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
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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

buildnetworks

Generating Network Matrix

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**

```r
# 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)
```

**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, sundays, event)
demographic_data

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 build-networks

- **labels**
  
names of each node in the network 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),]
# 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 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.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
survival_data

```r
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)
}
```

```r
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(data,k[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**

```r
survival_data
```

**Format**

100 rows and 2 column matrix
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