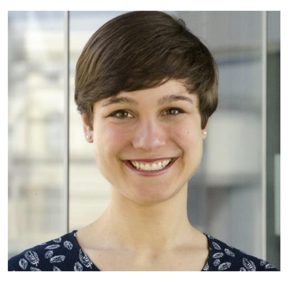

T191

Same brain, different look? – A scanner and preprocessing pipeline comparison for diffusion imaging

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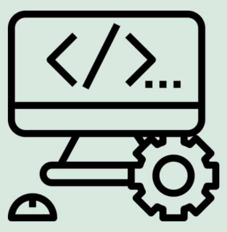
Problems

- **different MR imaging sites** or technical changes during **populational and longitudinal studies**
  → possible systematic errors biasing data analysis and interpretation

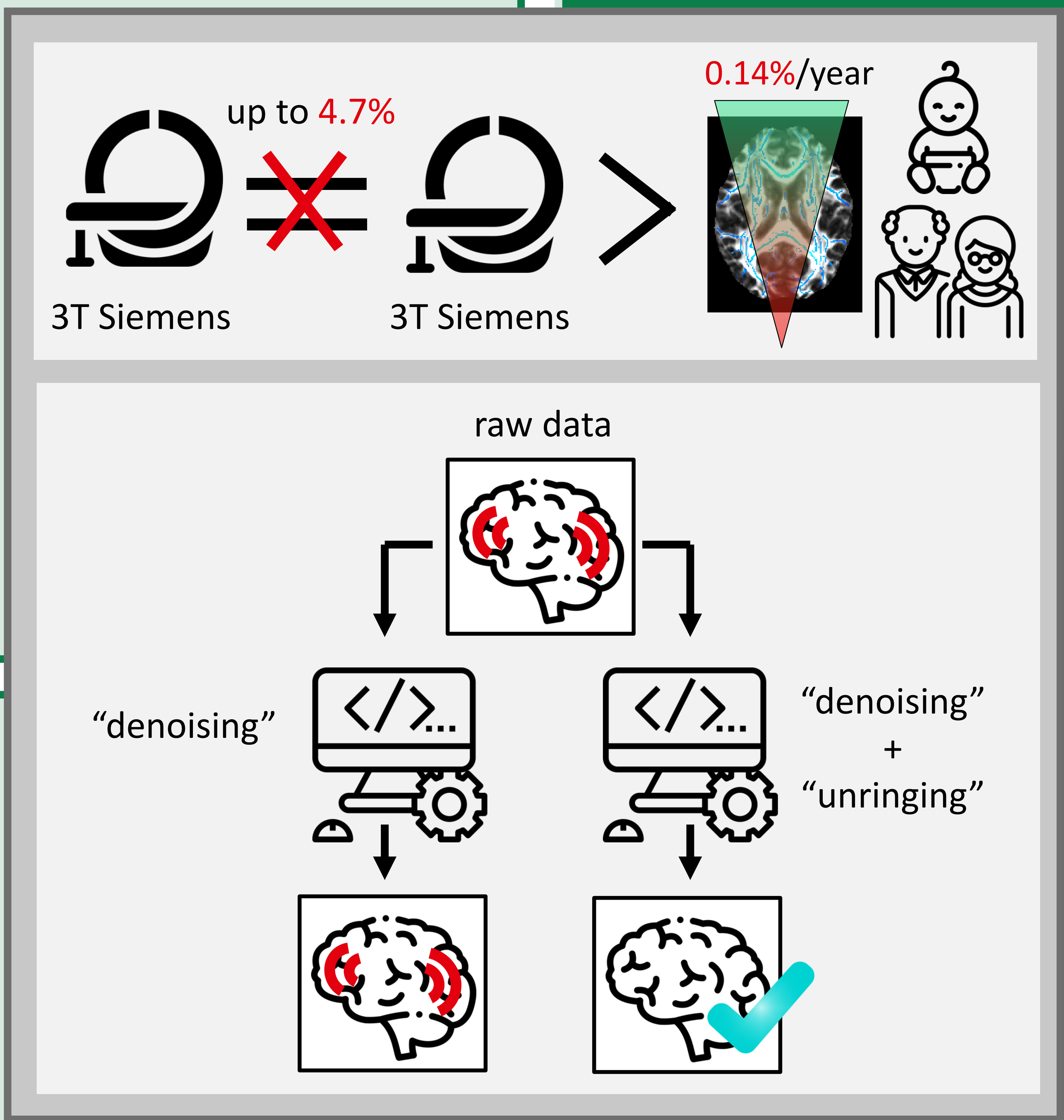
- **Gibbs-ringing** (GR), a common oscillation artefact, especially in diffusion-weighted imaging (DWI)
  → physically implausible negative diffusivity and **wrong fractional anisotropy** (FA) values



- **different preprocessing pipelines** for DWI data
  → can have severe influence on anatomical and structural measures

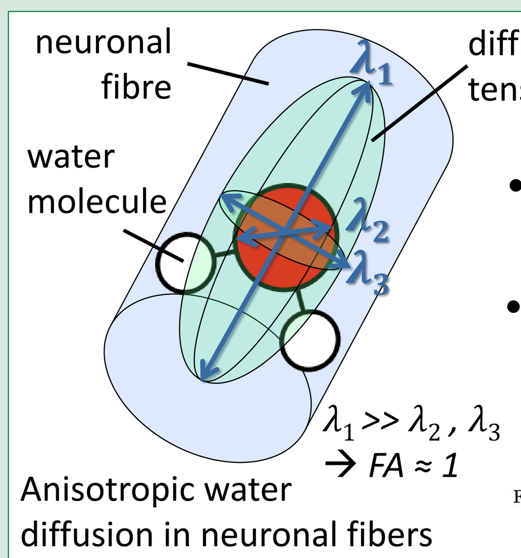
Approach

- same participants at different scanners
- two MRI scanners (3T Siemens Magnetom)
- preprocessing of DWI data with varying pipelines



Methods

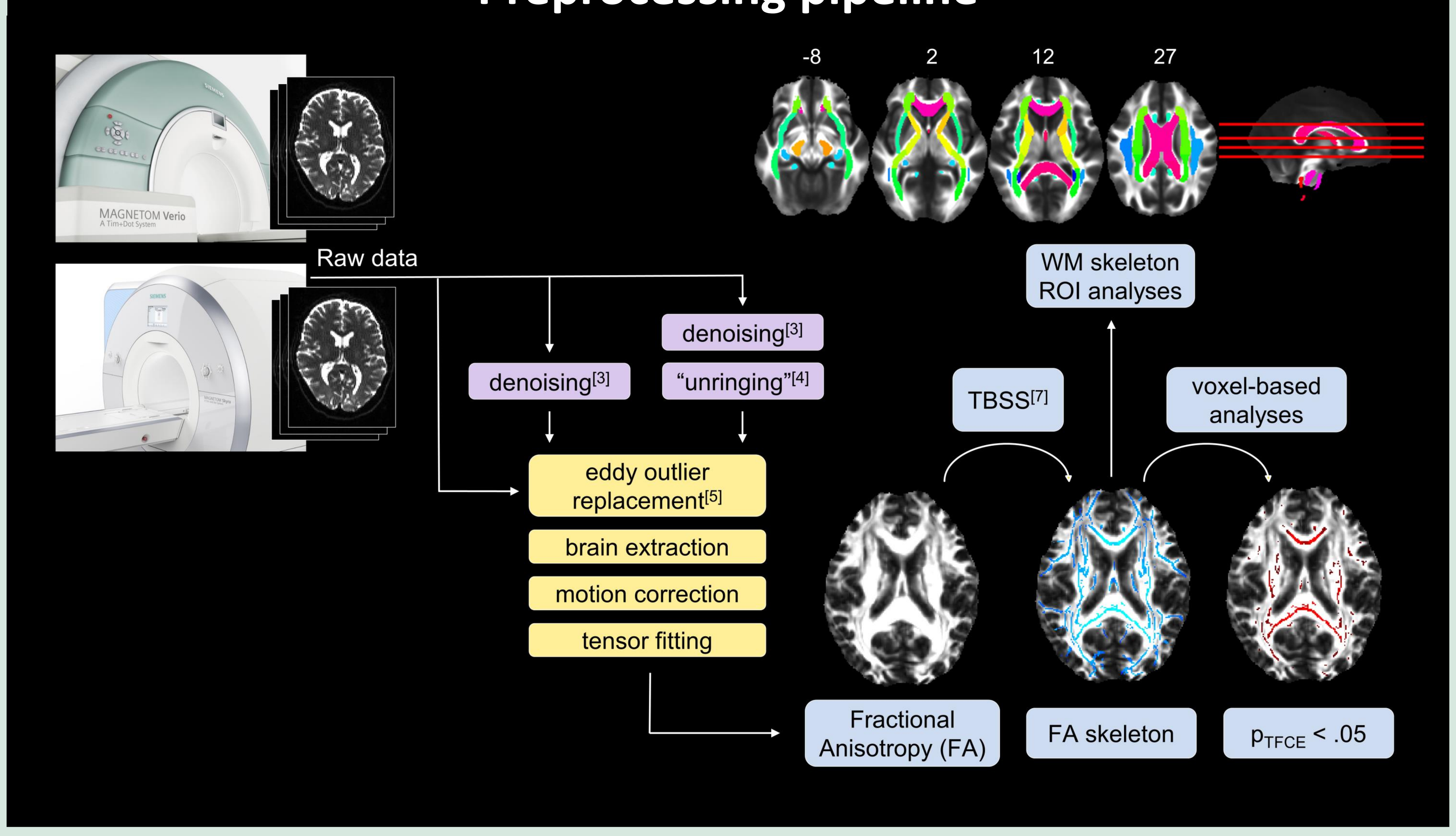
- DWI scans of 121 healthy participants (60f, 19-54 years)
- two different **3T Siemens Magnetom scanners** [1]: Verio and Skyra: b=1000, 60 dir, 7 b0, 1.7mm^3 isotropic, GRAPPA 2, bipolar, TE 100 ms, MB 1, raw filter, CMRR sequence [2]
- preprocessing pipelines include:
  - "denoising" (implemented in MRTRIX [3])
  - **removal of Gibbs-ringing** ("unringing" with Kellner tool [4])
  - eddy outlier replacement [5], motion correction and tensor fitting
- **FA values of whole brain WM skeleton** and within 8 regions of interest (ROI) (JHU DTI-based WM atlas [6] (1mm)^3): 4 in the corpus callosum (CC), superior longitudinal fasciculus and uncinate fasciculus (L and R respectively)
- tract-based spatial statistics (TBSS) [7] on WM skeleton
- statistics with Bayes Factor anova and Bayes Factor ttests



Fractional Anisotropy (FA)
- outcome measure from DWI
- information about white matter coherence

$$FA = \sqrt{\frac{1}{2}}\frac{\sqrt{(\lambda_1-\lambda_2)^2+(\lambda_2-\lambda_3)^2+(\lambda_3-\lambda_1)^2}}{\sqrt{\lambda_1^2+\lambda_2^2+\lambda_3^2}}$$

Preprocessing pipeline



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Conclusions

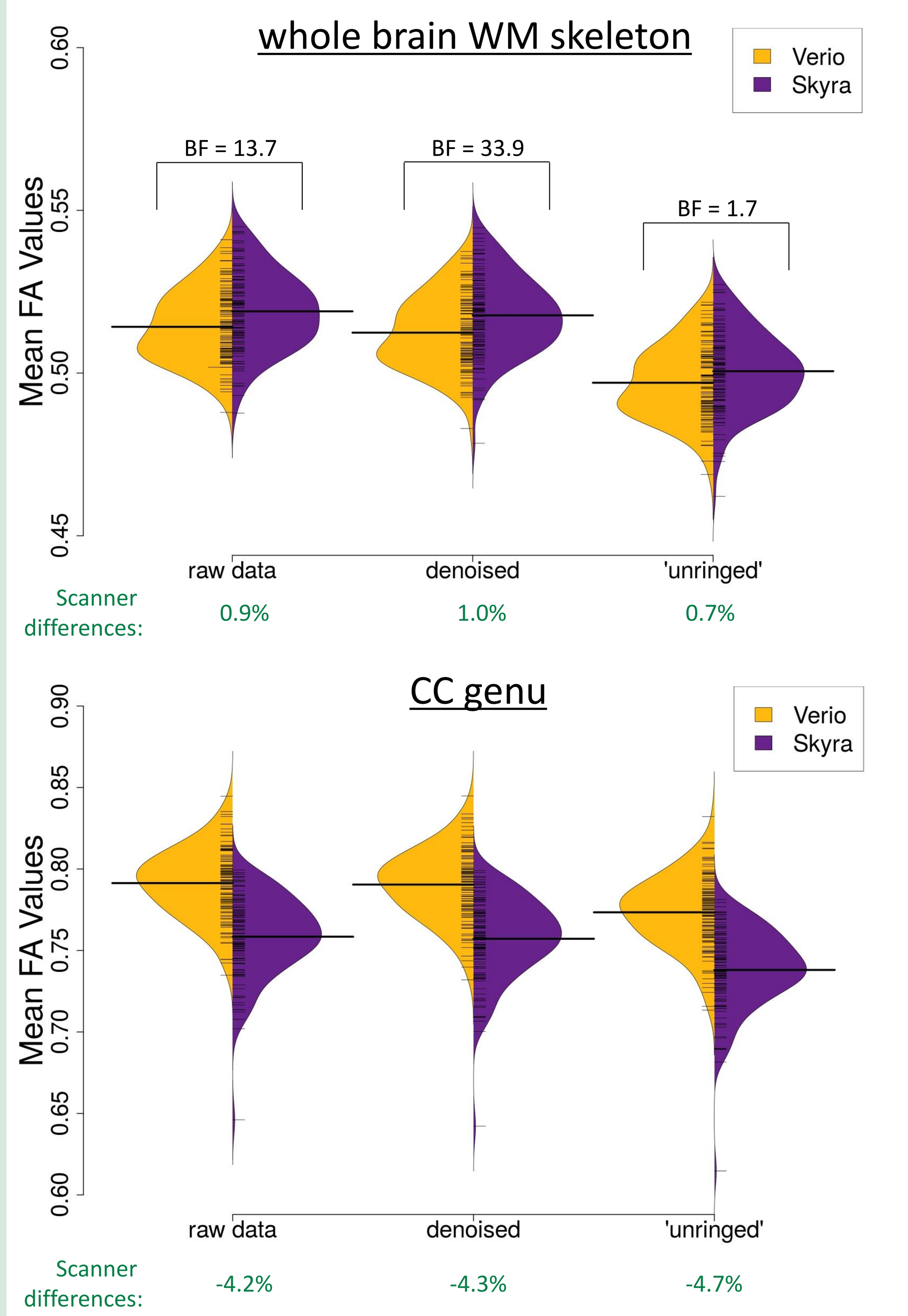
- MRI scanner of same manufacturer & field strength
  → large **difference of ~1%** of mean FA value on whole brain WM skeleton and up to 4.7% local difference
- use of whole brain **correction factor** not possible (suggested by Pohl et al. [9] to account for systematic error introduced by scanner differences) due to immense **regional variance** in differences across 8 ROIs
- effect size of scanner difference up to **33 times larger than age effect on FA** (decrease of 0.14%/year, estimated based on additional analysis of data from the LIFE Adult Study [8], n=1255)

- scanner differences in age effect strength
  → problematic for cross-sectional and longitudinal multi-site studies
- improvements by **reducing GR artefacts**
  → need of applying "unringing" with Kellner tool [4] as **standard step in processing DWI**

Results

- **global scanner difference up to 1%** in mean FA on whole brain WM skeleton (global)

Scanner comparison of mean FA values

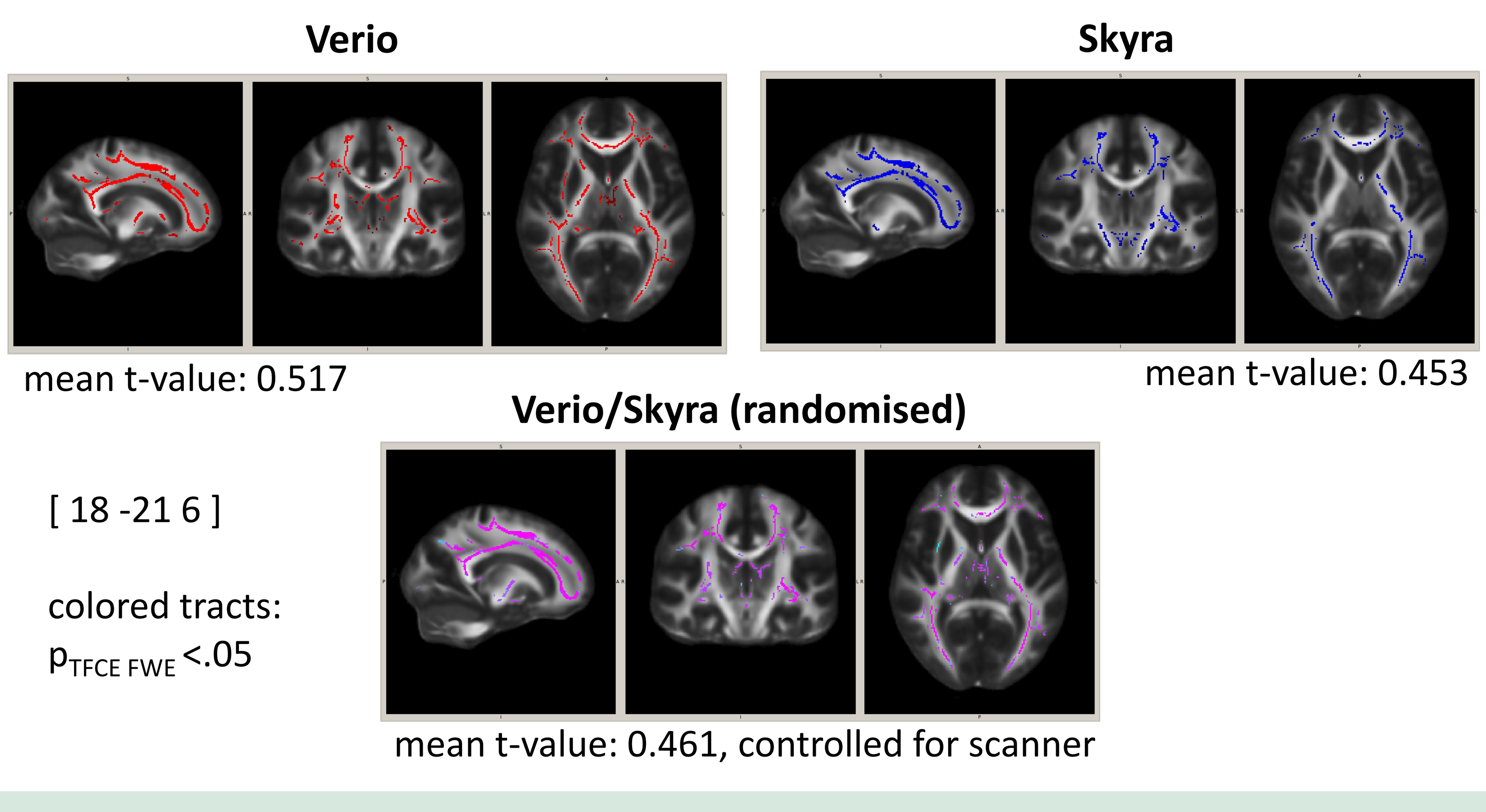


- **local scanner difference up to 4.7%** in CC genu (paired ttests: BF > 10^9)
- variations in sign and magnitude from ROI to ROI

- **GR artefacts** strongest in b0
- **"unringing"** [4] with Kellner tool reduces GR artefacts immensely
- # voxels with implausible FA values > 1 significantly lowered by "unringing" [4] (paired ttests: BF > 10^{10})

TBSS [7]:
- decrease of FA values as consequence of ageing
  → effect independent of preprocessing pipeline
  → **effect dependent of MRI scanners** (strongest in Verio, mean t-value: 0.517)

Negative age effect on FA compared between scanners (preprocessed with "unringing")



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