

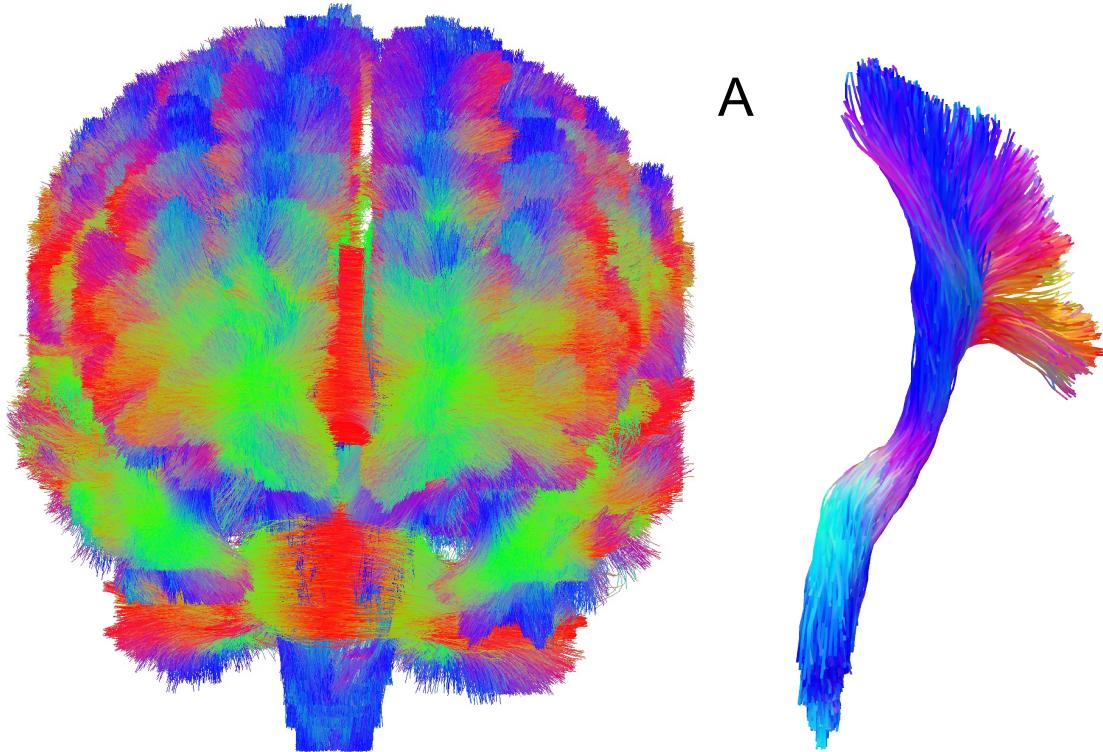
# Detecting microstructural deviations in individuals with deep diffusion MRI tractometry



Maxime Chamberland, PhD



## Along-tract profiling



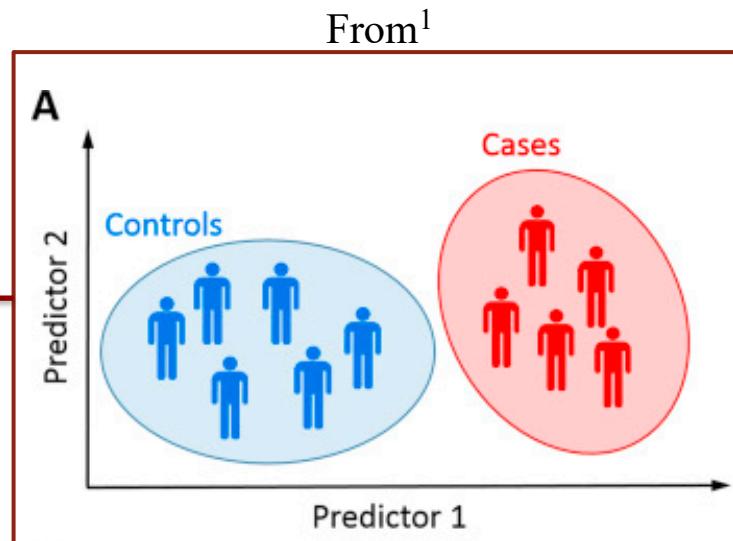
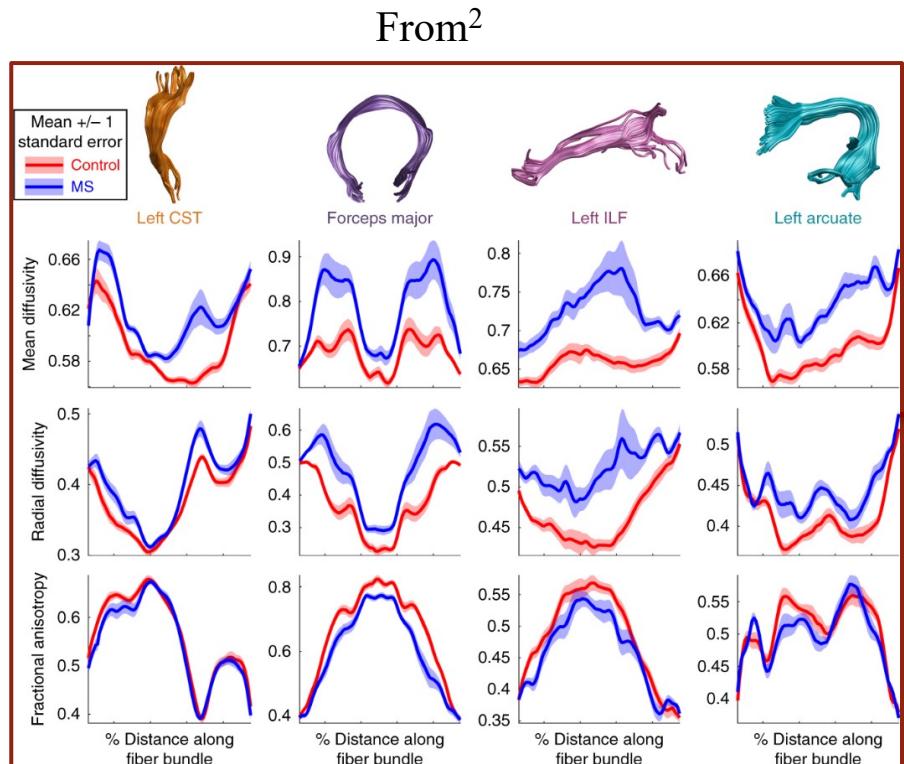
A. Bundle segmentation

Jones et al. **MRM** (2005); Corouge et al. **Media** (2006); Yeatman et al. **PLOS One** (2012);  
Colby et al. **Nimg** (2012); Cousineau et al. **Nimg Clin.** (2017); Yeatman et al. **Nat. Comms.** (2018)



# Understanding clinical heterogeneity

## Case-control approach



1. Marquand AF. et al. **Biological psychiatry** (2016)
2. Yeatman J. et al. **Nature Communications** (2018)



One of the main goal of neuroimaging is *personalized-medicine*

## Normative modeling



Idea: learn a set of  
**normative microstructural features**  
from healthy controls only



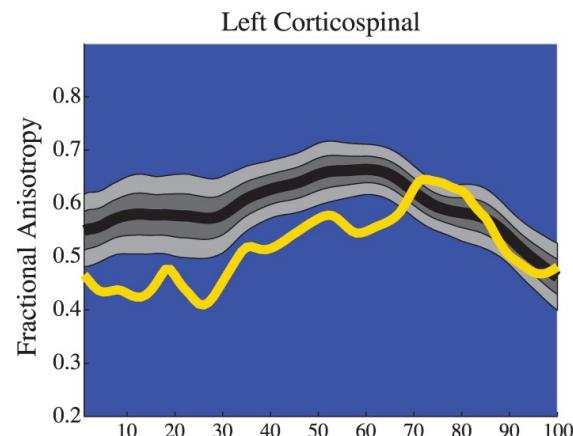
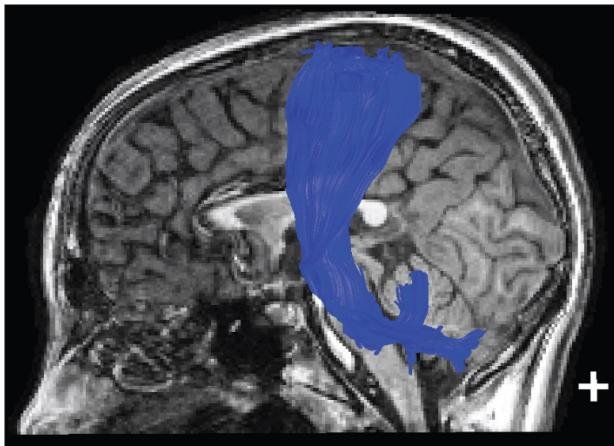
To shift from **group-wise comparisons<sup>1</sup>** (N vs M) to **individual diagnosis** (1 vs M) in diffusion MRI (**dMRI**) would enable the analysis of rare cases and clinically-heterogeneous groups<sup>2</sup>.

1. Jones DK., and Cercignani M. **NMR in Biomedicine** (2010)
2. Marquand AF. et al. **Biological psychiatry** (2016)

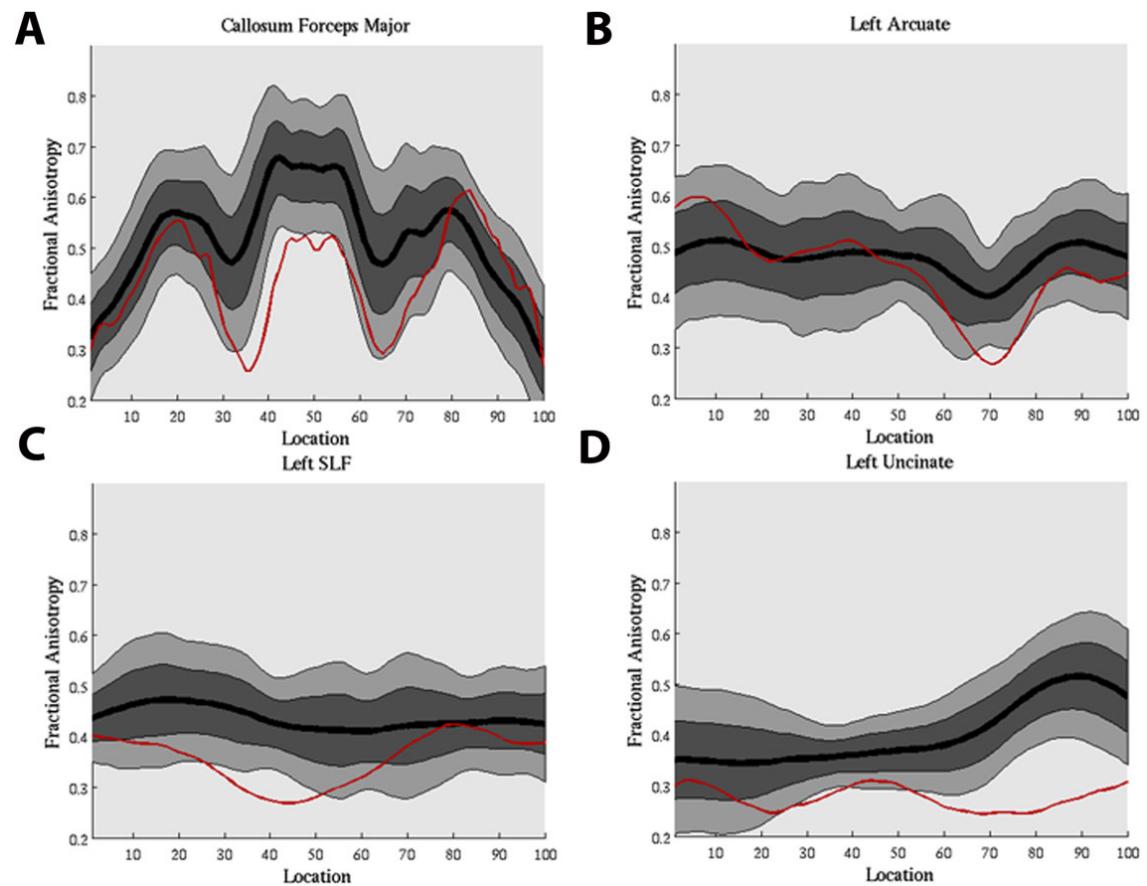
# Tract-profiling

## Univariate *z*-score approach

Cerebral palsy



Traumatic brain injury

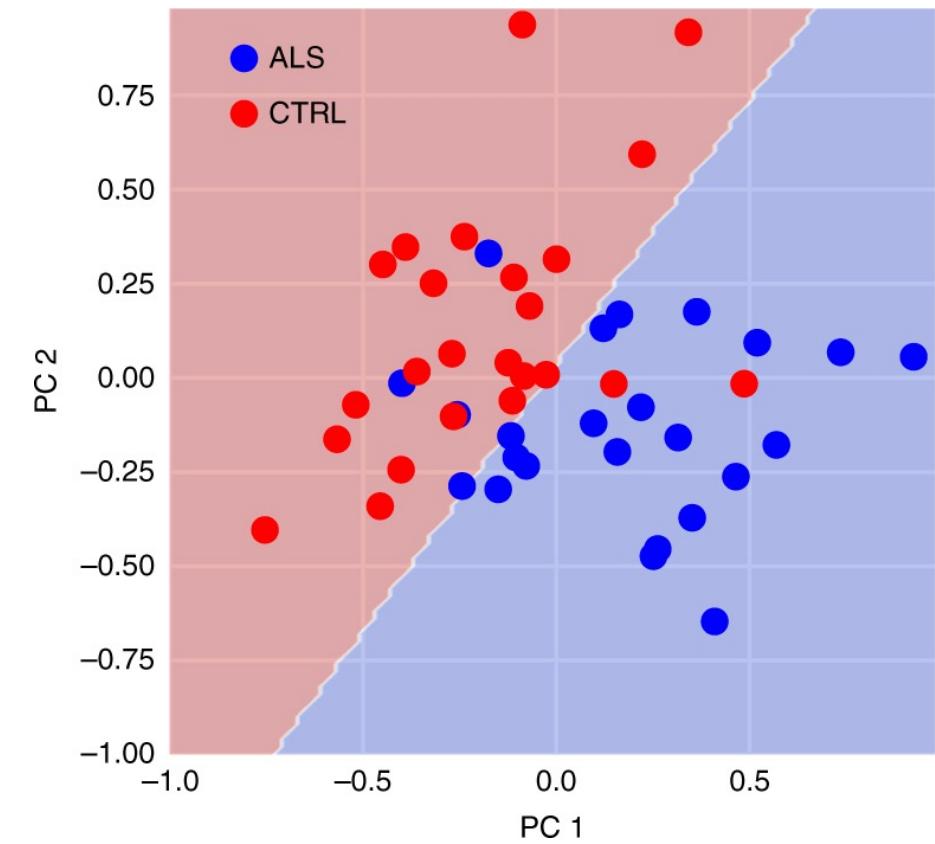
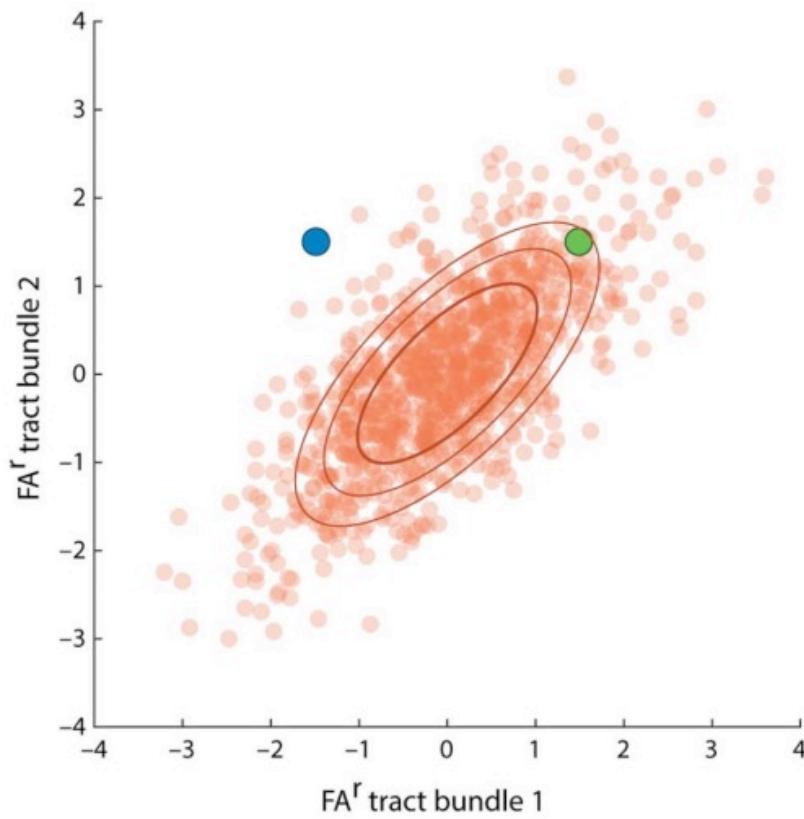


Left: Yeatman J. et al. PLOS One (2012)

Right: Yeh PH. et al. Human Brain Mapping (2017)

# Multivariate PCA approach

A

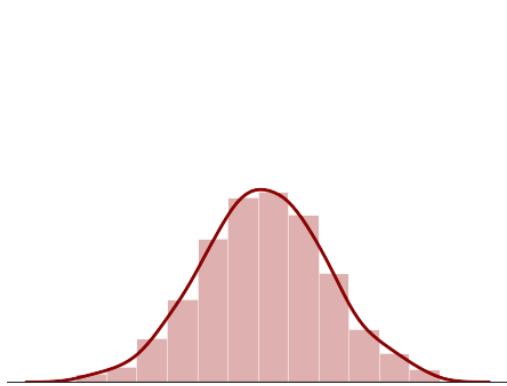


Left: Taylor PN. et al. *Neurology* (2020)

Right: Yeatman J. et al. *Nature Communications* (2018)

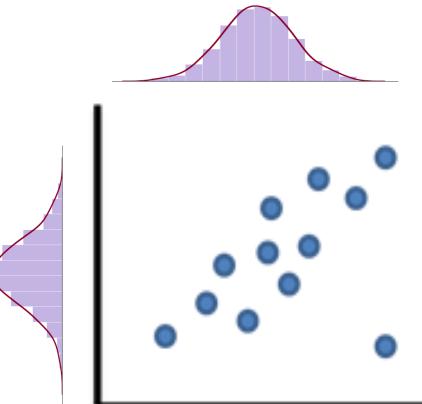
Multidimensional generalization

## Anomaly detection principle



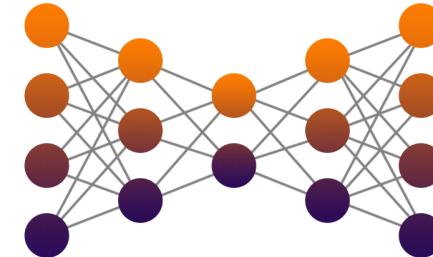
**Z**

Univariate  
Z-score



**M**

PCA +  
Mahalanobis Distance



**E**

Autoencoder +  
Reconstruction error

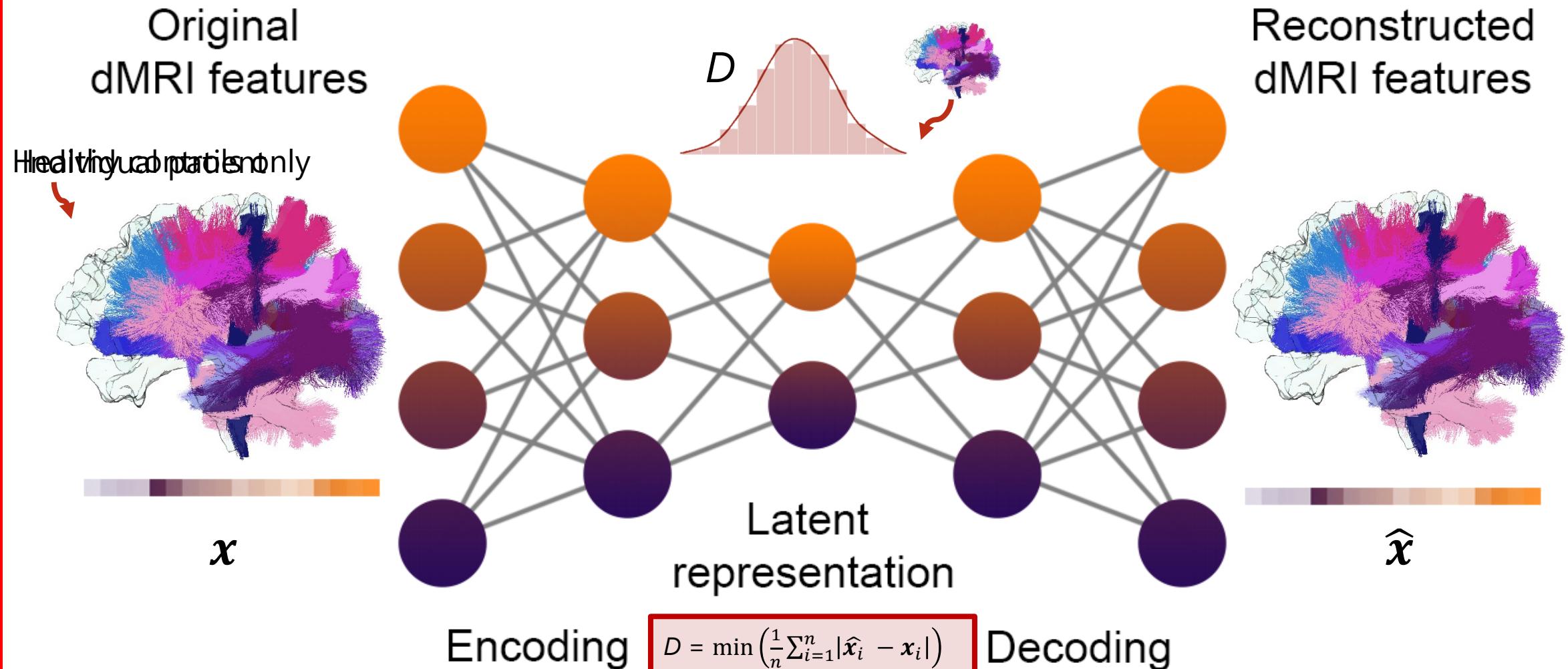
$$z = (x - \mu)/\sigma$$

$$M(x) = \sqrt{(x - \mu)' C^{-1} (x - \mu)},$$

$$\text{MAE} = \frac{1}{n} \sum_{j=1}^n |x_i - \hat{x}_i|,$$



## Unsupervised learning &amp; normative modeling



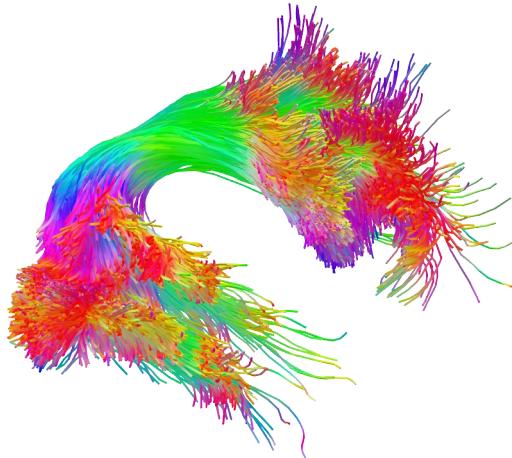
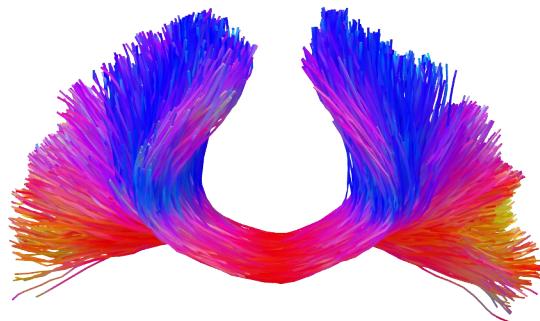


Tractometry approach

## Input features

- Automated tract segmentation using TractSeg<sup>1</sup>
- Tractometry:
  - FA, MD (low  $b = 1200$  s/mm $^2$ )
  - RISH0, RISH2 (high  $b = 6000$  s/mm $^2$ )
- Feature vector →  $n = 26$  tracts  $\times$  20 locations = 520 features for each subject.

Feature vector ( $\mathbf{x}$ )



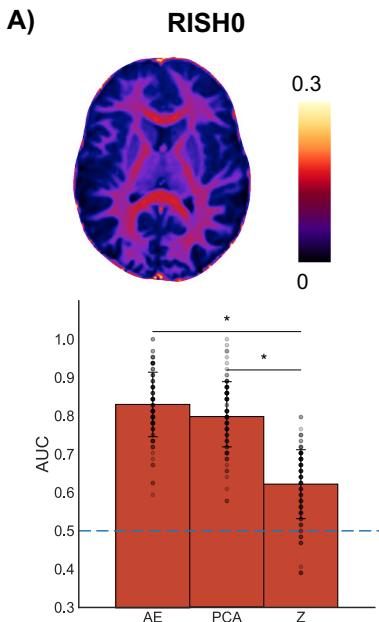
1. Wasserthal J. et al. *Neuroimage* (2018)

2. Chamberland M. et al. *Nature Computational Science* (2021)



Discriminating power

## White-matter anomaly detection in CNV participants



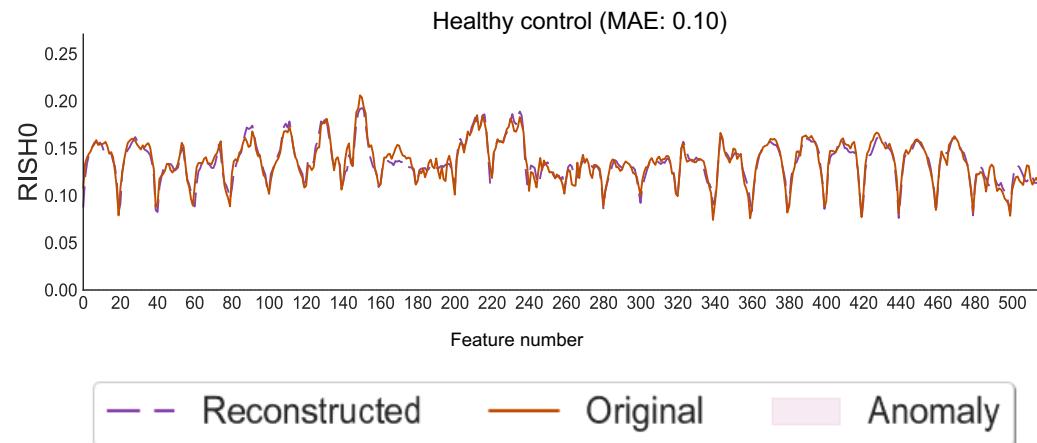
90 healthy controls children (HC)  
8 children with copy number variants (CNV)  
Train: 80% HC, repeat 100x

Consistent locations but not required

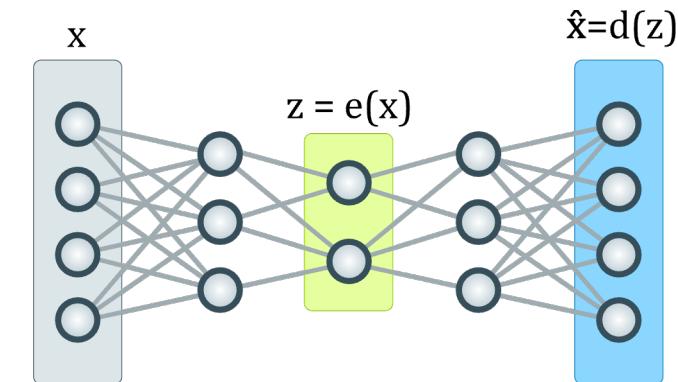


Tract-specific deviations

# White-matter anomaly detection in CNV participants



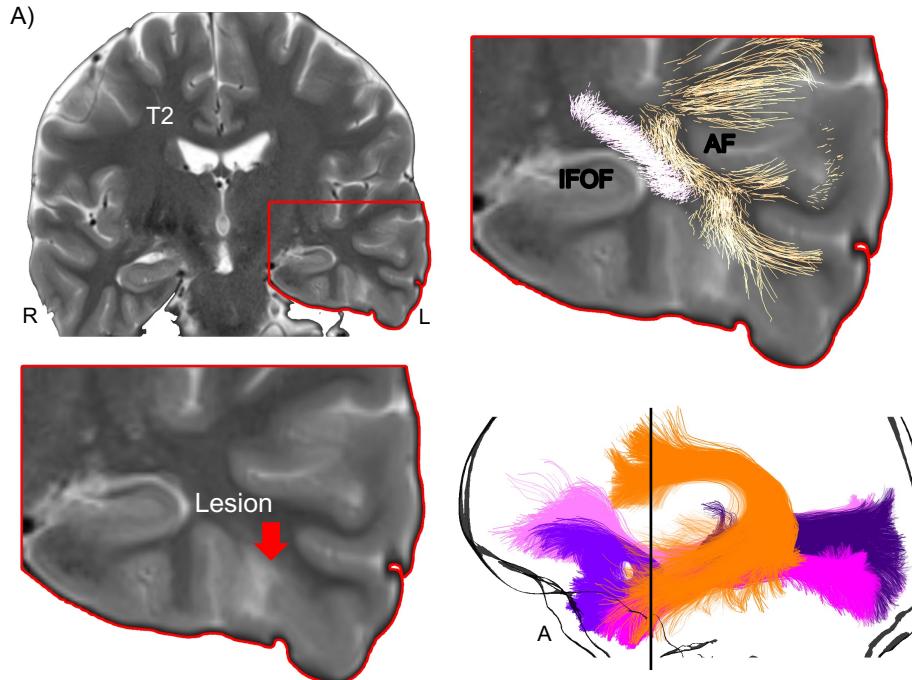
MAE: Mean Absolute Error





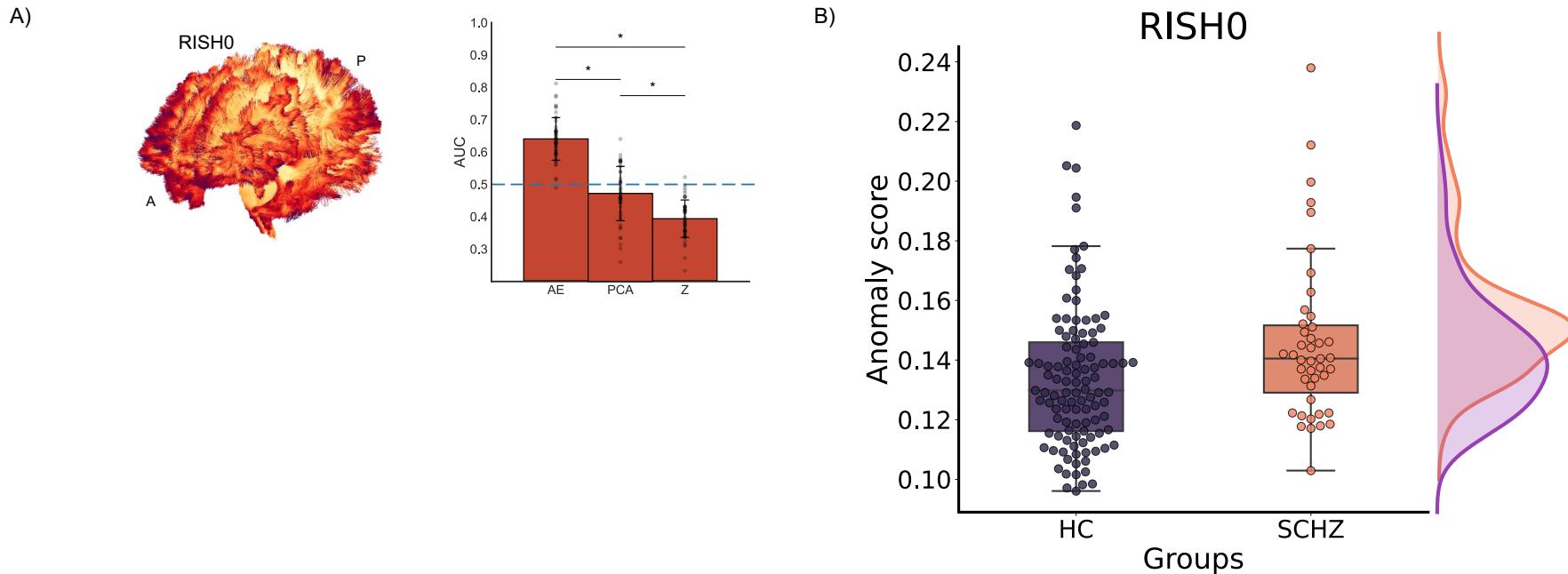
Focal cortical dysplasia

## White-matter anomaly detection in epilepsy



75 healthy controls  
1 epilepsy patient

# Linking brain heterogeneity with epidemiological findings in schizophrenia



Challenging task at hand → a supervised support vector machine classifier provides similar accuracy ( $AUC = 0.65 \pm 0.13$ )

109 healthy controls

43 schizophrenia patients

Train: 80% HC, repeat 100x

# Visual Analytics Framework

[github.com/chamberm/detect](https://github.com/chamberm/detect)



## Additional information

**Peer review information** *Nature Computational Science* thanks Laurent Petit, Daniel C. Alexander and the other, anonymous, reviewer(s) for their contribution to the peer review of this work.

**File Uploader**

Upload demographics  
Drop files here to upload or browse files

Upload profiles  
Drop files here to upload or browse files

Savename  
ANALYSIS\_01

Choose a metric below  
RISH0

Choose a patient group below  
2

Method  
 Z-score  
 PCA  
 AutoEncoder  
 SVM

Iterations  
50 - +

Regress confound?

**Run**

**Detect**

A deep learning based anomaly detection framework for Tractometry.  
Author: Maxime Chamberland ([chamberm.github.io](https://chamberm.github.io))

**1. Analysis**

**1. Visualisation section**

Show demographics  
 Show dataset

**Tract-profiles datasheet**

	Group	CID	AF_left_01	AF_left_02	AF_left_03	AF_left_04	AF_left_05
0	0	C010	0.0778	0.1207	0.1317	0.1329	0.1291
1	0	C011	0.0659	0.1002	0.1240	0.1274	0.1293
2	0	C012	0.0653	0.1031	0.1344	0.1438	0.1423
3	0	C013	0.0609	0.0931	0.1208	0.1286	0.1344
4	0	C014	0.1044	0.1223	0.1277	0.1341	0.1441
5	0	C015	0.0698	0.1152	0.1364	0.1439	0.1459
6	0	C016	0.0709	0.1211	0.1271	0.1283	0.1335
7	0	C017	0.0677	0.1265	0.1300	0.1063	0.1098
8	0	C020	0.0620	0.0994	0.1266	0.1349	0.1378

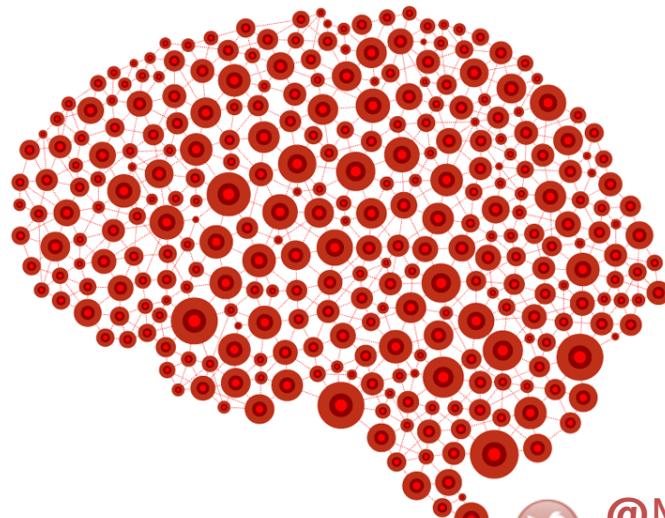
**2. Report**

**Model Loss**

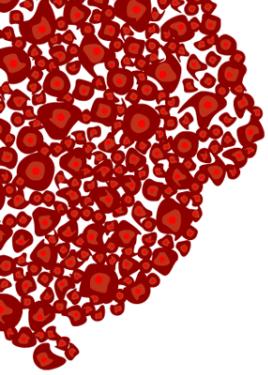
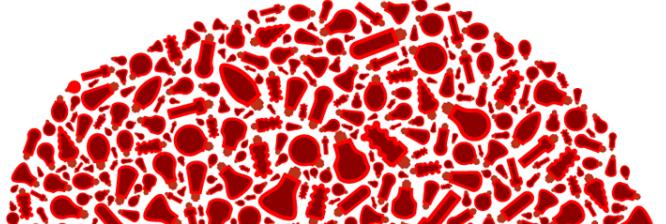
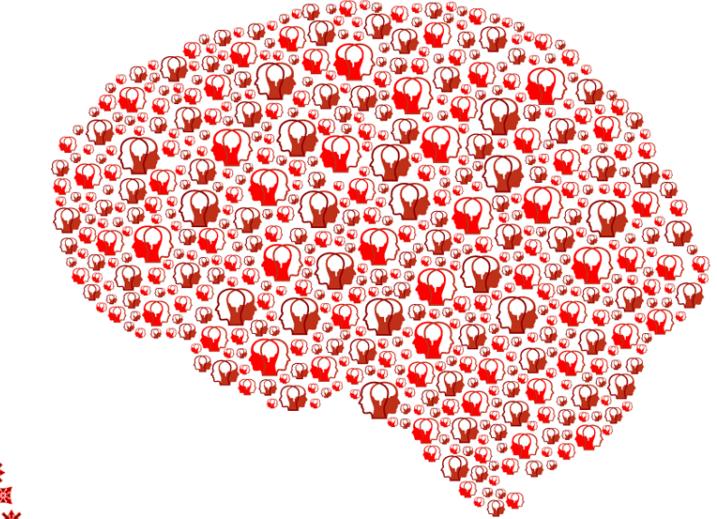
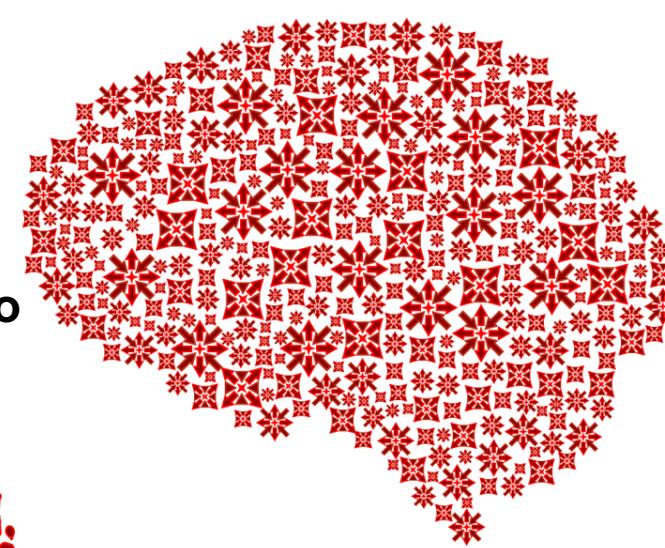
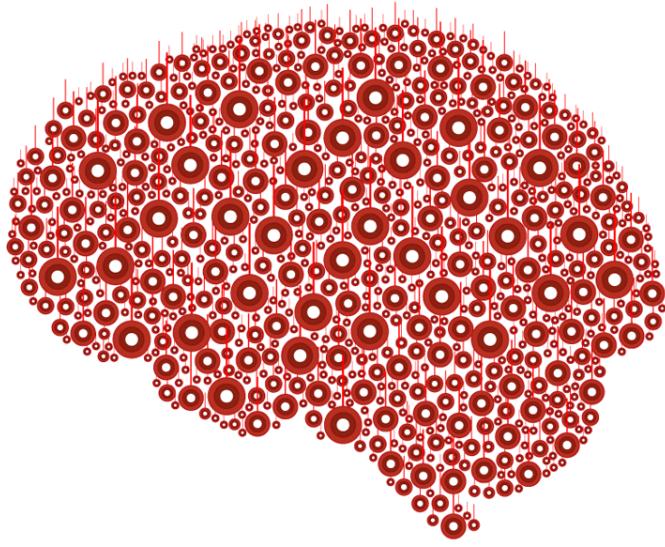
Loss  
Epoch

**AutoEncoder**

Density estimate  
Mean absolute error (MAE)  
Individuals



@MaxChamb  
[chamberm.github.io](https://chamberm.github.io)



[www.ru.nl/donders](http://www.ru.nl/donders)

[maxime.chamberland@donders.ru.nl](mailto:maxime.chamberland@donders.ru.nl)