

A full DTI pipeline with quality control steps in AFNI-FATCAT (and implementing other software)

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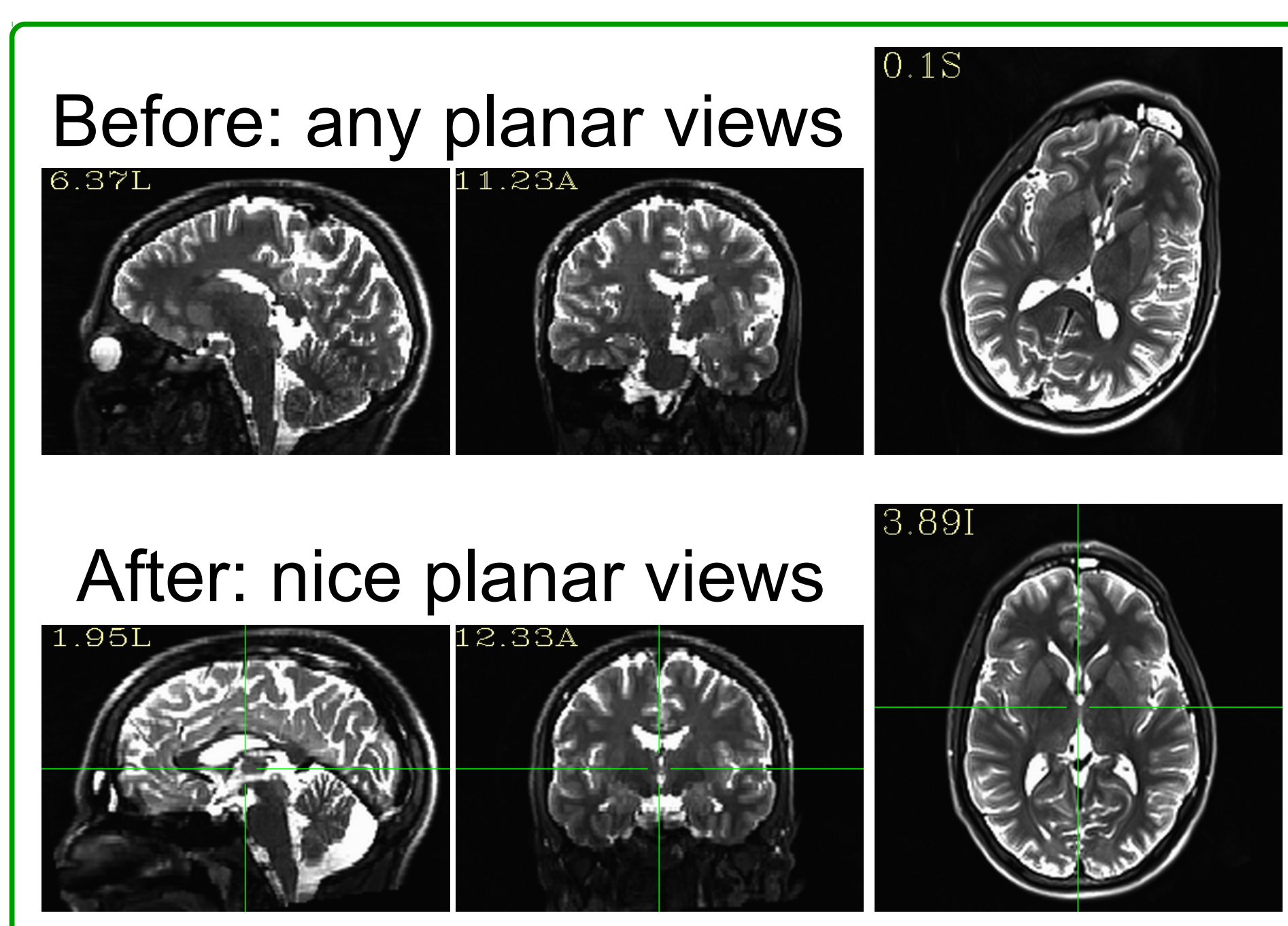


Scriptable pipelines are great. They facilitate clear reporting, reproducibility for others, redoing analyses, recording exact steps, and replicating steps across a study.

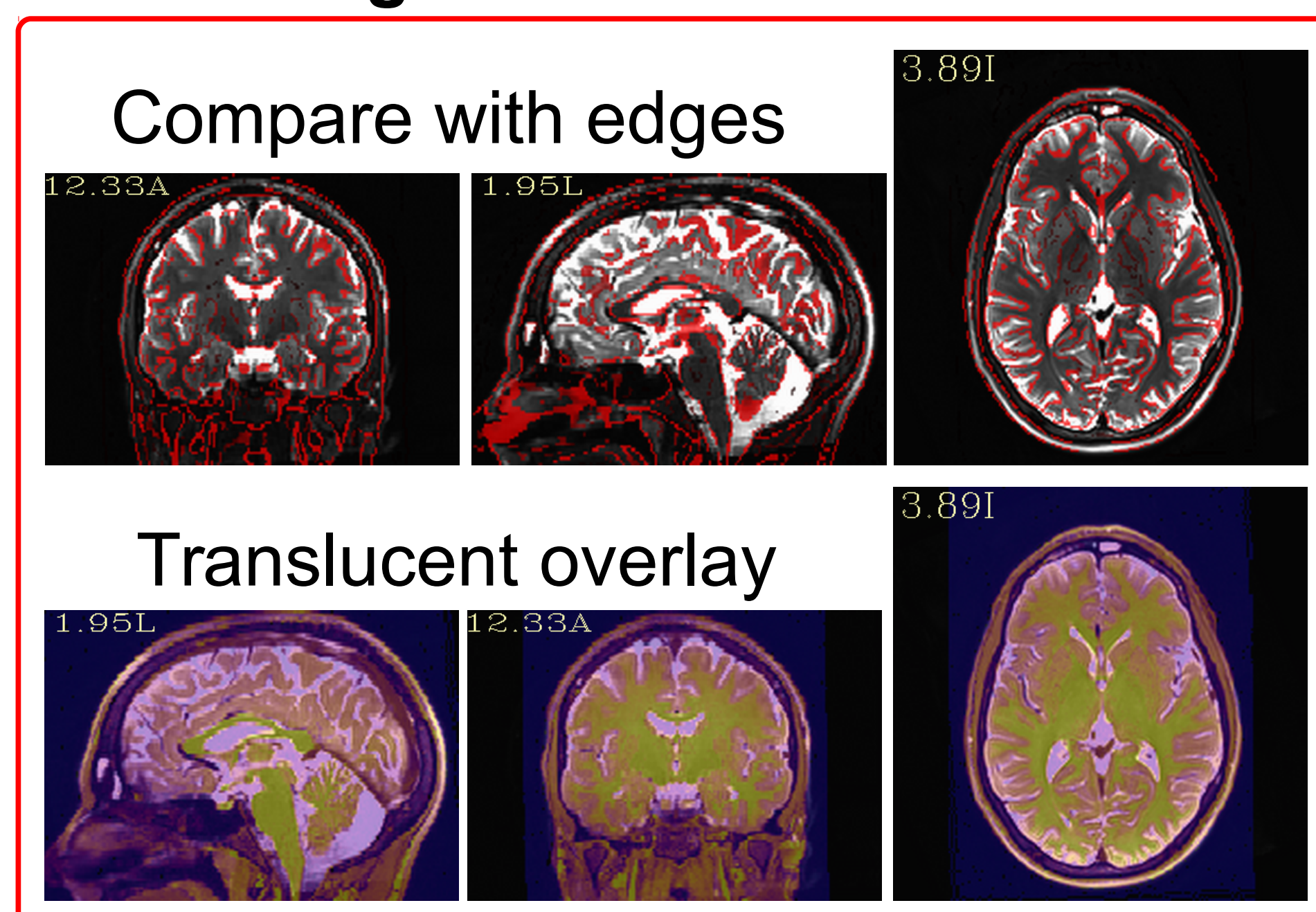
Here is a set of new, easy-to-use commands in AFNI-FATCAT^{1,2} to provide a full DTI analysis pipeline, integrating with SUMA^{3,4} and other scriptable software tools: *dcm2niix*⁵ (now distributed with AFNI), *TORTOISE*⁶ (yes, now scripty!) and *FreeSurfer*⁷.

The new tools include useful steps for preparing data for group analyses and quality control (QC), such as automated visual feedback (saving systematic images for easy comparison) and quantitative evaluation.

Axialization



Align anatomical vols



Select+filter bad DWI volumes

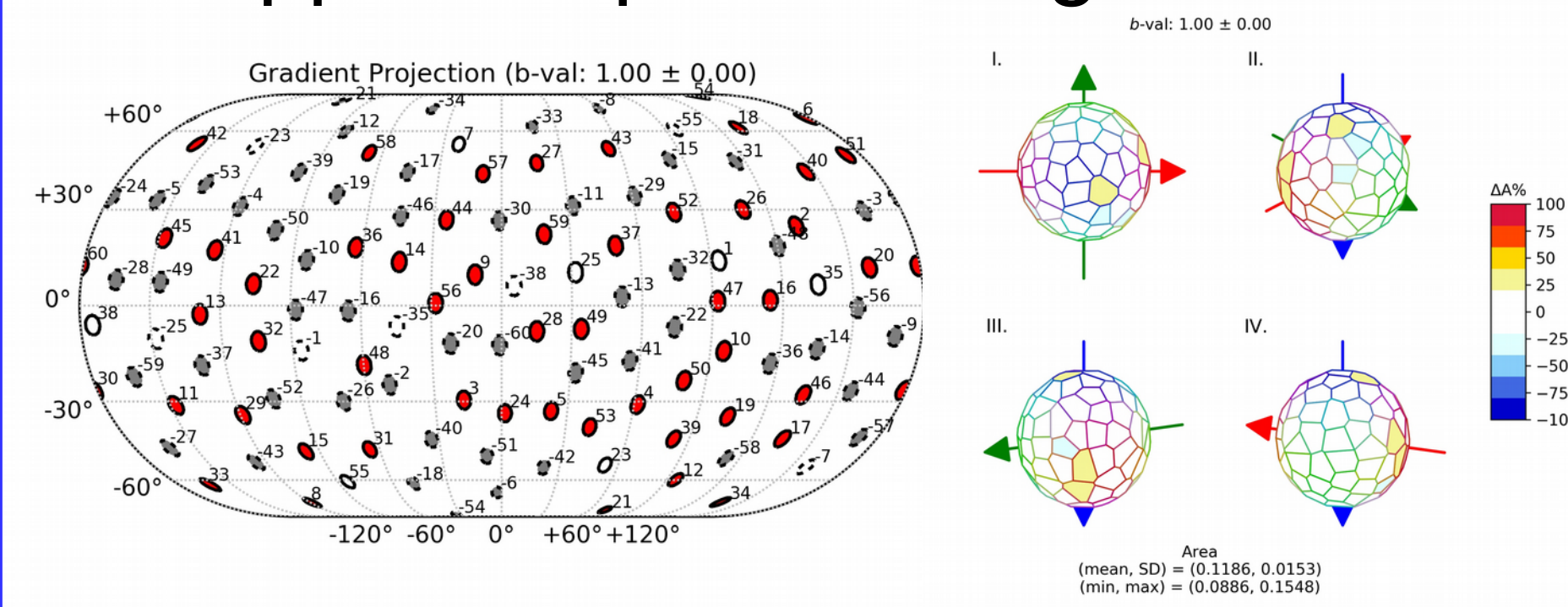
Interactive volume selection, create list combining AP+PA sets, apply to vols and bmatrix files



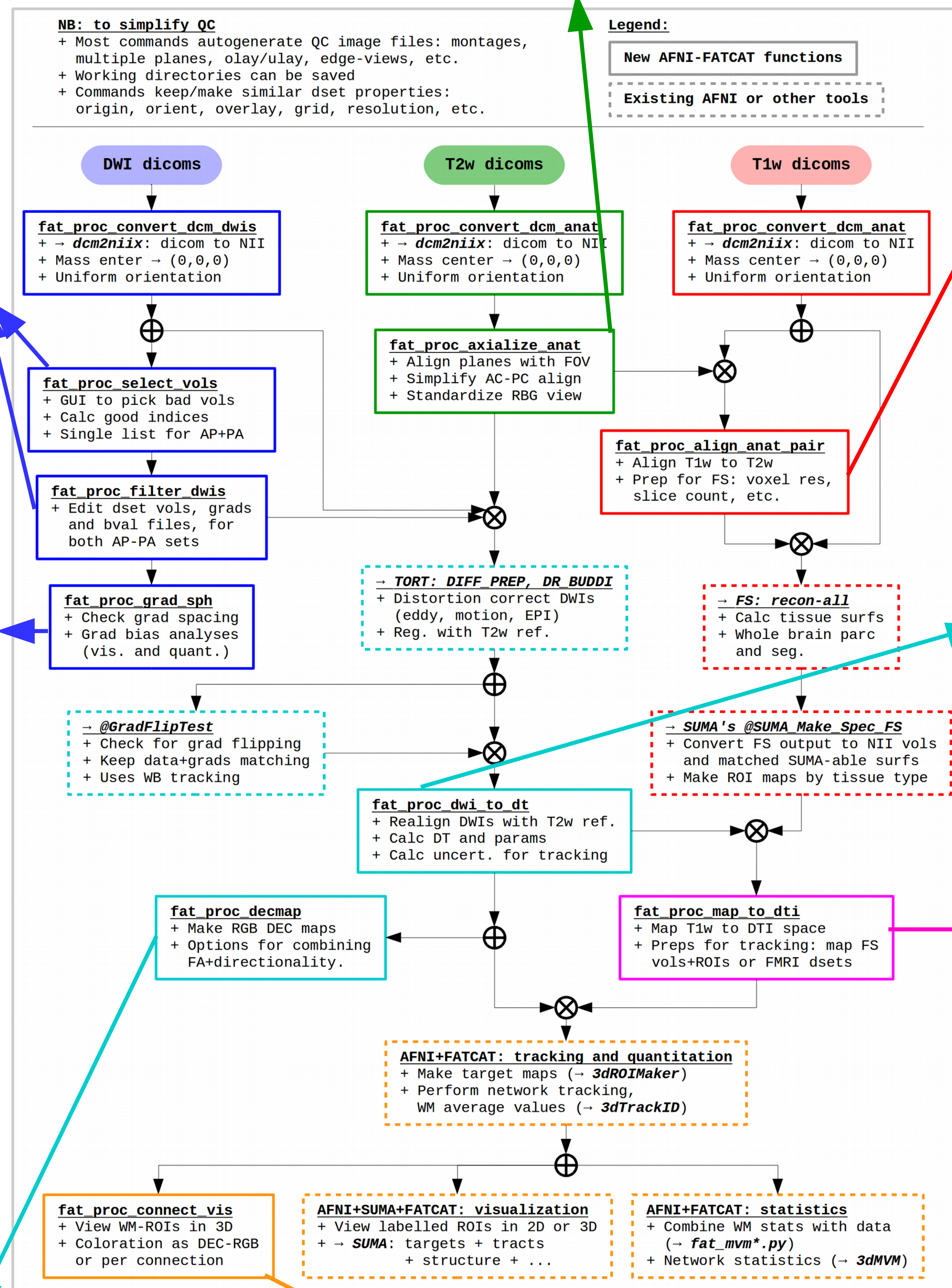
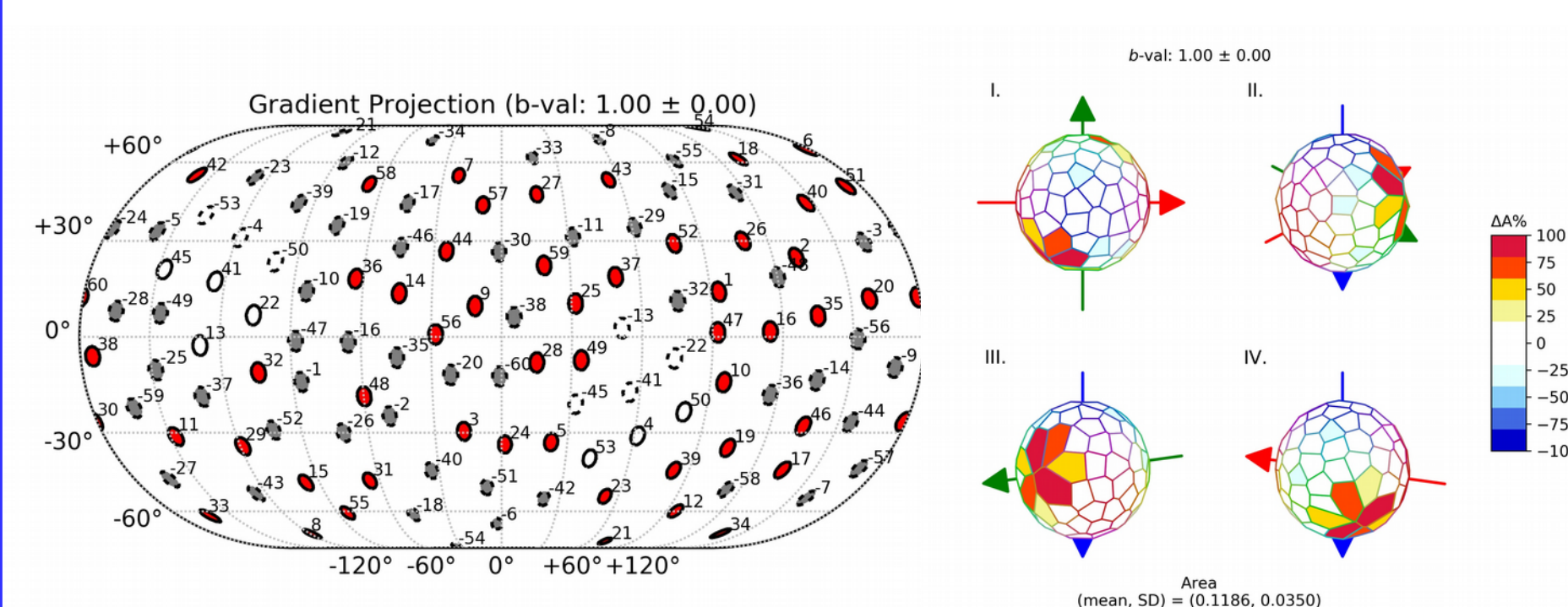
Check gradient coverage per subj

View and quantify isotropicity with spherical tessellation (can form regressors):

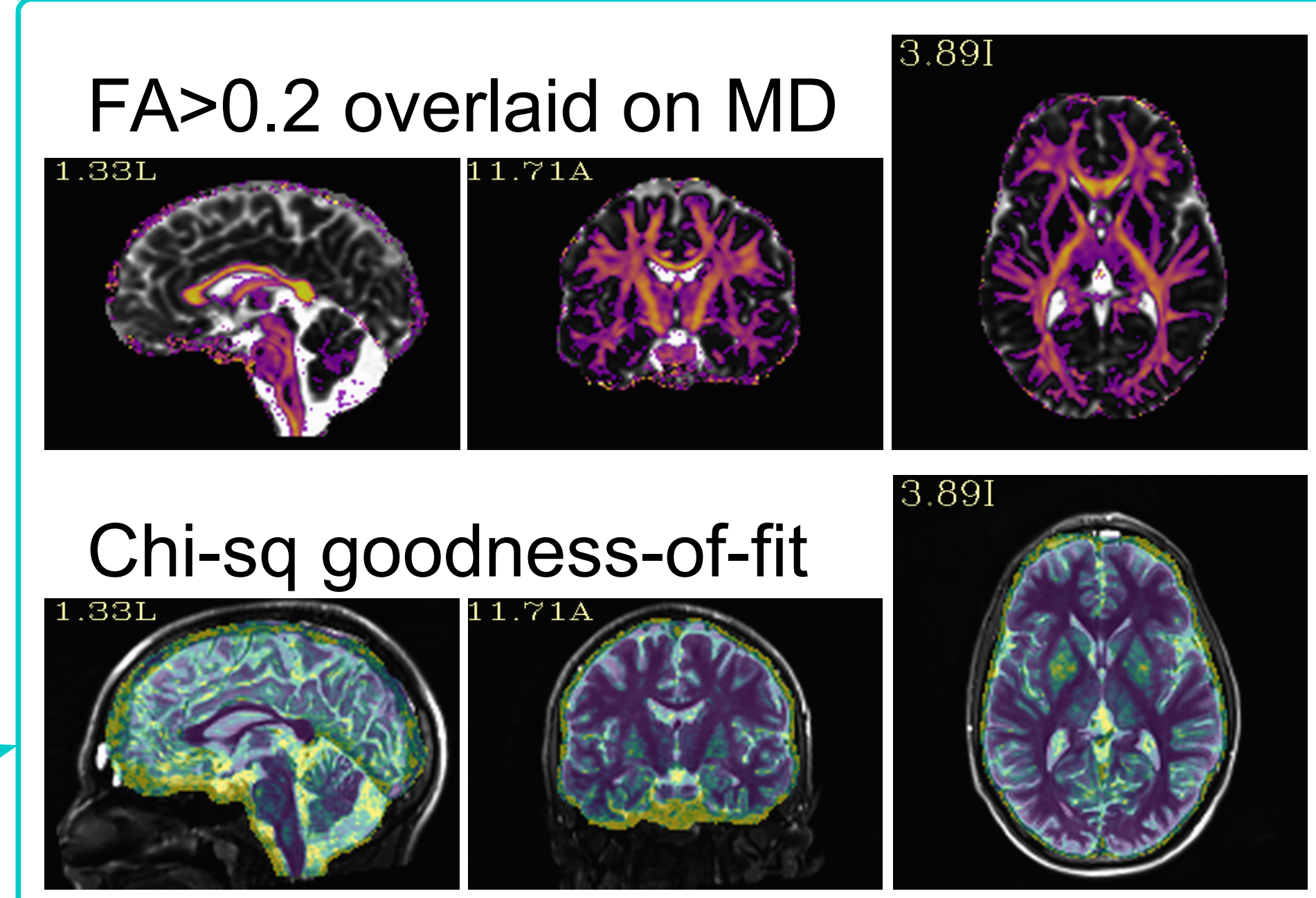
Ex. 1: random removal of 7/60 grads → approx. equal coverage



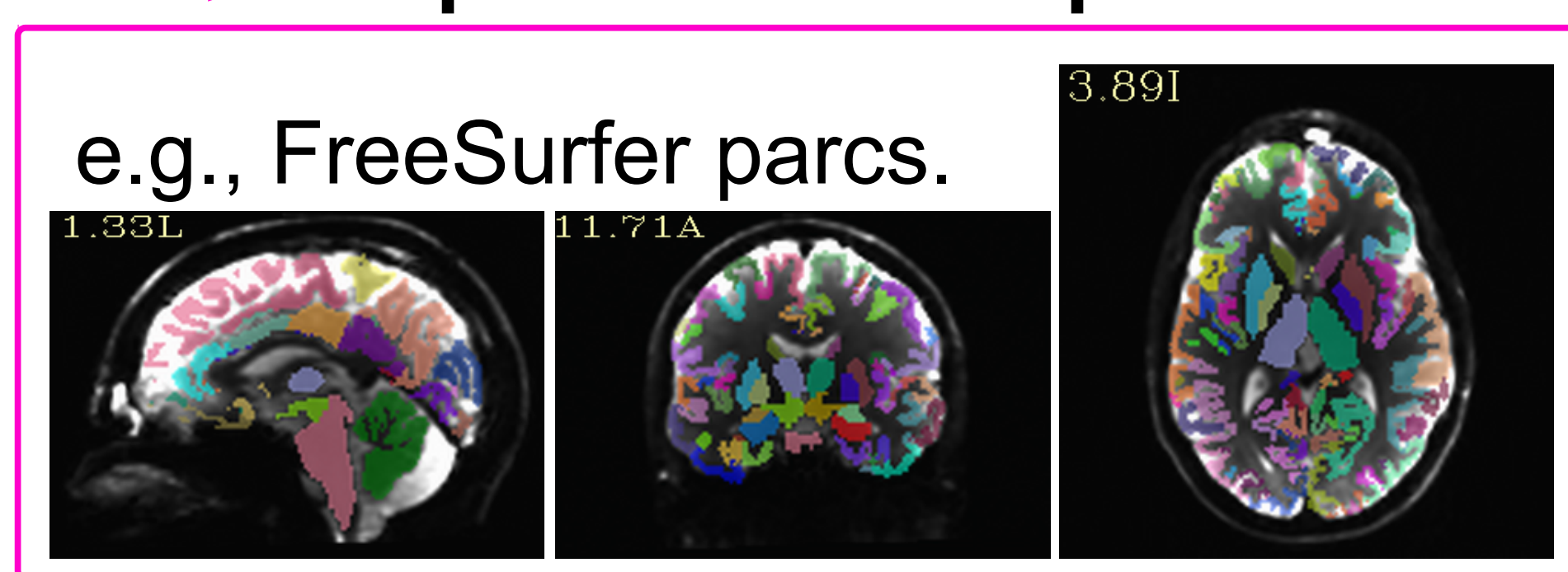
Ex. 2: "biased" removal of 7/60 grads → holes in coverage



DTI fitting and checking



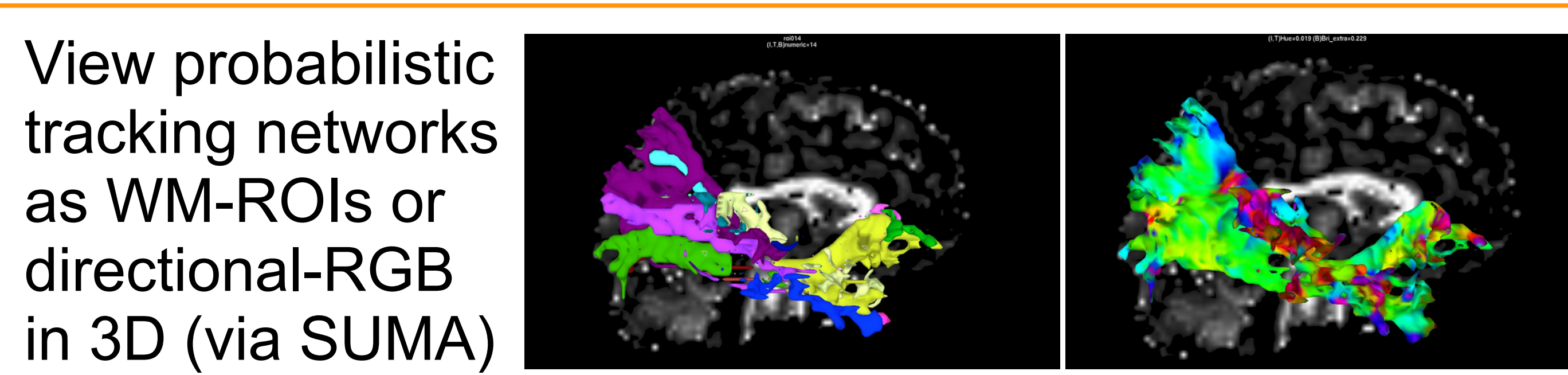
Map ROIs to DTI space



DEC maps



Volumetric WM viewing



References

- [1] Taylor PA, Saad ZS. 2013. Brain Connect 3:523-535.
- [2] Cox RW. 1996. Comput Biomed Res 29:162-173.
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- [4] Saad ZS, et al. 2004. IEEE ISBI, p. 1510.
- [5] Rorden C, Brett, M. 2000. Behav Neuro. 12, 191-200.
- [6] Pierpaoli C, et al. 2010. Proc. ISMRM 18, p. 1597.
- [7] Fischl B, et al. 2002. Neuron 33:341-355.

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