

```
[R.app GUI 1.30 (5511) i386-apple-darwin9.8.0]
```

```
Loading required package: sm
Package 'sm', version 2.2-3; Copyright (C) 1997, 2000, 2005, 2007 A.W.Bowman &
A.Azzalini
type help(sm) for summary information
Loading required package: splines
Loading required package: mgcv
This is mgcv 1.5-6 . For overview type `help("mgcv-package")'.
Loading required package: MASS
```

```
Attaching package: 'labdsv'
```

```
The following object(s) are masked from package:stats :
```

```
density
```

```
> data1<-read.table("T_sess_lgsq.txt", header=TRUE)
> attach(data1)
> data1<-na.omit(data1)
> data2<-read.table("T_schri_lgsq.txt", header=TRUE)
> attach(data2)
```

```
The following object(s) are masked from data1 :
```

```
CI EL ES EW FL HL HW LHL MFC PW SI SL
```

```
> data2<-na.omit(data2)
> pca1<-pca(data1, cor=FALSE)
> pca2<-pca(data2, cor=FALSE)
> PC1.1<-loadings(pca1)
> PC1.2<-loadings(pca2)
> PC1.1<-PC1.1[c(1:6)]
> PC1.2<-PC1.2[c(1:6)]
> Theta<-acos(PC1.1*%*%PC1.2)*57.29577951
> if(Theta>90) Theta<-180-Theta
> print(Theta)
      [,1]
[1,] 82.7628
> #prints angle between vectors
>
> n<-1000
> datapool<-merge(data1, data2, all=TRUE)
> n1<-nrow(data1)
> n2<-nrow(data2)
> Thetaperm<-NA
> while (n>0){
+ data1samp<-datapool[sample(nrow(datapool),n1, replace=FALSE),];
+ data2samp<-datapool[sample(nrow(datapool),n2, replace=FALSE),];
+ pca1samp<-pca(data1samp, cor=FALSE);
+ pca2samp<-pca(data2samp, cor=FALSE);
+ PC1.1samp<-loadings(pca1samp);
+ PC1.2samp<-loadings(pca2samp);
+ PC1.1samp<-PC1.1samp[c(1:6)];
```

```
+ PC1.2samp<-PC1.2samp[c(1:6)];
+ Thetasamp<-acos(PC1.1samp**PC1.2samp)*57.29577951;
+ if(Thetasamp>90) Thetasamp<-180-Thetasamp
+ Thetaperm<-append(Thetaperm, Thetasamp);
+ n<-n-1}
> Thetaperm<-na.omit(Thetaperm)
> cdf<-ecdf(Thetaperm)
> 1-cdf(Theta)
[1] 0.001
>
>
```