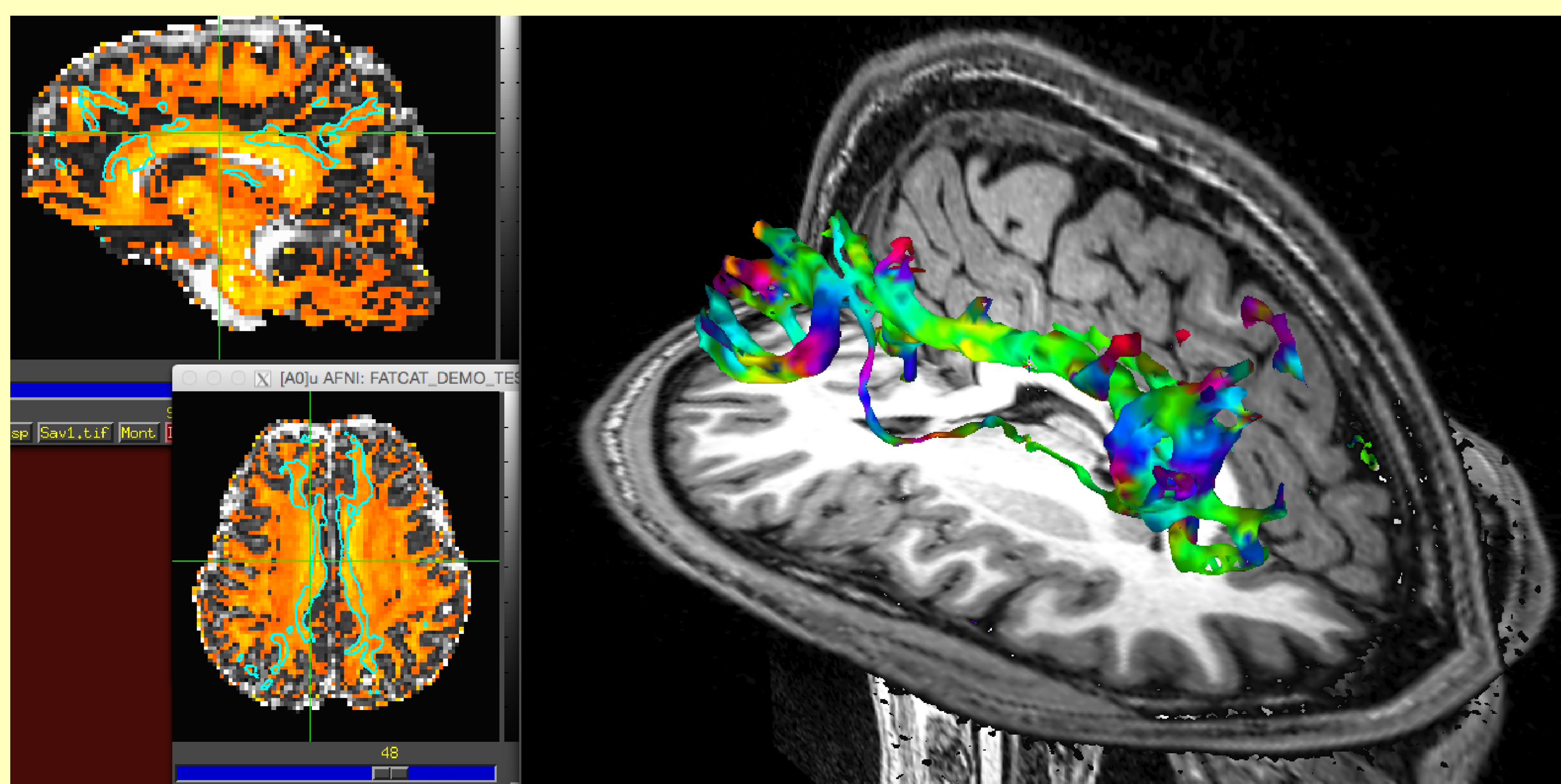


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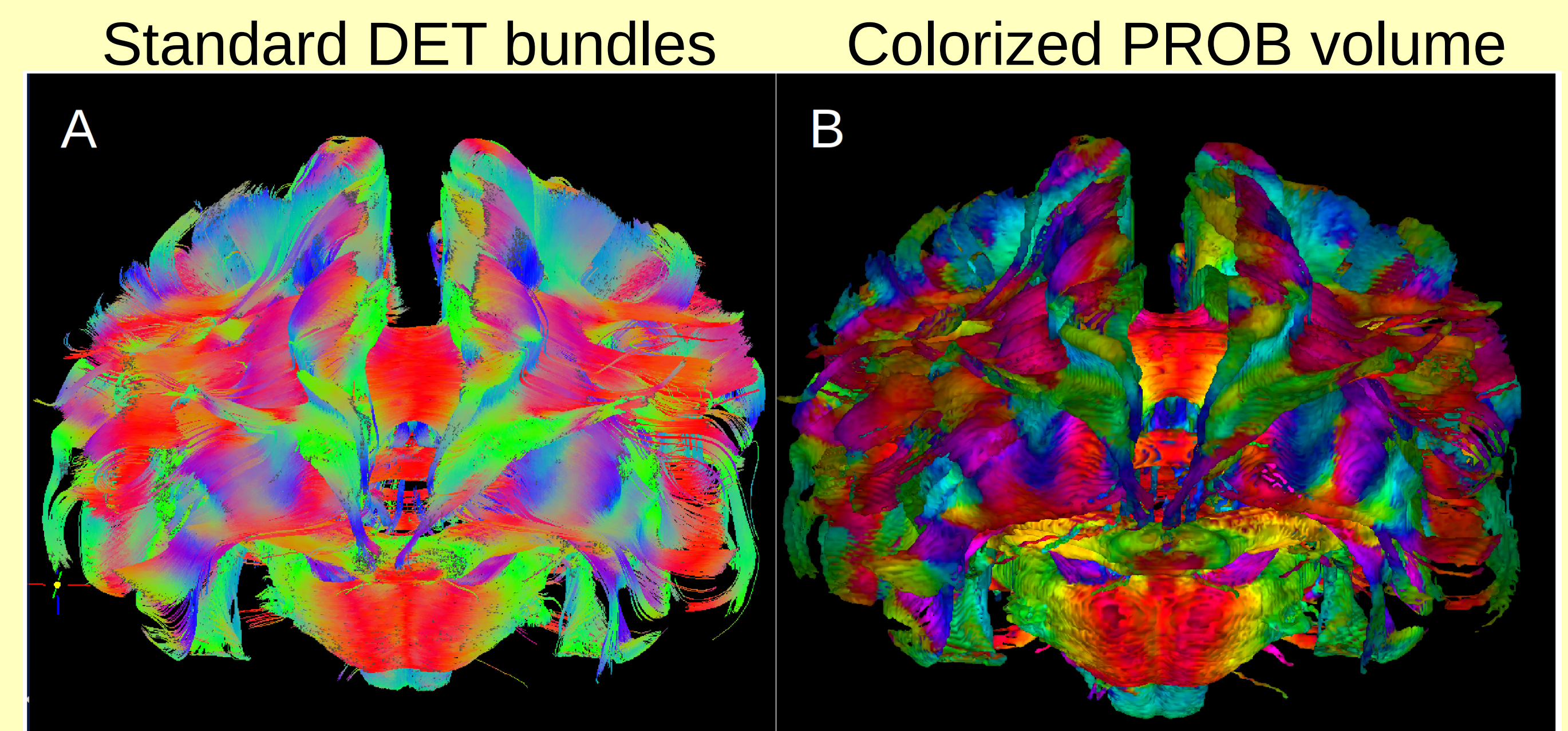
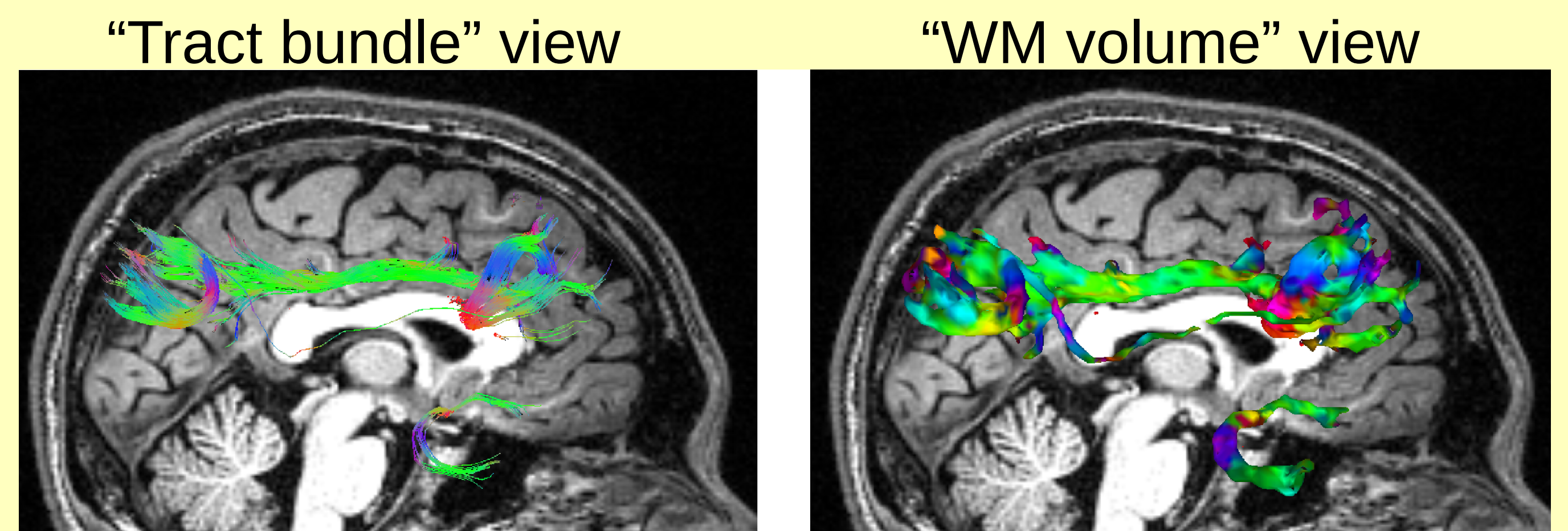


We describe new visualization and analysis tools for DTI and FMRI data in FATCAT¹, as part of AFNI² and interfacing with the 3D-viewer SUMA^{3,4}.

- In DTI analysis probabilistic tracking is more robust than deterministic⁵, but its outputs typically can't show information of directionality.
- New `@fat_tract_colorize` creates a smoothed surface of the tracked volume, converts V1 eigenvector to color representation, includes FA as optional brightness coloration, and opens AFNI+SUMA together with loaded volumes for viewing.



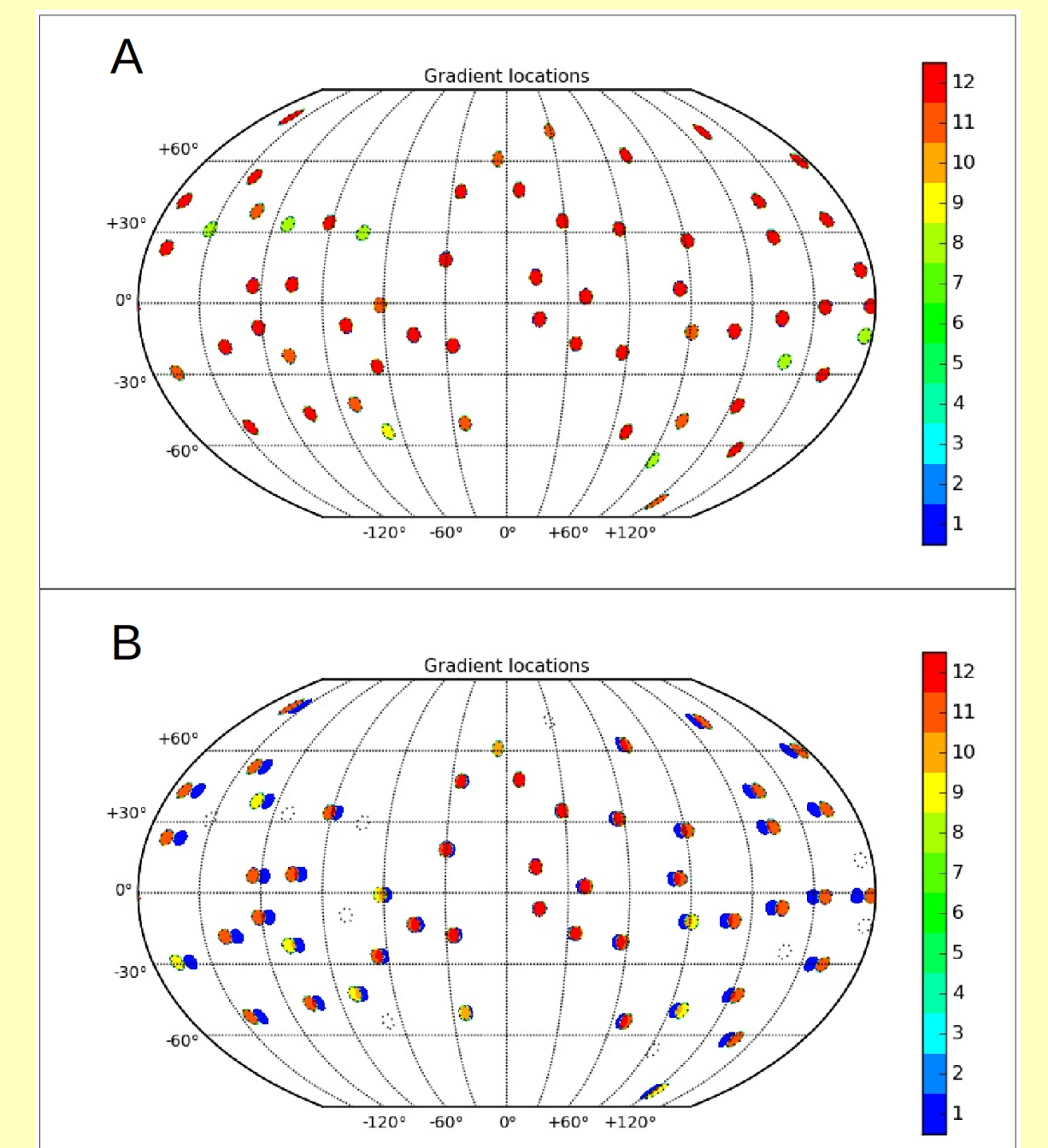
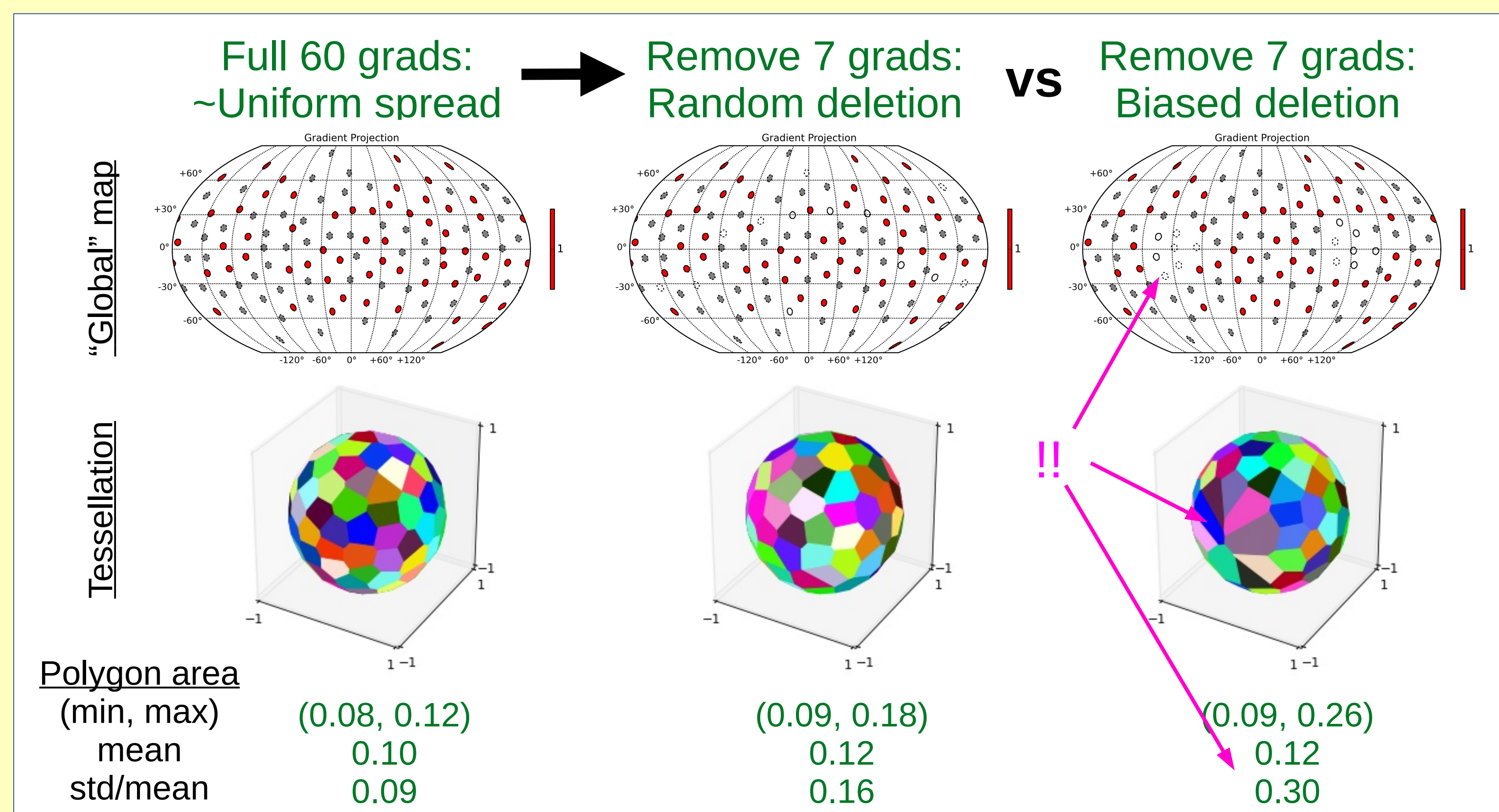
AFNI+SUMA: WM location, FA values and directionality.
FATCAT Demo subject, visualized using `@fat_tract_colorize`.



Whole brain tracking of a macaque brain⁶ for standard tract viewing and colored volumetric viewing, respectively. The high FA in the corpus callosum is highlighted, for example, in B using `@fat_tract_colorize`.

- In this imperfect world, DTI volumes often have to be removed (motion, distortion, etc.), which can bias tensor estimation at subject and group levels.
- `fat_grad_plot.py` allows user to:
 - visualize gradients in a 'global map' to show missing data,
 - highlight regions of many lost gradients (using spherical Voronoi tessellation polygons),
 - quantify amount of bias due to lost gradients (as variation in polygonal area).
- `fat_grad_plot.py` provides useful QA, plots and quantitative output.

Individual QA: show remaining gradients after removal, and quantify effects on 'evenness' of gradient distribution.

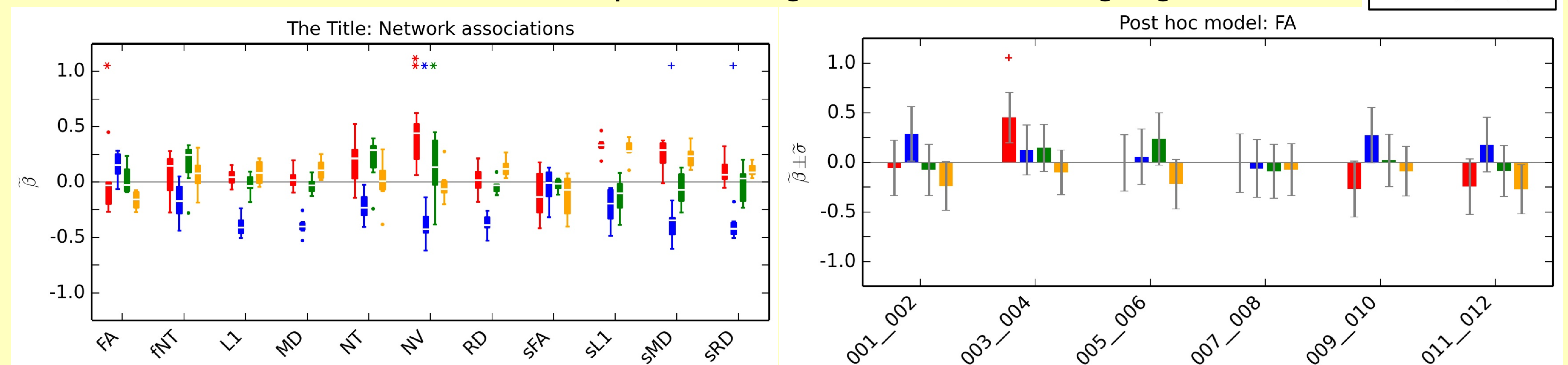


Group QA: show overlap of remaining gradients across group; check subject motion, etc.; table of quantities also output

- Summarize network statistics for either functional (FMRI) or structural (DTI) connectivity using `fat_mvm_review.py`.
- One useful analysis pipeline:
 - Calculate network connectivity matrices with 3dTrackID or 3dNetCorr,
 - Combine and model (using AFNI's 3dMVM⁷) with sample data using `fat_mvm*py` functions⁸,
 - Summarize and view results with `fat_mvm_review.py`,
 - Write paper and win Nobel prize*.

Example: statistical results from modeling DTI structural connectivity in terms of four variables (two categorical and two quantitative):

- Network level and all "within-network" post hoc model results are produced.
- Betas normalized for relative comparison; significance levels highlighted.



+p<0.1, *p<0.05, **p<0.01, ***p<0.001

*Not guaranteed, results may vary.

References

- [1] Taylor PA, Saad ZS. 2013. Brain Connect 3:523-535.
 [2] Cox RW. 1996. Comput Biomed Res 29:162-173.
 [3] Saad ZS, Reynolds RC. 2012. Neuroimage 62:768-777.
 [4] Saad ZS, et al. 2004. IEEE ISBI, p. 1510.
 [5] Moldrich RX, et al. 2010. Neuroimage 51:1027-1036.
 [6] Thomas C, et al. 2014. PNAS 111:16574-16579.
 [7] Chen G, et al. 2015. Front. Neurosci. 9:375.
 [8] Taylor PA, et al. 2016. Brain Connect 6(2):109-21.

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Poster #3534

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Stand By Time:
Wed, June 29
12:45 - 14:45

