

New Features

- Functionally Informed CBA (fCBA)** This version adds the possibility to use functionally defined regions as additional targets during cortex-based alignment (CBA). Weighting parameters are provided that balance purely anatomical (curvature-driven) and functional alignment forces. In case that homologue ROIs are available for all included subjects, fCBA allows to perform a single analysis integrating whole-cortex and ROI-based analysis instead of two separate analyses. See the topic "Functionally Informed CBA" in the "Cortex-Based Alignment" chapter of the User's Guide for further information.
- ASL Analysis** It is now possible to analyze arterial spin labelling (ASL) MRI data. The new slice-based and volume-based ASL plugins generate perfusion-weighted time-course data and absolute (quantitative) cerebral blood flow (CBF) maps for single- and multi-subject analyses. Absolute CBF quantification is especially useful for (patient) group studies. For details, consult the documentation provided by the plugins (select help link in short description available under "Plugins - Description Of Plugins" menu).
- EMEG: Realistic Head Model** Until this release, the EMEG tools used a spherical head model for distributed source modeling. This version supports a realistic head model potentially increasing the precision of topographic results in source space. Besides relying on standard segmentation tools, the new EEG-MEG forward model routines call the "OpenMEG" library (<http://openmeeg.gforge.inria.fr>) to fit the head model. For detailed instructions on how to obtain realistic individual head models, consult the users' guide (EEG-MEG chapter).
- GPU-Based Sinc Interpolation** While BrainVoyager uses CPU-based parallelization exploiting multiple processor cores to speed up performance since many years, modern graphics cards contain general purpose processing units (GPUs) that provide very powerful possibilities to parallelize calculations. This release is the first that offers the option to run non-graphical compute-intensive algorithms directly on the

graphics board. More specifically, sinc interpolation and sigma filtering can now be performed on the GPU. Sinc interpolation is especially important since it can be used in many compute-intensive routines, including motion correction and VMR/VMP/VTC spatial transformations. Depending on the graphics hardware, the new GPU implementation achieves results that lead from modest to dramatic reductions in calculation time. GPU-based sinc interpolation and sigma filtering can be enabled and tested using the "Speed" tab of the "Preferences" dialog. For more details, consult the "Exploiting the Power of GP-GPUs" topic of the "Additional Documentation" chapter in the User's Guide.

Sulcal Depth Maps

Sulcal depth volume and surface maps can now be created that provide information about the depth of voxels or vertices within sulci. Besides scientifically interesting macro-anatomical information (e.g. how sulcal depth differs in patient or age groups), the sulcal depth surface maps may also be used for surface visualization of folded, inflated and flattened cortex meshes as an alternative to the standard curvature-based visualizations. For further details, check the "Creating Sulcal Depth Maps" topic in the "Miscellaneous Tools" chapter of the User's Guide.

Enhancements

MVPA - Searchlight In previous versions the searchlight MVPA tool only provided descriptive information. With this release, BrainVoyager provides SVM-based and MANOVA-based searchlights: At each voxel a SVM classifier or a multivariate t test (Hotellings T) is now computed providing accuracy maps (from SVM version) and F statistics (from MANOVA version). For details, consult the "Multi-Voxel Pattern Analysis" chapter of the User's Guide.

MVPA - ROI-SVM It is now possible to run analyses in batch mode to reduce GUI interactions. The new batch mode tools allow, e.g. to perform and integrate results of all possible leave-N-out training testing combinations. For details consult the "Multi-Voxel Pattern Analysis"

- chapter of the User's Guide.
- Regular-Grid Cortical Depth Sampling** The visualization of high-resolution grid sampling results have been substantially improved now showing rectangular grids (instead of lines in only one dimension) as well as sampled functional data directly in 3D space. Furthermore display of grids (and meshes) can be constrained to be visible only close to the currently used cut plane; this is a useful option to precisely follow different depth level grids or meshes as they run along the cortex. For further details, consult the updated topic "Regular-Grid Cortical Depth Sampling" in the "Tools for High-Resolution Data" chapter of the User's Guide.
- VMP -> SMP, VTC -> MTC** The creation of surface maps (SMPs) from volume maps (VMPs) and mesh time courses (MTCs) from volume time courses (VTCs) has been improved allowing for better control how access of volume data should be performed from the vertices of a mesh. When clicking the "Create SMP" button in the "Surface Maps" dialog, a new "Depth Integration" dialog will appear that allows to specify whether volume data should be sampled at the 3D position of a vertex only (preferred choice for mesh-based cortical depth sampling) or whether functional data should be integrated along the depth of the cortex. The same options are also integrated in the "Create MTC from VTC" tab of the "Mesh Time Courses" dialog. Furthermore, it can be specified whether volume data sampling should use trilinear interpolation (default) or nearest neighbor interpolation. For details, consult the User's Guide.
- High-Resolution CBA** Cortex-based alignment (CBA) is now possible also with high-resolution spherical meshes. The new "Resolution" field in the first page of the CBA dialog allows to set one of three resolutions, high, standard and low. Based on the chosen setting, the creation of sphere meshes as well as parameters for morphing and alignment are adjusted in subsequent processing steps. Instead of standard SPH meshes with 81920 triangles (40962 vertices), the high-resolution meshes

use 327680 triangles (163842 vertices). Since CBA calculations are substantially slower with these high-resolution meshes, this option should only be used in cases that target alignment of *functional* data with (sub)-millimeter resolution. For details, consult the "Cortex-based alignment" chapter of the User's Guide.

GLM and ANOVA The default time series normalization method has been changed to percent signal change since this is most widely recommended in the literature for (multi-subject) GLM data analysis (see User's Guide for more details of provided normalization schemes). In previous versions, the beta values from the baseline condition was included as a level of a within-subjects factor when starting ANCOVA analysis from a GLM data file. Since the baseline predictor (and its beta and variance estimation) is not comparable to other main predictors, it does no longer appear as a within-factor level (this has been already changed for ROI GLMs in the previous release); without the baseline, the prerequisites for the 2-level mixed effects summary statistics model for balanced designs are met (for details, consult the User's Guide). To help users better judge what model is defined when changing the number of factors and covariates, the specified design is now also described directly in the "Design" tab (and as before in the "Table" tab). For designs with one main condition or one contrast, the single-group *t* test design is automatically chosen. It is now also possible to run a 1-between factor model (classical single-factor ANOVA) in case that only one main condition is available; in previous versions this could only be done by extracting betas for one level first in a VMP file that was then used as input. For ROI-based ANOVAs, the plotting function of betas has been improved now separating data from different groups with different line colors.

Plugin API - Plots and Documenten While plugins can be programmed with cross-platform complex GUI components (GUI plugins), it was not possible to provide graphical output to plot calculated values. This

tation version adds the possibility to draw bar graphs, line plots and scatter plots with a few simple commands. The produced plots look identical on Windows, Mac and Linux. For further information, run the "Plot Demo" plugin and inspect its source code; for a description of the new API functions, consult the new Developer Guide that is available under "Help -> Developer Guide".

Plugin API - FMR/MAPs and SRFs Plugin developers can access pointers to all major data formats except FMR and MAP data. New functions to access that data are now available. The commands for processing mesh (SRF) data have been extended by adding functions for loading and saving meshes and the possibility to remove meshes from scenes in a surface (OpenGL) window. For further information, consult the new Developer's Guide that is available under "Help -> Developer's Guide".

Centroid and Border POIs For some applications it is useful to calculate the centroid of a patch-of-interest (POI), e.g. to obtain representative mean (Talairach) coordinates of a surface area. This is especially relevant for anatomically defined regions since for functionally defined POIs the vertex with highest activity ("peak vertex") is usually used to represent the location of an area. It is also sometimes relevant to extract the border of a POI, e.g. in case that one wants to mark a region without interfering with the content within that region. The creation of centroid and border POIs is now possible by using the "Outline POIs" and "Centroid POIs" buttons in the new "Convert area POIs" field in the "Paths / CBA" tab of the "POI Analysis Options" dialog.

Group-To-Individual POI Projection It is often useful to visualize the result of alignment for specific POIs. While it was possible to map the location of a POI of one cortex mesh on another individual's cortex mesh it was not easily possible to visualize the location on individual cortex meshes that were defined on the group mesh. Using the new "" button in the "" field of the "" tab of the "" dialog, group-level POIs can now be projected back onto any individual cortex

mesh that participated in CBA. For details, see the "Cortex-based alignment" chapter of the User's Guide.

Fibers Fibers are now stored in binary format to increase reading and writing speed under the same ".fbr" extension. Old .fbr text files can still be loaded but should be saved once to convert them to the binary format. Fiber visualization has been improved to allow dynamic displays, e.g. animation of fibers in group bundles "growing" from start coordinates to end coordinates; the dynamic fiber displays also support slice-restricted fiber visualizations that are used e.g. in the context of high-resolution grid visualizations (see above).

Zooming and Tabbed Mode When using the "Zoom-In" and "Zoom-Out" icons in the toolbar on the left side, nothing happened when tabbed view mode was used; to zoom document views in or out, one needed first to switch from tabbed view mode to multi-window view mode. This is no longer necessary, i.e. when clicking on a zoom icon, the program automatically switches to multi-window view mode and positions the current sub-window in the left upper corner of the workspace; the latter increases the experience of the zooming effect. Note that this behavior is not implemented for OpenGL windows since they allow flexible content viewing also in tabbed view mode.

Touch-Based Navigation The viewpoint in surface windows can now also be controlled by using touch-based gestures on Mac and Windows PCs. Panning and pinch gestures allow to rotate and zoom using integrated or external (magic) track pads on Mac and touch-enabled screens on PCs running Windows 7.

Bug Fixes

Mixed ANOVA When specifying contrasts in a mixed ANOVA design with one between and one within factor, different error variances need to be used depending on the defined contrast. In previous versions, a more conservative error variance was always used if a contrast included cells across groups; if, however the

BrainVoyager QX 2.6 Release Notes

same balanced contrast is defined within groups, a more sensitive error variance can be used (the same as for the within-factor F test). This has been adjusted in the current version leading to more sensitive t maps in this case.

- POI-VMR Projection** When projecting POIs into VMRs with sub-millimeter resolution, the location of the created VOIs was not correct. This issue has been fixed.
- CBA - Single-Vertex POIs** When applying CBA to transform POIs with only one vertex into aligned group space the resulting POI could be empty. This issue has been fixed.
- GCM Plugin** In case that a VTC file did not had a protocol attached, the plugin would not work producing an empty GCM VMP file. This issue has been fixed.
- SVM - Optimal C Value** When using the cross-validation option to find the C value with best generalization performance, the value chosen was sometimes not the one with best performance. This issue has been fixed.
- VOI Dialog** VOIs were always marked as modified triggering a "Save VOIs" dialog when quitting the program. Furthermore, VTC files could sometimes not be removed from the VTC list. These issues have been fixed; the displayed VOI file name should now also correctly indicate (appended star symbol) whether VOIs have been modified or not. Furthermore the display of VOIs is now consistent with the available VOIs in the VOI dialog when switching between multiple open VMRs; in previous versions, VOIs might be shown from an old VOI file after loading a new VOI file. When VOI files were loaded containing voxel coordinates outside the VMR volume, the program could crash. This issue has been fixed.
- Create VTC Dialog** When transformation files were not found for native, ACPC or TAL transformations, the respective "To [space]" auto-fill options were disabled in previous versions. While this is useful behavior for many cases, it may be that the respective files are located in another directory, e.g. when using files from another

run. In order to avoid restrictions, the "To [space]" options are now always enabled but they indicate with the string "auto" whether a certain space is "reachable" with the "Auto-Fill" option with files in the local directory or not.

ROIs To VOIs When converting ROIs defined in FMR slice space to VOIs, the transformation always assumed that the target volume has 256 dimensions leading to wrong VOI definitions in case of native/ACPC space transformation. When not going to Talairach space (where this assumption is still made), the program now asks the user to select the desired native/ACPC space VMR file in order to extract the proper dimension values.

ROI-ANCOVA - Correlation When running correlation analysis between subject's contrast values and provided covariate values for ROIs in the ANCOVA dialog, the program could crash. This issue has been fixed.

Keyboard Shortcuts Sometimes keyboard shortcuts did not work properly, i.e. despite pressing the right key(s), the corresponding keyboard function was not invoked (e.g. opening a POI dialog). This issue has been fixed.

Convex/Concave Labels The labels for convex and concave curvature were flipped in the "Graded curvature colors" field of the "Background And Curvature Colors" dialog. This issue has been fixed.

GUI Plugin Dialogs on Mac When GUI plugins were invoked on the Mac by launching a GUI plugin, the window would disappear from view when clicking outside the dialog. This issue has been fixed.