R documentation

of ‘F:/documents/these/stat_R/R’ etc.

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`BrainMetabolism-package` *calculate brain metabolism rate from extracellular conentrations*

Description

calculate CMRO2, CMRgluc, mitochondrialPO2 ...
provide functions to process data from biosensors

Details

Package:	BrainMetabolism
Type:	Package
Version:	1.0
Date:	2015-03-03
License:	MIT

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References

Piilgaard Lauritzen JCBFM (2009) 29, 1517
Gjedde et al JCBFM (2005) 25(9), 1183
Gjedde et al JCBFM (2000) 20(4), 747
Du et al JCBFM 2012 32(9)
Gruetter et al J Neurochem 1998 70(1)
balanca et al (2016) in preparation

Examples

```
MyTPO2<-23 #mmHg
MyLDF<-95 #percent
MyL<-L.calc(CMR=219, TPO2=MyTPO2, P50=36, h=2.7, Ca=8, cbf=53 )
MyCMRO2<-CMRO2.calc(LDF=MyLDF, MyTPO2, P50=36, h=2.7, Ca=8, L=MyL,cbfbase=53)

MyGlucBrain<-1 #mM
MyGlucPlasma<-6 #mM
MyCRMgluc<-CMRGluc.calc(MyGlucbrain, Vd=0.77, Kt=13.4, Tmax=1.35, Gplasma=MyGlucPlasma)
```

`auc` *area under the curve*

Description

take a numeric vector and return the area under the curve (AUC)

Usage

```
auc(data, pos = TRUE)
```

Arguments

`data`	: a numeric vector
`pos`	: a logical value. if TRUE (default) AUC is calculated on positive values, if FALSE on negative values.

Value

auc : area under the curve

max/min : maxiaml value (or minimal if pos=FALSE) calibration *Sensor calibration*

Description

Fit an nth degree polynom

$$(y = C_n X^n + C_{n-1} X^{n-1} + \ldots + C_1 X + C_0)$$

to vectors x=volt and y=concentration

Usage

```
calibration(volt, mol, order = 1)
```

Arguments

`volt`	: a numeric vector of the biosensor voltage
`mol`	: a numeric vector of the molecule conentration in the medium (x and y must have the same length)
`order`	: a numeric value for the polynomial degree. default is one.

Value

Coef : coeficients in ascending order (i.e. C0, C1, C2, . . . , Cn)

R2 : goodness of fit

CMRGluc.calc *CMRGluc calculation*

Description

take extracellular glucose concentration and return brain metabolic rate of glucose, using a reversible Michaelis-Menten model equation:

Usage

```
CMRGluc.calc(Gbrain, Vd = 0.77, Kt = 13.4, Tmax = 1.35, Gplasma = 6)
```

Arguments

`Gbrain`	: a vector/numeric value of extracellular glucose concentration in mmol/L, time decay
`Vd`	: glucose brain space diffusion (default is 0.77 ml/g)
`Kt`	: glucose apparent maximal transport rate (default is 13.4 mmol/L)
`Tmax`	: the apparent maximal transport rate (default is 1.35 micormol/g/min)
`Gplasma`	: plasma glucose concentration (default=6mmol/L)

Details

$$G_{brain} = V_d \frac{\left(\frac{T_{max}}{CMR_{gluc}} - 1\right) \times G_{plasma} - K_t}{\frac{T_{max}}{CMR_{gluc}} + 1}$$

Value

CMRGlucose : numeric value of Cerebral metabolic rate of glucose in micromol/g/min

References

Du et al JCBFM 2012 32(9)

Gruetter et al J Neurochem 1998 70(1)

`CMRO2.calc` *CMRO2 calculation*

Description

take tissue oxygen pressure (tPO2) and cerebral blood flow (relative value, e.g. laser doopler lowmetry BPU)

Usage

```
CMRO2.calc(LDF, TPO2, P50 = 36, h = 2.7, Ca = 8, L = 4.03,
  cbfbase = 53)
```

Arguments

`LDF`	: a vector/numeric value of LDF (percentage of baseline, i.e: basal value is 100 %)
`TPO2`	: a vector/numeric value of brain oxygnen pressure (mmHg)
`P50`	: half-saturation tension of hemoglobine (default is 36 mmHg)
`h`	: hill's coeficient
`Ca`	: oxygen arterial concentration (default is 8 micromol/ml)
`L`	: effective diffusion coefficient of oxygen in brain tissue, default is 4.03 micomol/100g/mmHg, but one should use the L.calc function to calculate it from their data.
`cbfbase`	: basal expected value of CBF (default is 53 ml/100g/min wich was used to calculate L) LBF and TPO2 must be the same length

Details

$$PbtO_2 = P_{50} \cdot \sqrt[h]{\frac{2 \cdot C_a \cdot CBF}{CMRO_2} - 1} - \frac{CMRO_2}{2 \cdot L}$$

Value

CMRO2 : vector/numeric value of Cerebral Metabolic Rate of Oxygen in micromol/100g/min

References

Gjedde et al JCBFM (2005) 25(9), 1183

Piilgaard et al JCBFM (2009) 29, 1517

`correction.Temp` *Temperature correction*

Description

Biosensor enzymatic reaction, that underpin amperometric measures, has a sigmoid relation to temperature :

$$m(x, P) = \frac{P_1 + (P_2 - P_1)}{(1 + \exp((P_3 - x)/P_4))}$$

parameters are different for each enzyme and has been measured in vitro.
This function correct biosensor signal depending on temperature conditions during calibration and experimentation

Usage

```
correction.Temp(x, enz, temp.calib = 25, temp.exp = 37)
```

Arguments

`x`	: a numeric vector of the biosensor voltage
`enz`	: enzyme on the biosensor i.e. "glucose", "lactate", "glutamate, "daao"
`temp.calib`	: temperature of the medium where sensor has been calibrated the default is 25^{o}C (i.e. room temperature).
`temp.exp`	: temperature of the medium during experiment the default is 37^{o}C (i.e. animal central temperature)

Value

volt.temp.cor : a vector of corected x values for temperature

References

balanca et al 2015

`correction.TPO2` *Oxygen Tension correction*

Description

Biosensor enzymatic reaction, that underpin amperometric measures, has an asymptotic relation to oxygen tention in the medium :

$$m(PO_2, P) = P_1 + (P_2 - P_1) \times \exp(-\exp(P_3)PO_2)$$

parameters are different for each enzyme and has been measured in vitro
This function correct biosensor signal depending on PO2 conditions during calibration and experimentation

Usage

```
correction.TPO2(x, enz, TPO2 = 28)
```

Arguments

`x`	: a numeric vector of the biosensor voltage
`enz`	: enzyme on the biosensor i.e. "glucose", "lactate", "glutamate, "daao"
`TPO2`	: oxygene tension in the medium during the experiment. the default is 30mmHg measured in anesthetized rat brain.

Value

volt.O2.cor : a vector of corected x values for TPO2

References

balanca et al 2015

`IO2.calc` *Oxidative index calculation*

Description

take CMRO2 and LDF to give an oxidative index

Usage

```
IO2.calc(CMRO2, LDF, cbfbasal = 53)
```

Arguments

`CMRO2`	: vector/numeric value of Cerebral metabolic rate of oxygen in micromol/100g/min
`LDF`	: a vector/numeric value of LDF (percentage from baseline, baseline is 100 %)
`cbfbasal`	: basale expected value of CBF from the litterature (default is 53 ml/100g/min wich was used to calculate L)

Details

$$IO2 = CMRO2/(cbfbasal * LDF)$$

Value

IO2 : oxidative index, reflect the degree of flow metabolism coupling

References

Gjedde et al JCBFM (2000) 20(4), 747

L.calc — *Calculate the effective diffusion coefficient of oxygen in brain tissue, L.*

Description

take CMRO2 and cerebral blood flow (CBF) to calculate the effective diffusion coefficient of oxygen in brain tissue (L)

Usage

```
L.calc(CMR = 219, TPO2, P50 = 36, h = 2.7, Ca = 8, cbf = 53)
```

Arguments

`CMR`	: Cerebral Metabolic Rate of Oxygen, default is 219 micro mol/100
`TPO2`	: numeric value of brain oxygnen pressure (mmHg)
`P50`	: half-saturation tension of hemoglobine (default is 36 mmHg)
`h`	: hill's coeficient
`Ca`	: oxygen arterial concentration (default is 8 micromol/ml)
`cbf`	: expected value of CBF (default is 53 ml/100g/min wich was used to calculate L

Details

$$PbtO_2 = P_{50} \cdot \sqrt[h]{\frac{2 \cdot C_a \cdot CBF}{CMRO_2} - 1} - \frac{CMRO_2}{2 \cdot L}$$

Value

L : numeric value of the effective diffusion coefficient of oxygen in brain tissue micomol/100g/mmHg

References

Gjedde et al JCBFM (2005) 25(9), 1183

Piilgaard et al JCBFM (2009) 29, 1517

`noise.na` *Remove artifacts from biosensor signal, based on data's standar deviation*

Description

Remove artifacts from biosensor signal, based on data's standar deviation

Usage

```
noise.na(data, z = 20, width = 30)
```

Arguments

`data`	: a numeric vector
`z`	: a numeric value. Number of SD over which values should be exculded
`width`	: size of the window used to roll SD over data (see roll.funct)

Value

a vector with NA remplacing exculded values

`OGI.calc` *Oxygene Glucose index (OGI)*

Description

take CMRO2 and CMRGlucose to give an OGI

Usage

```
OGI.calc(CMRO2, CMRGluc)
```

Arguments

`CMRO2`	: vector (numeric value) of Cerebral metabolic rate of oxygen in micromol/100g/min
`CMRGluc`	: a vector (numeric value) of CMRGlucose in micromol/100g/min

Details

$$OGI = CMRO2/CMRGlucose$$

Value

OGI

polyfit *polynomial fit*

Description

Fit a nth degree polynom

$$(y = C_n X^n + C_{n-1} X^{n-1} + \ldots + C_1 X + C_0)$$

to vectors x and y

Usage

```
polyfit(x, y, order = 1)
```

Arguments

`x`	: a numeric vector
`y`	: a numeric vector (x and y must have the same length)
`order`	: a numeric value for the polynomial degree. default is one.

Value

model formula

Coef: coeficients in ascending order (i.e. C0, C1, C2, ..., Cn)

R2: Rsquare

polyval *polynomial evaluation*

Description

evaluation a nth degree polynom

$$(y = C_n X^n + C_{n-1} X^{n-1} + \ldots + C_1 X + C_0)$$

at given values of x

Usage

```
polyval(x, coef)
```

Arguments

`x`	: a numeric vector
`coef`	: a n dimention vector corresponding to the polynom coefficient (ascending order, i.e. C0, C1, C2, ... , Cn)

Value

y

`roll.funct` *apply a function FUN on a rooling windows of a vector*

Description

apply a function FUN on a rooling windows of a vector

Usage

```
roll.funct(data, width, FUN, size = T, ...)
```

Arguments

`data`	: a numeric vector
`width`	: the size of the rolling window
`FUN`	: the function to apply
`size`	: a logical value indicating if the returned vector have the same length as original data. default is TRUE.
`...`	: additional argument to pass to the FUN

Value

a vector with FUN result