Package 'DATforDCEMRI'

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Type Package

Title Deconvolution Analysis Tool for Dynamic Contrast Enhanced MRI

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Depends R (>= 2.11.0), xtable, akima, R.oo, R.methodsS3, matlab, lattice, locfit, graphics, grDevices, grid

Suggests R.matlab

Description This package performs voxel-wise deconvolution analysis of DCE-MRI contrast agent concentration versus time data and generates the Impulse Response Function, which can be used to approximate commonly utilized kinetic parameters such as Ktrans and ve. An interactive advanced voxel diagnosis tool (AVDT) is also provided to facilitate easy navigation of voxel-wise data.

LazyLoad yes

LazyData yes

NeedsCompilation no

Repository CRAN

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R topics documented:

DATforDCEMRI-package *Deconvolution Analysis Tool for DCE-MRI*

Description

Calculates the Impulse Response Function on a per-voxel basis for DCE-MRI data using numerical deconvolution, yielding the Impulse Response Function for each voxel analyzed. The Area under the Curve (AUC) and ratio of AUC to Mean Residence Time (MRT) provide estimates of the kinetic model parameters K^{trans} and v_e. A visualization tool is also included that allows the user to explore voxel-wise data in an interactive manner.

Details

Package:	DATforDCEMRI
Type:	Package
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LazyLoad:	yes

Author(s)

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References

Ferl GZ (2011) DATforDCEMRI: An R Package for Deconvolution Analysis and Visualization of DCE-MRI Data. *Journal of Statistical Software* **44**, 1-18.

Ferl GZ, Xu L, Friesenhahn M, Bernstein LJ, Barboriak DP, Port RE. (2010) An automated method for nonparametric kinetic analysis of clinical DCE-MRI data: application to glioblastoma treated with bevacizumab. *Magn Reson Med.* **63**, 1366-1375.

DAT *Deconvolution Analysis Tool*

Description

Calculates the Impulse Response Function on a per-voxel basis for DCE-MRI data using numerical deconvolution, yielding the Impulse Response Function for each voxel analyzed. The Area Under the Curve and ratio of AUC to Mean Residence Time provide estimates of the kinetic model parameters K^{trans} and v_e. A visualization tool is also included that allows the user to explore voxel-wise data in an interactive manner.

Usage

```
DAT(file = "nodata", slice = 0, vp = 0, border = 20, maxCt = 0.66,
parameter.plot = "AUCMRT", cutoff.map = 0.85, range.map = 1.5,
export.matlab = FALSE, batch.mode = FALSE, alpha.AIF=c(0,0,2000),
correct.trunc=TRUE, kep.nom=0.5, ...)
```

Arguments

file	RData file containing DCE-MRI data. May be generated manually or by the function DAT.checkData.
slice	Image slice to be extracted for analysis.
vp	Fractional plasma volume of tissue within Region of Interest. Default value is zero.
border	A border of image voxels around the Field of View to be excluded from analysis. Default is 20 voxels.
maxCt	Voxels will be excluded from analysis if the maximum contrast agent concentration exceed a threshold of maxCt times the maximum contrast agent concentration within the Arterial Input Function vector. Default value is 0.66.
parameter.plot	Which parameter will be described in the parametric maps? Two possible values are AUC and AUCMRT for the Area Under the Curve (AUC) and AUC divided by the Mean Residence Time of the Impulse Response Function (MRT). AUC is correlated with v_e and AUCMRT is correlated with K^{trans}. Default value is AUCMRT.
cutoff.map	Typically a number between 0.5 and 1. Represents the quantile at which parametric map values will be truncated in order to suppress very large AUC or AUCMRT values within the parametric maps. Default value is 0.85.
range.map	Typically a number between 1 and 2. The range of the color bar associated with the parametric map is set to the maximum value within the map times range.map. Default value is 1.5.
export.matlab	Will the deconvolution results be export as a matlab file in addition to an RData file? Default value is FALSE.
batch.mode	Will the interactive parametric maps normally displayed at the end of each run be suppressed? Default value is FALSE.
alpha.AIF	Vector of smoothing parameters utilized by the locfit function when smoothing the arterial input function. Default value is c(0,0,2000).
correct.trunc	Will a rough approximation of truncation error correction be performed on parametric maps of AUC and AUC/MRT? Default value is TRUE.
kep.nom	A nominal value of kep to be used for truncation correction, i.e., to estimate the AUC of the IRF from the end of the scanning period to infinity? Default value is 0.5.
...	Pass arguments.

Author(s)

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References

Ferl GZ (2011) DATforDCEMRI: An R Package for Deconvolution Analysis and Visualization of DCE-MRI Data. *Journal of Statistical Software* **44**, 1-18.

Ferl GZ, Xu L, Friesenhahn M, Bernstein LJ, Barboriak DP, Port RE. (2010) An automated method for nonparametric kinetic analysis of clinical DCE-MRI data: application to glioblastoma treated with bevacizumab. *Magn Reson Med.* **63**, 1366-1375.

See Also

See also `DAT.checkData`

`DAT.checkData` *Create and check data file.*

Description

The user loads DCE-MRI data into R using pre-existing functions such as `read.table`; `DAT.checkData` then saves all data into a single RData file which can be analyzed using `DAT`.

Usage

```
DAT.checkData(file.name, vector.times, map.CC, mask.ROI,
vector.AIF, slice.start=1, slice.stop="not.specified")
```

Arguments

`file.name`	Specify a name for the file that will be generated.
`vector.times`	Vector of time points at which contrast agent concentrations are measured (should have units of seconds).
`map.CC`	Array of voxel-wise contrast agent concentrations.
`mask.ROI`	Array containing the predefined Region of Interest.
`vector.AIF`	Vector containing the Arterial Input Function.
`slice.start`	For multislice data files, a range of slices must be specified. Slice numbers less than slice.start will not be included in the saved file. The default value for this argument is "1"; we recommend not changing this unless file size is a significant issue.
`slice.stop`	For multislice data files, a range of slices must be specified. Slice numbers grater than slice.stop will not be included in the RData file to be analyzed by `DAT`.

Author(s)

Gregory Zelinsky Ferl

Examples

```
data(DAT.simData, package="DATforDCEMRI")
myccarray <- (DAT.simData$mapCC)
mytimevector <- (DAT.simData$vectorTimes)
myroiarray <- (DAT.simData$maskROI)
myaifvector <- (DAT.simData$vectorAIF)
DAT.checkData(file.name="mydcemridata", vector.times=mytimevector, map.CC=myccarray,
mask.ROI=myroiarray, vector.AIF=myaifvector, slice.stop=2)
```

DAT.simData *Simulated DCE-MRI data*

Description

A simulated DCE-MRI data set to be used with DAT.

Usage

```
data(DAT.simData)
```

Format

The format is: List of 4

$ time: num [1:25] 0 12 24 36 48 60 72 84 96 108 ...

$ cc : num [1:256, 1:256, 1:2, 1:25] 0 0 0 0 0 0 0 0 0 0 ...

$ roi : int [1:256, 1:256, 1:2] 0 0 0 0 0 0 0 0 0 0 ...

$ aif : num [1:25] 0 0 2781 2120 1871 ...

Details

Simulated noisy data created using the Tofts version of the Kety model with a two compartment arterial input function.

Source

Simulated using R.

Examples

```
data(DAT.simData, package="DATforDCEMRI")
```

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