

Package ‘PDN’

July 21, 2025

Type Package

Title Personalized Disease Network

Version 0.1.0

Author Javier Cabrera <xavier.cabrera@gmail.com>, Fei Wang <cherry8177@gmail.com>

Maintainer Zhenbang Wang <bruce1edward@gmail.com>

Description Building patient level networks for prediction of medical outcomes and draw the cluster of network.
This package is based on paper Personalized disease networks for understanding and predicting cardiovascular diseases and other complex processes
(See Cabrera et al. <http://circ.ahajournals.org/content/134/Suppl_1/A14957>).

License GPL-2

Depends R (>= 2.3.0)

Imports survival, glmnet, ggplot2, network

LazyData TRUE

RoxygenNote 6.0.1

NeedsCompilation no

VignetteBuilder knitr

Suggests knitr, rmarkdown

Repository CRAN

Date/Publication 2017-11-03 23:27:43 UTC

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PDN-package	<i>Personized Disease Network</i>
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Description

Building patient level networks for prediction of medical outcomes and draw the cluster of network. This package is based on paper Personalized disease networks (PDN) for understanding and predicting cardiovascular diseases and other complex processes.

Details

Package: PDN
Type: Package
Version: 1.0
Date: 2017-08-14
License: GPL-2

Author(s)

Javier Cabrera and Fei Wang
Maintainer: Zhenbang Wang <bruce1edward@gmail.com>

References

Cabrera, Javier and Kostis, John B and Wang, Fei and Kostis, William J. (2016) *Personalized Disease Networks in Predicting Cardiovascular Outcomes*

buildnetworks	<i>Generating Network Matrix</i>
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Description

This function use data set with cut off information to create network matrix

Usage

buildnetworks(x, k1, del = 0)

Arguments

x	comorbidity data matrix with column correspond to ICD9 codes and row correspond to each patient
k1	the cut off point between Diagnosis/Procedure A to another Diagnosis/Procedure B, it can be fix number, NULL and datecut
del	number of character deleted for each name of the input

Value

Network Matrix

Examples

```
# Select a subset of data for toy example
comorbidity_data = comorbidity_data[c(1:10),]
survival_data = survival_data[c(1:10),]
k1 = datecut(comorbidity_data,survival_data[,1],survival_data[,2])
a = buildnetworks(comorbidity_data,k1)
```

comorbidity_data	<i>Sampele comorbidity data set</i>
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Description

This is the sample data set for Package PDN

Usage

```
comorbidity_data
```

Format

100 rows and 10 column matrix

datecut	<i>Generating Optimal cuts for the Data</i>
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Description

Performs Cox proportional hazards regression model on patients survival days based on different cutoffs

Usage

```
datecut(x, surdays, event)
```

Arguments

x	comorbidity data matrix with column correspond to ICD9 codes and row correspond to each patient
surdays	survival days for each patient
event	indicator variable 1 represent patient died 0 represent patient survive

Details

Building and draw personalized disease network

Value

a vector of cutoff points that maximize the Z statistics for cox model between each Diagnosis/Procedure A to another Diagnosis/Procedure B

Examples

```
comorbidity_data
survival_data
#Select a subset of data for toy example
comorbidity_data = comorbidity_data[c(1:10),]
survival_data = survival_data[c(1:10),]
k1 = datecut(comorbidity_data,survival_data[,1],survival_data[,2])
```

demographic_data	<i>Sampele demographic data set</i>
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Description

This is one of the sample data set. It contains the demographic information of each patients It has five variables which are sex, race, hispan, dshyr and prime

Usage

```
demographic_data
```

Format

100 rows and 5 column matrix

draw.PDN	<i>Draw Personalized Disease Network for one patient with network and ggplot2</i>
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Description

Draw Personalized Disease Network based on newtwork matrix

Usage

```
draw.PDN(tt, labels)
```

Arguments

tt	one row of network matrix generated from comorbidity data matrix using build-networks
labels	names of each node in the network matrix

Examples

```
#Select a subset of data for toy example
comorbidity_data = comorbidity_data[c(1:10),]
survival_data = survival_data[c(1:10),]
# Getting the names
k1 = datecut(comorbidity_data,survival_data[,1],survival_data[,2])
a = buildnetworks(comorbidity_data,k1)
#Plot PDN for patient 7
nn = names(comorbidity_data)
draw.PDN(a[7,],nn)
```

draw.PDN.circle	<i>Draw Personalized Disease Network for one patient</i>
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Description

Draw Personalized Disease Network based on newtwork matrix

Usage

```
draw.PDN.circle(a0, dak)
```

Arguments

a0	one row of network matrix generated from comorbidity data matrix using build-networks
dak	one row of Ranks matrix for corresponding comorbidity data matrix

Examples

```
#Select a subset of data for toy example
comorbidity_data = comorbidity_data[c(1:10),]
survival_data = survival_data[c(1:10),]
# Find date cuts
k1 = datecut(comorbidity_data,survival_data[,1],survival_data[,2])
# Build networks
a = buildnetworks(comorbidity_data,k1)

# Graph individual patients
datark = t(apply(comorbidity_data,1,rank))
dak = sort(datark[1,])
# draw PDN for the first patient
draw.PDN.circle(a[1,],dak)
# draw PDN for the whole comorbidity data set
par(mfrow=c(2,5))
for(i in 1 : nrow(a)){
  dak = apply(datark,2,sort)
  draw.PDN.circle(a[i,],dak[i,])
  title(main=paste("Patient",i))
}
```

draw.PDN.cluster

*Draw Personalized Disease Network for cluster of patients***Description**

Draw Personalized Disease Network based on cluster information

Usage

```
draw.PDN.cluster(a0, dak)
```

Arguments

a0	network matrix get from buildnetworks
dak	ranks data for comorbidity data matrix

Examples

```
#Select a subset of data for toy example
comorbidity_data = comorbidity_data[c(1:10),]
survival_data = survival_data[c(1:10),]
##Clustering Example
k1 = datecut(comorbidity_data,survival_data[,1],survival_data[,2])
a = buildnetworks(comorbidity_data,k1)
datark = t(apply(comorbidity_data,1,rank))
require(survival)
zsq = NULL
```

```

for(i in 1:ncol(a)){
  a1 = (summary(coxph(Surv(as.numeric(survival_data[,1]),survival_data[,2]) ~ a[,i],
    data=as.data.frame(a)))$coefficient[,4])^2
  zsq = cbind(zsq,a1)
}
zsq = as.numeric(zsq)
wi=zsq/sum(zsq,na.rm=TRUE)
wi[wi<10^-3]=10^-3
wi[is.na(wi)]=10^-3
#weighted matrix
wa = NULL
for(i in 1:ncol(a)){
  wa = cbind(wa,a[,i]*wi[i])
}
#PCA
pr.out=prcomp(wa)
x.svd=svd(wa)
x.score1 <- wa %*% x.svd$v
x.score2 <- x.svd$u %*% diag(x.svd$d)
##HC cluster using the first 8 PCA scores
dp<-dist(x.score2[,1:8])
hcp<-hclust(dp, method="ward.D")
##Plot Network
s1=rev(sort(apply(a[cutree(hcp,3)==2,],2,mean)))[1:50]
dak = sort(apply(datark[cutree(hcp,3)==2,],2,mean,na.rm=TRUE))
names(dak) = unlist(strsplit(names(dak),"DAT"))
draw.PDN.cluster(s1,dak)

```

survival_data

*Sampele Survival data set***Description**

This is the sample data set for function datecut. The first column is the time difference between the patient admission date and death date The second column is the indicator variable with 1 corresponding to patient death, 0 corresponding to patient alive

Usage

survival_data

Format

100 rows and 2 column matrix

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