Package ‘GAprediction’

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Type Package
Title Prediction of gestational age with Illumina HumanMethylation450 data
Version 1.0.0
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Description [GAprediction] predicts gestational age using Illumina HumanMethylation450 CpG data.
License GPL (>=2)
LazyData TRUE
Depends R (>= 3.3)
Imports glmnet, stats, utils, Matrix
biocViews DNAMethylation, Epigenetics, Regression, BiomedicalInformatics
Suggests knitr, rmarkdown
VignetteBuilder knitr
NeedsCompilation no

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extractSites

**Extract CpG sites for gestational age prediction**

**Description**

The function allows the user to extract CpG sites used for gestational age prediction with the function `predictGA`.

**Usage**

```r
extractSites(type="se")
```

**Arguments**

- `type=c("se", "min", "all")` can be used to specify which CpGs are to be extracted. "se" designates the CpGs needed by the `predictGA` function if the penalty term lambda is to be set to one standard error within the minimum, "min" specifies the minimum lambda, while "all" returns the complete sets of CpGs in the `UL.mod.cv` object.

- a string that can be "se" (default), "min" or "all", depending on which CpGs is wanted by the user.

**Details**

**type**

Use this function if `predictGA` fails due to missing predictor CpGs, or to see which CpGs are used by `predictGA` for gestational age prediction.

**Value**

Returns a vector with the requested CpG sites.

**Author(s)**

Jon Bohlin

**See Also**

`predictGA`, `UL.mod.cv`

**Examples**

```r
CpGs <- extractSites( type="se" )
```
**predictGA**

**Predict gestational age in days from conception**

### Description

The function `predictGA` takes a matrix with Illumina HumanMethylation450 type DNA methylation data. Column names must designate CpG sites (i.e. 'cgXXXXXX', X=number) and row names samples IDs.

### Usage

```r
predictGA(mldat, transp=TRUE, se=TRUE)
```

### Arguments

- `mldat`: A matrix containing DNA methylation beta values (0<=beta<=1)
- `transp`: If TRUE (default), the transpose is automatically taken if the number of rows is greater than the number of columns.
- `se`: If se=TRUE, the estimated coefficients are based on the prediction model with the lambda penalty term being allowed to vary up to one standard error within the minimum. If se=FALSE, the minimum lambda is assumed.

### Details

The minimum lambda (se=FALSE) may result in slightly better predictions, however substantially more CpG sites are needed for estimation. Since the prediction difference is hardly noticeable se=TRUE is the default option.

### Value

The function returns estimated gestational age predictions, together with samples IDs as row names, in a data.frame object.

### Note

Requires quite a bit of memory due to the large DNA methylation matrix required for the prediction model.

### Author(s)

Jon Bohlin

### References


Examples

```r
## Make a mock Illumina HumanMethylation450 type DNA methylation matrix
cpgs <- extractSites( type="se" )
allcpgs <- extractSites( type="all" )
numsamples <- 100
mlmatr <- matrix( NA, ncol=length( allcpgs ), nrow=numsamples )
mlmatr <- data.frame( mlmatr )
for( i in cpgs )
  mlmatr[,i] <- runif( numsamples, min=0, max=1 )
## Perform gestational age prediction
mypred <- predictGA( mlmatr )
```

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**UL.mod.cv**

A glmnet-object trained to perform gestational age prediction.

**Description**

The glmnet-object consists of a Lasso-regression model 'trained' to perform gestational age predictions. It is called by the wrapper function `predictGA`, which is more user-friendly.

**Details**

The trained Lasso-model contains cross-validated estimates of the penalty term lambda that regulates the number of CpG sites needed for gestational age prediction. It is called by the glmnet-inherited predict function with a matrix of CpG betas (with values between 0 and 1) that conforms to the Illumina HumanMethylation450 platform. The gestational age estimates used to train the regression model were taken from the MoBa cohort and are based on ultrasound.

**Source**


**References**


**Examples**

```r
## Extract all non-zero regression coefficients
temp <- as.matrix( coef( UL.mod.cv ) )
allNonZeroCoefs <- rownames( temp )[ temp[,1]!=0 ]
allNonZeroCoefs[ -1 ]
```
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