

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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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.
- Hornik, K., and Gruen, B. **movMF**: Mixtures of von Mises-Fisher Distributions, 2012. R package version 0.1-0.
- Hankin, R. K. S. Special functions in R: introducing the **gsl** package. *R News* 6 (October 2006).
- 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 tessellation, 2012. R package version 0.3-2.
- R Core Team. **R**: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria, 2012. ISBN 3-900051-07-0.
- 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.
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- Tabelow K., Polzehl J.: **dti**: DTI/DWI Analysis, 2012. R package version 1.1-0.
- 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., Ugurbil 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.

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](#), [htable](#)

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.odfvf` (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](#)

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>.

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_V1](#), [data_gfa](#),

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

<code>gdi</code>	method of ODF reconstruction to use <code>c("gqi", "gqi2")</code> (default: "gqi").
<code>run</code>	logical variable enabling loading previously processed data (default: TRUE).
<code>fbase</code>	Directory where the required input data files are located.
<code>roi</code>	Region of Interest (ROI) to use as mask; default mask (<code>roi=NULL</code>) uses an all brain mask for the supplied data set.
<code>rg</code>	range of slices to process (default option <code>rg=c(1,1)</code>); <code>rg=NULL</code> processes all slices.
<code>swap</code>	toggle radiological/neurological orientation (default: FALSE).
<code>lambda</code>	diffusion sampling length in <code>gdi="gqi"</code> and <code>gdi="gqi2"</code> . By default the following default values are used when <code>lambda=NULL</code> is specified: 1.24 in "gqi", 3 in "gqi2".
<code>depth</code>	sampling density on the hemisphere used in simulation (default <code>N=321</code> ; <code>depth=3</code>).
<code>btoption</code>	b-table selection between 'btable.txt' (<code>btoption=1</code>), 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 (<code>btoption=2</code>).
<code>threshold</code>	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
<code>kdir</code>	maximum number of fibre directions to map (default: 2).
<code>zfactor</code>	parameter controlling z-value in relief overlay maps (default: 5).
<code>showglyph</code>	logical variable controlling visualization of voxel glyphs (default: FALSE).
<code>showimage</code>	object controlling visualization of line-maps (default: "linesgfa"). Alternative options are: <code>c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata")</code> (see Details).
<code>bview</code>	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
<code>savendir</code>	directory for saving/loading processed results (default: <code>tempdir()</code>).
<code>bg</code>	map background colour (default "white")
<code>texture</code>	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
<code>aniso</code>	anisotropic parameter in the range "[0,1]" or NULL to use in ODF pos-processing default: NULL.
<code>...</code>	additional material properties for geometry appearance as specified in <code>rgl.material</code> .

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 overlaid on line map; "linesrgbmap" - lines overlaid on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlaid on line map;

Value

`gqi.odfpeaklines` produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlaid 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.fantasia](#), [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 <code>gdi="gqi"</code> and <code>gdi="gqi2"</code> . By default the following default values are used when <code>lambda=NULL</code> is specified: 1.24 in "gqi", 3 in "gqi2".
depth	sampling density on the hemisphere used in simulation (default <code>N=321</code> ; <code>depth=3</code>).
btoption	b-table selection between 'btable.txt' (<code>btoption=1</code>), and 3D-DSI grid b-table supplied with the diffusion data set (default <code>btoption=2</code>).
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").
savendir	directory for saving/loading processed results (default: <code>tempdir()</code>).
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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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.odfvvmf](#), [gqi.odfvvmflines](#), [gqi.odfvxgrid](#), [s2tessel.zorder](#), [rgbvolmap](#), [simulglyph.vmf](#), [simul.fantasia](#), [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 `nii_norm`.

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.

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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.

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.fandtasias](#), [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

<code>gdi</code>	method of ODF reconstruction to use <code>c("gqi", "gqi2")</code> (default: "gqi").
<code>run</code>	logical variable enabling loading previously processed data (default: TRUE).
<code>fbase</code>	Directory where the required input data files are located.
<code>roi</code>	Region of Interest (ROI) to use as mask; default mask (<code>roi=NULL</code>) uses an all brain mask for the supplied data set.
<code>rg</code>	range of slices to process (default option <code>rg=c(1,1)</code>); <code>rg=NULL</code> processes all slices.
<code>swap</code>	toggle radiological/neurological orientation (default: FALSE).
<code>lambda</code>	diffusion sampling length in <code>gdi="gqi"</code> and <code>gdi="gqi2"</code> . By default the following default values are used when <code>lambda=NULL</code> is specified: 1.24 in "gqi", 3 in "gqi2".
<code>depth</code>	sampling density on the hemisphere used in simulation (default <code>N=321</code> ; <code>depth=3</code>).
<code>btoption</code>	b-table selection between 'btable.txt' (<code>btoption=1</code>), 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 (<code>btoption=2</code>).
<code>threshold</code>	thresholding generalized fractional anisotropy (GFA) value at each voxel (default: 0.4).
<code>kdir</code>	maximum number of fibre directions to map (default: 6).
<code>zfactor</code>	parameter controlling z-value in relief overlay maps (default: 5).
<code>showglyph</code>	logical variable controlling visualization of voxel glyphs (default: FALSE).
<code>showimage</code>	object controlling visualization of line-maps (default: "linesgfa"). Alternative options are: <code>c("none", "gfa", "lines", "linesgfa", "linesrgbmap", "linesdata")</code> (see Details).
<code>bview</code>	MRI slice view selection in {axial, coronal, sagittal} (default: "coronal").
<code>savedir</code>	directory for saving/loading processed results (default: <code>tempdir()</code>).
<code>bg</code>	map background colour (default "white").
<code>texture</code>	name of the PNG file to be used as RGB map overlay in some 'showimage' options (default NULL - no texture).
<code>clusterthr</code>	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
<code>aniso</code>	anisotropic parameter in the range "[0,1]" or NULL to use in ODF pos-processing default: NULL.
<code>...</code>	additional material properties for geometry appearance as specified in <code>rgl.material</code> , or specification of non-default control parameters as detailed in <code>movMF</code> .

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 overlaid on line map; "linesrgbmap" - lines overlaid on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlaid on line map.

Value

`gqi.odfvmflines` produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlaid 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.fantasia](#), [simul.simplefield](#), [data](#), [data.bval](#), [data.bvec](#), [htable](#)

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 <code>rgl.material</code> .

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

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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 tessellation, 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.odfvmlines](#), [s2tessel.zorder](#), [plotglyph](#), [rgbvolmap](#), [simulglyph.vmf](#), [simul.fantasia](#), [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	<i>Normalization of Principal Diffusion Directions</i>
---------	--

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

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

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)

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

References

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

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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)

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

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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.

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.odfvvmf](#), [gqi.odfvvmfines](#), [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.odfvmf](#), [lines](#), [rgbvolmap](#), [gqi.odfpeaks](#), [gqi.odfpeaklines](#), [gqi.odfvxgrid](#), [plotglyph](#), [simulglyph.vmf](#), [simul.fandtasias](#), [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.fandtasias	<i>Simulation of Curved Fibre Bundles for von Mises-Fisher Fibre Orientation Mapping</i>
------------------	--

Description

The synthesized field of diffusion profiles generated by `simul.fandtasias` 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.fandtasias(gdi="gqi", gridsz=32, b=4000, depth=3, sigma=0.01,
  clusterthr=0.6, showglyph=FALSE, savedir=tempdir(), ...)
```

Arguments

<code>gdi</code>	method of ODF reconstruction to use <code>c("gqi", "gqi2")</code> (default: "gqi").
<code>gridsz</code>	dimension of squared grid to use in simulation (default 32)
<code>b</code>	strength of the magnetic diffusion gradient (default b-value=4000).
<code>depth</code>	sampling densities on the hemisphere used in simulation (default N=321; depth=3).
<code>sigma</code>	Rician noise level used in simulation; (default 0.01).
<code>clusterthr</code>	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
<code>showglyph</code>	logical variable controlling visualization of voxel glyphs (default: FALSE).
<code>savedir</code>	directory for saving/loading processed results (default: <code>tempdir()</code>).
<code>...</code>	optional specification of non-default control parameters as detailed in <code>movMF</code> .

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 Barmoutis' code to generate synthetic tensor diffusion-weighted MRI fields. The procedure is very time intensive for grids of size 32x32.

Value

`simul.fandtasias` 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>.

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

See Also

[simul.fandtasiasignal](#), [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	<i>Simulation of a Simple Field of Diffusion Profiles for von Mises-Fisher Fibre Orientation Mapping</i>
-------------------	--

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 customize 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)

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

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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 tessellation, 2012. R package version 0.3-2.

See Also

[simulglyph.vmf](#), [simul.fantasia](#), [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

<code>gdi</code>	method of ODF reconstruction to use <code>c("gqi", "gqi2", "sph")</code> (default: "gqi").
<code>s2grid</code>	S2 shell grid, or other equivalent user specified grid. By default <code>s2grid=NULL</code> means that the grid is generated by <code>s2tessel.zorder</code> .
<code>angles</code>	angles in degrees of fibres to be used in simulation (default: two fibres with angles <code>c(20,100)</code>).
<code>depth</code>	sampling densities on the hemisphere used in simulation (default <code>N=321</code> ; <code>depth=3</code>).
<code>b</code>	strength of the magnetic diffusion gradient (default <code>b-value=3000</code>).
<code>lambda</code>	model parameter: diffusion sampling length in <code>gdi="gqi"</code> and <code>gdi="gqi2"</code> ; Aganj's regularization parameter in <code>gdi="sph"</code> . By default the following default values are used when <code>lambda=NULL</code> is specified: 1.24 in "gqi", 3 in "gqi2", and 0.006 in "sph".
<code>order</code>	parameter associated with the order of the spherical harmonics approximation for <code>gdi="sph"</code> (default: 4).
<code>sigma</code>	Rician noise level used in simulation; (default <code>NULL</code>).
<code>clusterthr</code>	thresholding orientations based on ODF values at each voxel for directional clustering (default: 0.6).
<code>savedir</code>	directory for saving/loading processed results (default: <code>tempdir()</code>).
<code>showglyph</code>	logical variable controlling visualization of voxel glyphs (default: <code>TRUE</code>).
<code>aniso</code>	anisotropic parameter in the range "[0,1]" or <code>NULL</code> to use in ODF pos-processing (default: <code>NULL</code>).
<code>logplot</code>	logical variable for selecting log-scale (default <code>TRUE</code>).
<code>wi</code>	weight given to fiber's volume fraction. Example for two fibers with different weights <code>wi=c(0.7, 0.3)</code> (default <code>NULL</code> gives equal weight to all fibers.)
<code>...</code>	optional specification of non-default control parameters as detailed in <code>movMF</code> .

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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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.fandtasias](#), [simul.simplefield](#)

Examples

```
## Not run:
## Examples of synthesized 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)

```

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

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sph.odfpeaklines	<i>Fibre Orientation Mapping Based on Local Peak Detection with QBI Reconstruction</i>
------------------	--

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").
savendir	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.odfvmlines`.

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 overlaid on line map; "linesrgbmap" - lines overlaid on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlaid on line map.

Value

sph.odfpeaklines produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlaid 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>

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.

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.odfvmfines](#), [gqi.odfvxgrid](#), [s2tessel.zorder](#), [plotglyph](#), [rgbvolmap](#), [simulglyph.vmf](#), [simul.fantasia](#), [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 overlaid 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	<i>Main Fibre Orientation Determination via Peak Detection with Q-ball Reconstruction</i>
--------------	---

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>.

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.

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.odfvmlines](#), [gqi.odfvxgrid](#), [s2tessel.zorder](#), [rgbvolmap](#), [simulglyph.vmf](#), [simul.fandtasias](#), [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=temppdir())
##-----
## Process whole volume: generate NIfTI files
##  data_gfa_sph.nii.gz and data_V1_sph.nii.gz
sph.odfpeaks(rg=NULL)
rgbvolmap(fbase=temppdir(), 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=temppdir(), 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: temppdir()).
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)

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

References

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- 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.fandtasias](#), [simul.simplefield](#), [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	<i>Fibre Orientation Mapping Based on von Mises-Fisher Distributions with QBI reconstruction</i>
-----------------	--

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 <code>rgl.material</code> .

Details

The function `sph.odfvmfines` 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 overlaid on line map; "linesrgbmap" - lines overlaid on RGB map (if available); "linesdata" - 'data_brain.nii.gz' is overlaid on line map.

Value

`sph.odfvmfines` produces line-maps of ODF profiles for diffusion data slices. The line-maps may be overlaid 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>

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.odfvmf](#), [sph.odfpeaks](#), [sph.odfvmfines](#), [gqi.odfvxgrid](#), [plotglyph](#), [rgbvolmap](#), [s2tessel.zorder](#), [simulglyph.vmf](#), [simul.fantasia](#), [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").
savendir	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 <code>rgl.material</code> .

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.odfvmfines](#), [s2tessel.zorder](#), [plotglyph](#), [rgbvolmap](#), [simulglyph.vmf](#), [simul.fandtasias](#), [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

<code>g0</code>	matrix of 3D points on the S2 shell used in simulation.
<code>angles</code>	angles in degrees of fibres to be used in simulation (default: two fibres with angles <code>c(20,100)</code>).
<code>b</code>	strength of the magnetic diffusion gradient (default <code>b-value=3000</code>).
<code>S0</code>	signal intensity without the diffusion weighting (default: 1).
<code>sigma</code>	Rician noise level used in simulation (default <code>NULL</code>).
<code>logplot</code>	logical variable for selecting log-scale (default <code>TRUE</code>).
<code>pos</code>	3D positional coordinate (default <code>c(0,0,0)</code>).
<code>showglyph</code>	logical variable controlling visualization of voxel glyph (default: <code>TRUE</code>).
<code>new</code>	starts a new figure if <code>TRUE</code> (default <code>new=TRUE</code>).
<code>wi</code>	weight given to fiber's volume fraction. Example for two fibers with different weights <code>wi=c(0.7,0.3)</code> (default <code>NULL</code> gives equal weight 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 $\{1700, 200, 200\} \times 10^{-6}$ 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.

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

Alexander, D. C., Barker, G. J., and Arridge, S. R. Detection and Modeling of Non-Gaussian Apparent Diffusion Coefficient Profiles in Human Brain Data. *Magnetic Resonance in Medicine* 48 (2002), 331-340.

See Also

[simulglyph.vmf](#), [plotglyph.gqi.odfvmflines](#), [rgbvolmap](#), [gqi.odfpeaks](#), [gqi.odfpeaklines](#), [gqi.odfvxgrid](#), [simulglyph.vmf](#), [simul.fandtasias](#), [simul.simplefield](#)

Examples

```
## Not run:
## S2 grid
s2 <- s2tessel.zorder(depth=3)
g0 <- s2$pc
## synthesize diffusion signal (two crossing fibres)
open3d()
angles=c(20,100); b=3000
S <- synthfiberss2z(g0=g0, angles=angles, b=b)
## synthesize 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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