Package ‘planet’

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Description  This package contains R functions to predict biological variables to from placental 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.
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Description

This package contains R functions to predict biological variables to from placental 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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Other contributors:

- Wendy P. Robinson [contributor]

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**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coefficients from the three placental gestational age clocks from Lee Y et al. 2019.</td>
</tr>
</tbody>
</table>


### Usage

```r
data(ageCpGs)
```

### Format

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

### ethnicityCpGs

**CpGs to predict ethnicity**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1860 CpGs used to predict ethnicity.</td>
</tr>
</tbody>
</table>

See Yuan et al. 2019 for details.

### Usage

```r
data(ethnicityCpGs)
```

### Format

A character vector of length 1860

### Source

### 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.


**Usage**

```r
data(plBetas)
```

**Format**

A matrix

**Source**

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

**Description**


Contains colors for:

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

**Usage**

```r
data(plColors)
```

**Format**

An object of class character of length 6.

### plPhenoData

**Description**

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

Downloaded from the GEO accession:

- GSE75196


**Usage**

```r
data(plPhenoData)
```

**Format**

A tibble
**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**

```r
# 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
tibble

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

# Load placenta DNAm data
data(plBetas)
predictEthnicity(plBetas)
Pipe operator

Description

See magrittr::%>% for details.

Usage

lhs %>% rhs

Value

lhs

Examples

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