Group Studies of Diffusion Data   **Steve Smith, FMRIB, Oxford**

Who will benefit from this information?

Researchers wanting to learn the basics of analyzing Diffusion MRI data from group studies. I will discuss the major challenges and goals of such analyses, and the main approaches that are taken for analysis.

How was a problem determined?

The major challenge is to achieve good correspondence (alignment) of images across different subjects, so that any local (e.g., voxelwise) cross-subject analysis (e.g., comparing patients and controls) is meaningful – we need to be sure that a given point in the image corresponds to the same anatomical structure in all subjects.

Examples of how this issue has been addressed

The most common approach initially used was to apply *voxel-based morphometry*, meaning that generic nonlinear registration is applied to align FA images into a "standard space", and then voxelwise statistics are computed across subjects [Ashburner]. However, this does not robustly generate perfect alignment between subjects, and so *tract-based spatial statistics* was developed, to try to improve further the robustness/accuracy of the alignment, and to only test those parts of the image deemed most reliable and interpretable [Smith]. Other approaches have attacked the correspondence problem in other ways, for example, some have used tractography to identify corresponding anatomical features in different subjects [e.g., Goodlett, Yendiki, Yushkevich, Gong].

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What will learners be able to do differently because of this information?

Attendees at this talk will be made aware of some of the important problems associated with analysis of multi-subject diffusion datasets, and learn something about the (conceptual and software) options available for analyzing such datasets.