Package ‘oro.pet’

February 20, 2015

Version 0.2.3
Date 2014-01-19
Title Rigorous - Positron Emission Tomography
Author Brandon Whitcher
Maintainer Brandon Whitcher <bwhitcher@gmail.com>
Description Image analysis techniques for positron emission tomography (PET) that form part of the Rigorous Analytics bundle.
Depends R (>= 2.14.0)
Suggests minpack.lm, msm
Imports grDevices, methods, oro.dicom (>= 0.3.7), oro.nifti (>= 0.3.9), utils
License BSD_3_clause + file LICENSE
LazyData no
NeedsCompilation no
Repository CRAN
Date/Publication 2014-09-27 07:36:55

R topics documented:

  compartmentalModel ................................................................. 2
  expConv ................................................................................. 3
  hillEquation ........................................................................... 3
  LeanBodyMass .......................................................................... 5
  multilinearReferenceTissueModel ................................................. 6
  occupancy ................................................................................ 7
  plotBindingPotential ................................................................. 8
  QIBA ....................................................................................... 10
  simplifiedReferenceTissueModel .................................................. 11
  Summarizing SUVs ................................................................... 13

Index 14
compartmentalModel

Compartmental Models for Kinetic Parameter Estimation

Description

A selection of parametric models are provided that combine a compartmental model for tissue and empirical versions of the arterial input function or reference region time activity curve.

Usage

compartmentalModel(type)

Arguments

type is a character string that identifies the type of compartmental model to be used. Acceptable models include:

“srtm” Simplified Reference Tissue Model
“srtm2” Simplified Reference Tissue Model in two steps

Details

Parametric models from the PET literature are provided to the user for kinetic parameter estimation.

Value

A function.

Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

References


See Also

simplifiedReferenceTissueModel
### expConv

**Empirical Convolution Between an Input Function and a Single Exponential**

#### Description

Computationally efficient method to convolve a vector of observations and a single exponential function with two parameters.

#### Usage

```r
expConv(input, k1, k2)
```

#### Arguments

- **input**: is the so-called input function.
- **k1**: is the scaling parameter in the single exponential function.
- **k2**: is the decay parameters in the single exponential function.

#### Details

Assuming the input function has been sampled (or interpolated) to a high temporal resolutions, say one Hertz, a simple for loop is used to perform the convolution.

#### Value

The vector containing the result from the convolution operation.

#### Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

### hillEquation

**Estimation of the Half Maximal Inhibitory Concentration**

#### Description

The half maximal inhibitory concentration (IC50) is a measure of the effectiveness of a compound in inhibiting biological or biochemical function. This quantitative measure indicates how much of a particular drug or other substance (inhibitor) is needed to inhibit a given biological process (or component of a process) by half.

#### Usage

```r
hillEquation(conc, occ, guess = c(1, 100), control = minpack.lm::nls.lm.control())
```
Arguments

conc   a vector of drug concentrations in plasma (example units are ng/mL).
occ   a vector of PET occupancy values that correspond to the measured drug concentrations in plasma.
guess   a length-two vector of starting values for the nonlinear optimization.
control is a list of parameters used by nls.lm.control that are set by default, but may be customized by the user.

Details

See reference(s).

In this version of the function the maximal occupancy (rmax) is estimated automatically. This should be optional.

Value

IC50         Half maximal inhibitory concentration
rmax         Estimated maximal occupancy
IC50SE       Approximate standard error for IC50
rmaxSE       Approximate standard error for rmax
hessian      Hessian matrix from the Levenburg-Marquardt procedure
info         Return value from the Levenburg-Marquardt procedure
deviance     Deviance from the Levenburg-Marquardt procedure
message      Text message from the Levenburg-Marquardt procedure

Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

References


See Also

nls.lm
LeanBodyMass

Calculating the Lean Body Mass

Description

The lean body mass (LBM) is calculated according to the formula

\[
1.1 \cdot \text{weight} - 128 \cdot \left(\frac{\text{weight}}{\text{height}}\right)^2
\]

if male and

\[
1.07 \cdot \text{weight} - 148 \cdot \left(\frac{\text{weight}}{\text{height}}\right)^2
\]

if female.

Usage

\[
\text{leanBodyMass}(\text{height}, \text{weight}, \text{gender})
\]

Arguments

\begin{itemize}
  \item \text{height} is a vector of heights in centimeters.
  \item \text{weight} is a vector of weights in kilograms.
  \item \text{gender} is a character vector (may be of length one) with the value “male” or “female”.
\end{itemize}

Value

Vector of lean body mass values in kilograms.

Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

References


See Also

\texttt{standardUptakeValue}

Examples

\begin{verbatim}
n <- 11
h <- seq(200, 150, length=n)
w <- seq(80, 120, length=n)
cbind(h, w, leanBodyMass(h, w, "male"), leanBodyMass(h, w, "female"))
\end{verbatim}
**Description**

The multilinear reference tissue model (MRTM) estimates the binding potential from an observed time activity curve without the need for arterial sampling. Instead, a second time activity curve must be provided from a suitable reference region where there is negligible binding.

**Usage**

```r
multilinearReferenceTissueModel(tac, ref, time, tstar, MRTM2 = TRUE, k2prime = NULL)
```

**Arguments**

- `tac`: a vector corresponding to the time activity curve from the tissue (in Bq/mL).
- `ref`: a vector corresponding to the time activity curve from the reference region (in Bq/mL).
- `time`: a vector of average frame times (in minutes).
- `tstar`: the time (in minutes) where the linear relationship between the response and covariates may be assumed to be true.
- `MRTM2`: a logical value that selects the three-parameter model (MRTM) or the two-parameter model (MRTM2), where k2prime is fixed.
- `k2prime`: the value of k2prime that has been fixed.

**Details**

See the references.

The numeric integration required to construct the design matrix is performed by interpolating the time activity curves, both for the tissue and reference region, to one-second resolution and then performing the `cumsum` operation on them.

Given the nonlinear relationship between binding potential and the regression parameters, the `deltamethod` is used to approximate its standard error.

**Value**

- `BP`: Binding potential
- `BP.error`: Approximate standard error of the binding potential
- `R1`: Ratio of the volumes of distribution for the tissue and reference region (assumes a one-tissue model is valid)
- `R1.error`: Approximate standard error for the ratio
- `k2`: Clearance rate constant from the tissue to plasma (assumes a one-tissue model is valid)
occupancy

k2.error                   Approximate standard error for k2
X                       Design matrix used in the linear regression
beta                     Regression coefficients

Author(s)
Brandon Whitcher <bwhitcher@gmail.com>

References

See Also
cumsum, deltamethod

occupancy                  Compute Drug Occupancy with Approximate Standard Errors

Description
Receptor occupancy is calculated from positron emission tomography (PET) data as the treatment-induced relative change in the concentration of available (not occupied) receptors.

Usage
occupancy(base, drug, baseSE = NULL, drugSE = NULL, base.drug.corr = 0)

Arguments
base                 is the baseline binding potential (BPND).
drug                 is the post-treatment binding potential (BPND).
baseSE               is the standard error for the baseline BPND.
drugSE               is the standard error for the post-treatment BPND.
base.drug.corr       is the user-specified correlation between baseline and post-treatment binding potentials.
Details

Occupancy is calculated using the straightforward and well-known formula. If the standard errors for the two binding potentials are provided, then the delta method is used to approximate the standard error for the estimate of occupancy.

Value

OCC is the percent drug occupancy.
SE is the approximate standard error of the parameter estimate.

Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

References


See Also

deltamethod

plotBindingPotential  Plot Baseline Versus Post-Treatment Binding Potentials

Description

Inspired by the Lassen plot (Cunningham et al., 2010) this is a straightforward graphical summary of pre-treatment versus post-treatment binding potentials for a single subject across multiple brain regions.

Usage

plotBindingPotential(base, drug, lty45=2, lty=1, lwd45=2, lwd=3, col45="darkgrey", col="orange", pch=1, cex=1, xlim=range(0, base, 0.5), ylim=range(0, drug, 0.5), xlab=expression(BP[ND]^{Base}), ylab=expression(BP[ND]^{Drug}), ...)
plotBindingPotential

Arguments

base is the vector of baseline binding potentials across brain regions.
drug is the vector of post-treatment binding potentials across brain regions.
lty45 is the line type for the 45-degree line.
lty is the line type for the estimated regression line.
lwd45 is the line width for the 45-degree line.
lwd is the line width for the estimated regression line.
col45 is the color for the 45-degree line.
col is the color for the estimated regression line.
pch is the plotting character symbol.
cex is the size of the plotting symbol.
xlim is the range of values on the x-axis.
ylim is the range of values on the y-axis.
xlab is the label on the x-axis.
ylab is the label on the y-axis.
... for additional arguments to be passed to the plot function.

Details

See the reference below.

Value

A plot.

Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

References


See Also

par, plot
Calculating SUVs for PET Using QIBA Pseudocode

Description

The standard uptake value (SUV) is calculated based on an 18F-FDG-PET acquisition using ancillary information contained in the DICOM data.

Usage

```bash
## S4 method for signature 'array'
standardUptakeValue(pixelData, mask = NULL, CSV = NULL,
                      seriesNumber = NULL, method = c("qiba", "user"),
                      prior = NULL, decayedDose = NULL)
## S4 method for signature 'array'
activityConcentration(pixelData, CSV = NULL, seriesNumber = NULL,
                        method = "qiba")
```

Arguments

- **pixelData**: is a multidimensional array of signal intensities of class `nifti`.
- **mask**: is a multidimensional array of logical values (only used when `method = "user"`).
- **CSV**: is a data frame that is the output from `dicomTable` and contains all necessary DICOM header fields.
- **seriesNumber**: is the SeriesNumber that corresponds to the PET acquisition.
- **method**: takes on two possible values (qiba and user), where QIBA pseudocode is used to calculate the SUVs or user-defined parameters are used.
- **prior**: is a list of DICOM header field names that are necessary for the SUV calculation under `method = "user"` or may be used to replace values from the DICOM header information when `method = "qiba"`.
- **decayedDose**: is the amount of the RadionuclideTotalDose after being corrected for residual dose in the syringe. This value is NOT usually corrected in the DICOM data.

Details

[MORE]

Note, for GE scanners it is common for the RescaleSlope DICOM field to vary on a slice-by-slice basis. This is taken into account if a GE scanner is detected from the Modality DICOM field. However, the InstanceNumber is used to reorder the slices so they match the incoming NIfTI file of PixelData. If this is not correct it may be necessary to manually re-order the RescaleSlope field in the CSV data frame so that the activity concentration is calculated correctly.
Value

A list containing the following items

- **SUUVbw**: is a multidimensional array, the same dimension as `pixelData`, that contains the standard uptake values.
- **hdr**: is a list of DICOM header fields used in the SUV calculation.
- **decayTime**: is the decay time calculated from the DICOM header information.
- **decayedDose**: is the RadionuclideTotalDose, if taken from the DICOM header information, or the user-specified value.
- **SUUVbwScaleFactor**: is `PatientsWeight \cdot 1000 / decayedDose`.

Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

References


See Also

- `dicomTable`, `nifti`

---

**simplifiedReferenceTissueModel**

*The Simplified Reference Tissue Model*

**Description**

The simplified reference tissue model (SRTM) estimates the binding potential from an observed time activity curve without the need for arterial sampling. It assumes a one-tissue compartment model to describe the influx and efflux in the tissue region of interest and the reference region.

**Usage**

```r
simplifiedReferenceTissueModel(tac, ref, time, SRTM2 = TRUE, k2prime = NULL,
   guess = c(R1 = 0.5, k2 = 0.01),
   control = minpack.lm::nls.lm.control())
```
### simplifiedReferenceTissueModel

**Arguments**

- `tac` a vector corresponding to the time activity curve from the tissue (in Bq/mL).
- `ref` a vector corresponding to the time activity curve from the reference region (in Bq/mL).
- `time` a vector of average frame times (in minutes).
- `SRTM2` a logical value that selects the three-parameter model (SRTM) or the two-parameter model (SRTM2), where k2prime is fixed.
- `k2prime` the value of k2prime that has been fixed.
- `guess` values for the initial parameter estimates for R1 and k2.
- `control` a list of parameters used by `nls.lm.control` that are set by default, but may be customized by the user.

**Details**

See the references.

The model has been parameterized in the manner of Wu and Carson (2002). That is, the nonlinear regression estimates R1, k2 and k'2 for the three-parameter model (SRTM) and R1 and k 2 for the two-parameter model (SRTM2).

The convolution is performed after interpolating the time activity curves, both for the tissue and the reference region, to one-second resolution then downsampling them back to the original sampling rate.

**Value**

- `BP` Binding potential
- `R1` Ratio of the volumes of distribution for the tissue and reference region
- `k2` Clearance rate constant from the tissue to plasma
- `BP.error` Approximate standard error of the binding potential
- `R1.error` Approximate standard error for the ratio
- `k2.error` Approximate standard error for k2

**Author(s)**

Brandon Whitcher <b.whitcher@gmail.com>

**References**


**See Also**

deltamethod, expConv, nls.lm
Summarizing SUVs for PET

Description
The standard uptake value (SUV) is summarized using the hotspot method or by calculating total volume of the high values.

Usage

hotSpotSUV(suv, radius = 10, type = "3D")  
totalSUV(suv, mask, z, bg, local = TRUE)

Arguments

- `suv` is the standard uptake value (SUV).
- `radius` is the desired hotspot radius (units = voxels).
- `type` is a character string (acceptable values are 2D or 3D) that determines the dimension of the hot spot (default = 3D).
- `mask` is a multidimensional array of logical values.
- `z` is the slice index.
- `bg` is the estimated background SUV.
- `local` is a logical value.

Details

...

Value

...

Author(s)

Brandon Whitcher <bwhitcher@gmail.com>

See Also

- `leanBodyMass`
Index

*Topic hillequation
  multilinearReferenceTissueModel, 6
  occupancy, 7
  plotBindingPotential, 8
  simplifiedReferenceTissueModel, 11

*Topic misc
  compartmentalModel, 2
  expConv, 3

activityConcentration (QIBA), 10
activityConcentration, array-method (QIBA), 10

compartmentalModel, 2

cumsum, 7

deltamethod, 7, 8, 12
dicomTable, 11

expConv, 3, 12

hillEquation, 3
hotSpotSUV (Summarizing SUs), 13

LeanBodyMass, 5
leanBodyMass, 13
leanBodyMass (LeanBodyMass), 5

multilinearReferenceTissueModel, 6

nifti, 11
nls.lm, 4, 12

occupancy, 7

par, 9
plot, 9
plotBindingPotential, 8

QIBA, 10

standardUptakeValue, 5
standardUptakeValue (QIBA), 10
standardUptakeValue, array-method (QIBA), 10
Summarizing SUVs, 13
totalSUV (Summarizing SUVs), 13