Package: MAP (via r-universe)

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Type Package

Title Multimodal Automated Phenotyping

Version 0.1.3

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Description Electronic health records (EHR) linked with
biorepositories are a powerful platform for translational
studies. A major bottleneck exists in the ability to phenotype
patients accurately and efficiently. Towards that end, we
developed an automated high-throughput phenotyping method
integrating International Classification of Diseases (ICD)
codes and narrative data extracted using natural language
processing (NLP). Specifically, our proposed method, called MAP
(Map Automated Phenotyping algorithm), fits an ensemble of
latent mixture models on aggregated ICD and NLP counts along
with healthcare utilization. The MAP algorithm yields a
predicted probability of phenotype for each patient and a
threshold for classifying subjects with phenotype yes/no (See
Katherine P. Liao, et al. (2019) <doi:10.1101/587436>.).

License GPL-2

Encoding UTF-8

LazyData true

Depends R (>= 3.4.0), flexmix (>= 2.3-14), Matrix(>= 1.2-10)

Suggests knitr, rmarkdown

NeedsCompilation no

RoxygenNote 6.1.1

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Repository https://jjr1234.r-universe.dev

RemoteUrl https://github.com/cran/MAP

RemoteRef HEAD

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Contents

MAP *MAP algorithm*

Description

Main function to perform MAP algorithm to calculate predicted probabilities of positive phenotype for each patient based on NLP and ICD counts adjusted for healthcare utilization.

Usage

```
MAP(mat = NULL, note = NULL, yes.con = FALSE, full.output = FALSE)
```

Arguments

mat	Count data (sparse matrix). One of the columns has to be ICD data with name being ICD.
note	Note count (sparse matrix) indicating health utilization.
yes.con	A logical variable indicating if concomitant is desired. Not used for now.
full.output	A logical variable indicating if full outputs are desired.

Value

Returns a list with following objects:

scores	indicates predicted probabilities.
cut.MAP	the cutoff value that can be used to derive binary phenotype.

References

High-throughput Multimodal Automated Phenotyping (MAP) with Application to PheWAS. Katherine P. Liao, Jiehuan Sun, Tianrun A. Cai, Nicholas Link, Chuan Hong, Jie Huang, Jennifer Huffman, Jessica Gronsbell, Yichi Zhang, Yuk-Lam Ho, Victor Castro, Vivian Gainer, Shawn Murphy, Christopher J. O'Donnell, J. Michael Gaziano, Kelly Cho, Peter Szolovits, Isaac Kohane, Sheng Yu, and Tianxi Cai with the VA Million Veteran Program (2019) <doi:10.1101/587436>.

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Examples

```
## simulate data to test the algorithm
n = 400
ICD = c(rpois(n/4,10), rpois(n/4,1), rep(0,n/2) )
NLP = c(rpois(n/4,10), rpois(n/4,1), rep(0,n/2) )
mat = Matrix(data=cbind(ICD,NLP),sparse = TRUE)
note = Matrix(rpois(n,10)+5,ncol=1,sparse = TRUE)
res = MAP(mat = mat,  note=note)
head(res$scores)
res$cut.MAP
```

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