

ER-flow Application Description Template

Application Name: Freesurfer Pial
Application domain: Medical Imaging
Brief description of application Freesurfer is a set of automated tools for reconstruction of the brain's cortical surface from structural MRI data, and overlay of functional MRI data onto the reconstructed surface. It also segments brain regions automatically. After Freesurfer has been applied once on the MRI data, it may be needed to apply some corrections and re-run Freesurfer. This application can then be used to recalculate what has gone wrong in the first run.
Data: input data format: nifty / dicom (image) or archive (with image and other data) output data format: an archive containing the results of the various steps sample data: lfn:/grid/vlmed/AMC-e-BioScience/medical-imaging/freesurfer/sample-data/Freesurfer-input.zip application http://surfer.nmr.mgh.harvard.edu/ documentation http://surfer.nmr.mgh.harvard.edu/fswiki publication https://surfer.nmr.mgh.harvard.edu/fswiki/Publications
Execution environment DCI: (EGI, SRM/LFC, vlmed VO) middleware: gLite, CVMFS workflow system: WS-PGRADE, MOTEUR
Execution characteristics input: 100MB, 1 to hundreds output: 150MB, many organized processing time (per unit): 24 - 36 hours memory usage: n.a. disk usage: ~2GB
Target users Neuroscientists, radiologists, psychiatrists of the AMC Brain Imaging Center http://www.lebic-amc.nl number of users: 10+ user type: end-user
Usage scenario for workflow in the ER-FLOW Various workflows have been implemented to port this application to EGI for the vlmed VO. These workflows are published on the SHIWA repository with appropriate documentation, metadata and sample data. Due to licensing of Freesurfer, only vlmed VO members can run application. Users start Freesurfer from the AMC science gateways. Additionally, the Freesurfer_recon-all workflow can be accessed and executed via the SHIWA Portal by external users.
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