

Package ‘SKNN’

October 8, 2024

Type Package

Title A Super K-Nearest Neighbor (SKNN) Classification Algorithm

Version 4.1

Date 2024-10-09

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Depends methods, stats

Description It's a Super K-Nearest Neighbor classification method with using kernel density to describe weight of the distance between a training observation and the testing sample.

Collate SKNN.R Dist.R PCAY.R AllClasses.R KNN.R

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NeedsCompilation no

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Repository CRAN

Date/Publication 2024-10-08 20:10:01 UTC

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SKNN-package

*Super K-Nearest Neighbor (SKNN) Classification***Description**

It's a Super K-Nearest Neighbor classification method with using kernel density to describe the weight of the distance between a training observation and the sample to be classified.

Details

Package: SKNN
 Type: Package
 Version: 4.1
 Date: 2024-10-09
 License: GPL-2

Author(s)

Yarong Yang, Nader Ebrahimi, Yoram Rubin, and Jacob Zhang

References

Yarong Yang, Nader Ebrahimi, and Yoram Rubin.(2024) SKNN: A Super K-Nearest Neighbor Classification Algorithm.

Yarong Yang, Matt Over, and Yoram Rubin.(2012) Strategic Placement of Localization Devices (such as Pilot Points and Anchors) in Inverse Modeling Schemes. *Water Resources Research*, 48, W08519, doi:10.1029/2012WR011864.

B.B.W. Silverman.(1986) *Density Estimation for Statistics and Data Analysis*. London: Chapman and Hall.

Examples

```
Sepal.Length<-c(4.8, 5.1, 4.6, 5.3, 5.0, 5.7, 5.7, 6.2, 5.1, 5.7, 6.7, 6.3, 6.5, 6.2, 5.9)
Sepal.Width<-c(3.0, 3.8, 3.2, 3.7, 3.3, 3.0, 2.9, 2.9, 2.5, 2.8, 3.0, 2.5, 3.0, 3.4, 3.0)
Petal.Length<-c(1.4, 1.6, 1.4, 1.5, 1.4, 4.2, 4.2, 4.3, 3.0, 4.1, 5.2, 5.0, 5.2, 5.4, 5.1)
Petal.Width<-c(0.3, 0.2, 0.2, 0.2, 0.2, 1.2, 1.3, 1.3, 1.1, 1.3, 2.3, 1.9, 2.0, 2.3, 1.8)
Species<-as.factor(c(rep("red",5),rep("blue",5),rep("green",5)))
iris<-cbind(Sepal.Length,Sepal.Width,Petal.Length,Petal.Width)
Res<-length(nrow(iris))
k<-10
for(i in 1:nrow(iris))
  Res[i]<-SKNN(data=iris,Class=as.vector(Species),k=k,test=iris[i,])
accuracy<-length(which(Res==Species))/length(Species)
plot(x=1:15,y=rep(1,15),col=as.vector(Species),lwd=4,ylim=c(0,3),xlab="",ylab="",
```

```
yaxt = "n",xaxt="n")
par(new=TRUE)
plot(x=1:15,y=rep(2,15),col=Res,lwd=4,ylim=c(0,3),xlab="",ylab="",yaxt = "n",xaxt="n")
ind<-which(Res!=Species)
if(length(ind)>0) {
  for(j in 1:length(ind))
    lines(x=c(ind[j],ind[j]),y=c(1+0.05,2-0.05))
}
text(5,0.3,paste("SKNN Misclassified:",length(ind)))
axis(2,at=2,labels="SKNN",las=1)
text(10,2.5,paste("k: ",k))
```

Dist

Finding the distance between two observations.

Description

It's a function of finding the distance between two observations.

Usage

```
Dist(x,y)
```

Arguments

| | |
|---|--|
| x | Numeric. A vector denoting an observation. |
| y | Numeric. A vector denoting an observation. |

Value

A list.

Author(s)

Yarong Yang

Description

It's implementation of the K-Nearest Neighbor classification method for data of any number of dimentionions.

Usage

```
KNN(data, Class, k, test)
```

Arguments

| | |
|-------|--|
| data | Numeric. The training data set, matrix. |
| Class | Character. Class of the training observations, vector. |
| k | Integer. The number of K to be used. |
| test | Numeric. The sample to be classified. |

Value

A character.

Author(s)

Yarong Yang

References

A.T. Covert and P. Hart. Nearest Neighbor Pattern Classification. IEEE Transactions on Information Theory, 13(1): 21-27, 1967.

Examples

```
Sepal.Length<-c(4.8, 5.1, 4.6, 5.3, 5.0, 5.7, 5.7, 6.2, 5.1, 5.7, 6.7, 6.3, 6.5, 6.2, 5.9)
Sepal.Width<-c(3.0, 3.8, 3.2, 3.7, 3.3, 3.0, 2.9, 2.9, 2.5, 2.8, 3.0, 2.5, 3.0, 3.4, 3.0)
Petal.Length<-c(1.4, 1.6, 1.4, 1.5, 1.4, 4.2, 4.2, 4.3, 3.0, 4.1, 5.2, 5.0, 5.2, 5.4, 5.1)
Petal.Width<-c(0.3, 0.2, 0.2, 0.2, 0.2, 1.2, 1.3, 1.3, 1.1, 1.3, 2.3, 1.9, 2.0, 2.3, 1.8)
Species<-as.factor(c(rep("red",5),rep("blue",5),rep("green",5)))
iris<-cbind(Sepal.Length,Sepal.Width,Petal.Length,Petal.Width)
Res<-length(nrow(iris))
k<-10
for(i in 1:nrow(iris))
  Res[i]<-KNN(data=iris,Class=as.vector(Species),k=k,test=iris[i,])
accuracy<-length(which(Res==Species))/length(Species)
plot(x=1:15,y=rep(1,15),col=as.vector(Species),lwd=4,ylim=c(0,3),xlab="",ylab="",
yaxt = "n",xaxt="n")
par(new=TRUE)
```

```
plot(x=1:15,y=rep(2,15),col=Res,lwd=4,ylim=c(0,3),xlab="",ylab="",yaxt = "n",xaxt="n")
ind<-which(Res!=Species)
if(length(ind)>0) {
  for(j in 1:length(ind))
    lines(x=c(ind[j],ind[j]),y=c(1+0.05,2-0.05))
}
text(5,0.3,paste("KNN Misclassified:",length(ind)))
axis(2,at=2,labels="KNN",las=1)
text(10,2.5,paste("k: ",k))
```

PCAy

Revised PCA analysis

Description

It's a revised PCA analysis.

Usage

PCAy(data)

Arguments

data Numeric. Data matrix for revised PCA analysis.

Value

An object of class "PCAy".

Author(s)

Yarong Yang and Yoram Rubin

References

Yarong Yang, Matt Over, and Yoram Rubin.(2012) Strategic Placement of Localization Devices (such as Pilot Points and Anchors) in Inverse Modeling Schemes. *Water Resources Research*, 48, W08519, doi:10.1029/2012WR011864.

Yarong Yang, Nader Ebrahimi, and Yoram Rubin.(2024) SKNN: A Super K-Nearest Neighbor Classification Algorithm.

Examples

```

Sepal.Length<-c(4.8, 5.1, 4.6, 5.3, 5.0, 5.7, 5.7, 6.2, 5.1, 5.7, 6.7, 6.3,
6.5, 6.2, 5.9)
Sepal.Width<-c(3.0, 3.8, 3.2, 3.7, 3.3, 3.0, 2.9, 2.9, 2.5, 2.8, 3.0, 2.5,
3.0, 3.4, 3.0)
Petal.Length<-c(1.4, 1.6, 1.4, 1.5, 1.4, 4.2, 4.2, 4.3, 3.0, 4.1, 5.2, 5.0,
5.2, 5.4, 5.1)
Petal.Width<-c(0.3, 0.2, 0.2, 0.2, 0.2, 1.2, 1.3, 1.3, 1.1, 1.3, 2.3, 1.9,
2.0, 2.3, 1.8)
dat<-cbind(Sepal.Length,Sepal.Width,Petal.Length,Petal.Width)
Res<-PCAy(dat)

```

PCAyD

Class to contain the results from revised PCA analysis.

Description

The function PCAy returns object of class PCAyD.

Objects from the Class

```
new("PCAyD",Var=new("numeric"),PC=new("matrix"),Scores=new("matrix"),IScores=new("numeric"))
```

Slots

Var: An numeric vector giving the variance of each PC.

PC: A numeric matrix about the coefficients of each PC.

Scores: A numeric matrix showing the loading coefficients of each PC.

IScores: A numeric vector with each element being the rowsum of Scores.

Author(s)

Yarong Yang and Yoram Rubin

References

Yarong Yang, Matt Over, and Yoram Rubin.(2012) Strategic Placement of Localization Devices (such as Pilot Points and Anchors) in Inverse Modeling Schemes. Water Resources Research, 48, W08519, doi:10.1029/2012WR011864.

Yarong Yang, Nader Ebrahimi, and Yoram Rubin.(2024) SKNN: A Super K-Nearest Neighbor Classification Algorithm.

Examples

```
showClass("PCAyD")
```

Description

It's a Super K-Nearest Neighbor classification method with using kernel density to describe weight of the distance between a training observation and the testing sample.

Usage

```
SKNN(data, Class, k, test)
```

Arguments

| | |
|-------|--|
| data | Numeric. The training data set, matrix. |
| Class | Character. Class of the training observations, vector. |
| k | Integer. The number of K to be used. |
| test | Numeric. The sample to be classified. |

Value

A character.

Author(s)

Yarong Yang, Nader Ebrahimi, and Yoram Rubin

References

Yarong Yang, Nader Ebrahimi, and Yoram Rubin.(2024) SKNN: A Super K-Nearest Neighbor Classification Algorithm.

Yarong Yang, Matt Over, and Yoram Rubin.(2012) Strategic Placement of Localization Devices (such as Pilot Points and Anchors) in Inverse Modeling Schemes. *Water Resources Research*, 48, W08519, doi:10.1029/2012WR011864.

B.B.W. Silverman. *Density Estimation for Statistics and Data Analysis*. London: Chapman and Hall, 1986.

Examples

```
Sepal.Length<-c(4.8, 5.1, 4.6, 5.3, 5.0, 5.7, 5.7, 6.2, 5.1, 5.7, 6.7, 6.3, 6.5, 6.2, 5.9)
Sepal.Width<-c(3.0, 3.8, 3.2, 3.7, 3.3, 3.0, 2.9, 2.9, 2.5, 2.8, 3.0, 2.5, 3.0, 3.4, 3.0)
Petal.Length<-c(1.4, 1.6, 1.4, 1.5, 1.4, 4.2, 4.2, 4.3, 3.0, 4.1, 5.2, 5.0, 5.2, 5.4, 5.1)
Petal.Width<-c(0.3, 0.2, 0.2, 0.2, 0.2, 1.2, 1.3, 1.3, 1.1, 1.3, 2.3, 1.9, 2.0, 2.3, 1.8)
Species<-as.factor(c(rep("red",5),rep("blue",5),rep("green",5)))
iris<-cbind(Sepal.Length,Sepal.Width,Petal.Length,Petal.Width)
Res<-length(nrow(iris))
k<-10
```

```
for(i in 1:nrow(iris))
  Res[i]<-SKNN(data=iris,Class=as.vector(Species),k=k,test=iris[i,])
accuracy<-length(which(Res==Species))/length(Species)
plot(x=1:15,y=rep(1,15),col=as.vector(Species),lwd=4,ylim=c(0,3),xlab="",ylab="",
yaxt = "n",xaxt="n")
par(new=TRUE)
plot(x=1:15,y=rep(2,15),col=Res,lwd=4,ylim=c(0,3),xlab="",ylab="",yaxt = "n",xaxt="n")
ind<-which(Res!=Species)
if(length(ind)>0) {
  for(j in 1:length(ind))
    lines(x=c(ind[j],ind[j]),y=c(1+0.05,2-0.05))
}
text(5,0.3,paste("SKNN Misclassified:",length(ind)))
axis(2,at=2,labels="SKNN",las=1)
text(10,2.5,paste("k: ",k))
```


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