Package ‘PDN’

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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 for understanding and predicting cardiovascular diseases and other complex processes (See Cabrera et al. <http://circ.ahajournals.org/content/134/Suppl_1/A14957>.
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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
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### Author(s)

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### References

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

### Description

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

### Usage

`buildnetworks(x, k1, del = 0)`
comorbidity_data

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    Sample comorbidity data set

Description

This is the sample data set for Package PDN

Usage

comorbidity_data

Format

100 rows and 10 column matrix

datecut    Generating Optimal cuts for the Data

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 personized 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  Sample demographic data set

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**

*Draw Personalized Disease Network for one patient with network and ggplot2*

**Description**

Draw Personalized Disease Network based on network matrix

**Usage**

draw.PDN(tt, labels)

**Arguments**

- **tt**
  - one row of network matrix generated from comorbidity data matrix using buildnetworks

- **labels**
  - names of each node in the network matrix

**Examples**

```r
# Select a subset of data for toy example
comorbidity_data = comorbidity_data[10],
survival_data = survival_data[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**

*Draw Personalized Disease Network for one patient*

**Description**

Draw Personalized Disease Network based on network matrix

**Usage**

draw.PDN.circle(a0, dak)

**Arguments**

- **a0**
  - one row of network matrix generated from comorbidity data matrix using buildnetworks

- **dak**
  - one row of Ranks matrix for corresponding comorbidity data matrix
**Examples**

```r
# 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)

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**

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

**Arguments**

- `a0`: network matrix get from buildnetworks
- `dak`: ranks data for comorbidity data matrix

**Examples**

```r
# 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**

Sample 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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