

A Freely available Anatomist/BrainVISA Package for Analysis of diffusion MR data

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Abstract

Analysis of MR diffusion data in a research or clinical framework requires the use of various processing tools and the possibility to merge the diffusion related data with other kinds of data. A diffusion dedicated package has been developed for this purpose in the context of the Anatomist/BrainVISA platform [1,2]. The package can accept as input series of diffusion weighted data including any number of gradient directions and B values.

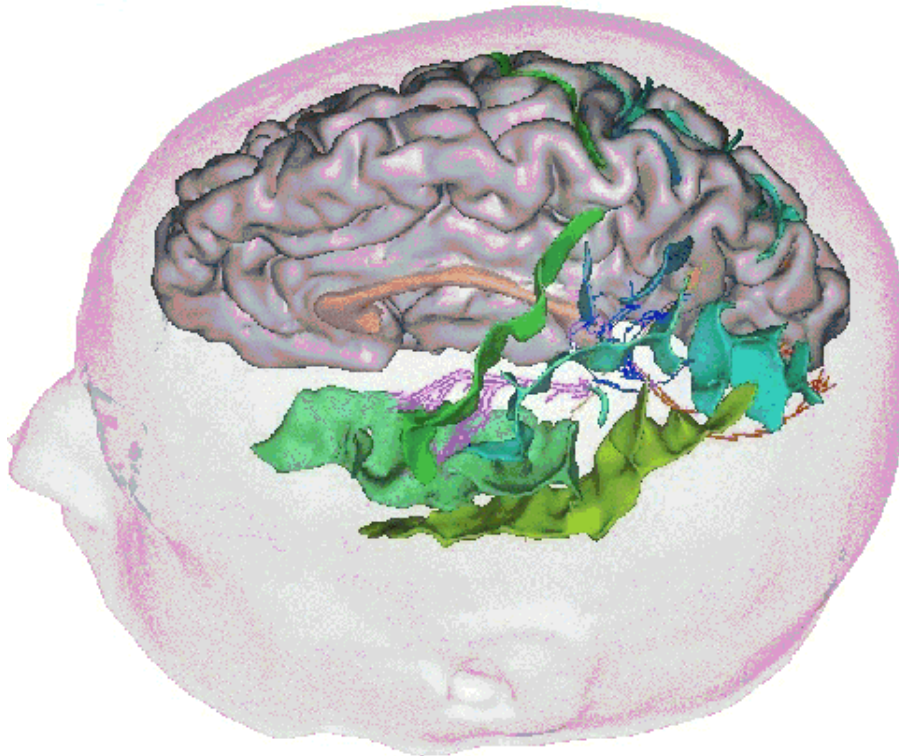
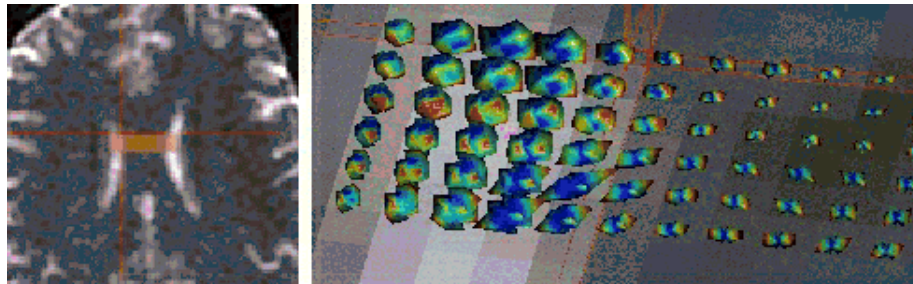
The processing tools are the following:

- 1) Correction of the Eddy current related spatial distortions induced by the diffusion gradients. The method warps each 2D slice on the corresponding T2-weighted slice using the optimal affine transformation according to mutual information [3].
- 2) Estimation of the diffusion tensor using least square based or robust estimators [3].
- 3) Computation of various diffusion related maps including fractional anisotropy, volume ratio, maximum eigenvector (direction or RGB coded), etc...
- 4) A module for the 3D drawing of Volumes of Interest (VOI) made up of sets of voxels.
- 5) The computation of various statistics for each VOI.
- 6) Dedicated visualization tools for the various diffusion weighted maps, including the high angular resolution data leading to visualize for each voxel a "diffusoid", namely a spherical mesh deformed and colored according to the diffusion directional properties (see Fig.up).
- 7) The tracking of the putative bundles of fascicles connecting the VOIs using a method including regularization of the bundle directions in the voxels of low anisotropy [4,5]. This method is updated regularly in order to provide a better management of the fiber crossing [6]. The different tracking approaches provided in the package belong to the same inverse problem framework, which leads to reconstruct the geometry of white matter as the lowest energy configuration of a spin glass [7]. The spins represent pieces of fascicle that orient themselves according to diffusion data and interact in order to create low curvature fascicles.

The integration of the diffusion package into the Anatomist/BrainVISA platform results in a user friendly interface which allows the combination of multimodal data (aMRI, fMRI, dMRI, EEG/MEG, etc.). For instance, the trajectory of the tracked bundles can be localized relatively to the main cortical sulci automatically recognized by an other package of the same platform (see Fig.down). The volumes of interest can be inferred from Statistical Parametric Maps (SPMs) obtained from functional data using for instance the Brainvisa's embedding of SPM's fMRI analysis software. The package should be rapidly extended with a statistical module in order to perform comparison of the matrices of connectivities obtained for each subject. Other extensions are planned relatively to the comparison with matrices of functional connectivity obtained from fMRI.

All the tools mentioned above are freely available. They can be downloaded from the following web page: <http://brainvisa.info>.

- [1] Rivière et al., HBM, NeuroImage 11(5),2000
- [2] Cointepas et al., HBM, Neuroimage, 13(6):98,2001
- [3] Mangin et al., Med Image Anal, 6:191-198,2002
- [4] Poupon et al., MICCAI, LNCS-1496:489-498,1998
- [5] Poupon et al., Neuroimage, 12(2):184-195,2000
- [6] Cointepas et al., MICCAI, LNCS-2448:475-482,2002
- [7] Mangin et al., NMR in Biomedicine, 15(7-8):481-492,2002



Up: visualization of high angular resolution data. Right: Merging fiber bundles and cortical sulci