DHT_vignette

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```r
source("~/Downloads/Dispersion/pvalue_combinations_v2/DHT.R")
```

```
## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.6-8

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

## Loading required package: Rcpp

## Loading required package: RcppZiggurat

## Loading required package: RcppParallel

##
## Attaching package: 'RcppParallel'

## The following object is masked from 'package:Rcpp':
##
##     LdFlags

##
## Rfast: 2.1.0
```

```
## ___ __ __ __ __     __ __ __ __ __ _          _                   __ __ __ __ __   __ __ __ __ __ _
## |  __ __ __ __  |  |  __ __ __ __ _/         /  \                 |  __ __ __ __ /  /__ __ _  _ __ _
## | |          | | | |                        / _  \                | |                       / /
## | |          | | | |                       / / \  \               | |                      / /
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## |  \          | |                      /  __ _ _ _    \                         | |      \/  / /
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## |_|    \__ __ __\ |_|              /_/                    \_\ /_ __ __ __ ___|     \/
##
## Attaching package: 'Rfast'
```

```
## The following object is masked from 'package:dplyr':
##
##     nth
```

```
##
## Attaching package: 'data.table'
```

```
## The following object is masked from 'package:Rfast':
##
##     transpose
```

```
## The following objects are masked from 'package:dplyr':
##
##     between, first, last
```

```
##
## Attaching package: 'psych'
```

```
## The following object is masked from 'package:Rfast':
##
##     skew
```

```
## The following object is masked from 'package:vegan':
##
##     pca
```

We implement DHT on sparrows data and Tikus Coral Data. Input the groupwise data as a list in the function `DHT.pval()`. The function uses all but 2 cores of your machine for parallel computation of permutation p-values, so please adjust external wrapper accordingly. You can manually adjust the number of cores used in the permutation by editing the process_permutation function in the function perm_final(). If Euclidean distance is used, the cailliez function will issue a warning - "Warning: Euclidean distance found : no correction needed" - you can ignore this.

Sparrows Data

```
DATA <- read.table("sparrows.csv", sep = ";", dec = ".", header=TRUE);


# Standardized data
DATA[,1:5] <- scale(DATA[,1:5])
ident.sparrows <- DATA$status
group1 = DATA %>% filter(status == "Survived") %>% select(-status)
group2 = DATA %>% filter(status == "Non-survived")%>% select(-status)
DHT.pval(list(group1, group2), n.perm = 999, distance = "euclidean", binary = FALSE)
```

```
## Warning in cailliez(D): Euclidean distance found : no correction needed
```

```
## [1] 0.031
```

Tikus Coral Data

```
load("tikus.RData")
group = list()
group[[1]] = tikus$abund[tikus$x$time == 81,]
group[[2]] = tikus$abund[tikus$x$time == 83,]
group[[3]] = tikus$abund[tikus$x$time == 84,]
group[[3]] = tikus$abund[tikus$x$time == 85,]
group[[4]] = tikus$abund[tikus$x$time == 87,]
group[[5]] = tikus$abund[tikus$x$time == 84,]
DHT.pval(group, n.perm = 999, distance = "bray", binary = FALSE)
```

```
## [1] 0.002
```