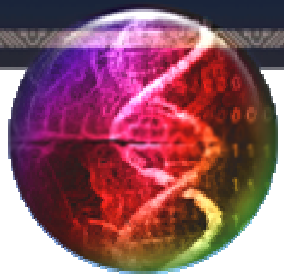
LABORATORY OF NEURO IMAGING, UCLA

Center for Computational Biology (CCB)



Presents

Guido Gerig, PhD

UNC Chapel Hill, Departments of Computer Science and Psychiatry

Friday, October 21, 2005 at 11 AM

Brain Mapping Center #221, 660 Charles E. Young Drive South

Quantitative analysis of structural MRI and DTI to assess trajectory of early brain development

Tissue segmentation and lobe parcellation: We have developed a new fully automatic brain segmentation and tissue segmentation technique that uses probabilistic brain atlases (neonate, 2yrs, 4yrs) as spatial priors. The tool incorporates brain stripping, bias correction, atlas-registration, multi-channel MRI registration, and probabilistic segmentation including separation of myelinated and non-myelinated white matter into one package.

Computational anatomy tools for building spatio-temporal 4-D atlases of brain growth: A new computational anatomy tool is based on the concept of unbiased atlas building. A population of 3-D images is simultaneously deformed to build a new average center image, which is a sharp MR image encoding the average structures of the whole population. Group differences and longitudinal change are assessed by quantifying local deformation between pairs of atlases, which provides a fully volumetric description of the growth pattern.

White matter development measured by DTI: Local diffusion properties in white matter are associated with axon density, degree of myelination and density of white matter. We have developed new tools for quantitative analysis of DTI by statistical analysis of distributions of tensor data in regions or interest, and by quantitative tractography which uses Riemannian symmetric space for tensor interpolation and averaging. As a result, diffusion properties are represented as a function of geodesic arc-length along major fiber tracts.

For information, please contact Ivo Dinov, PhD at 310.206.2101

http://www.ccb.ucla.edu

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