Package 'planet'

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Title Placental DNA methylation analysis tools

Version 1.21.0

URL http://github.com/wvictor14/planet, http://victoryuan.com/planet/

BugReports http://github.com/wvictor14/planet/issues

Description This package contains R functions to predict biological variables to from placnetal DNA methylation data generated from infinium arrays. This includes inferring ethnicity/ancestry, gestational age, and cell composition from placental DNA methylation array (450k/850k) data.

Depends R (>= 4.3)

Imports methods, tibble, magrittr, dplyr

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License GPL-2

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Contents

`planet-package` *planet: Placental DNA methylation analysis tools*

Description

This package contains R functions to predict biological variables to from placnetal DNA methylation data generated from infinium arrays. This includes inferring ethnicity/ancestry, gestational age, and cell composition from placental DNA methylation array (450k/850k) data.

Author(s)

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See Also

Useful links:

- https://victor.rbind.io/planet
- http://github.com/wvictor14/planet
- Report bugs at http://github.com/wvictor14/planet/issues

ageCpGs *Placental gestational age CpGs*

Description

Coefficients from the three placental gestational age clocks from Lee Y et al. 2019.

Reference: Lee Y, Choufani S, Weksberg R, et al. Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging (Albany NY). 2019;11(12):4238–4253. doi:10.18632/aging.102049. PMID: 31235674

Usage

```
data(ageCpGs)
```

Format

A tibble with coefficients for the RPC, CPC, and refined RPC.

ethnicityCpGs *CpGs to predict ethnicity*

Description

1860 CpGs used to predict ethnicity.

See Yuan et al. 2019 for details.

Usage

```
data(ethnicityCpGs)
```

Format

A character vector of length 1860

Source

https://pubmed.ncbi.nlm.nih.gov/31399127/

plBetas *Example placental DNA methylation data*

Description

6 DNA methylation profiles from preeclampsia and healthy control placentas. This data was downloaded from:

- GSE75196

"Genome wide DNA methylation profiling of normal and preeclampsia placental samples. Illumina Infinium HumanMethylation450 BeadChip (450K array) was used to obtain DNA methylation profiles in placental samples. Samples included 16 samples from healthy uncomplicated pregnancies and 8 samples from pregnancies affected by preeclampsia." - from Yeung et al.

The DNA methylation data for 24 placental samples were downloaded from GSE75196. After normalizing using `minfi::preprocessNoob` and `wateRmelon::BMIQ`, the data were filtered to 6/24 samples and 10,000 random CpGs + those CpGs used in the gestational age clock and ethnicity classifier.

Reference: Yeung KR, Chiu CL, Pidsley R, Makris A et al. DNA methylation profiles in preeclampsia and healthy control placentas. Am J Physiol Heart Circ Physiol 2016 May 15;310(10):H1295-303. PMID:26968548

Usage

```
data(plBetas)
```

Format

A matrix

Source

https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE75196

plCellCpGsFirst *First trimester placental cell type coefficients*

Description

First trimester coefficients for placental cellular deconvolution from `YuanVetal.2020`.

Reference: to be edited PMID: to be edited

Usage

```
data(plCellCpGsFirst)
```

Format

A matrix with coefficients for Trophoblasts, Stromal, Endothelial, Hofbauer cells, nRBCs, and Syncytiotrophoblasts.

plCellCpGsThird *Third trimester placental cell type coefficients*

Description

Third trimester coefficients for placental cellular deconvolution from `YuanVetal.2020`.

Reference: to be edited PMID: to be edited

Usage

```
data(plCellCpGsThird)
```

Format

A matrix with coefficients for Trophoblasts, Stromal, Endothelial, Hofbauer cells, nRBCs, and Syncytiotrophoblasts.

plColors *A color palette for placental cell types*

Description

A nice color palette for placental cell types.

Used in `YuanVetal.2020`.

Contains colors for:

- Syncytiotrophoblast
- Trophoblast
- Stromal
- Hofbauer
- Endothelial
- nRBCs

Usage

```
data(plColors)
```

Format

An object of class `character` of length 6.

plPhenoData *Sample information accompanying* pl_betas

Description

Sex, disease, and gestational age information associated with pl_betas.

Downloaded from the GEO accession:

- GSE75196

Reference: Yeung KR, Chiu CL, Pidsley R, Makris A et al. DNA methylation profiles in preeclampsia and healthy control placentas. Am J Physiol Heart Circ Physiol 2016 May 15;310(10):H1295-303. PMID: 26968548

Usage

```
data(plPhenoData)
```

Format

A tibble

Source

https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE75196

predict *predict mixxo from*

Description

copied from mixOmicsTeam/mixOmics/refs/heads/master/R/predict.R on 2025 Jan 30. Some components omitted that are not used in planet.

Usage

```
## S3 method for class 'mixo_pls'
predict(
  object,
  newdata,
  study.test,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  multilevel = NULL,
  ...
)

## S3 method for class 'mixo_spls'
predict(
  object,
  newdata,
```

```
  study.test,
  dist = c("all", "max.dist", "centroids.dist", "mahalanobis.dist"),
  multilevel = NULL,
  ...
)
```

Arguments

object	object of class inheriting from "(mint).(block).(s)pls(da)".
newdata	data matrix in which to look for for explanatory variables to be used for prediction. Please note that this method does not perform multilevel decomposition or log ratio transformations, which need to be processed beforehand.
study.test	For MINT objects, grouping factor indicating which samples of newdata are from the same study. Overlap with object$study are allowed.
dist	distance to be applied for discriminant methods to predict the class of new data, should be a subset of "centroids.dist", "mahalanobis.dist" or "max.dist" (see Details). Defaults to "all".
multilevel	Design matrix for multilevel analysis (for repeated measurements). A numeric matrix or data frame. For a one level factor decomposition, the input is a vector indicating the repeated measures on each individual, i.e. the individuals ID. For a two level decomposition with splsda models, the two factors are included in Y. Finally for a two level decomposition with spls models, 2nd AND 3rd columns in design indicate those factors (see example in ?splsda and ?spls).
...	not used currently.

Value

predict produces a list with the following components:

predict	predicted response values. The dimensions correspond to the observations, the response variables and the model dimension, respectively. For a supervised model, it corresponds to the predicted dummy variables.
variates	matrix of predicted variates.
B.hat	matrix of regression coefficients (without the intercept).
AveragedPredict	if more than one block, returns the average predicted values over the blocks (using the predict output)
WeightedPredict	if more than one block, returns the weighted average of the predicted values over the blocks (using the predict and weights outputs)
class	predicted class of newdata for each 1, ...,ncomp components.
MajorityVote	if more than one block, returns the majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.
WeightedVote	if more than one block, returns the weighted majority class over the blocks. NA for a sample means that there is no consensus on the predicted class for this particular sample over the blocks.
weights	Returns the weights of each block used for the weighted predictions, for each nrepeat and each fold

centroids	matrix of coordinates for centroids.
dist	type of distance requested.
vote	majority vote result for multi block analysis (see details above).

Author(s)

Florian Rohart, Sébastien Déjean, Ignacio González, Kim-Anh Lê Cao, Al J Abadi

References

Rohart F, Gautier B, Singh A, Lê Cao K-A. mixOmics: an R package for 'omics feature selection and multiple data integration. PLoS Comput Biol 13(11): e1005752

Tenenhaus, M. (1998). *La regression PLS: theorie et pratique*. Paris: Editions Technic.

See Also

http://www.mixOmics.org for more details.

Examples

```
# example code
```

---

predictAge — *Predicts gestational age using placental DNA methylation microarray data*

Description

`predictAge` Multiplies the coefficients from one of three epigenetic gestational age clocks, by the corresponding CpGs in a supplied betas `data.frame`.

Usage

```
predictAge(betas, type = "RPC")
```

Arguments

betas	An n by m dataframe of methylation values on the beta scale (0, 1), where the CpGs are arranged in rows, and samples in columns. Should contain all CpGs used in each clock
type	One of the following: "RPC" (Robust), "CPC", (Control) or "RRPC" (Refined Robust).

Details

Predicts gestational age using one of 3 placental gestational age clocks: RPC, CPC, or refined RPC. Requires placental DNA methylation measured on the Infinium 27K/450k/EPIC methylation array. Ensure as many predictive CpGs are present in your data, otherwise accuracy may be impacted.

It's recommended that you have all predictive CpGs, otherwise accuracy may vary.

Value

A vector of length m, containing inferred gestational age.

Examples

```
# Load placenta DNAm data
library(dplyr)
data(plBetas)
data(plPhenoData)

plPhenoData %>%
    mutate(inferred_ga = predictAge(plBetas, type = "RPC"))
```

`predictEthnicity` *Predicts ethnicity using placental DNA methylation microarray data*

Description

Uses 1860 CpGs to predict self-reported ethnicity on placental microarray data.

Usage

```
predictEthnicity(betas, threshold = 0.75, force = FALSE)
```

Arguments

`betas`	n x m dataframe of methylation values on the beta scale (0, 1), where the variables are arranged in rows, and samples in columns. Should contain all 1860 predictors and be normalized with NOOB and BMIQ.
`threshold`	A probability threshold ranging from (0, 1) to call samples 'ambiguous'. Defaults to 0.75.
`force`	run even if missing predictors. Default is `FALSE`.

Details

Predicts self-reported ethnicity from 3 classes: Africans, Asians, and Caucasians, using placental DNA methylation data measured on the Infinium 450k/EPIC methylation array. Will return membership probabilities that often reflect genetic ancestry composition.

The input data should contain all 1860 predictors (cpgs) of the final GLMNET model.

It's recommended to use the same normalization methods used on the training data: NOOB and BMIQ.

Value

a tibble

Examples

```
## To predict ethnicity on 450k/850k samples

# Load placenta DNAm data
data(plBetas)
predictEthnicity(plBetas)
```

`predictPreeclampsia` *predictPreeclampsia*

Description

Uses 45 CpGs to predict early preeclampsia (PE delivered before or at 34 weeks of gestation) on placental DNA methylation microarray data.

Usage

```
predictPreeclampsia(betas, ...)
```

Arguments

`betas`	matrix or array of methylation values on the beta scale (0, 1), where the variables are arranged in rows, and samples in columns.
`...`	feeds into outersect function

Details

Assigns the class labels "early-PE" or "normotensive" to each sample and returns a class probability.

Value

produces a list with components detailed in the `mixOmics::predict` R documentation

It is recommended that users apply beta-mixture quantile normalization (BMIQ) to their data

prior to prediction. This was the normalization method used on the training data.

Examples

```
# To predict early preeclampsia on 450k/850k samples

# Load data
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "eoPredData")

# test object
x_test <- eh[['EH8403']]
x_test %>% predictPreeclampsia()
```

`%>%` *Pipe operator*

Description

See `magrittr::%>%` for details.

Usage

```
lhs %>% rhs
```

Value

lhs

Examples

```
c(1, 2, 3) %>% sum()
```

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