Package 'gdimap'

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Title Generalized Diffusion Magnetic Resonance Imaging

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Depends R (>= 3.0.0), rgl

Imports oro.nifti, movMF, grid, gridExtra, colorspace, geometry, gsl, abind

Description Diffusion anisotropy has been used to characterize white matter neuronal pathways in the human brain, and infer global connectivity in the central nervous system. The package implements algorithms to estimate and visualize the orientation of neuronal pathways in model-free methods (q-space imaging methods). For estimating fibre orientations two methods have been implemented. One method implements fibre orientation detection through local maxima extraction. A second more robust method is based on directional statistical clustering of ODF voxel data. Fibre orientations in multiple fibre voxels are estimated using a mixture of von Mises-Fisher (vMF) distributions. This statistical estimation procedure is used to resolve crossing fibre configurations.
Reconstruction of orientation distribution function (ODF) profiles may be performed using the standard generalized q-sampling imaging (GQI) approach, Garyfallidis' GQI (GQI2) approach, or Aganj's variant of the Q-ball imaging (CSA-QBI) approach. Procedures for the visualization of RGB-maps, line-maps and glyph-maps of real diffusion magnetic resonance imaging (dMRI) data-sets are included in the package.

LazyData yes

NeedsCompilation no

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R topics documented:

`gdimap-package` *Generalized Diffusion Magnetic Resonance Imaging*

Description

The package implements algorithms to estimate and visualize the orientation of neuronal pathways in model-free methods (q-space imaging methods). For fibre orientation estimation based on mixtures of von Mises-Fischer (vMF) distributions see `gqi.odfvmflines`, `gqi.odfvmf`, `sph.odfvmflines`, and `sph.odfvmf`. For fibre orientation estimation based on local peak detection procedures see `gqi.odfpeaklines`, `gqi.odfpeaks`, `sph.odfpeaklines`, and `sph.odfpeaks`. In these names, the prefix 'gqi' references functions using the standard GQI method (Yeh et.al. 2010), or the GQI2 variant (Garyfallidis 2012) for ODF reconstruction. The prefix 'sph' references functions using spherical harmonics approximations based on Aganj's ODF reconstruction (CSA-QBI). Visualization of RGB-maps and glyph-maps is implemented through `rgbvolmap` and `gqi.odfvxgrid`, respectively. Various types of simulations of diffusion and ODF profiles, illustrating the application of vMF mixtures for fibre orientation estimation are implemented in `simulglyph.vmf`, `simul.simplefield`, `simul.fandtasia`. Data sets used in the examples are documented.

Details

For a complete list of functions type `library(help=gdimap)`.

Note

For reasons of limited CRAN storage space, a trimmed down data set with just 4 coronal slices was selected. Coronal slices (29:32) were extracted from the original data set. Hence, the argument `bview="coronal"` is used in the examples, and the range of coronal slices is (1:4). User specified complete data sets may be used without restrictions.

Commonly used acronyms:
GFA - Generalized Fractional Anisotropy
ODF - Orientation Distribution Function
GQI - Generalized q-Sampling Imaging
GQI2 - Generalized q-Sampling Imaging variant
QBI - Q-ball Imaging
CSA-QBI - Constant Solid Angle QBI MRI - Magnetic Resonance Imaging
dMRI - Diffusion Magnetic Resonance Imaging
RGB maps - Red:Green:Blue color maps
HARDI - High Angular Resolution Diffusion Imaging
vMF - von Mises-Fisher

Author(s)

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References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

Ferreira da Silva, A. R. Facing the Challenge of Estimating Human Brain White Matter Pathways. In *Proc. of the 4th International Joint Conference on Computational Intelligence* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress, pp. 709-714.

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Adler, D., and Murdoch, D. **rgl**: 3D visualization device system (OpenGL), 2012. R package version 0.92.880.

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Barber, C. B., Habel, K., Grasman, R., Gramacy, R. B., Stahel, A., and Sterratt, D. C. **geometry**: Mesh generation and surface tesselation, 2012. R package version 0.3-2.

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Polzehl J., Tabelow K., dti: Beyond the Gaussian Model in Diffusion-Weighted Imaging. *Journal of Statistical Software* 44, 12 (2011).

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626-1635.

Garyfallidis E., Towards an Accurate Brain Tractography, 2012, PhD Thesis, University of Cambridge.

Aganj I., Lenglet C., Sapiro G., Yacoub E., Ugurbill K. and Harel N. Reconstruction of the orientation distribution function in single- and multiple-shell q-ball imaging within constant solid angle, *Magnetic Resonance in Medicine*, 64(2) (2010), 554-566.

`btable` *b-Table File for Shell Data*

Description

'`btable.txt`' is an alias for '`dsi203_bmax4000`', a (nx4) b-table data file used in conjunction with the data set '`data.nii.gz`' (alias "DSI 203-point 3mm"), as provided by the *Advanced Biomedical MRI Lab, National Taiwan University Hospital*, and referenced in the package **DSI_Studio** developed by Fang-Cheng Yeh. The first column specifies the b-values, and the remaining 3 columns specify the b-vectors.

'`btable.txt`' The sampling points in '`btable.txt`' ('`dsi203_bmax4000`') are distributed in a S2 shell with 203 points. The b-values range from 0 to 4000.

References

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q- Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626–1635.

NITRC repository, http://www.nitrc.org.

`data` *A Real Dataset for Diffusion MRI Analysis*

Description

The data set '`data.nii.gz`' is a gzipped NIfTI data set converted from the original DICOM data set provided by the *Advanced Biomedical MRI Lab, National Taiwan University Hospital*, under the designation '`DSI 203-point 3mm`'.

For reasons of limited CRAN storage space, a trimmed down data set with just 4 coronal slices was selected. Coronal slices (29:32) were extracted from the original data set. Hence, the argument `bview="coronal"` is used in the examples, and the range of coronal slices is (1:4). User specified complete data sets may be used without restrictions.

Format

The file '`data.nii.gz`' is in gzipped NIfTI format. The R-package **oro.nifti** is required to read NIfTI files.

Details

The data set is included in the **DSI Studio** package, publicly available from the NITRC repository. This data set is from a normal 24-year-old male volunteer, and has been provided as a demonstration data set in connection with the *DSI Studio* software for diffusion MR image analysis. The data set was obtained with an echo planar imaging diffusion sequence with twice-refocused echo, dimension 64x64x40, and slice thickness 2.9mm. Further details on the data set specification are available from the NITRC repository.

References

Whitcher, B., Schmid, V. J., and Thornton, A. Working with the DICOM and NIfTI data standards in R. *Journal of Statistical Software* 44, 6 (2011), 1-28.

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626–1635.

NITRC repository, http://www.nitrc.org.

See Also

`data_brain_mask`, `data.bval`, `data.bvec`, `data_V1`, `data_V2`, `data_gfa`, `btable`

data.bval *b-Table File*

Description

b-values file for the 3D-DSI sampling scheme used in the DICOM data acquisition process for file 'data.nii.gz'.

Format

'data.bval' is in ASCII format

Details

The b-values in 'data.bval' range from 0 to 4000. The data set 'data.nii.gz' is NIfTI-converted from the DICOM data set provided by the *Advanced Biomedical MRI Lab, National Taiwan University Hospital*, under the designation 'DSI 203-point 3mm'. The corresponding file 'data.bvec' has 203 points uniformly distributed on a 3D (DSI) grid limited to the volume of the unit sphere.

References

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626–1635.

data.bvec *3D b-table Vectors for Data Acquisition*

Description

3D grid file containing the sampling points used in diffusion data acquisition for file 'data.nii.gz'.

Format

'data.bvec' is in ASCII format, specified as a sequence of values, as produced by the 'dcm2nii' tool, and compatible with the formats used in the 'DSI_Studio' and 'Dipy' toolboxes.

Details

The file 'data.bvec' has 203 points uniformly distributed on a 3D (DSI) grid limited to the volume of the unit sphere. The data set 'data.nii.gz' is NIfTI-converted from the DICOM data set provided by the *Advanced Biomedical MRI Lab, National Taiwan University Hospital*, under the designation 'DSI 203-point 3mm'.

References

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626–1635.

data_brain_mask *Example of Mask File Used in Diffusion MRI Processing*

Description

The 'data_brain_mask.nii.gz' dataset defines the mask used in the diffusion MRI analysis for 'data.nii.gz'.

Format

The file 'data_brain_mask.nii.gz' is in gzipped NIfTI format. The R-package **oro.nifti** is required to read NIfTI files. This file may be obtained from 'data.nii.gz' by applying FSL/BET pre-processing tools.

Details

For reasons of limited CRAN storage space, a trimmed down data set with just 4 coronal slices was selected. Coronal slices (29:32) were extracted from the original data set.

The mask used here is an all-brain mask; it just removes non-brain regions, as the result of applying a brain extraction tool to the 'data.nii.gz' dataset. However, other masks may be defined to select regions of interest (ROIs).

References

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626–1635.

Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. Fsl. *NeuroImage* 62, 2 (2012), 782-790.

NITRC repository, http://www.nitrc.org.

See Also

data, data.bval, data.bvec, data_V1, data_V2, data_gfa, btable

data_gfa *Generalized Fractional Anisotropy (GFA) File*

Description

The 'data_gfa' summarizes anisotropic properties of the Orientation Distribution Function (ODF) of the fibres using the generalized fractional anisotropy (GFA) metric, based on the GQI method.

Format

The file 'data.nii.gz' is in gzipped NIfTI format. The R-package **oro.nifti** is required to read NIfTI files.

Details

The file 'data_gfa' was produced by the function gqi.odfvmf (using the default arguments) included in **gdimap**. Functions for visualization of RGB maps and line-maps are included in **gdimap**. The output files 'data_V1.nii.gz' and 'data_gfa.nii.gz' are compatible with the "FSL/fslview" tool for RGB map and line map visualization.

For reasons of limited CRAN storage space, the source data set contains just 4 coronal slices as indicated in data.

References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

Ferreira da Silva, A. Facing the challenge of estimating human brain white matter pathways. *In Proc. of NCTA 2012 - Int. Conf. on Neural Computation Theory and Applications* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress.

Whitcher, B., Schmid, V. J., and Thornton, A. Working with the DICOM and NIfTI data standards in R. *Journal of Statistical Software* 44, 6 (2011), 1-28.

Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. Fsl. *NeuroImage* 62, 2 (2012), 782-790.

See Also

data_V1, data_V2

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data_V1 *ODF First Principal Directions File*

Description

The 'data_V1' contains the first principal directions of the Orientation Distribution Function (ODF)of the fibres at each 'data' voxel, based on the GQI method.

Format

The file 'data.nii.gz' is in gzipped NIfTI format. The R-package **oro.nifti** is required to read NIfTI files.

Details

The file 'data_V1' was produced by the function gqi.odfvmf (using the default arguments). Functions for visualization of RGB maps and line-maps are included in **gdimap**. The output files 'data_V1.nii.gz' and 'data_gfa_gqi.nii.gz' are compatible with the "FSL/fslview" tool for RGB map and line map visualization.

For reasons of limited CRAN storage space, the source data set contains just 4 coronal slices as indicated in data.

References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

Ferreira da Silva, A. Facing the challenge of estimating human brain white matter pathways. *In Proc. of NCTA 2012 - Int. Conf. on Neural Computation Theory and Applications* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress.

Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. Fsl. *NeuroImage* 62, 2 (2012), 782-790.

See Also

data_V2, data_gfa

`data_V2` *ODF Second Principal Directions File*

Description

The 'data_V2' contains the second principal directions of the Orientation Distribution Function (ODF) of the fibres at each 'data' voxel, based on the GQI method.

Format

The file 'data.nii.gz' is in gzipped NIfTI format. The R-package **oro.nifti** is required to read NIfTI files.

Details

The file 'data_V2' was produced by the function `gqi.odfvmf` (using the default arguments) included in **gdimap**.

For reasons of limited CRAN storage space, the source data set contains just 4 coronal slices as indicated in data.

References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

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Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. Fsl. *NeuroImage* 62, 2 (2012), 782-790.

See Also

data_V1, data_gfa,

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dec *Directionally-Encoded Color (DEC) Representation*

Description

dec illustrates the RGB encoding used in DEC representations

Usage

```
dec(depth=4, new=TRUE)
```

Arguments

depth	codedepth controls the sampling density on the hemisphere (default depth=4).
new	start a new plot with new=TRUE (default).

Details

The DEC encoding is the standard colouring scheme to represent the orientation of anisotropic tissue, as originally proposed by Pajevic, et.al.

Author(s)

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References

Pajevic, S., and Pierpaoli, C. Color Schemes to Represent the Orientation of Anisotropic Tissues From Diffusion Tensor Data: Application to White Matter Fiber Tract Mapping in the Human Brain. Magnetic Resonance in Medicine 42 (1999), 526-540.

Examples

```
## Not run:
    dec()

## End(Not run)
```

gqi.odfpeaklines *Fibre Orientation Mapping Based on Local Peak Detection*

Description

gqi.odfpeaklines produces line-maps of ODF profiles for diffusion data slices.

Usage

```
gqi.odfpeaklines(gdi="gqi", run=TRUE, fbase=NULL, roi=NULL, rg=c(1,1),
 swap=FALSE, lambda=NULL, depth=3, btoption=2, threshold=0.4, kdir=2,
 zfactor=5, showglyph=FALSE, showimage="linesgfa", bview="coronal",
 savedir=tempdir(), bg="white", texture=NULL, aniso=NULL, ...)
```

Arguments

gdi	method of ODF reconstruction to use c("gqi", "gqi2") (default: "gqi").
run	logical variable enabling loading previously processed data (default: TRUE).
fbase	Directory where the required input data files are located.
roi	Region of Interest (ROI) to use as mask; default mask (roi=NULL) uses an all brain mask for the supplied data set.
rg	range of slices to process (default option rg=c(1,1)); rg=NULL processes all slices.
swap	toggle radiological/neurological orientation (default: FALSE).
lambda	diffusion sampling length in gdi="gqi" and gdi="gqi2". By default the following default values are used when lambda=NULL is specified: 1.24 in "gqi", 3 in "gqi2".
depth	sampling density on the hemisphere used in simulation (default N=321; depth=3).
btoption	b-table selection between 'btable.txt' (btoption=1), and the 3D-DSI grid b-table extracted from the diffusion data set ('data.bvec' and 'data.bval'). By default, the 3D-DSI grid b-table is used (btoption=2).
threshold	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
kdir	maximum number of fibre directions to map (default: 2).
zfactor	parameter controlling z-value in relief overlay maps (default: 5).
showglyph	logical variable controlling visualization of voxel glyphs (default: FALSE).
showimage	object controlling visualization of line-maps (default: "linesgfa"). Alternative options are: c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata") (see Details).
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir().

bg	map background colour (default "white")
texture	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
aniso	anisotropic parameter in the range "[0,1)" or NULL to use in ODF pos-processing default: NULL.
...	additional material properties for geometry appearance as specified in rgl.material.

Details

The identification of fibre directions is performed by extracting the local maxima of the reconstructed ODF, where this function surpasses a certain threshold. GQI (Yeh et.al. 2010) or GQI2 (Garyfallidis 2012) may be used for ODF reconstruction. gqi.odfpeaklines implements the standard method of fibre orientation detection. Local maxima of the reconstructed ODF are located simply by selecting a large number of sampled points on the sphere and searching within a fixed radius neighbourhood. For a single main fibre orientation the method performs well. However, for crossing fibres and other complex fibre configurations the peaks of the ODF profiles identified by the methods do not necessarily match the orientations of the distinct fibre populations. A more robust method is implemented in gqi.odfvmflines.

Starting with the raw high angular resolution diffusion signal acquired on a grid of q-space, the ODF profile is reconstructed at each voxel, considering a sampling density of unit vectors on a unit S2 grid. Generalized q-Sampling Imaging (GQI) is used for orientation distribution function (ODF) reconstruction. Two b-tables defining the acquisition setup are specified. One is a b-table for a S2-like grid denoted by 'btable.txt'. The other is the b-table for the 3D-DSI sampling scheme used in the DICOM data acquisition. This b-table has 203 points uniformly distributed on a 3D grid limited to the volume of the unit sphere. In both tables, the b-values range from 0 to 4000.

Slice map display and overlay selection is controlled by specifying one the arguments c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata") for showimages. Meanings are as follows: "none" - no visualization; "gfa" - GFA map only; "lines" - line map only; "linesgfa" - GFA overlayed on line map; "linesrgbmap" - lines overlayed on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlayed on line map;

Value

gqi.odfpeaklines produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlayed with generalized fractional anisotropy (GFA) relief maps, diffusion data maps or ROI maps. The file 'V1list.RData' containing the first main orientation directions for all processed voxels is output for further posterior orientation processing.

Author(s)

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References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

Ferreira da Silva, A. R. Facing the Challenge of Estimating Human Brain White Matter Pathways. In *Proc. of the 4th International Joint Conference on Computational Intelligence* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress, pp. 709-714.

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626-1635.

Garyfallidis E., Towards an Accurate Brain Tractography, 2012, PhD Thesis, University of Cambridge.

See Also

gqi.odfpeaks, gqi.odfvmf, gqi.odfvmflines, gqi.odfvxgrid, s2tessel.zorder, plotglyph, rgbvolmap, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
  ##-------------
  ## Line map using ODF peak detection
  gqi.odfpeaklines(run=TRUE, showimage="lines")
  ## idem with "gqi2"
  gqi.odfpeaklines(gdi="gqi2", run=TRUE, showimage="lines")
  ## display line-map overlayed on GFA map
  gqi.odfpeaklines(run=FALSE, showimage="linesgfa")
  ##-------------
  ## generate slice texture first from default data file
  texturefname <- file.path(tempdir(),"rgbmap.png")
  rgbvolmap(texture=texturefname, bg="transparent")
  ## Line map with RGB map overlay
  gqi.odfpeaklines(run=TRUE, showimage="linesrgbmap",
    texture=texturefname)
  ##-------------
  ## Show examples of reconstructed glyphs in ODF processing
  gqi.odfpeaklines(showimage="lines", showglyph=TRUE)
  ##------------
  ## using a ROI overlay
  gqi.odfpeaklines(roi="slfcst.nii.gz", showimage="linesgfa")
  ## using data overlay
  gqi.odfpeaklines(showimage="linesdata")

## End(Not run)
```

---

gqi.odfpeaks *Main Fibre Orientation Determination via Peak Detection with GQI Reconstruction*

Description

Generalized q-Sampling Imaging (GQI) is used for orientation distribution function (ODF) reconstruction. For identifying voxel fibre directions, the local maxima of the reconstructed ODF are identified, where this function surpasses a certain threshold.

Usage

```
gqi.odfpeaks(gdi="gqi", fbase=NULL, rg=NULL, swap=FALSE, lambda=NULL,
 depth=3, btoption=2, threshold=0.4, showglyph=FALSE, bview="coronal",
 savedir=tempdir(), aniso=NULL)
```

Arguments

gdi	method of ODF reconstruction to use c("gqi", "gqi2") (default: "gqi").
fbase	Directory where the required input data files are located.
rg	range of slices to process; default option rg=NULL processes all slices.
swap	toggle radiological/neurological orientation (default: FALSE).
lambda	diffusion sampling length in gdi="gqi" and gdi="gqi2". By default the following default values are used when lambda=NULL is specified: 1.24 in "gqi", 3 in "gqi2".
depth	sampling density on the hemisphere used in simulation (default N=321; depth=3).
btoption	b-table selection between 'btable.txt' (btoption=1), and 3D-DSI grid b-table supplied with the diffusion data set (default btoption=2).
threshold	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
showglyph	logical variable controlling visualization of voxel glyphs (default: FALSE).
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir().
aniso	anisotropic parameter in the range "[0,1)" or NULL to use in ODF pos-processing default: NULL.

Details

GQI specifies an operational sampling scheme in q-space from which the ODF can be estimated. The most commonly used approach for identifying fibre directions is to extract the local maxima of the reconstructed ODF, where this function surpasses a certain threshold. The application of the approach is based on the assumption that the principal directions extracted from the ODF can be interpreted as principal directions of the underlying fibre architecture. Thresholding avoids selecting smaller ODF peaks that may appear due to noise. Local maxima of the reconstructed ODF are located simply by selecting a large number of sampled points on the sphere and searching within a fixed radius neighbourhood. GQI (Yeh et.al. 2010) or GQI2 (Garyfallidis 2012) may be used for ODF reconstruction.

Starting with the raw high angular resolution diffusion signal acquired on a grid of q-space, the ODF profile is reconstructed at each voxel, considering a sampling density of unit vectors on a unit S2 grid. Generalized q-Sampling Imaging (GQI) is used for orientation distribution function (ODF)

reconstruction. Two b-tables defining the acquisition setup are specified. One is a b-table for a S2-like grid denoted by 'btable.txt'. The other is the b-table for the 3D-DSI sampling scheme used in the DICOM data acquisition. This b-table has 203 points uniformly distributed on a 3D grid limited to the volume of the unit sphere. In both tables, the b-values range from 0 to 4000.

The output files 'data_V1_gqi.nii.gz' and 'data_gfa_gqi.nii.gz' are used to visualize RGB maps through rgbvolmap() or via the "FSL/fslview" tool. These files may also be used to perform white matter fibre tractography.

Value

gqi.odfpeaks outputs two data files in NIfTI format named 'data_V1_gqi.nii.gz' and 'data_gfa_gqi.nii.gz'. The first main fibre directions per voxel are contained in 'data_V1_gqi.nii.gz'. The file 'data_gfa_gqi.nii.gz' contains the GFA values per voxel.

Author(s)

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References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

Ferreira da Silva, A. R. Facing the Challenge of Estimating Human Brain White Matter Pathways. In *Proc. of the 4th International Joint Conference on Computational Intelligence* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress, pp. 709-714.

Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. FSL. *NeuroImage* 62, 2 (2012), 782-790.

See Also

gqi.odfpeaklines, plotglyph, gqi.odfvmf, gqi.odfvmflines, gqi.odfvxgrid, s2tessel.zorder, rgbvolmap, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
    ##-------------
    ## Generate ODF volumes (GQI volume processing) for
    ## range of slices using deterministic find peaks algorithm
    gqi.odfpeaks(rg=c(1,1), bview="coronal", showglyph=FALSE)
    ## Show RGB maps for range of slices processed by gqi.odfpeaks()
    rgbvolmap(fbase=tempdir())
    ##-------------
    ## Process whole volume: generate NIfTI files
    ##   data_gfa_gqi.nii.gz and data_V1_gqi.nii.gz
    gqi.odfpeaks(rg=NULL)
```

```
    rgbvolmap(fbase=tempdir(), rg=NULL, bview="coronal")
    ##-------------
    ## Visualization of RBG maps based on processed volumes
    ## "data_gfa_gqi.nii.gz and "data_V1_gqi.nii.gz"
    ## (visualization compatible with the FSL/fslview tool)
    rgbvolmap(rg=NULL, bview="coronal")
    ##-------------
    ## Show reconstructed glyphs in ODF processing
    ## for principal direction determination
    gqi.odfpeaks(rg=c(1,1), bview="coronal", showglyph=TRUE, depth=3)

## End(Not run)
```

`gqi.odfvmf` *Fibre Orientation Estimation Based on von Mises Distributions with GQI Reconstruction*

Description

Fibre orientations in multiple fibre voxels are estimated using a mixture of von Mises-Fisher (vMF) distributions. This statistical estimation procedure is used to resolve crossing fibre mappings.

Usage

```
gqi.odfvmf(gdi="gqi", run=TRUE, fbase=NULL, savedir=tempdir(), rg=NULL, swap=FALSE,
 lambda=NULL, depth=3, btoption=2, threshold=0.4, showglyph=FALSE, bview="coronal",
 clusterthr=0.6, aniso=NULL, ...)
```

Arguments

`gdi`	method of ODF reconstruction to use `c("gqi", "gqi2")` (default: `"gqi"`).
`run`	logical variable enabling loading previously processed data (default: `TRUE`).
`fbase`	Directory where the required input data files are located.
`savedir`	directory for saving/loading processed results (default: `tempdir()`.
`rg`	range of slices to process; default option `rg=NULL` processes all slices.
`swap`	toggle radiological/neurological orientation (default: `FALSE`).
`lambda`	diffusion sampling length in `gdi="gqi"` and `gdi="gqi2"`. By default the following default values are used when `lambda=NULL` is specified: 1.24 in "gqi", 3 in "gqi2".
`depth`	sampling density on the hemisphere used in simulation (default N=321; depth=3).
`btoption`	b-table selection between '`btable.txt`' (`btoption=1`), and the 3D-DSI grid b-table extracted from the diffusion data set ('`data.bvec`' and '`data.bval`'). By default, the 3D-DSI grid b-table is used (`btoption=2`).
`threshold`	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).

bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
showglyph	logical variable controlling visualization of voxel glyphs (default: FALSE).
clusterthr	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
aniso	anisotropic parameter in the range "[0,1)" or NULL to use in ODF pos-processing default: NULL.
...	optional specification of non-default control parameters as detailed in movMF.

Details

GQI methods specify an operational sampling scheme in q-space from which the ODF can be estimated. GQI (Yeh et.al. 2010) or GQI2 (Garyfallidis 2012) may be used for ODF reconstruction. For directional clustering estimation gqi.odfvmf uses a mixture of 2 and 4 von Mises-Fisher (vMF) distributions that serves as a model for directional ODF profile data, corresponding to multiple fibre orientations. Statistical orientation estimation in gqi.odfvmf is based on von Mises clustering procedures provided by the R-package **movMF**, by Kurt Hornik and Bettina Gruen.

Starting with the raw diffusion signal acquired on a grid of q-space, the ODF profile is estimated at each voxel, considering a sampling density of unit vectors on a unit S2 grid. When a threshold is applied to the estimated ODF at each voxel, the non-thresholded unit vectors provide directional statistics information about the estimated ODF profile. The main ODF orientations at each voxel relevant for fibre tracking may be estimated by clustering the non-thresholded unit vectors.

The main diffusion data set used in the examples is a DICOM data set provided by the "Advanced Biomedical MRI Lab, National Taiwan University Hospital", which is included in the "DSI Studio" package, publicly available from the NITRC repository (http://www.nitrc.org). Two b-tables defining the acquisition setup are specified. One is a b-table for a S2-like grid denoted by 'btable.txt'. The other is the b-table for the 3D-DSI sampling scheme used in the DICOM data acquisition. This b-table has 203 points uniformly distributed on a 3D grid limited to the volume of the unit sphere. In both tables, the b-values range from 0 to 4000. Sampling densities of N=81 (depth=2) and N=321 (depth=3) on the hemisphere are often used in ODF profile reconstruction from diffusion acquisitions.

The output files 'data_V1_gqi.nii.gz', 'data_V2_gqi.nii.gz', 'data_V3_gqi.nii.gz', and 'data_gfa_gqi.nii.gz' may be used for probabilistic white matter tractography. These principal diffusion direction (PDD) files retain information about the 'theta' and 'alpha' parameters of the von Mises-Fisher mixture at each voxel. The file 'data_V123_gqi.nii.gz' joins all three PDD files in a single NIfTI file. For visualization purposes via a external tool such as "FSL/fslview" the voxel PDDs must be normalized to the unit sphere beforehand by using niinorm.

Value

gqi.odfvmf outputs three data files in NIfTI format named 'data_V1_gqi.nii.gz', 'data_V2_gqi.nii.gz', and 'data_gfa_gqi.nii.gz'. The first and second main fibre directions per voxel are contained in 'data_V1_gqi.nii.gz', 'data_V2_gqi.nii.gz', respectively. The file 'data_gfa_gqi.nii.gz' contains the GFA metric per voxel.

Author(s)

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References

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Ferreira da Silva, A. R. Facing the Challenge of Estimating Human Brain White Matter Pathways. In *Proc. of the 4th International Joint Conference on Computational Intelligence* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress, pp. 709-714.

Hornik, K., and Gruen, B. **movMF**: Mixtures of von Mises-Fisher Distributions, 2012. R package version 0.1-0.

Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626-1635.

Garyfallidis E., Towards an Accurate Brain Tractography, 2012, PhD Thesis, University of Cambridge.

Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. FSL. *NeuroImage* 62, 2 (2012), 782-790.

See Also

gqi.odfvmflines, gqi.odfpeaklines, gqi.odfvxgrid, rgbvolmap, gqi.odfpeaks, s2tessel.zorder, plotglyph, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
    ## Generate ODF volumes (GQI volume processing)
    ## for a range of slices using von Mises-Fisher clustering
    gqi.odfvmf(depth=2, showglyph=FALSE, threshold=0.5, savedir=tempdir())
    ## RGB maps for range of slices processed by gqi.odfvmf()
    rgbvolmap(fbase=tempdir(), rg=c(1,4), bview="coronal")
    ##-------------
    ## Show reconstructed glyphs in ODF processing
    ## for first and second main fibre direction determination
    gqi.odfvmf(gdi="gqi", rg=c(1,1), bview="coronal", depth=3,
      showglyph=TRUE, threshold=0.5)
    gqi.odfvmf(gdi="gqi2", rg=c(1,1), bview="coronal", depth=3,
      showglyph=TRUE, threshold=0.5)
    ##-------------
    ## speeded up approximations: hardmax and numeric kappa
    gqi.odfvmf(depth=2, showglyph=FALSE, threshold=0.5, savedir=tempdir(),
      E="hardmax", kappa=20)
    rgbvolmap(fbase=tempdir(), rg=c(1,4), bview="coronal")

## End(Not run)
```

`gqi.odfvmflines` *Fibre Orientation Mapping Based on von Mises-Fisher Distributions with GQI Reconstruction*

Description

In order to enable mapping complex white matter fibres in the brain, `gqi.odfvmflines` implements a new methodology based on directional statistics to estimate fibre profiles from high angular resolution diffusion imaging data. Statistical orientation estimation in `gqi.odfvmf` and `gqi.odfvmflines` is based on von Mises-Fisher clustering procedures provided by the R-package **movMF**, by Kurt Hornik and Bettina Gruen.

Usage

```
gqi.odfvmflines(gdi="gqi", run=TRUE, fbase=NULL, savedir=tempdir(), roi=NULL, rg=c(1,1),
 swap=FALSE, lambda=NULL, depth=3, btoption=2, threshold=0.4, kdir=6, zfactor=5,
 showglyph=FALSE, showimage="linesgfa", bview="coronal", bg="white", texture=NULL,
 clusterthr=0.6, aniso=NULL, ...)
```

Arguments

`gdi`	method of ODF reconstruction to use `c("gqi", "gqi2")` (default: `"gqi"`).
`run`	logical variable enabling loading previously processed data (default: `TRUE`).
`fbase`	Directory where the required input data files are located.
`roi`	Region of Interest (ROI) to use as mask; default mask (`roi=NULL`) uses an all brain mask for the supplied data set.
`rg`	range of slices to process (default option `rg=c(1,1)`); `rg=NULL` processes all slices.
`swap`	toggle radiological/neurological orientation (default: `FALSE`).
`lambda`	diffusion sampling length in `gdi="gqi"` and `gdi="gqi2"`. By default the following default values are used when `lambda=NULL` is specified: 1.24 in "gqi", 3 in "gqi2".
`depth`	sampling density on the hemisphere used in simulation (default N=321; depth=3).
`btoption`	b-table selection between '`btable.txt`' (`btoption=1`), and the 3D-DSI grid b-table extracted from the diffusion data set ('`data.bvec`' and '`data.bval`'). By default, the 3D-DSI grid b-table is used (`btoption=2`).
`threshold`	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
`kdir`	maximum number of fibre directions to map (default: 6).
`zfactor`	parameter controlling z-value in relief overlay maps (default: 5).
`showglyph`	logical variable controlling visualization of voxel glyphs (default: `FALSE`).

showimage	object controlling visualization of line-maps (default: "linesgfa"). Alternative options are: c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata") (see Details).
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir().
bg	map background colour (default "white").
texture	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
clusterthr	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
aniso	anisotropic parameter in the range "[0,1)" or NULL to use in ODF pos-processing default: NULL.
...	additional material properties for geometry appearance as specified in rgl.material, or specification of non-default control parameters as detailed in movMF.

Details

The function gqi.odfvmflines implements a mixture-model approach to clustering orientation distribution functions (ODFs) based on the von Mises-Fisher distributions. The method focus on clustering data on the unit sphere, where complexity arises from representing ODF profiles as directional data. GQI (Yeh et.al. 2010) or GQI2 (Garyfallidis 2012) may be used for ODF reconstruction.

Starting with the raw diffusion signal acquired on a grid of q-space, the ODF profile is estimated at each voxel, considering a sampling density of unit vectors on a unit S2 grid. When a threshold is applied to the estimated ODF at each voxel, the non-thresholded unit vectors provide directional statistics information about the estimated ODF profile. The main ODF orientations at each voxel relevant for fibre tracking may be estimated by clustering the non-thresholded unit vectors.

The main diffusion data set used in the examples is a DICOM data set provided by the "Advanced Biomedical MRI Lab, National Taiwan University Hospital", which is included in the "DSI Studio" package, publicly available from the NITRC repository (http://www.nitrc.org). Two b-tables defining the acquisition setup are specified. One is a b-table for a S2-like grid denoted by 'btable.txt'. The other is the b-table for the 3D-DSI sampling scheme used in the DICOM data acquisition. This b-table has 203 points uniformly distributed on a 3D grid limited to the volume of the unit sphere. In both tables, the b-values range from 0 to 4000.

Slice map display and overlay selection is controlled by specifying one the arguments
c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata")
for showimages. Meanings are as follows: "none" - no visualization; "gfa" - GFA map only; "lines" - line map only; "linesgfa" - GFA overlayed on line map; "linesrgbmap" - lines overlayed on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlayed on line map.

Value

gqi.odfvmflines produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlayed with generalized fractional anisotropy (GFA) relief maps, diffusion data maps or ROI maps. The file 'V1list.RData' containing the first main orientation directions for all processed voxels is output for further posterior orientation processing.

Author(s)

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References

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Yeh, F.-C., Wedeen, V. J., and Tseng, W.-Y. I. Generalized q-Sampling Imaging. *IEEE Transactions on Medical Imaging* 29, 9 (2010), 1626-1635.

Garyfallidis E., Towards an Accurate Brain Tractography, 2012, PhD Thesis, University of Cambridge.

See Also

gqi.odfvmf, gqi.odfpeaks, gqi.odfvmflines, gqi.odfvxgrid, plotglyph, rgbvolmap, s2tessel.zorder, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
  ##-------------
  ## von Mises-Fisher fibre orientation mapping
  ## for a range of slices
  gqi.odfvmflines(gdi="gqi", run=TRUE, rg=c(1,1), depth=2,
    showimage="linesdata", threshold=0.5)
  gqi.odfvmflines(gdi="gqi2", run=TRUE, rg=c(1,1), depth=2,
    showimage="linesdata", threshold=0.5)
  ## display line-maps only
  gqi.odfvmflines(run=FALSE, depth=2, showimage="lines")
  ## using GFA overlay
  gqi.odfvmflines(run=FALSE, depth=2, showimage="linesgfa")
  ##-------------
  ## Show reconstructed glyphs in ODF processing
  ## for principal direction determination
  gqi.odfvmflines(run=TRUE, depth=3,
    showimage="linesdata", showglyph=TRUE, threshold=0.5)
  ## show glyphs with using 'aniso' parameter
  gqi.odfvmflines(run=TRUE, depth=3,
    showimage="linesdata", showglyph=TRUE, threshold=0.5, aniso=0.3)
  ##-------------
  ## using a ROI overlay
  gqi.odfvmflines(run=TRUE, depth=3, roi="slfcst.nii.gz")
```

```
  ##-------------
  ## coronal view with texture for a single slice
  texturefname <- file.path(tempdir(),"rgbmap.png")
  rgbvolmap(texture=texturefname, bg="transparent")
  gqi.odfvmflines(threshold=0.5, showimage="linesrgbmap",
    texture=texturefname)
  ##-------------
  ## speeded up approximations: hardmax and common/numeric kappa
  gqi.odfvmflines(gdi="gqi", run=TRUE, rg=c(1,1), depth=2,
    showimage="linesdata", threshold=0.5,
    E="hardmax", kappa=list(common = TRUE))
  gqi.odfvmflines(gdi="gqi", run=TRUE, rg=c(1,1), depth=2,
    showimage="linesdata", threshold=0.5, E="hardmax", kappa=20)

## End(Not run)
```

---

gqi.odfvxgrid *Glyph Maps*

Description

gqi.odfvxgrid produces glyph-map fields of reconstructed ODF profiles for voxels in slices.

Usage

```
gqi.odfvxgrid(gdi="gqi", fbase=NULL, rg=c(1,1), swap=FALSE, lambda=NULL,
 depth=3, btoption=2, threshold=0.4, kdir=4, zfactor=5,
 showimage="glyphgfa", bview="coronal",
 savedir=tempdir(), bg="white", texture=NULL, aniso=NULL, ...)
```

Arguments

gdi	method of ODF reconstruction to use c("gqi", "gqi2") (default: "gqi").
fbase	Directory where the required input data files are located.
rg	range of slices to process (default option rg=c(1,1)); rg=NULL processes all slices.
swap	toggle radiological/neurological orientation (default: FALSE).
lambda	diffusion sampling length in gdi="gqi" and gdi="gqi2". By default the following default values are used when lambda=NULL is specified: 1.24 in "gqi", 3 in "gqi2".
depth	sampling density on the hemisphere used in simulation (default N=321; depth=3).
btoption	b-table selection between 'btable.txt' (btoption=1), and the 3D-DSI grid b-table extracted from the diffusion data set ('data.bvec' and 'data.bval'). By default, the 3D-DSI grid b-table is used (btoption=2).
threshold	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).

kdir	maximum number of fibre directions to map (default: 4).
zfactor	parameter controlling z-value in relief overlay maps (default: 5).
showimage	object controlling visualization of line-maps (default: "glyphgfa"). Alternative options are: c("none", "gfa", "glyph", "glyphgfa", "glyphrgbmap", "glyphdata") (see Details).
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir().
bg	map background colour (default "white")
texture	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
aniso	anisotropic parameter in the range "[0,1)" or NULL to use in ODF pos-processing default: NULL.
...	additional material properties for geometry appearance as specified in rgl.material.

Details

GQI (Yeh et.al. 2010) or GQI2 (Garyfallidis 2012) may be used for ODF reconstruction. Slice glyph map display and overlay selection is controlled by specifying one the arguments c("none", "gfa", "glyph", "glyphgfa", "glyphrgbmap", "glyphdata") for showimages. Meanings are as follows: "none" - no overlay; "gfa" - GFA map only; "glyph" - glyph map only; "glyphgfa" - GFA overlayed on glyph map; "glyphrgbmap" - glyphs overlayed on RGB map (if available); "glyphdata" - 'data_brain.nii.gz' is overlayed on line map.

Author(s)

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References

Adler, D., and Murdoch, D. **rgl**: 3D visualization device system (OpenGL), 2012. R package version 0.92.880.

Auguie, B. **gridExtra**: functions in Grid graphics, 2012. R package version 0.9.1.

Barber, C. B., Habel, K., Grasman, R., Gramacy, R. B., Stahel, A., and Sterratt, D. C. **geometry**: Mesh generation and surface tesselation, 2012. R package version 0.3-2.

Zeileis, A., Hornik, K., and Murrell, P. Escaping RGBland: Selecting colors for statistical graphics. Computational Statistics & Data Analysis 53 (2009), 3259-3270.

See Also

gqi.odfpeaks, gqi.odfvmf, gqi.odfvmflines, s2tessel.zorder, plotglyph, rgbvolmap, simulglyph.vmf, simul.fandtasia, simul.simplefield

Examples

```
## Not run:
  ## show glyph-map for selected slice
  gqi.odfvxgrid(threshold=0.5, depth=2, showimage="glyphgfa")
  gqi.odfvxgrid(gdi="gqi", threshold=0.5, depth=2, showimage="glyphgfa")
  ##----
  ## generate slice RGB map as texture
  texturefname <- file.path(tempdir(),"rgbmap.png")
  rgbvolmap(texture=texturefname, bg="transparent")
  ## coronal glyphs + RGBmap
  gqi.odfvxgrid(threshold=0.5, depth=2, showimage="glyphrgbmap",
    texture=texturefname)

## End(Not run)
```

`niinorm` *Normalization of Principal Diffusion Directions*

Description

`niinorm` normalizes Principal Diffusion Directions (PDDs) in NIfTI files. The unnormalized PDD values produced by `gqi.odfvmf` retain information about the estimated von Mises-Fisher parameters at each voxel, which are useful in probabilistic tractography. On the other hand, normalized PDD values are useful for visualization and seed mask creation, namely using the 'FSL/fslview' tool.

Usage

```
niinorm(srcdir=tempfile(), filename="data_V1", savedir=tempdir())
```

Arguments

`srcdir`	directory where loading files are located (default: `tempdir()`.)
`filename`	name of the NIfTI file with PDD values to be normalized (default: '`"data_V1")`'.)
`savedir`	directory for saving processed results (default: `tempdir()`.)

Value

`niinorm` accepts NIfTI files with incorporated PDD values as produced by `gqi.odfvmf`, and outputs NIfTI files with normalized PDD values in the unit sphere. The output NIfTI filenames receive the suffix 'n', e.g., '`data_V1n`' and '`data_V2n`'.

Author(s)

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See Also

gqi.odfvmf

Examples

```
## Not run:
## Example using the PDD files in gdimap
## normalize vector data generated by vMF functions
## before visualization with FSL/fslview
fi1 <- "data_V1.nii.gz"
p <- system.file(file.path("extdata", fi1), package = "gdimap")
p1 <- strsplit(p,fi1)[[1]][1]
niinorm(srcdir=p1, filename=fi1, savedir=tempdir())
fi2 <- "data_V2.nii.gz"
niinorm(srcdir=p1, filename=fi2, savedir=tempdir())
## try fslview if installed
fo1 <- file.path(tempdir(),"data_V1n.nii.gz")
fo2 <- file.path(tempdir(),"data_V2n.nii.gz")
fo3 <- file.path(p1, "data_gfa.nii.gz")
if(Sys.which("fslview") != "") system(paste("fslview", fo3, fo2, fo1, "&"))

## End(Not run)
```

---

plotglyph *3D Glyph Visualization*

Description

The ODF profiles reconstructed at each voxel by GQI are visualized as 3D glyphs using **rgl**. The estimated fibre orientations per voxel are also depicted.

Usage

```
plotglyph(odf, grad, pk, kdir=6, vmfglyph=TRUE, pos=c(0,0,0))
```

Arguments

odf	slice ODFs.
grad	ODF vertices generated by the selected shell tessellation.
pk	coordinates of voxel main directions.
kdir	maximum number of directions to use (default: 6).
vmfglyph	logical variable for glyph visualization in two situations: statistical vMF glyphs (default: TRUE), and deterministic glyphs.
pos	3D positional coordinate (default c(0,0,0)).

Details

plotglyph is used by gqi.odfvxgrid, gqi.odfpeaklines, and gqi.odfvmflines.

Author(s)

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References

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Adler, D., and Murdoch, D. **rgl**: 3D visualization device system (OpenGL), 2012. R package version 0.92.880.

Auguie, B. **gridExtra**: functions in Grid graphics, 2012. R package version 0.9.1.

Barber, C. B., Habel, K., Grasman, R., Gramacy, R. B., Stahel, A., and Sterratt, D. C. **geometry**: Mesh generation and surface tesselation, 2012. R package version 0.3-2.

See Also

simulglyph.vmf, simulglyph.vmf, gqi.odfpeaks, gqi.odfvmf, gqi.odfvmflines, gqi.odfvxgrid, s2tessel.zorder, plotglyph, rgbvolmap

Examples

```
## Not run:
    gqi.odfvmflines(showglyph=TRUE, thr=0.7)
    ## noise-free simulations and vMF estimation (2 directions)
    simulglyph.vmf(angles=c(20,110),b=1500)

## End(Not run)
```

---

rgbvolmap *Generalized Fractional Anisotropy (GFA) Maps (RGB Maps)*

Description

Using GFA data and the main direction of ODF profiles produced by gqi.odfpeaks or gqi.odfvmf, rgbvolmap displays RGB maps.

Usage

```
rgbvolmap(fbase=NULL, rg=c(1,1),  bview="coronal",
 texture=NULL, bg="black")
```

Arguments

fbase	Directory where the required input data files are located.
rg	range of slices to process (default option rg=c(1,1)); rg=NULL processes all slices.
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
texture	PNG file name and location to store image, to be used as texture in overlay maps (defaultNULL).
bg	background colour (default "black").

Details

The standard convention for colour assignment when combining GFA values with directional information is adopted (see Pajevic, et.al.; Jellison et.al.). Colour hue indicates direction as follows: red, left-right; green, antero-posterior; blue, superior-inferior. Brightness is proportional to GFA. The output files 'data_V1.nii.gz' and 'data_gfa.nii.gz' are compatible with the "FSL/fslview" tool for RGB map and line map visualization.

Note

Commonly used acronyms:
GFA - Generalized Fractional Anisotropy
ODF - Orientation Distribution Function
GQI - Generalized q-Sampling Imaging
dMRI - Diffusion Magnetic Resonance Imaging
RGB maps - Red-Green-Blue colour maps

Author(s)

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References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

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Pajevic, S., and Pierpaoli, C. Color Schemes to Represent the Orien- tation of Anisotropic Tissues From Diffusion Tensor Data: Application to White Matter Fiber Tract Mapping in the Human Brain. Magnetic Resonance in Medicine 42 (1999), 526-540.

Jellison, B. J., Field, A. S., Medow, J., Lazar, M., Salamat, M. S., and Alexander, A. L. Diffusion tensor imaging of cerebral white matter: A pictorial review of physics, fiber tract anatomy, and tumor imaging patterns. *AJNR Am. J. Neuroradiology* 25 (2004), 356-369.

See Also

gqi.odfpeaks, gqi.odfpeaklines, gqi.odfvmf, gqi.odfvmflines, gqi.odfvxgrid, plotglyph, s2tessel.zorder

Examples

```
## Not run:
    ##-------------
    ## Generate ODF volumes (GQI volume processing) for
    ## range of slices using deterministic find peaks algorithm
    gqi.odfpeaks(rg=c(1,1), showglyph=FALSE)
    ## Show RGB maps for range of slices processed by gqi.odfpeaks()
    rgbvolmap(fbase=tempdir(), rg=c(1,1))
    ## Changing background colour
    rgbvolmap(fbase=tempdir(), rg=c(1,1), bg="transparent")
    ##-------------
    ## Process whole volume: generates NIfTI files
    ##   data_gfa_gqi.nii.gz and data_V1_gqi.nii.gz
    gqi.odfpeaks(rg=NULL)
    ## Visualization of RBG maps generated by vMF function "gqi.odfvmf"
    ## (cf. FSL/fslview tool)
    rgbvolmap(fbase=tempdir(), rg=NULL, bview="coronal")

## End(Not run)
```

---

s2tessel.zorder *3D Shell Grid Tessellation*

Description

3D shell grid tessellation of the icosahedron by Delaunay triangulation. Point are sorted in ZZ to enable hemi-sphere sampling.

Usage

```
s2tessel.zorder(depth=3, viewgrid=FALSE, saveg=FALSE)
```

Arguments

depth	sampling density on the hemisphere used in simulation (default N=321; depth=3).
viewgrid	logical variable controlling shell grid visualization (default: FALSE).
saveg	logical variable controlling grid data storage (default: FALSE).

Details

Sampling densities of N=81 (depth=2) and N=321 (depth=3) on the hemisphere are often used in ODF profile reconstruction from raw diffusion acquisitions.

Author(s)

Adelino Ferreira da Silva, Universidade Nova de Lisboa, Faculdade de Ciencias e Tecnologia, Portugal, <afs at fct.unl.pt>

References

Adler, D., and Murdoch, D. **rgl**: 3D visualization device system (OpenGL), 2012. R package version 0.92.880.

Barber, C. B., Habel, K., Grasman, R., Gramacy, R. B., Stahel, A., and Sterratt, D. C. **geometry**: Mesh generation and surface tessellation, 2012. R package version 0.3-2.

See Also

gqi.odfvmflines, rgbvolmap, gqi.odfpeaks, gqi.odfpeaklines, gqi.odfvxgrid, plotglyph, simulglyph.vmf, simul.fandtasia, simul.simplefield

Examples

```
## Not run:
  s2tessel.zorder(depth=2, viewgrid=TRUE) # 162 shell points
  s2tessel.zorder(depth=3, viewgrid=TRUE) # 642 shell points

## End(Not run)
```

---

simul.fandtasia *Simulation of Curved Fibre Bundles for von Mises-Fisher Fibre Orientation Mapping*

Description

The synthesized field of diffusion profiles generated by simul.fandtasia are used to reconstruct ODF profiles using the GQI method. ODF profiles and fibre directions are estimated by relying on von Mises-Fisher (vMF) distributions for directional mapping.

Usage

```
simul.fandtasia(gdi="gqi", gridsz=32, b=4000, depth=3, sigma=0.01,
 clusterthr=0.6, showglyph=FALSE, savedir=tempdir(), ...)
```

Arguments

gdi	method of ODF reconstruction to use c("gqi", "gqi2") (default: "gqi").
gridsz	dimension of squared grid to use in simulation (default 32)
b	strength of the magnetic diffusion gradient (default b-value=4000).
depth	sampling densities on the hemisphere used in simulation (default N=321; depth=3).
sigma	Rician noise level used in simulation; (default 0.01).

clusterthr	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
showglyph	logical variable controlling visualization of voxel glyphs (default: FALSE).
savedir	directory for saving/loading processed results (default: tempdir().
...	optional specification of non-default control parameters as detailed in movMF.

Details

Noisy profiles may be simulated by adding Rician noise to the simulated diffusion profile, with a user defined standard deviation level specified as σ (SNR=1/σ). The procedure is adapted from Barmpoutis' code to generate synthetic tensor diffusion-weighted MRI fields. The procedure is very time intensive for grids of size 32x32.

Value

simul.fandtasia returns a field of 32x32 diffusion profiles in NIfTI format.

Author(s)

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References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

Ferreira da Silva, A. R. Facing the Challenge of Estimating Human Brain White Matter Pathways. In *Proc. of the 4th International Joint Conference on Computational Intelligence* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress, pp. 709-714.

Hornik, K., and Gruen, B. **movMF**: Mixtures of von Mises-Fisher Distributions, 2012. R package version 0.1-0.

Barmpoutis, A. Tutorial on Diffusion Tensor MRI using Matlab. Electronic Edition, University of Florida, 2010,
http://www.mathworks.com/matlabcentral/fileexchange/file_infos/26997-fandtasia-toolbox.

See Also

simul.fandtasiaSignal, simulglyph.vmf, simul.simplefield

Examples

```
## Not run:
    ## simulation with a new generated field of profiles,
    ## of size 16x16 (for speed), with added noise
    simul.fandtasia(gridsz=16, sigma=0.01)
    simul.fandtasia(gdi="gqi2", gridsz=16, sigma=0.01)
```

```
    ## same as before, but showing crossing-fibre glyphs
    simul.fandtasia(gridsz=16, sigma=0.01, showglyph=TRUE)
    simul.fandtasia(gdi="gqi2", gridsz=16, sigma=0.01, showglyph=TRUE)
    ## using a 32x32 data field as in the original reference
    ## Warning: time-consuming example
    simul.fandtasia()
    ## speeded up approximations: hardmax and numeric kappa
    simul.fandtasia(gridsz=16, sigma=0.01, E="hardmax", kappa=20)

## End(Not run)
```

`simul.fandtasiaSignal` *Simulation of Crossing-Fibre Diffusion Profiles*

Description

`simul.fandtasiaSignal` generates a synthesized field of diffusion profiles following Barmpoutis's algorithm.

Usage

```
simul.fandtasiaSignal(g, gridsz=32, b=4000, sigma=NULL, savedir=tempdir())
```

Arguments

`g`	matrix of 3D points on the S2 shell used in simulation.
`gridsz`	dimension of squared grid to use in simulation (default 32).
`b`	strength of the magnetic diffusion gradient (default b-value=4000).
`sigma`	Rician noise level used in simulation; (default `NULL`).
`savedir`	directory for saving/loading processed results (default: `tempdir()`).

Details

The diffusion field simulates a field of dimension `gridsz x gridsz` of diffusion profiles for testing crossing fibre orientation mapping. The procedure `simul.fandtasiaSignal` is an adaptation of Barmpoutis' MATLAB code to generate synthetic tensor diffusion-weighted MRI fields.

Value

`simul.fandtasiaSignal` returns a field of 32x32 diffusion profiles in NIfTI format.

Author(s)

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References

Ferreira da Silva, A. R. Facing the Challenge of Estimating Human Brain White Matter Pathways. In *Proc. of the 4th International Joint Conference on Computational Intelligence* (Oct. 2012), K. Madani, J. Kacprzyk, and J. Filipe, Eds., SciTePress, pp. 709-714.

Hornik, K., and Gruen, B. **movMF**: Mixtures of von Mises-Fisher Distributions, 2012. R package version 0.0-2.

Barmpoutis, A. Tutorial on Diffusion Tensor MRI using Matlab. Electronic Edition, University of Florida, 2010, http://www.mathworks.com/matlabcentral/fileexchange/file_infos/26997-fandtasia-toolbox.

See Also

simul.fandtasia, simul.simplefield

Examples

```
## Not run:
    ## shell grid
    s2 <- s2tessel.zorder(depth=3)
    simul.fandtasiaSignal(g=s2$pc, gridsz=16, sigma=0.01)

## End(Not run)
```

---

simul.simplefield *Simulation of a Simple Field of Diffusion Profiles for von Mises-Fisher Fibre Orientation Mapping*

Description

ODF profiles and fibre directions are estimated using mixtures of von Mises-Fisher (vMF) distributions for directional mapping. The synthesized field of diffusion profiles generated by `simul.simplefield` are used to reconstruct ODF profiles using GQI or GQI2.

Usage

```
simul.simplefield(gdi="gqi", b=3000, sigma=NULL,
 clusterthr=0.6, logplot=TRUE, savedir=tempdir(),
 fmask="m1", ang=NULL, ...)
```

Arguments

`gdi`	method of ODF reconstruction to use `c("gqi", "gqi2")` (default: `"gqi"`).
`b`	strength of the magnetic diffusion gradient (default b-value=3000).
`sigma`	Rician noise level used in simulation; (default `NULL`).
`clusterthr`	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).

logplot	logical variable for selecting log-scale (default TRUE).
savedir	directory for saving processed results (default: tempdir().
fmask	choice of field mask among a table of pre-defined mask models for simple field simulations. Models are built by indexing array masks. Models c("m1","m2","m3") simulate single fiber fields. Models c("mx1","mx2", "mx3" simulates crossing-fiber fields.
ang	angle in degrees to be cutomize fmask models (default: NULL - pre-defined angles are used).
...	optional specification of non-default control parameters as detailed in movMF.

Details

The number of fibres is automatically estimated from the diffusion profile. Noisy profiles may be simulated by adding Rician noise to the simulated diffusion profile, with a user defined standard deviation level specified as σ (SNR=1/σ).

Value

simul.simplefield plots the reconstructed field of ODF profiles together with the vMF-estimated fiber directions. It outputs three data files in NIfTI format named 'data_V1_gqi.nii.gz', 'data_V2_gqi.nii.gz', and 'data_gfa_gqi.nii.gz'. The first and second main fibre directions per voxel are contained in 'data_V1_gqi.nii.gz', 'data_V2_gqi.nii.gz', respectively. The file 'data_gfa_gqi.nii.gz' contains the GFA metric per voxel.

Author(s)

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References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

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Hornik, K., and Gruen, B. **movMF**: Mixtures of von Mises-Fisher Distributions, 2012. R package version 0.1-0.

Adler, D., and Murdoch, D. **rgl**: 3D visualization device system (OpenGL), 2012. R package version 0.92.880.

Barber, C. B., Habel, K., Grasman, R., Gramacy, R. B., Stahel, A., and Sterratt, D. C. **geometry**: Mesh generation and surface tessellation, 2012. R package version 0.3-2.

See Also

simulglyph.vmf, simul.fandtasia, synthfiberss2z, plotglyph, gqi.odfvmflines, rgbvolmap, gqi.odfpeaks, gqi.odfpeaklines, gqi.odfvxgrid

Examples

```
## Not run:
  simul.simplefield(fmask="m1")
  simul.simplefield(gdi="gqi2", fmask="m1")
  ##
  simul.simplefield(logplot=FALSE, fmask="m3")
  simul.simplefield(gdi="gqi2", logplot=FALSE, fmask="m3")
  ##
  simul.simplefield(sigma=0.033, logplot=FALSE, fmask="mx1")
  simul.simplefield(gdi="gqi2", sigma=0.033, logplot=FALSE, fmask="mx1")

## End(Not run)
```

`simulglyph.vmf` *Voxel Diffusion Profile Simulation and von Mises-Fisher Fibre Mapping*

Description

The synthesized diffusion voxel profiles generated by `synthfiberss2z` are used to reconstruct ODF profiles. Three methods may be used for reconstruction: GQI, GQI2, and Q-ball. ODF profiles and fibre directions are estimated by relying on von Mises-Fisher (vMF) distributions for directional mapping.

Usage

```
simulglyph.vmf(gdi="gqi", s2grid=NULL, angles=c(20,100), depth=3, b=3000,
 lambda=NULL, order=4, sigma=NULL, clusterthr=0.6, savedir=tempdir(),
 showglyph=TRUE, aniso=NULL, logplot=TRUE, wi=NULL, ...)
```

Arguments

`gdi`	method of ODF reconstruction to use `c("gqi", "gqi2", "sph")` (default: `"gqi"`).
`s2grid`	S2 shell grid, or other equivalent user specified grid. By default `s2grid=NULL` means that the grid is generated by `s2tessel.zorder`.
`angles`	angles in degrees of fibres to be used in simulation (default: two fibres with angles `c(20,100)`).
`depth`	sampling densities on the hemisphere used in simulation (default N=321; depth=3).
`b`	strength of the magnetic diffusion gradient (default b-value=3000).
`lambda`	model parameter: diffusion sampling length in `gdi="gqi"` and `gdi="gqi2"`; Aganj's regularization parameter in `gdi="sph"`. By default the following default values are used when `lambda=NULL` is specified: 1.24 in "gqi", 3 in "gqi2", and 0.006 in "sph".
`order`	parameter associated with the order of the spherical harmonics approximation for `gdi="sph"` (default: 4).

sigma	Rician noise level used in simulation; (default NULL).
clusterthr	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
savedir	directory for saving/loading processed results (default: tempdir()).
showglyph	logical variable controlling visualization of voxel glyphs (default: TRUE).
aniso	anisotropic parameter in the range "[0,1)" or NULL to use in ODF pos-processing default: NULL.
logplot	logical variable for selecting log-scale (default TRUE).
wi	weight given to fiber's volume fraction. Example for two fibers with different weights wi=c(0.7,0.3) (default NULL gives equal weigth to all fibers.)
...	optional specification of non-default control parameters as detailed in movMF.

Details

The "gdi" argument specifies the method of ODF reconstruction to use in the list c("gqi", "gqi2", "sph"). The number of fibres is automatically estimated from the diffusion profile. To decide on the number of components to select the Bayesian information criterion (BIC) is applied.

Value

simulglyph.vmf plots the reconstructed ODF profile together with the vMF-estimated fiber directions.

Author(s)

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References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

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Hornik, K., and Gruen, B. **movMF**: Mixtures of von Mises-Fisher Distributions, 2012. R package version 0.0-2.

Adler, D., and Murdoch, D. **rgl**: 3D visualization device system (OpenGL), 2012. R package version 0.92.880.

Barber, C. B., Habel, K., Grasman, R., Gramacy, R. B., Stahel, A., and Sterratt, D. C. **geometry**: Mesh generation and surface tessellation, 2012. R package version 0.3-2.

Tabelow K., Polzehl J.: **dti**: DTI/DWI Analysis, 2012. R package version 1.1-0.

See Also

synthfiberss2z, plotglyph, gqi.odfvmflines, rgbvolmap, gqi.odfpeaks, gqi.odfpeaklines, gqi.odfvxgrid, simul.fandtasia, simul.simplefield

Examples

```
## Not run:
    ## Examples of synthetized voxel diffusion glyphs
    ## ODF glyphs, and vMF fiber orientation mapping
    ## noise-free simulations and vMF estimation by GQI and QBI
    b <- 3000; angles <- c(20,110)
    simulglyph.vmf(angles=angles,b=b, gdi="gqi")
    simulglyph.vmf(angles=angles,b=b, gdi="gqi", logplot=FALSE)
    simulglyph.vmf(angles=angles,b=b, gdi="gqi2")
    simulglyph.vmf(angles=angles,b=b, gdi="gqi2", logplot=FALSE)
    ## test reconstruction with aniso factor
    simulglyph.vmf(angles=angles,b=b, gdi="gqi", aniso=0.5)
    ## Spherical harmonics model
    simulglyph.vmf(angles=angles,b=b, gdi="sph")
    simulglyph.vmf(angles=angles,b=b, gdi="sph", aniso=0.5)
    ## plot diffusion signal with "logplot=FALSE"
    angles <- 45; b <- 1500
    simulglyph.vmf(angles=angles,b=b, gdi="gqi",  logplot=FALSE)
    simulglyph.vmf(angles=angles,b=b, gdi="gqi2", logplot=FALSE)
    ## 2 direction, lower crossing-angles, higher b
    angles <- c(20,80); b <- 6000
    simulglyph.vmf(angles=angles,b=b, gdi="gqi")
    simulglyph.vmf(angles=angles,b=b, gdi="sph")
    ## 2 direction, different volume fractions
    simulglyph.vmf(angles=angles, b=b, wi=c(0.7, 0.3), clusterthr=0.4)
    ## 2 direction, low croosing angle
    angles <- c(20,65); b <- 6000
    simulglyph.vmf(angles=angles,b=b)
    ## 3 directions
    angles <- c(20,80,140); b <- 3000
    simulglyph.vmf(angles=angles,b=b)
    # 3 directions
    angles <- c(0,60,120); b <- 3000
    simulglyph.vmf(angles=angles,b=b)
    # 3 directions, different weights
    simulglyph.vmf(angles=angles,b=b, wi=c(0.25,0.25,0.5), clusterthr=0.4)
    ##------------------
    ## noisy simulations and vMF estimation by GQI and QBI
    b <- 3000; sigma <- 0.033
    angles <- c(20,110)
    simulglyph.vmf(angles=angles,b=b, sigma=sigma, gdi="gqi")
    simulglyph.vmf(angles=angles,b=b, sigma=sigma, gdi="sph")
    # 2 direction, lower crossing-angles, higher b
    angles <- c(20,80)
    simulglyph.vmf(angles=angles,b=b, sigma=sigma)
    ## 2 direction, low croosing angle
    angles <- c(20,65)
```

```
simulglyph.vmf(angles=angles,b=b, sigma=sigma)
# 3 directions
angles <- c(20,80,140)
simulglyph.vmf(angles=angles,b=b, sigma=sigma)
# 3 directions
angles <- c(0,60,120)
simulglyph.vmf(angles=angles,b=b, sigma=sigma)
##------------------
## speeded up approximations: hardmax and common kappa
## 2 direction, low croosing angle
b <- 4000; angles <- c(20,65)
simulglyph.vmf(angles=angles,b=b, clusterthr=0.4,
  E="hardmax", kappa = list(common = TRUE))
## 3 directions, different weights
b <- 6000; angles <- c(0,60,120)
simulglyph.vmf(angles=angles,b=b, wi=c(0.25,0.25,0.5),
  clusterthr=0.4, E="hardmax", kappa = list(common = TRUE))
## hardmax; numeric kappa
simulglyph.vmf(angles=angles,b=b, wi=c(0.25,0.25,0.5),
  clusterthr=0.4, E="hardmax", kappa = 40)

## End(Not run)
```

`slfcst` *A Region-of-Interest (ROI) File for Diffusion MRI Analysis*

Description

The '`slfcst.nii.gz`' is a region-of-interest (ROI) file that was formed by extracting the superior longitudinal fasciculus (SLF) and corticospinal tract (CST) regions from the main data diffusion set '`data.nii.gz`'.

For reasons of limited CRAN storage space, a trimmed down data set with just 4 coronal slices was selected. Coronal slices (29:32) were extracted from the original data set. Hence, the argument `bview="coronal"` is used in the examples, and the range of coronal slices is (1:4). User specified complete data sets may be used without restrictions.

Format

The file '`slfcst.nii.gz`' is in gzipped NIfTI format. The R-package **oro.nifti** is required to read NIfTI files.

Details

The extracted regions were registered to the DSI data set using the FSL/FLIRT tool. The procedure uses the '`JHU-ICBM-labels-2mm.nii.gz`' atlas included in the FSL toolbox.

The ROI file '`slfcst.nii.gz`' depicts brain regions where anatomic white matter fibre crossings are known to exist, forming multiple pathway bundles connected to the cerebral cortex.

References

Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. Fsl. *NeuroImage* 62, 2 (2012), 782-790.

Whitcher, B., Schmid, V. J., and Thornton, A. Working with the DICOM and NIfTI data standards in R. *Journal of Statistical Software* 44, 6 (2011), 1-28.

`sph.odfpeaklines` *Fibre Orientation Mapping Based on Local Peak Detection with QBI Reconstruction*

Description

`sph.odfpeaklines` produces line-maps of ODF profiles for diffusion data slices using a regularized spheric harmonics method for ODF reconstruction.

Usage

```
sph.odfpeaklines(run=TRUE, fbase=NULL, roi=NULL, rg=c(1,1), btoption=2,
 swap=FALSE, threshold=0.4, kdir=2,  zfactor=5, showglyph=FALSE,
 showimage="linesgfa", bview="coronal", savedir=tempdir(),
 bg="white", order=4, texture=NULL, ...)
```

Arguments

`run`	logical variable enabling loading previously processed data (default: `TRUE`).
`fbase`	Directory where the required input data files are located.
`roi`	Region of Interest (ROI) to use as mask; default mask (`roi=NULL`) uses an all brain mask for the supplied data set.
`rg`	range of slices to process (default option `rg=c(1,1)`); `rg=NULL` processes all slices.
`btoption`	b-table selection between '`btable.txt`' (`btoption=1`), and the 3D-DSI grid b-table extracted from the diffusion data set ('`data.bvec`' and '`data.bval`'). By default, the 3D-DSI grid b-table is used (`btoption=2`).
`swap`	toggle radiological/neurological orientation (default: `FALSE`).
`threshold`	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
`kdir`	maximum number of fibre directions to map (default: 2).
`zfactor`	parameter controlling z-value in relief overlay maps (default: 5).
`showglyph`	logical variable controlling visualization of voxel glyphs (default: `FALSE`).
`showimage`	object controlling visualization of line-maps (default: `"linesgfa"`). Alternative options are: `c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata")` (see Details).

bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir()).
bg	map background colour (default "white")
order	parameter associated with the order of the spherical harmonics approximation (default: 4).
texture	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
...	additional material properties for geometry appearance as specified in rgl.material, or specification of non-default control parameters as detailed in movMF.

Details

The identification of fibre directions is performed by extracting the local maxima of the reconstructed ODF, where this function surpasses a certain threshold. The Q-ball reconstruction method with Aganj regularization as implemented in **dti** (Tabelow and Polzehl) is used for orientation distribution function (ODF) reconstruction. sph.odfpeaklines implements the standard method of fibre orientation detection. Local maxima of the reconstructed ODF are located simply by selecting a large number of sampled points on the sphere and searching within a fixed radius neighbourhood. For a single main fibre orientation the method performs well. However, for crossing fibres and other complex fibre configurations the peaks of the ODF profiles identified by the methods do not necessarily match the orientations of the distinct fibre populations. A more robust method is implemented in sph.odfvmflines.

Starting with the raw high angular resolution diffusion signal acquired on a S2-shell of q-space, the ODF profile is reconstructed at each voxel, considering a sampling density of unit vectors on a unit S2 shell. Q-ball imaging (QBI) is used for orientation distribution function (ODF) reconstruction. For comparison with GQI, the b-table 'btable.txt' has been used in the examples. This b-table has 203 points distributed on a S2-shell.

Slice map display and overlay selection is controlled by specifying one the arguments c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata") for showimages. Meanings are as follows: "none" - no visualization; "gfa" - GFA map only; "lines" - line map only; "linesgfa" - GFA overlayed on line map; "linesrgbmap" - lines overlayed on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlayed on line map.

Value

sph.odfpeaklines produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlayed with generalized fractional anisotropy (GFA) relief maps, diffusion data maps or ROI maps. The file 'V1list.RData' containing the first main orientation directions for all processed voxels is output for further posterior orientation processing.

Author(s)

Adelino Ferreira da Silva, Universidade Nova de Lisboa, Faculdade de Ciencias e Tecnologia, Portugal, <afs at fct.unl.pt>

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Tuch D. S., Q-Ball Imaging, *Magnetic Resonance in Medicine* 52 (2004), 1358-1372.

Tabelow K., Polzehl J.: **dti**: DTI/DWI Analysis, 2012. R package version 1.1-0.

See Also

sph.odfpeaks, sph.odfvmf, sph.odfvmflines, gqi.odfvxgrid, s2tessel.zorder, plotglyph, rgbvolmap, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
  ##-------------
  ## Line map using ODF peak detection
  sph.odfpeaklines(run=TRUE, showimage="lines")
  ## display line-map overlayed on GFA map
  sph.odfpeaklines(run=FALSE, showimage="linesgfa")
  ##-------------
  ## Show examples of reconstructed glyphs in ODF processing
  sph.odfpeaklines(showimage="lines", showglyph=TRUE)
  ##------------
  ## using a ROI overlay
  sph.odfpeaklines(roi="slfcst.nii.gz", showimage="linesgfa")
  ## using data overlay
  sph.odfpeaklines(showimage="linesdata")

## End(Not run)
```

---

sph.odfpeaks *Main Fibre Orientation Determination via Peak Detection with Q-ball Reconstruction*

Description

The Q-ball reconstruction method with Aganj regularization as implemented in **dti** (Tabelow and Polzehl) is used for orientation distribution function (ODF) reconstruction. For identifying voxel fibre directions, the local maxima of the reconstructed ODF are identified, where this function surpasses a certain threshold.

Usage

```
sph.odfpeaks(fbase=NULL, rg=NULL, swap=FALSE, btoption=2,
 threshold=0.4, showglyph=FALSE, bview="coronal", savedir=tempdir(), order=4)
```

Arguments

fbase	Directory where the required input data files are located.
rg	range of slices to process; default option rg=NULL processes all slices.
swap	toggle radiological/neurological orientation (default: FALSE).
btoption	b-table selection between 'btable.txt' (btoption=1), and 3D-DSI grid b-table supplied with the diffusion data set (default btoption=2).
threshold	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
showglyph	logical variable controlling visualization of voxel glyphs (default: FALSE).
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir()).
order	parameter associated with the order of the spherical harmonics approximation (default: 4).

Details

The most commonly used approach for identifying fibre directions is to extract the local maxima of the reconstructed ODF, where this function surpasses a certain threshold. The application of the approach is based on the assumption that the principal directions extracted from the ODF can be interpreted as principal directions of the underlying fibre architecture. Thresholding avoids selecting smaller ODF peaks that may appear due to noise. Local maxima of the reconstructed ODF are located simply by selecting a large number of sampled points on the sphere and searching within a fixed radius neighbourhood.

Starting with the raw high angular resolution diffusion signal acquired on a S2-shell of q-space, the ODF profile is reconstructed at each voxel, considering a sampling density of unit vectors on a unit S2 shell. Q-ball imaging (QBI) is used for orientation distribution function (ODF) reconstruction. For comparison with GQI, the b-table 'btable.txt' has been used in the examples. This b-table has 203 points distributed on a S2-shell.

The output files 'data_V1_sph.nii.gz' and 'data_gfa_sph.nii.gz' are used to visualize RGB maps through rgbvolmap() or via the "FSL/fslview" tool. These files may also be used to perform white matter fibre tractography.

Value

sph.odfpeaks outputs two data files in NIfTI format named 'data_V1_sph.nii.gz' and 'data_gfa_sph.nii.gz'. The first main fibre directions per voxel are contained in 'data_V1_sph.nii.gz'. The file 'data_gfa_sph.nii.gz' contains the GFA values per voxel.

Author(s)

Adelino Ferreira da Silva, Universidade Nova de Lisboa, Faculdade de Ciencias e Tecnologia, Portugal, <afs at fct.unl.pt>

References

Ferreira da Silva, A. R. Computational Representation of White Matter Fiber Orientations, *International Journal of Biomedical Imaging*, Vol. 2013, Article ID 232143, Hindawi Publishing Corporation http://dx.doi.org/10.1155/2013/232143.

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Tuch D. S., Q-Ball Imaging, *Magnetic Resonance in Medicine* 52 (2004), 1358-1372.

Tabelow K., Polzehl J.: **dti**: DTI/DWI Analysis, 2012. R package version 1.1-0.

See Also

sph.odfpeaklines, plotglyph, sph.odfvmf, sph.odfvmflines, gqi.odfvxgrid, s2tessel.zorder, rgbvolmap, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
    ##-------------
    ## Generate ODF volumes (GQI volume processing) for
    ## range of slices using deterministic find peaks algorithm
    sph.odfpeaks(rg=c(1,1), bview="coronal", showglyph=FALSE)
    ## Show RGB maps for range of slices processed by sph.odfpeaks()
    rgbvolmap(fbase=tempdir())
    ##-------------
    ## Process whole volume: generate NIfTI files
    ##   data_gfa_sph.nii.gz and data_V1_sph.nii.gz
    sph.odfpeaks(rg=NULL)
    rgbvolmap(fbase=tempdir(), rg=NULL, bview="coronal")
    ##-------------
    ## Show reconstructed glyphs in ODF processing
    ## for principal direction determination
    sph.odfpeaks(rg=c(1,1), bview="coronal", showglyph=TRUE)

## End(Not run)
```

`sph.odfvmf` *Fibre Orientation Estimation Based on von Mises Distributions with Q-ball Reconstruction*

Description

Fibre orientations in multiple fibre voxels are estimated using a mixture of von Mises-Fisher (vMF) distributions. This statistical estimation procedure is used to resolve crossing fibre mappings.

Usage

```
sph.odfvmf(run=TRUE, fbase=NULL, savedir=tempdir(), rg=NULL, swap=FALSE,
 btoption=2, threshold=0.4, showglyph=FALSE, bview="coronal", order=4,
 clusterthr=0.6, aniso=NULL, ...)
```

Arguments

`run`	logical variable enabling loading previously processed data (default: `TRUE`).
`fbase`	Directory where the required input data files are located.
`savedir`	directory for saving/loading processed results (default: `tempdir()`.
`rg`	range of slices to process; default option `rg=NULL` processes all slices.
`swap`	toggle radiological/neurological orientation (default: `FALSE`).
`btoption`	b-table selection between '`btable.txt`' (`btoption=1`), and the 3D-DSI grid b-table extracted from the diffusion data set ('`data.bvec`' and '`data.bval`'). By default, the 3D-DSI grid b-table is used (`btoption=2`).
`threshold`	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
`bview`	MRI slice view selection in {`axial, coronal, sagittal`} (default: `"coronal"`).
`showglyph`	logical variable controlling visualization of voxel glyphs (default: `FALSE`).
`order`	parameter associated with the order of the spherical harmonics approximation (default: 4).
`clusterthr`	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
`aniso`	anisotropic parameter in the range "[0,1)" or `NULL` to use in ODF pos-processing default: `NULL`.
`...`	optional specification of non-default control parameters as detailed in `movMF`.

Details

For directional clustering estimation `sph.odfvmf` uses a mixture of 2 and 4 von Mises-Fisher (vMF) distributions that serves as a model for directional ODF profile data, corresponding to multiple fibre orientations. Statistical orientation estimation in `sph.odfvmf` is based on von Mises clustering procedures provided by the R-package **movMF**, by Kurt Hornik and Bettina Gruen.

Starting with the raw diffusion signal acquired on a grid of q-space, the ODF profile is estimated at each voxel, considering a sampling density of unit vectors on a unit S2 grid. When a threshold is applied to the estimated ODF at each voxel, the non-thresholded unit vectors provide directional statistics information about the estimated ODF profile. The main ODF orientations at each voxel relevant for fibre tracking may be estimated by clustering the non-thresholded unit vectors. The Q-ball reconstruction method with Aganj regularization as implemented in **dti** (Tabelow and Polzehl) is used for orientation distribution function (ODF) reconstruction.

The main diffusion data set used in the examples is a DICOM data set provided by the "Advanced Biomedical MRI Lab, National Taiwan University Hospital", which is included in the "DSI Studio" package, publicly available from the NITRC repository (http://www.nitrc.org). One QBI-compatible b-table defining the acquisition setup on a S2-shell is included in the package. The b-table for the shell acquisition used in For comparison with GQI, the b-table 'btable.txt' has been used in the examples. This b-table has 203 points distributed on a S2-shell.

The output files 'data_V1_sph.nii.gz', 'data_V2_sph.nii.gz' and 'data_gfa_sph.nii.gz' are used to visualize RGB maps through rgbvolmap() or via the "FSL/fslview" tool. These files may be used to perform white matter fibre tractography.

Value

sph.odfvmf outputs three data files in NIfTI format named 'data_V1_sph.nii.gz', 'data_V2_sph.nii.gz', and 'data_gfa_sph.nii.gz'. The first and second main fibre directions per voxel are contained in 'data_V1_sph.nii.gz', 'data_V2_sph.nii.gz', respectively. The file 'data_gfa_sph.nii.gz' contains the GFA metric per voxel.

Author(s)

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References

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Hornik, K., and Gruen, B. **movMF**: Mixtures of von Mises-Fisher Distributions, 2012. R package version 0.1-0.

Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M. FSL. *NeuroImage* 62, 2 (2012), 782-790.

Tuch D. S., Q-Ball Imaging, *Magnetic Resonance in Medicine* 52 (2004), 1358-1372.

Tabelow K., Polzehl J.: **dti**: DTI/DWI Analysis, 2012. R package version 1.1-0.

See Also

sph.odfvmflines, sph.odfpeaklines, gqi.odfvxgrid, rgbvolmap, sph.odfpeaks, s2tessel.zorder, plotglyph, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
    ## Generate ODF volumes (QBI volume processing)
    ## for a range of slices using von Mises-Fisher clustering
    sph.odfvmf(showglyph=FALSE, threshold=0.5, savedir=tempdir())
    ## RGB maps for range of slices processed by sph.odfvmf()
    rgbvolmap(fbase=tempdir(), rg=c(1,4), bview="coronal")
    ##-------------
    ## Show reconstructed glyphs in ODF processing
    ## for first and second main fibre direction determination
    sph.odfvmf(rg=c(1,1), bview="coronal", showglyph=TRUE, threshold=0.5)

## End(Not run)
```

---

sph.odfvmflines *Fibre Orientation Mapping Based on von Mises-Fisher Distributions with QBI reconstruction*

Description

In order to enable mapping complex white matter fibres in the brain, sph.odfvmflines implements a new methodology based on directional statistics to estimate fibre profiles from high angular resolution diffusion imaging data. Statistical orientation estimation in sph.odfvmf is based on von Mises-Fisher clustering procedures provided by the R-package **movMF**, by Kurt Hornik and Bettina Gruen.

Usage

```
sph.odfvmflines(run=TRUE, fbase=NULL, savedir=tempdir(), roi=NULL,  rg=c(1,1), swap=FALSE,
 btoption=2, threshold=0.4, kdir=4, zfactor=5, showglyph=FALSE, showimage="linesgfa",
 bview="coronal", bg="white", order=4, texture=NULL, clusterthr=0.6, aniso=NULL, ...)
```

Arguments

run	logical variable enabling loading previously processed data (default: TRUE).
fbase	Directory where the required input data files are located.
roi	Region of Interest (ROI) to use as mask; default mask (roi=NULL) uses an all brain mask for the supplied data set.
rg	range of slices to process (default option rg=c(1,1)); rg=NULL processes all slices.
swap	toggle radiological/neurological orientation (default: FALSE).

btoption	b-table selection between 'btable.txt' (btoption=1), and the 3D-DSI grid b-table extracted from the diffusion data set ('data.bvec' and 'data.bval'). By default, the 3D-DSI grid b-table is used (btoption=2).
threshold	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
kdir	maximum number of fibre directions to map (default: 4).
zfactor	parameter controlling z-value in relief overlay maps (default: 5).
showglyph	logical variable controlling visualization of voxel glyphs (default: FALSE).
showimage	object controlling visualization of line-maps (default: "linesgfa"). Alternative options are: c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata") (see Details).
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir().
bg	map background colour (default "white")
order	parameter associated with the order of the spherical harmonics approximation (default: 4).
texture	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
clusterthr	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
aniso	anisotropic parameter in the range "[0,1)" or NULL to use in ODF pos-processing default: NULL.
...	additional material properties for geometry appearance as specified in rgl.material.

Details

The function sph.odfvmflines implements a mixture-model approach to clustering orientation distribution functions (ODFs) based on the von Mises-Fisher distributions. The method focus on clustering data on the unit sphere, where complexity arises from representing ODF profiles as directional data.

Starting with the raw high angular resolution diffusion signal acquired on a S2-shell of q-space, the ODF profile is reconstructed at each voxel, considering a sampling density of unit vectors on a unit S2 shell. Q-ball imaging (QBI) is used for orientation distribution function (ODF) reconstruction. For comparison with GQI, the b-table 'byable.txt' has been used in the examples. This b-table has 203 points distributed on a S2-shell.

Slice map display and overlay selection is controlled by specifying one the arguments
c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata")
for showimages. Meanings are as follows: "none" - no visualization; "gfa" - GFA map only; "lines" - line map only; "linesgfa" - GFA overlayed on line map; "linesrgbmap" - lines overlayed on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlayed on line map.

Value

sph.odfvmflines produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlayed with generalized fractional anisotropy (GFA) relief maps, diffusion data maps or ROI maps. The file 'V1list.RData' containing the first main orientation directions for all processed voxels is output for further posterior orientation processing.

Author(s)

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References

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Tuch D. S., Q-Ball Imaging, *Magnetic Resonance in Medicine* 52 (2004), 1358-1372.

Tabelow K., Polzehl J.: **dti**: DTI/DWI Analysis, 2012. R package version 1.1-0.

See Also

sph.odfvmf, sph.odfpeaks, sph.odfvmflines, gqi.odfvxgrid, plotglyph, rgbvolmap, s2tessel.zorder, simulglyph.vmf, simul.fandtasia, simul.simplefield, data, data.bval, data.bvec, btable

Examples

```
## Not run:
  ##-------------
  ## von Mises-Fisher fibre orientation mapping
  ## for a range of slices
  sph.odfvmflines(run=TRUE, rg=c(1,1), showimage="linesdata",
    threshold=0.5)
  ## display line-maps only
  sph.odfvmflines(run=FALSE, showimage="lines")
  ## using GFA overlay
  sph.odfvmflines(run=FALSE, showimage="linesgfa")
  ##-------------
  ## Show reconstructed glyphs in ODF processing
  ## for principal direction determination
  sph.odfvmflines(run=TRUE, showimage="linesdata",
    showglyph=TRUE, threshold=0.5)
  ##-------------
  ## using a ROI overlay
  sph.odfvmflines(run=TRUE, roi="slfcst.nii.gz")
```

```
  ##-------------
  ## speeded up approximations: hardmax and common/numeric kappa
  sph.odfvmflines(run=TRUE, rg=c(1,1), showimage="linesdata",
    E="hardmax", kappa=list(common = TRUE))
  sph.odfvmflines(run=TRUE, rg=c(1,1), showimage="linesdata",
    E="hardmax", kappa=20)

## End(Not run)
```

---

sph.odfvxgrid *Glyph Maps*

Description

sph.odfvxgrid produces glyph-map fields of reconstructed ODF profiles for voxels in slices.

Usage

```
sph.odfvxgrid(fbase=NULL, rg=c(1,1), swap=FALSE, btoption=2, threshold=0.4,
 kdir=4, zfactor=5, showimage="glyphgfa", bview="coronal",
 savedir=tempdir(), bg="white", order=4, texture=NULL, ...)
```

Arguments

fbase	Directory where the required input data files are located.
rg	range of slices to process (default option rg=c(1,1)); rg=NULL processes all slices.
swap	toggle radiological/neurological orientation (default: FALSE).
btoption	b-table selection between 'btable.txt' (btoption=1), and the 3D-DSI grid b-table extracted from the diffusion data set ('data.bvec' and 'data.bval'). By default, the 3D-DSI grid b-table is used (btoption=2).
threshold	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
kdir	maximum number of fibre directions to map (default: 4).
zfactor	parameter controlling z-value in relief overlay maps (default: 5).
showimage	object controlling visualization of line-maps (default: "glyphgfa"). Alternative options are: c("none", "gfa", "glyph", "glyphgfa", "glyphrgbmap", "glyphdata") (see Details).
bview	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
savedir	directory for saving/loading processed results (default: tempdir().
bg	map background colour (default "white")
order	parameter associated with the order of the spherical harmonics approximation (default: 4).
texture	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
...	additional material properties for geometry appearance as specified in rgl.material.

Details

Slice glyph map display and overlay selection is controlled by specifying one the arguments `c("none", "gfa", "glyph", "glyphgfa", "glyphrgbmap", "glyphdata")` for `showimages`. Meanings are as follows: `"none"` - no overlay; `"gfa"` - GFA map only; `"glyph"` - glyph map only; `"glyphgfa"` - GFA overlayed on glyph map; `"glyphrgbmap"` - glyphs overlayed on RGB map (if available); `"glyphdata"` - 'data_brain.nii.gz' is overlayed on line map.

Q-ball imaging (QBI) is used for orientation distribution function (ODF) reconstruction. One QBI-compatible b-table defining the acquisition setup on a S2-shell is included in the package. The b-table 'btable.txt' has 203 points distributed on a S2-shell.

Author(s)

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References

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Tuch D. S., Q-Ball Imaging, *Magnetic Resonance in Medicine* 52 (2004), 1358-1372. Tabelow K., Polzehl J.: **dti**: DTI/DWI Analysis, 2012. R package version 1.1-0.

See Also

sph.odfpeaks, sph.odfvmf, sph.odfvmflines, s2tessel.zorder, plotglyph, rgbvolmap, simulglyph.vmf, simul.fandtasia, simul.simplefield

Examples

```
## Not run:
  ## show glyph-map for selected slice
  sph.odfvxgrid(threshold=0.5, showimage="glyphgfa")
  ##----
  ## generate slice RGB map as texture
  rgbvolmap(texture=TRUE, transp=TRUE)
  ## coronal glyphs + RGBmap
  sph.odfvxgrid(threshold=0.5, showimage="glyphrgbmap",
    texture=file.path(tempdir(),"rgbmap.png"))

## End(Not run)
```

`synthfiberss2z` *Voxel Diffusion Profiles for Multiple Fibre Simulation*

Description

`synthfiberss2z` simulates apparent diffusion coefficient (ADC) profiles in multi-direction, diffusion-weighted MR data, for testing ODF reconstruction and fibre orientation estimation.

Usage

```
synthfiberss2z(g0, angles=c(20,100), b=3000, S0=1, sigma=NULL,
 logplot=TRUE, pos=c(0,0,0), showglyph=FALSE, new=TRUE, wi=NULL)
```

Arguments

`g0`	matrix of 3D points on the S2 shell used in simulation.
`angles`	angles in degrees of fibres to be used in simulation (default: two fibres with angles `c(20,100)`).
`b`	strength of the magnetic diffusion gradient (default b-value=3000).
`S0`	signal intensity without the diffusion weighting (default: 1).
`sigma`	Rician noise level used in simulation (default `NULL`).
`logplot`	logical variable for selecting log-scale (default `TRUE`).
`pos`	3D positional coordinate (default `c(0,0,0)`).
`showglyph`	logical variable controlling visualization of voxel glyph (default: `TRUE`).
`new`	starts a new figure if `TRUE` (default `new=TRUE`).
`wi`	weight given to fiber's volume fraction. Example for two fibers with different weights `wi=c(0.7,0.3)` (default `NULL` gives equal weigth to all fibers.)

Details

The simulation models the profile of the ADC over the sphere. Prolate diffusion tensor (DT) white matter profiles are estimated with eigenvalues {1700, 200, 200}(x 10^(-6) mm2/s) (see D.C. Alexander, 2002). Diffusion profiles for crossing fibres are simulated from prolate DTs in equal proportions, where each fibre is represented by a prolate DT. Noisy profiles may be simulated by adding Rician noise to the simulated diffusion profile, with a user defined standard deviation level specified as σ (SNR=1/σ). Typically, noise values of SNR~30 are used in simulated dMRI.

Value

`synthfiberss2z` plots the diffusion profile and returns the synthesized diffusion signal.

Author(s)

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See Also

simulglyph.vmf, plotglyph gqi.odfvmflines, rgbvolmap, gqi.odfpeaks, gqi.odfpeaklines, gqi.odfvxgrid, simulglyph.vmf, simul.fandtasia, simul.simplefield

Examples

```
## Not run:
    ## S2 grid
    s2 <- s2tessel.zorder(depth=3)
    g0 <- s2$pc
    ## synthetize diffusion signal (two crossing fibres)
    open3d()
    angles=c(20,100); b=3000
    S <- synthfiberss2z(g0=g0, angles=angles, b=b)
    ## synthetize signal with different volume fractions
    S <- synthfiberss2z(g0=g0, angles=angles, b=b, wi=c(0.7,0.3))
    ## synthesize diffusion signal (three crossing fibres)
    angles <- c(0,60,120); b <- 3000
    S <- synthfiberss2z(g0=g0, angles=angles, b=b)

## End(Not run)
```

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