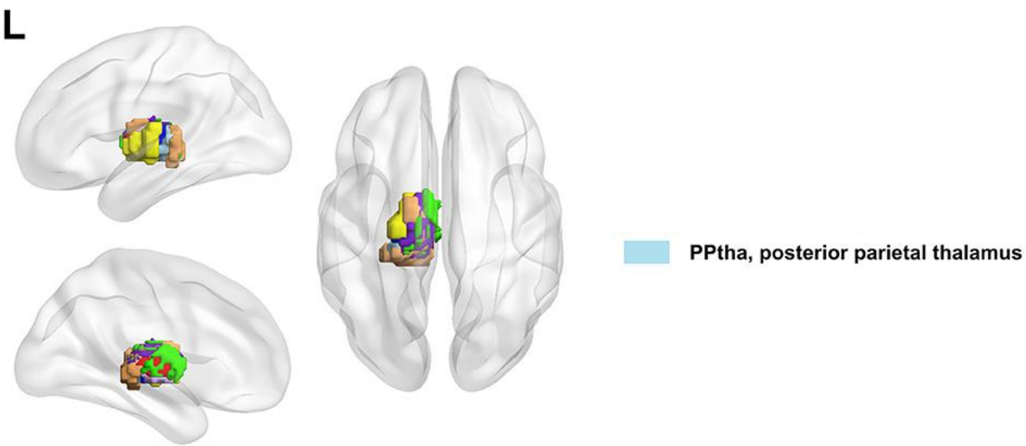
- Part of the hippocampus
- Function: Functional specificity of caudal hippocampus lies in exploratory behaviour and spatial learning, major role in learning and memory

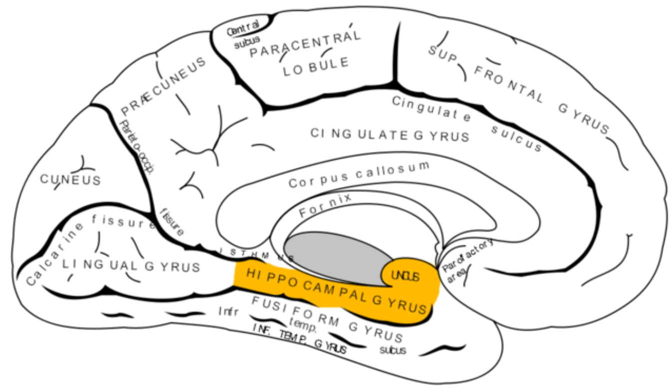
Input | Preprocessing | Models | Evaluation | **Interpretation**

Source: Morosan et al (2001), TE1.0 and TE1.2, Benarroch (2019), Agranular Insular, Plaskacheva et al (2009), Caudal Hippocampus

Identified Brain subregions with key importance for Alzheimer

Identified Brain Areas: Posterior Parahippocampal Gyrus and Posterior Parietal Thalamus





Posterior Parietal Thalamus

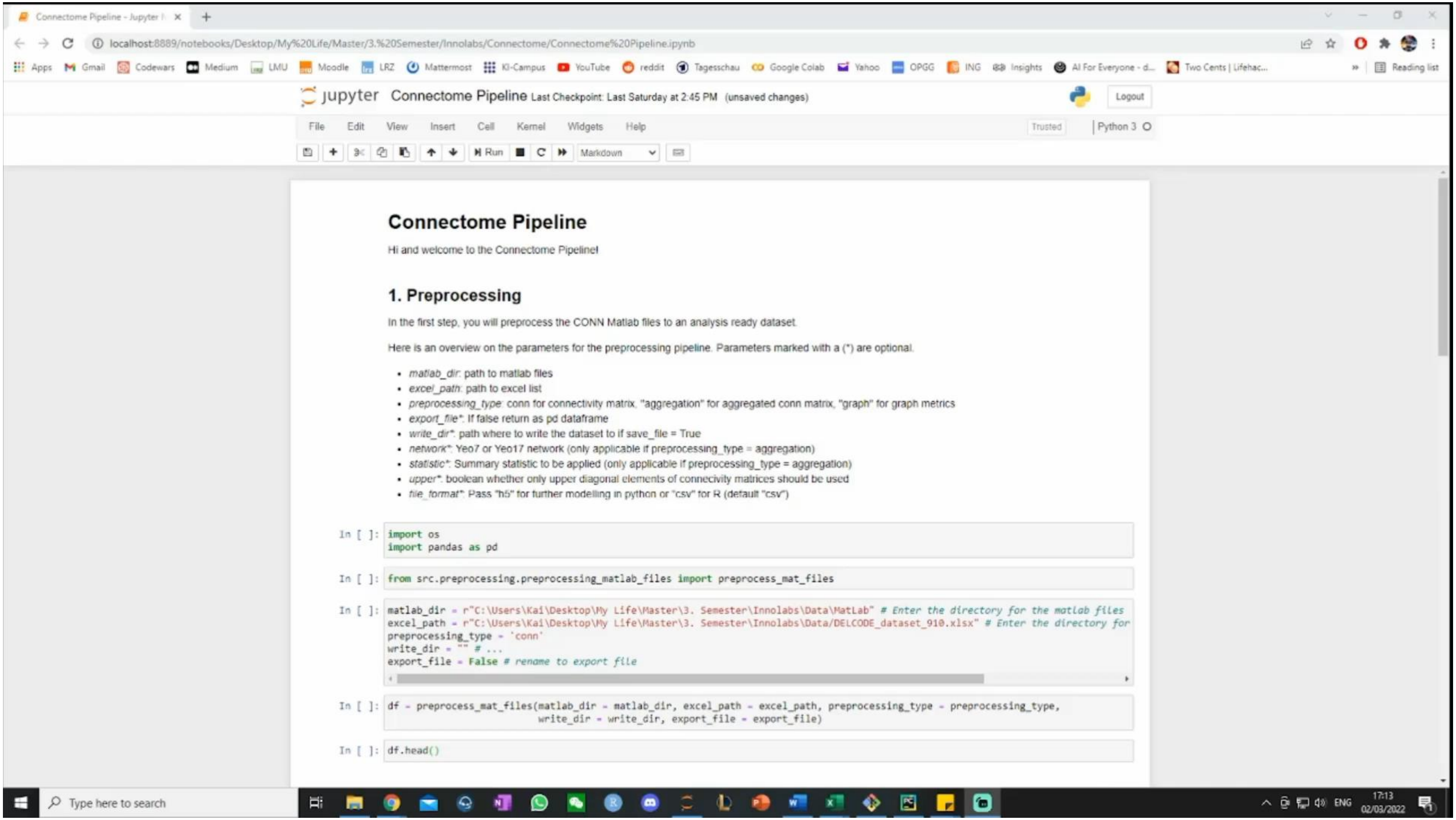
- Part of the Posterior Thalamus
- Function: the Posterior Parietal Thalamus enables skilled Forelimb Movement and Tool Use. The Thalamus roles as a sensory relay in visual, auditory, somatosensory, motor activity, emotion, memory, arousal, and other sensorimotor association functions.

Posterior Parahippocampal Gyrus

- Part of the parahippocampal gyrus
- Function: parahippocampal gyrus plays an important role in memory encoding and retrieval

Source: Parahippocampal Gyrus, Bohbot et al (2015), Posterior Parietal Thalamus, Mayer et al (2019)

Video about full Connectome Pipeline



Input | Preprocessing | Models | Evaluation | Interpretation

6. Use and potential benefits of our final product

Continuation options

Connectome can support further research in dementia and related diseases

Adaptable to new ideas

- Open to new models like SVMs
- Possibility to add other types of feature importance
- Similar diseases of the brain can also be researched
- Further interpretation methods can be added to the pipeline

Available to everyone

- Fully published on GitHub
- Available to all researchers worldwide to use

Easy to use

- Pipeline kept as simple as possible with clear instructions
- Required Data and model choice are sufficient to receive a fitted model to predict on
- Detailed understanding of the chosen models setup not necessary

Publications

- Publishing findings in a medical journal is an option after more results have been found

Thank you for your attention!

Kai

Jana

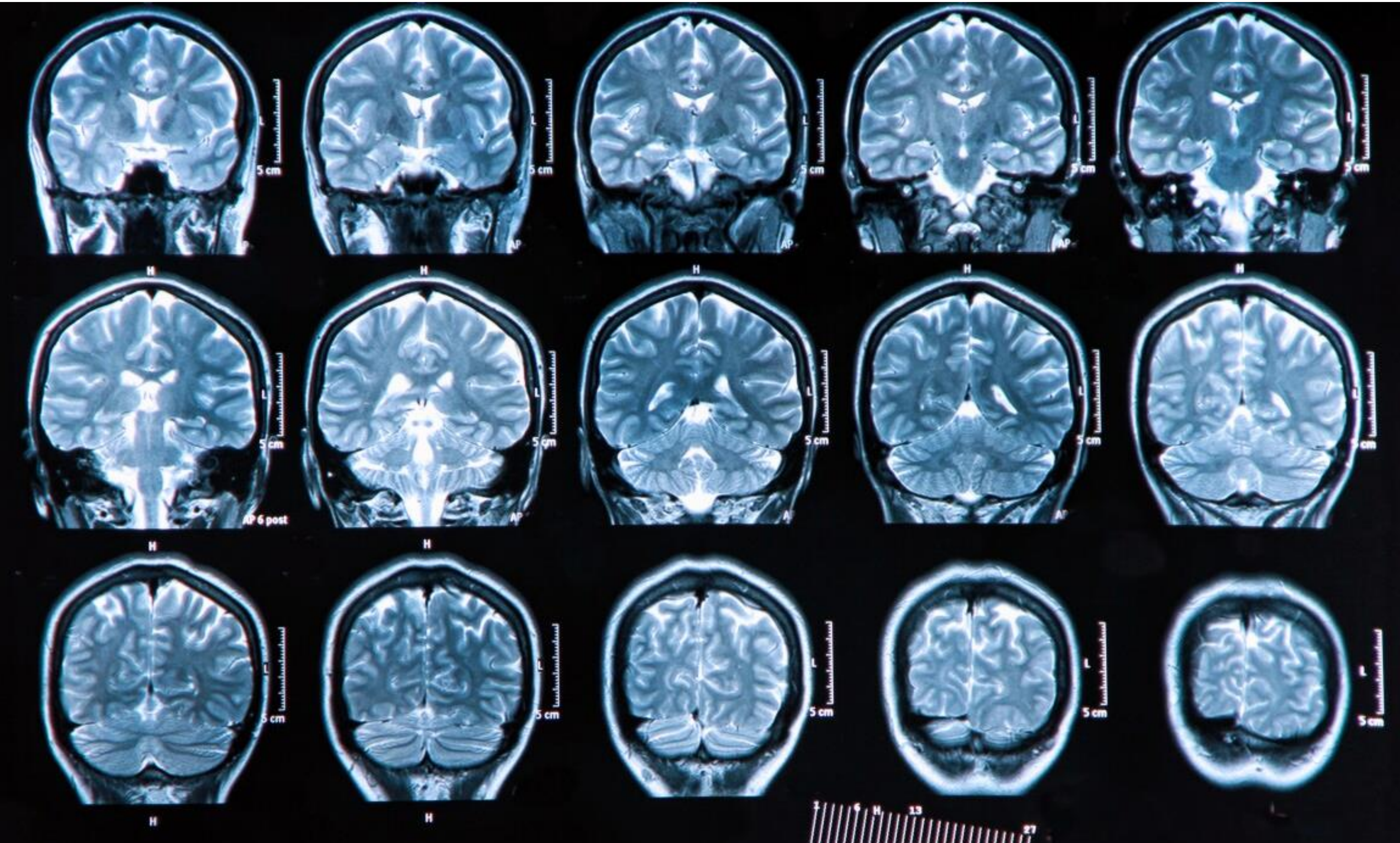
Leo

Jonas

Kathi

Do you have any questions?

Appendix



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