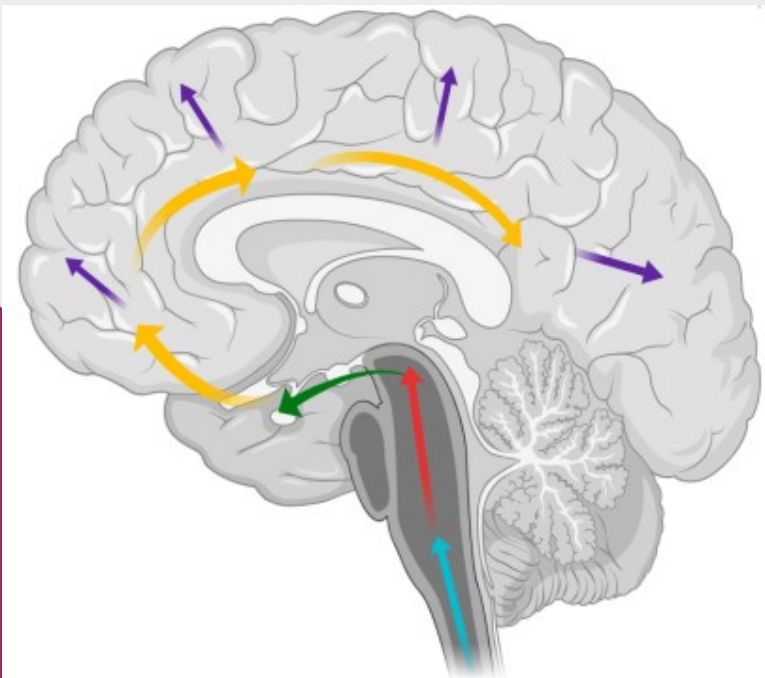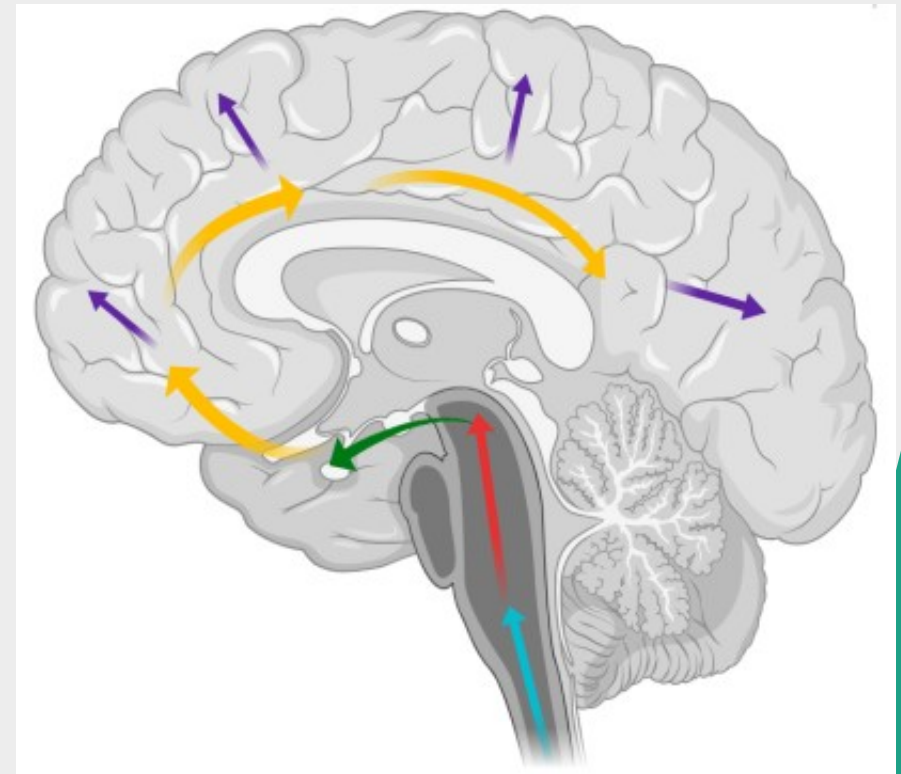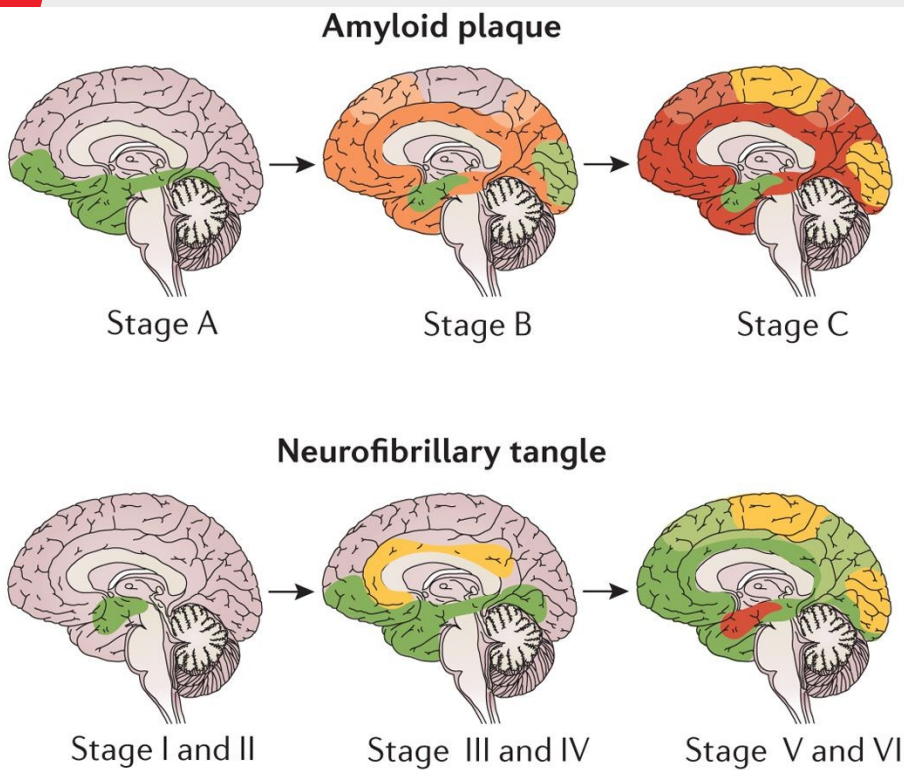# Spreading Models of Misfolded Proteins on Connectomes at the time of Pasta Cacio e Pepe
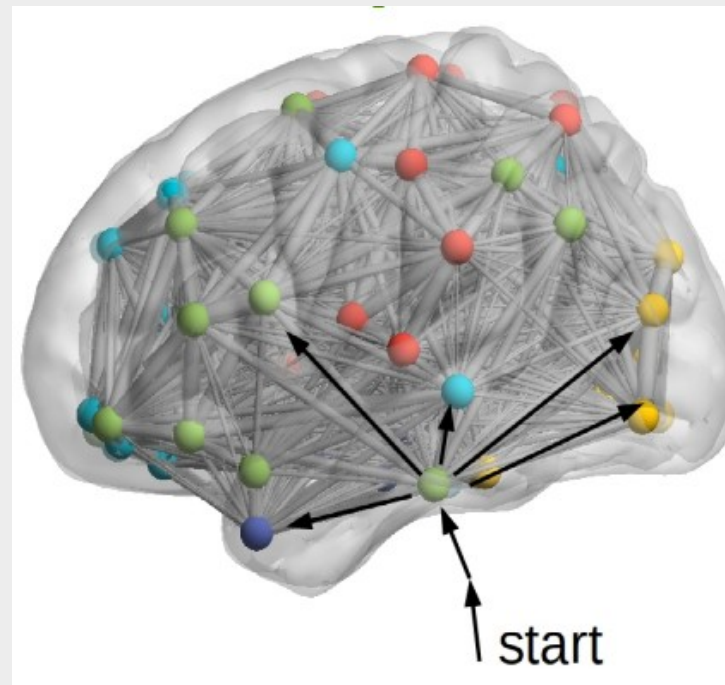
Alessandro Crimi   Eleanna Kara

Alzheimer and Parkinson dynamics

- Parkinson and Alzheimer disease are neurodegenerative diseases characterized by spreading of misfolded proteinsacross the brain.
- We would like to study how this spreading occur.

Amyloid plaque

Stage A → Stage B → Stage C

Neurofibrillary tangle

Stage I and II → Stage III and IV → Stage V and VI

Braak Hypothesis

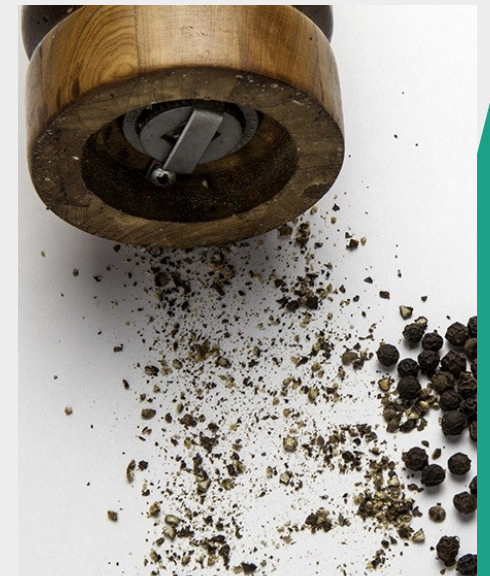## Studied in Autopsies but still controversial

What we can do?

- We have the structural connectomes from the ADNI and PPMI dataset

- We can validate spreading models (Python/Matlab)

$$X(t) = \exp^{-\beta L t} X(t-1) + X(t-1)$$

- And compare them to PET tracers or brain atrophy.

- There are also genetic data on the ADNI and PPMI dataset so, we can cross-validate

  spreading with known genes or GWAS.

- Or?

Crimi and Kara, «Spreading model for patients with Parkinson disease based on Connectivity differences»
IEEE ISBI 2019

https://github.com/alecrimi/misfoldedproteins_connectome
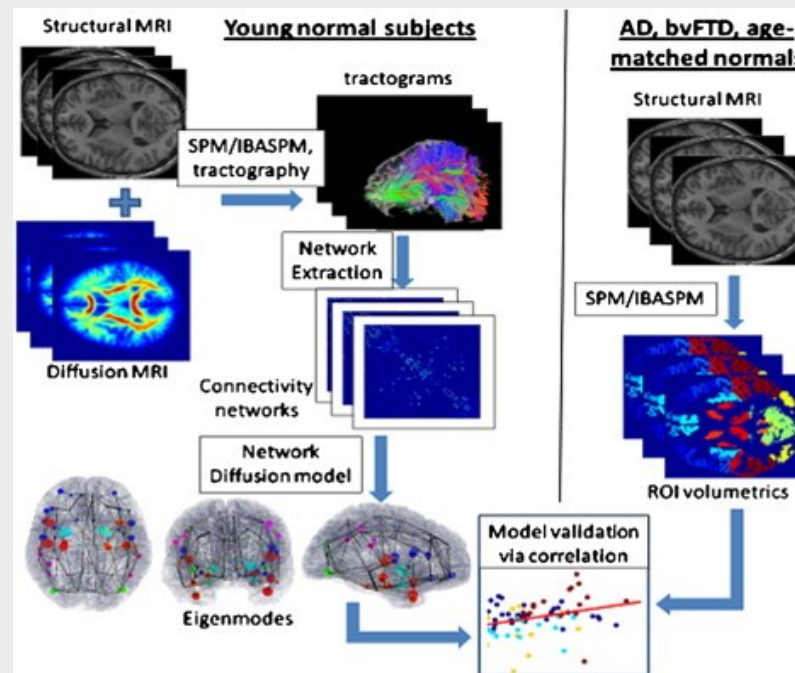
 @dr.alecrimi

 @Dr_Alex_Crimi

alessandro.crimi@usz.ch

BrainHackZurich

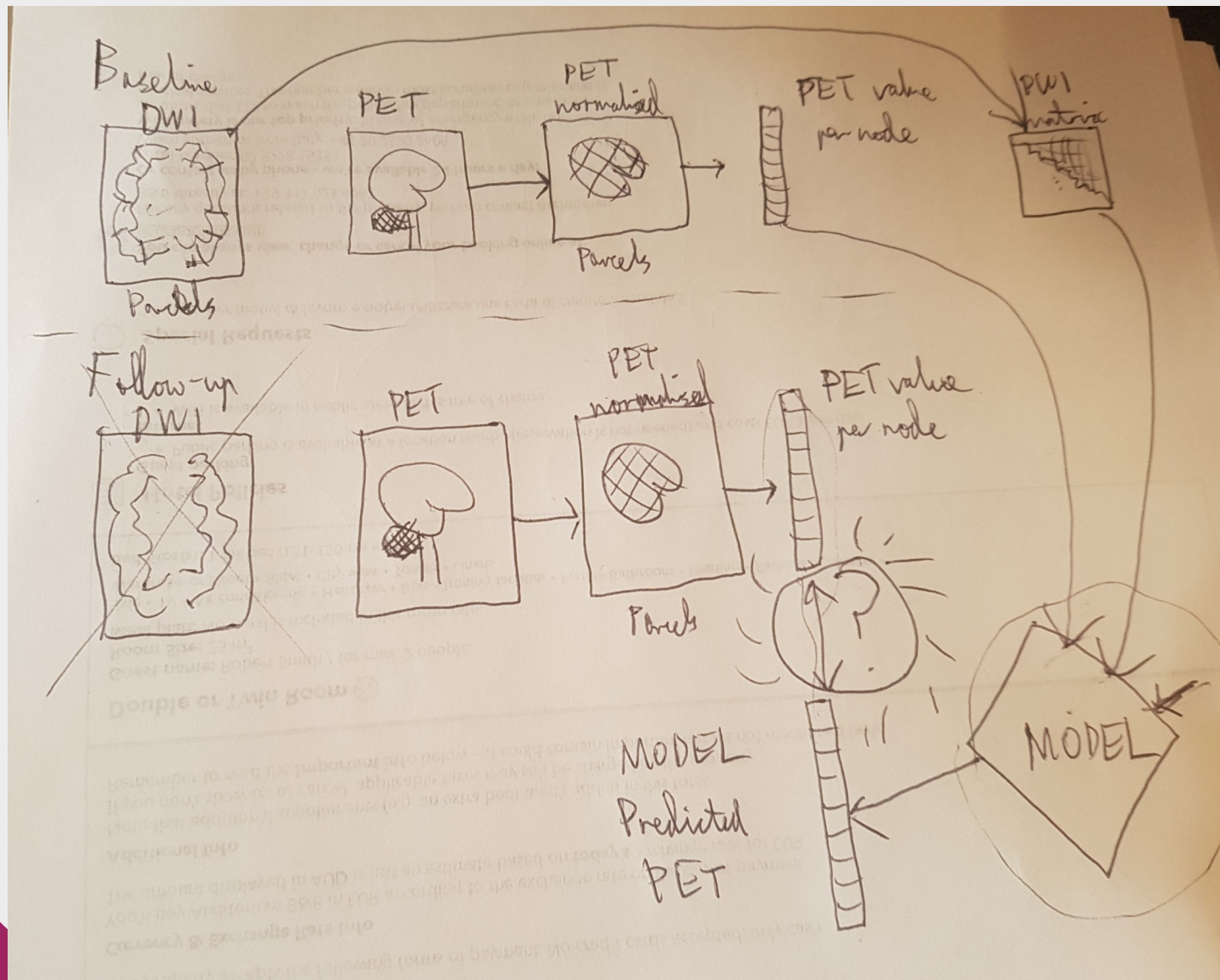## October 3rd/4th 2019

www.brainhackzurich.ch

What we have learnt

- Many things still unkown from neuropathology
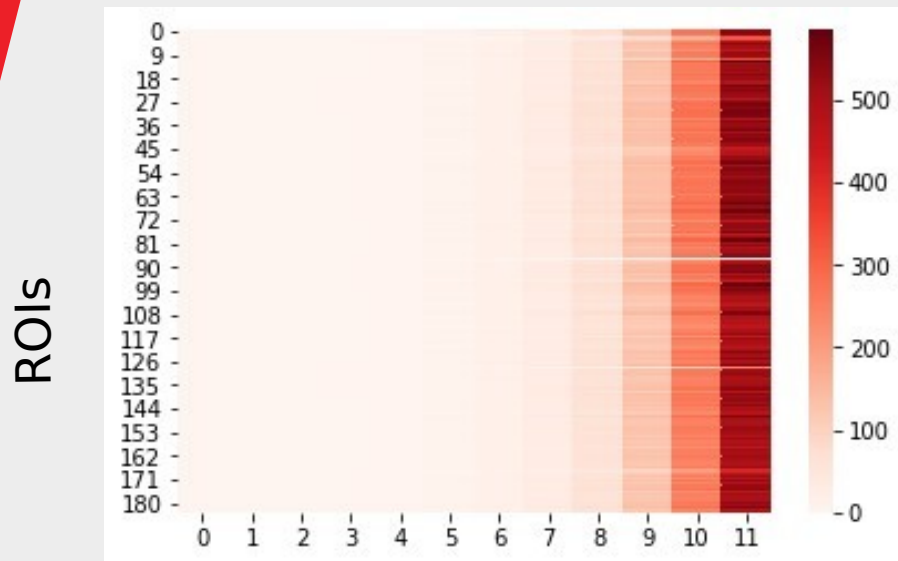- Validation of pathological spreading can still improved

What we came up
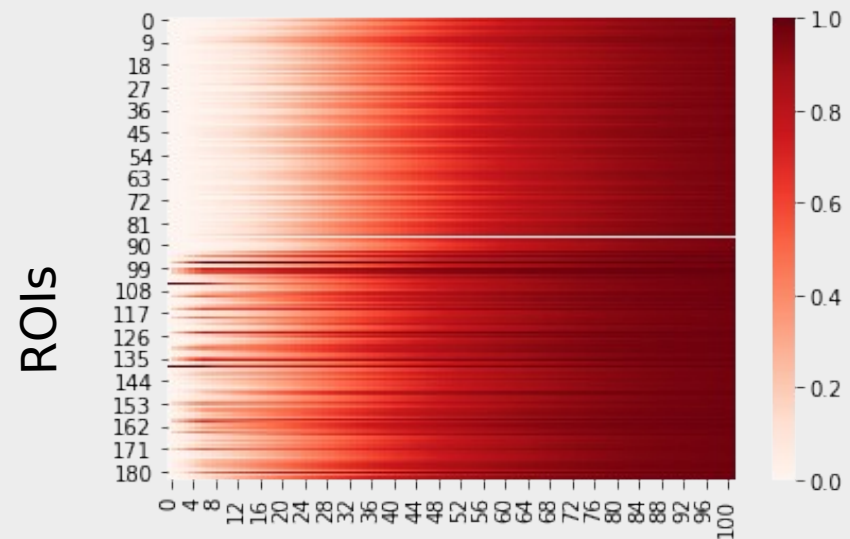
- Analog workflow from Robert

HeatKernel based spreading

- Tested only on ADNI dataset (subset)

Next steps

- Fix the other code(s)

- Compare all methods

- Do the same on the Parkinson and ALS dataset

- https://github.com/alecrimi/misfoldedproteins_connectome