

Package: PheNorm (via r-universe)

August 20, 2024

Type Package

Title Unsupervised Gold-Standard Label Free Phenotyping Algorithm for EHR Data

Version 0.1.1

Description The algorithm combines the most predictive variable, such as count of the main International Classification of Diseases (ICD) codes, and other Electronic Health Record (EHR) features (e.g. health utilization and processed clinical note data), to obtain a score for accurate risk prediction and disease classification. In particular, it normalizes the surrogate to resemble gaussian mixture and leverages the remaining features through random corruption denoising. Background and details about the method can be found at Yu et al. (2018) [doi:10.1093/jamia/ocx111](https://doi.org/10.1093/jamia/ocx111).

License GPL-3

Encoding UTF-8

RoxygenNote 7.1.1

URL <https://celehs.github.io/PheNorm/>

BugReports <https://github.com/celehs/PheNorm/issues>

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Repository <https://celehs.r-universe.dev>

RemoteUrl <https://github.com/celehs/phenorm>

RemoteRef HEAD

RemoteSha 7ea2ecee5b4ce88c029eee22341cc5536167effc

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PheNorm.Prob

Fit the phenotyping algorithm PheNorm using EHR features

Description

The function requires as input: * a surrogate, such as the ICD code * the healthcare utilization It can leverage other EHR features (optional) to assist risk prediction.

Usage

```
PheNorm.Prob(
  nm.logS.ori,
  nm.utl,
  dat,
  nm.X = NULL,
  corrupt.rate = 0.3,
  train.size = 10 * nrow(dat)
)
```

Arguments

nm.logS.ori	name of the surrogates (log(ICD+1), log(NLP+1) and log(ICD+NLP+1))
nm.utl	name of healthcare utilization (e.g. note count, encounter_num etc)
dat	all data columns need to be log-transformed and need column names
nm.X	additional features other than the main ICD and NLP
corrupt.rate	rate for random corruption denoising, between 0 and 1, default value=0.3
train.size	size of training sample, default value 10 * nrow(dat)

Value

list containing probability and beta coefficient

Examples

```
## Not run:
set.seed(1234)
fit.dat <- read.csv("https://raw.githubusercontent.com/celehs/PheNorm/master/data-raw/data.csv")
fit.phenorm=PheNorm.Prob("ICD", "utl", fit.dat, nm.X = NULL,
                        corrupt.rate=0.3, train.size=nrow(fit.dat));
head(fit.phenorm$probs)

## End(Not run)
```

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