

Package ‘HierDpart’

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Title Partitioning Hierarchical Diversity and Differentiation Across Metrics and Scales, from Genes to Ecosystems

Description Miscellaneous R functions for calculating and decomposing hierarchical diversity metrics, including hierarchical allele richness, hierarchical exponential Shannon entropy (true diversity of order $q=1$), hierarchical heterozygosity and genetic differentiation (Jaccard dissimilarity, Delta D, Fst and Jost's D). In addition, a new approach to identify population structure based on the homogeneity of multivariate variances of Shannon differentiation is presented. This package allows you to analyse spatial structured genetic data or species data under a unifying framework (Gaggiotti, O. E. et al, 2018, *Evol Appl*, 11:1176-1193; <DOI:10.1111/eva.12593>), which partitions diversity and differentiation into any hierarchical levels. It helps you easily structure and format your data. In summary, it implements the analyses of true diversity profiles ($q=0,1,2$), hierarchical diversities and differentiation decomposition, visualization of population structure, as well as the estimation of correlation between geographic distance and genetic differentiation.

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Depends R (>= 3.0)

License GPL (>= 3)

SystemRequirements GNU make

URL <https://github.com/xinghuq/HierDpart>

BugReports <https://github.com/xinghuq/HierDpart/issues>

Imports GGally, adegenet, diveRsity, entropart, mmod, ggplot2, hierfstat, reshape2, tibble, ade4, vegan, ape, pegas, permute

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boot.ppDeltaD	<i>Bootstrapping test of pairwise allelic differentiation (Delta D) between populations</i>
---------------	---

Description

Do bootstrapping on pairwise allelic differentiation (Delta D) between populations and get the confidence interval.

Usage

```
boot.ppDeltaD(dat, ncode, nboot, quant = c(0.025, 0.975), diploid = TRUE, ...)
```

Arguments

dat	Genetic file
ncode	Genotype coding type
nboot	Number of bootstraps

quant	confidence interval
diploid	Ploidy
...	

Details

Do bootstrapping on pairwise allelic differentiation (Delta D) between populations and get the confidence interval

Value

lower1	lower confidence interval of pairwise allelic differentiation
uper1	uper confidence interval of pairwise allelic differentiation
DeltaD.per.loc	Delta D per locus

Author(s)

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References

Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution*, 39(4), 783-791.

Examples

```
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
boot.ppDeltaD(infile, ncode=3, nboot=999, quant = c(0.025, 0.975), diploid = TRUE)
```

CorDdPlot	<i>Plot the relation between genetic differentiation (Delta D) and geographic distance</i>
-----------	--

Description

This function plots the linear regression of genetic differentiation (Delta D) against geographic distance.

Usage

```
CorDdPlot(x, d, ncode)
```

Arguments

x	The genetic file, here is genepop format file.
d	Geographic distance.If D is TRUE, you should input the matrix of geographic distance; if no realistic distance,d should be set as NULL, then the default distance will be generated according to the order of the population sequence.
ncode	The type of your coding allele

Value

plot	Return to a linear plot for the relation between genetic differentiation (Delta D) and geographic distance.
lm	Return to details of linear regression between genetic differentiation (Delta D) and geographic distance.

Author(s)

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References

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

Examples

```
# example genepop file
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
CorDdPlot(infile,d=NULL,ncode=3)
```

COR_DeltaDd

Function for calculating pairwise Delta D and correlation between genetic differentiation (Delta D) and geographic distance

Description

This function calculates new pairwise genetic differentiation, Delta D (Gaggiotti OE, et al, 2018), as well as the correlation between genetic differentiation (Delta D) and geographic distance.

Usage

```
COR_DeltaDd(f, d, ncode, nrepet)
```

Arguments

f	A genetic data files, the format is genepop format.
d	Pairwise geographic distance for calculating correlations. If no actual geographic distance, d=NULL. If TRUE, the geographic distance should be a matrix that corresponds to the pairwise genetic differentiation matrix.
ncode	The coding type of your genetic data.
nrepet	Number of permutations.

Details

This function returns to lists of pairwise Delta D matrix, and a matrix of theoretical geographical distance if d is NULL, as well as the correlation coefficient.

Value

PairwiseDeltaD	The pairwise genetic differentiation matrix (Delta D).
Dgeo	The pairwise geographical distance matrix.
CorDeltaDd	Pearson correlation coefficient between genetic differentiation (Delta D) and geographic distance.

Author(s)

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References

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

See Also

COR_Fst

Examples

```
# example genepop file
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
d1=COR_DeltaDd(infile,d=NULL,ncode=3,nrepet=999)
print(d1)
```

COR_Fstd *Function for calculating pairwise Fst and correlation coefficient between Fst (Weir and Cockerham, 1984) and geographic distance*

Description

This function calculates pairwise genetic differentiation (Fst), as well as the correlation coefficient between genetic differentiation (Fst) and geographic distance.

Usage

```
COR_Fstd(x, d, ncode, nrepet)
```

Arguments

x	A genetic data files, here the format is genepop format.
d	Pairwise geographic distance for calculating correlations. If no actual geographic distance, d=NULL. The geographic distance should be a matrix that corresponds to the pairwise genetic differentiation matrix.
ncode	The code type of the genotype.
nrepet	Number of permutations.

Details

This function returns lists of pairwise Fst matrix, and a matrix of theoretical geographical distance if d is NULL, as well as the correlation coefficient.

Value

pwFst	The pairwise genetic differentiation (Fst) matrix.
COR_Fstd	Pearson correlation coefficient between genetic differentiation (Fst) and geographic distance.

Author(s)

qinxinghu@gmail.com

References

- Goudet, J. (2005). Hierfstat, a package for R to compute and test hierarchical F-statistics. *Molecular Ecology Notes*, 5(1), 184-186.
- Jombart, T. (2008). adegenet: a R package for the multivariate analysis of genetic markers. *Bioinformatics*, 24 (11), 1403-1405.
- Weir, B.S. (1996) *Genetic Data Analysis II*. Sinauer Associates.
- Weir B.S. and Cockerham C.C. (1984) Estimating F-Statistics for the Analysis of Population Structure. *Evolution* 38:1358

Evolution and the Genetics of Populations Volume 2: the Theory of Gene Frequencies, pg 294-295, S. Wright, Univ. of Chicago Press, Chicago, 1969.

See Also

COR_detaDd

Examples

```
# example genepop file, the example file is a complicated hierarchical island model
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
#d2=COR_Fstd(infile,d=NULL,ncode=3,nrepet=999)
#print(d2)
```

DeltaDcorplot

Plot correlation matrix for pairwise Delta D

Description

This function plots the pairwise genetic differentiation (Delta D).

Usage

```
DeltaDcorplot(x, ncode)
```

Arguments

x	The genetic data file, genepop format.
ncode	The coding type of the genetic data.

Details

This function returns the pairwise genetic differentiation (Delta D) plot.

Value

The result will return a genetic differentiation (Delta D) correlation plot.

Author(s)

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References

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

See Also

HierD; CorDdplot

Examples

```
# example genepop file
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
DeltaDcorplot(infile,ncode=3)
```

HierAr

Calculating hierarchical allelic richness

Description

This function calculates hierarchical allelic richness for populations structured in any hierarchy.

Usage

```
HierAr(x, nreg, r, ncode)
```

Arguments

x	The data file, genepop format.
nreg	Number of aggregate in your hierarchical structure.
r	The number of subaggregate in your hierarchical structure.
ncode	Coding type of genetic data.

Details

This function calculates the hierarchical allelic richness for metapopulations structured in any hierarchy. In this function, you can input your genepop file (x) and structure (nreg, r) of your data in the arguments, and then returns a matrix of your hierarchical Ar. This is very efficient than other functions.

Value

Ar_pop	Allelic richness for each population per locus
Hierareco	Total allelic richness
Ar_reg	Allelic richness for each aggregate (eg. region)
Hierar_loc	Allelic richness per locus for each aggregate (eg. region)
Ar_overall	Hierarchical allelic richness at different hierarchical levels

Author(s)

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References

- El Mousadik A. and Petit R.J. (1996) High level of genetic differentiation for allelic richness among populations of the argan tree *argania spinosa* skeys endemic to Morocco. *Theoretical and Applied Genetics*, 92:832-839
- Goudet, J. (2005). Hierfstat, a package for R to compute and test hierarchical F-statistics. *Molecular Ecology Notes*, 5(1), 184-186.

See Also

HierHe; HierFst; HierD

Examples

```
#we want to calculate the hierarchical allelic richness of
#16 populations structured in a 4 regions.
#Each region contains 7,4,2,3 populations.
# example genepop file
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
HAr=HierAr(infile, nreg=4, r=c(7,4,2,3), ncode=3)
HAr
```

HierD	<i>Function for calculating and decomposing genetic diversity (D, q=1) and differentiation (Delta D)</i>
-------	--

Description

This function calculates and decomposes genetic diversity (Hill number $q=1$) and differentiation (Delta D) (Oscar, E et al, 2018) into alpha, beta, gamma diversity, as well as Delta D2 and Delta D1 differentiation.

Usage

```
HierD(x, nreg, r, ncode)
```

Arguments

x	The genotypic data, genepop format
nreg	Number of aggregate in the hierarchical structure.
r	The number of subaggregate in the hierarchy.
ncode	Coding type of genetic data.

Details

This function calculates the hierarchical genetic differentiation (Delta D) for metapopulations structured in any hierarchy. In this function, you can input genepop file (x) and define structure (nreg, r) in the arguments, and then returns a list of your hierarchical genetic diversity and differentiation (Delta D). The result contains D_gamma, D_alpha.2, D_alpha.1, D_beta.2, D_beta.1, Differentiation.2, Differentiation.1, which corresponds to the diversity at different hierarchical levels.

Value

Dst Result returns to a list of hierarchical diversities (q=1) and genetic differentiations, including D_gamma (total diversity), D_alpha.2 (average total diversity between aggregates (eg. regions) within the ecosystem), D_alpha.1 (average diversity between subaggregates (eg.subpopulations)), D_beta.2 (number of aggregate equivalent), D_beta.1 (number of subaggregate equivalent), Differentiation.2 (genetic differentiation between aggregates), Differentiation.1 (genetic differentiation between subaggregates).

Author(s)

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References

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

See Also

HierAr; HierFst; HierHe

Examples

```
# example genepop file
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
hierD=HierD(infile,nreg=4,r=c(7,4,2,3),ncode=3)
print(hierD)
```

HierDjost

Hierarchical DJost

Description

This function partitions the DJost into hierarchical levels

Usage

```
HierDjost(x, nreg, r, ncode)
```

Arguments

x	Input file, genepop format
nreg	The number of aggregates
r	The number of subaggregates in each aggregates
ncode	The integer used to code an allele

Details

This function partitions genetic differentiation, DJost, into different hierarchical levels

Value

HierDjost_perloc	DJost per locus
HieDjost_overall	Overall DJost
pairDjostp	Pairwise DJost between subaggregates (populations)
pairDjostr	Pairwise DJost between aggregates (regions)

Author(s)

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References

Jost, L. O. U. (2008). GST and its relatives do not measure differentiation. *Molecular ecology*, 17(18), 4015-4026.

Examples

```
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
HierDjost_Island=HierDjost(infile,nreg=4,r=c(7,4,2,3),ncode=3)
print(HierDjost_Island)
```

HierFst *Function for calculating hierarchical genetic differentiation (Fst)*
(Weir B.S., 1996; Yang R.C.,1998)

Description

This function calculates hierarchical genetic differentiation (Fst) based on Weir B.S., 1996 and Yang R.C., 1998). The hierarchy that set in the input arguments (nreg, r) will automatically generate your hierarchical structure. Based on the parameters you set, the result returns to a F-statistics matrix displaying one level (rows) of Fst within a higher level hierarchy (columns).

Usage

```
HierFst(x, nreg, r, ncode)
```

Arguments

x	The name of the data file, or the string giving the path to the file. The file should be a genepop object, with the appropriate extension.
nreg	The number of aggregate in the hierarchy.
r	A vector specifying number of subaggregate (eg.subpopulations) within each aggregate.
ncode	An integer indicating the number of characters used to code an allele.

Details

This function was modified and improved from the `varcomp.glob` function from the `hierfstat` package (Jerome Goudet & Thibaut Jombart 2015). It was optimized to easily set the hierarchical structure while `varcom.glob` requires the structure data should be already correctly formatted in accordance with `hierfstat` data. In this function, you can input your genetic file (`x`) and set the structure (`nreg`, `r`) of your data in the arguments. The result will return a matrix of hierarchical Fst.

Value

The result returns a matrix of hierarchical F-statistics type-coefficients at different levels.

Note

Note that you should arrange your population in the order corresponding to your structure set in `nreg`.

Author(s)

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References

- Weir, B.S. (1996) Genetic Data Analysis II. Sinauer Associates.
- Yang, R.C. (1998). Estimating hierarchical F-statistics. *Evolution* 52 (4):950-956
- Goudet J. (2005). Hierfstat, a package for R to compute and test variance components and F-statistics. *Molecular Ecology Notes*. 5:184-186

See Also

HierAr

Examples

```
#
# example genepop file
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
hFst=HierFst(infile, nreg=4, r=c(7,4,2,3), ncode=3)
print(hFst)
```

 HierHe

Function for calculating hierarchical heterozygosity

Description

This function calculates and decomposes hierarchical heterozygosity into different levels. We can obtain allelic diversity (H_e) in any hierarchy.

Usage

```
HierHe(x, nreg, r, ncode)
```

Arguments

x	Genetic data, the format should be genepop file with proper extension.
nreg	Number of aggregate in the hierarchy.
r	The number of subaggregate in the hierarchy.
ncode	Coding type of genetic data, whether 3, or 2.

Details

In line with other genetic metrics, this function obtains hierarchical expected heterozygosity (H_e) for metapopulations. The result gives us hierarchical allelic diversity at different levels that you set in the input argument.

Value

HierHe_perloc	List of hierarchical allelic diversity (heterozygosity) at different levels per locus.
HierHr	Hierarchical allelic diversity (heterozygosity) at aggregate/regional levels.
Hrperloc	Hierarchical allelic diversity (heterozygosity) per locus at aggregate/regional levels.
HieHr_overall	Overall (mean) hierarchical allelic diversity (heterozygosity) at different levels.

Author(s)

qinxinghu@gmail.com

References

- Goudet, J. (2005). Hierfstat, a package for R to compute and test hierarchical F-statistics. *Molecular Ecology Notes*, 5(1), 184-186.
- Jombart, T. (2008). adegenet: a R package for the multivariate analysis of genetic markers. *Bioinformatics*, 24(11), 1403-1405.
- Nei, M. (1977). F-statistics and analysis of gene diversity in subdivided populations. *Annals of human genetics*, 41(2), 225-233.

See Also

HierAr, HierD, HierFst

Examples

```
# example genepop file
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
HiHe=HierHe(infile, nreg=4, r=c(7, 4, 2, 3), ncode=3)
print(HiHe)
```

HierJd

Hierarchical Jaccard dissimilarity

Description

This function calculates hierarchical genetic Jaccard dissimilarity

Usage

```
HierJd(f, ncode, nreg, r)
```

Arguments

f	Input file, genepop format
ncode	The integer used to code an allele
nreg	The number of aggregates (regions)
r	The number of subaggregates in each aggregate

Details

This function partitions genetic Jaccard dissimilarity into different hierarchical levels

Value

Jdpop	Jaccard dissimilarity between subaggregates
Jdr	Jaccard dissimilarity between aggregates
HierJd	The partitioning of Jaccard dissimilarity at different hierarchical levels

Author(s)

qinxinghu@gmail.com

References

Jaccard, P. (1901). Etude comparative de la distribution florale dans une portion des Alpes et des Jura. Bull Soc Vaudoise Sci Nat, 37, 547-579. Jaccard, P. (1912). The distribution of the flora in the alpine zone. 1. New phytologist, 11(2), 37-50.

Examples

```
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
HierJd_Island=HierJd(infile, nreg=4, r=c(7, 4, 2, 3), ncode=3)
print(HierJd_Island)
```

 Hierptest

Test the significance among aggregates (regions, ecosystems...)

Description

Permutation test of the significance among aggregates, e.g., test the significance of the allelic differentiation within ecosystem among different regions

Usage

```
Hierptest(f, ncode, level, permutations)
```

Arguments

f	Input file, genepop format
ncode	Genotype coding type, whether 2 digital or 3 digital
level	The hierarchical level you want to test
permutations	permutations

Value

perptest	Permutation test result for the level you specified
----------	---

Author(s)

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References

Anderson, M. J. (2014). Permutational multivariate analysis of variance (PERMANOVA). Wiley StatsRef: Statistics Reference Online, 1-15.

Examples

```
# example genepop file
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
region1=paste("region",rep(1,time=6))
region2=paste("region",rep(2,time=6))
region3=paste("region",rep(3,time=2))
region4=paste("region",rep(4,time=2))

level1=data.frame(matrix(data=0,nrow=16,ncol=1))
level1[1:6,1]=region1
level1[7:12,1]=region2
level1[13:14,1]=region3
level1[15:16,1]=region4
colnames(level1)=c("region")

hiertest=Hierpertest(infile,ncode=3,level1$region,permutations=999)
hiertest
```

IDIP

Function for decomposing diversity (genetic or species diversity) and differentiation into different hierarchical levels

Description

This function comes from Information-based Diversity Partitioning (Chao et al, 2017). It allows you to decompose diversity under a specified multi-level hierarchical structure.

Usage

```
IDIP(abun, struc)
```

Arguments

abun	The count or frequency data, raw or relative species/allele abundances.
struc	The hierarchial structure.

Details

This function is definitely an useful tool to do analysis of any information based diversity decomposition. Whether the data is genetic allele/species count/abundance or other frequency data in ecology, chemistry or economy.

Value

IDIP can be applied to any arbitrary number of hierarchical levels. The output consists of a basic data summary and decomposition results, with the latter including (1) gamma (or total) diversity; alpha and beta diversity at each level; (2) proportion of total beta information (Shannon information) found at each level; (3) mean differentiation (dissimilarity) among aggregates at each level (Chao et al, 2017).

Author(s)

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References

Chao, A., & Chiu, C. H. User's Guide for Online program iDIP (Information-based Diversity Partitioning).

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

Examples

```
str=Str(nreg=4,r=c(7,4,2,3),n=16)
abu=matrix(data=runif(16*3,min=0,max=1),nrow = 20,ncol = 16)
IDIP(abu,str)
```

Ldisper

Test significance of dispersion among subaggregate within aggregate

Description

Test significance of dispersion among subaggregate within aggregate. Here we used dispersion for testing the variance within the aggregate

Usage

```
Ldisper(f, ncode, group)
```

Arguments

f	genepop file
ncode	genotype coding type
group	the level of aggregate you want to test

Value

dispersion	Multivariate homogeneity of group dispersions
pertestdis	Permutation test of significance among groups(aggregate)

Author(s)

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References

- Anderson, M.J. (2006) Distance-based tests for homogeneity of multivariate dispersions. *Biometrics* 62, 245-253.
- Anderson, M.J., Ellingsen, K.E., McArdle, B.H. (2006) Multivariate dispersion as a measure of beta diversity. *Ecology Letters* 9, 683-693.
- ONeill, M.E. (2000) A Weighted Least Squares Approach to Levene's Test of Homogeneity of Variance. *Australian and New Zealand Journal of Statistics* 42, 8-100.

Examples

```
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
region1=paste("region",rep(1,time=6))
region2=paste("region",rep(2,time=6))
region3=paste("region",rep(3,time=2))
region4=paste("region",rep(4,time=2))

level1=data.frame(matrix(data=0,nrow=16,ncol=1))
level1[1:6,1]=region1
level1[7:12,1]=region2
level1[13:14,1]=region3
level1[15:16,1]=region4
colnames(level1)=c("region")

ldis=Ldisper(infile,ncode=3,group=level1$region)
ldis$dispersion
ldis$pertestdis
```

permutate.DeltaD *Permutation test for allelic differentiation (Delta D)*

Description

This function performs permutations for pairwise comparison of allelic differentiation.

Usage

```
permutate.DeltaD(file, ncode, permutations)
```

Arguments

file	Genepop file
ncode	Genotype coding
permutations	Number of permutations

Details

This function runs slowly because the permutations work on the random sampling of the individuals from raw data and calculating the statistics every iteration. The permutation test here shuffles the individuals and samples the individuals to calculate the Delta D every permutation. Significance of the allelic differentiation is obtained from Monte-Carlo test.

Value

pwDeltaD.obs The observed value of allelic differentiation Delta D
pwalltests The test results of pairwise Delta D

Author(s)

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References

Thioulouse, J., & Dray, S. (2007). Interactive multivariate data analysis in R with the ade4 and ade4TkGUI packages. *Journal of Statistical Software*, 22(5), 1-14.

Examples

```
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
permutate.DeltaD=function(infile, ncode=3, permutations=999)
```

plot.aggregates *Plot aggregates with dispersions (variances)*

Description

Plot the aggregates by groups

Usage

```
plot.aggregates(disper, hull = FALSE, ellipse = TRUE)
```

Arguments

disper The dispersion data
hull whether plot hull shape
ellipse whether plot ellipse by group

Examples

```
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
region1=paste("region",rep(1,time=6))
region2=paste("region",rep(2,time=6))
region3=paste("region",rep(3,time=2))
region4=paste("region",rep(4,time=2))

level1=data.frame(matrix(data=0,nrow=16,ncol=1))
level1[1:6,1]=region1
level1[7:12,1]=region2
level1[13:14,1]=region3
level1[15:16,1]=region4
colnames(level1)=c("region")

ldis=Ldisper(infile,ncode=3,group=level1$region)
plot(ldis$dispersion,hull=FALSE, ellipse=TRUE)
```

plotdiff1

Plot genetic differentiation (Delta D) across loci

Description

Plot genetic differentiation (Delta D, Gaggiotti OE, et al, 2018) across loci.

Usage

```
plotdiff1(x, ncode)
```

Arguments

x	Genetic data, should be genepop format
ncode	The coding type of your genetic data.

Details

Function generates two genetic differentiation (Delta D) plots, a box plot and a scatter plot

Author(s)

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References

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

See Also

DeltaDcorplot

Examples

```
##plot genetic differentiation across loci
# example genepop file
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
plotdiff1(infile,ncode=3)
```

plot_pcoa_aggregate *Draw the aggregation plot for allelic differentiation*

Description

Ordination plot of the allelic differentiation. Draw the aggregation groups according to the hierarchical level.

Usage

```
plot_pcoa_aggregate(f, ncode, level, label = TRUE)
```

Arguments

f	Input files, genepop format
ncode	Genotype coding type
level	Hierarchical level (group)
label	Whether lable the aggregates or not, TRUE or FALSE

Details

PcoA ordination plot of the allelic differentiation between aggregates. If there is distinguishable difference between aggregates, the plot identifies the different aggregations

Author(s)

qinxinghu@gmail.com

Examples

```
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
region1=paste("region",rep(1,time=6))
region2=paste("region",rep(2,time=6))
region3=paste("region",rep(3,time=2))
region4=paste("region",rep(4,time=2))
```

```

level1=data.frame(matrix(data=0,nrow=16,ncol=1))
level1[1:6,1]=region1
level1[7:12,1]=region2
level1[13:14,1]=region3
level1[15:16,1]=region4
colnames(level1)=c("region")
plot_pcoa_aggregate(infile, ncode=3, level=level1$region, label = TRUE)

```

```

print_boot_ppDeltaD    Print the bootstrapping result for pairwise allelic differentiation
                      (Delta D)

```

Description

Print the confidence interval of pairwise allelic differentiation (Delta D)

Usage

```
print_boot_ppDeltaD(x, ...)
```

Arguments

x boot.ppDeltaD object
 ...

Details

Print the bootstrapping result for pairwise allelic differentiation (Delta D)

Value

value print the confidence interval of the pairwise allelic differentiation

Examples

```

f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
boottest=boot.ppDeltaD(infile, ncode=3, nboot=999, quant = c(0.025, 0.975), diploid = TRUE)
print_boot_ppDeltaD(boottest)

```

pwag.permutest	<i>Permutation test for allelic differentiation (Delta D) among subaggregates within aggregate</i>
----------------	--

Description

This test examines the allelic differentiation (Delta D) among subaggregates within aggregate. The permutation works on the pairwise allelic differentiation between subaggregates within different aggregates.

Usage

```
pwag.permutest(f, ncode, group, permutations)
```

Arguments

f	Genepop file
ncode	The number coding genotypes
group	The group or level of the aggregates
permutations	Number of permutations

Value

pwpermutest.detail	Permutation test detail of the pairwise difference between aggregates
pwtest.aggregate	Pairwise permutation P-value between aggregates

Author(s)

qinxinghu@gmail.com

References

Anderson, M. J. (2014). Permutational multivariate analysis of variance (PERMANOVA). Wiley StatsRef: Statistics Reference Online, 1-15.

Examples

```
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
region1=paste("region", rep(1, time=6))
region2=paste("region", rep(2, time=6))
region3=paste("region", rep(3, time=2))
region4=paste("region", rep(4, time=2))

level1=data.frame(matrix(data=0, nrow=16, ncol=1))
level1[1:6,1]=region1
```

```

level1[7:12,1]=region2
level1[13:14,1]=region3
level1[15:16,1]=region4
colnames(level1)=c("region")
pwag.permutest(infile, ncode=3, group=level1$region, permutations=999)

```

pwDeltaD

Pairwise Shannon differentiation (Delta D)

Description

Estimating pairwise Shannon differentiation (Delta D)

Usage

```
pwDeltaD(x, para)
```

Arguments

x	Input file, data matrix or data frame
para	Indicating whether using parallel process

Details

Calculating pairwise Shannon differentiation, Delta D (Gaggiotti, O. E., et al, 2018).

Value

PairwiseDeltaD Pairwise Delta D

Note

Note that for windows system, the parallel doesn't work for multiple cores. In that case, users should set para=FALSE.

Author(s)

qinxinghu@gmail.com

References

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary applications*, 11(7), 1176-1193.

Examples

```
### Users can test the example in their own computer,
###as this is pairwise differentiation, using parallel
# will save more time
#f <- system.file('extdata',package='HierDpart')
#infile <- file.path(f, "Island.gen")
#library(adegenet)
#Islandfile=read.genepop(infile,ncode=3)
#Islandfreq=tab(Islandfile,freq=TRUE)
#IslandpD=pwDeltaD(Islandfreq,para=FALSE)
#print(IslandpD)
```

qD

Function for calculating genetic diversity profile (q=0,1,2)

Description

This function calculates genetic diversity profile (q=0, 1, 2).

Usage

```
qD(x, q, ncode)
```

Arguments

x	Input data, genepop format.
q	Hill numbers, q=0,1,2.
ncode	The coding type of the genetic file.

Details

This function returns different genetic diversities, q is the order of Hill number, specifically, richness (q=0), exponential Shannon entropy (q=1), and heterozygosity related measure (q=2, $^2D=1/(1-He)$).

Value

Result returns to the diversity profile (q) as you defined.

Author(s)

qinxinghu@gmail.com

References

Marcon, E., & Herault, B. (2015). entropart: An R package to measure and partition diversity. *Journal of Statistical Software*, 67(8).

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

Examples

```
# example genepop file
f <- system.file('extdata',package='HierDpart')
infile <- file.path(f, "Island.gen")
qD(infile,q=0,ncode=3)
```

qDplot

Plot the genetic diversity profiles (q=0,1,2)

Description

This function calculates the diversity profiles and generates a line plot. You can get either one of the diversity index plot, richness (q=0), exponential Shannon entropy (q=1), and heterozygosity related measure of diversity (q=2), or all of them.

Usage

```
qDplot(x, q, ncode)
```

Arguments

x	The input genetic files, genepop format
q	The order of Hill numbers, q =0,1,2, or "all".If q= "all", this will return plot including three diversities.
ncode	The coding type of your data.

Details

Result returns a diversity plot.

Author(s)

qinxinghu@gmail.com

References

Marcon, E., & Herault, B. (2015). entropart: An R package to measure and partition diversity. *Journal of Statistical Software*, 67(8).

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*.

See Also

qD

Examples

```
# example genepop file
f <- system.file('extdata', package='HierDpart')
infile <- file.path(f, "Island.gen")
# plot allelic richness
qDplot(infile, q=0, ncode=3)
#plot all three diversity profiles
qDplot(infile, q="all", ncode=3)
```

Str

Function for generating the structure for HierDpart format

Description

This function allows you to easily and automatically generate the hierarchical structure for your data. The structure files are HierDpart format working for function IDIP which is easy to construct by defining your aggregates and total number of subaggregate.

Usage

```
Str(nreg, r, n)
```

Arguments

nreg	The number of aggregates in your hierarchy.
r	A vector specifying number of populations or subpopulations within each aggregate.
n	An integer indicating the number of subaggregate.

Details

This function is designed to fit the input format for function IDIP (Chao et al, 2017). It is more easy to understand and set the hierarchical structure using this function.

Value

A matrix that displays your hierarchical structure.

Author(s)

qinxinghu@gmail.com

References

Gaggiotti, O. E., Chao, A., Peres-Neto, P., Chiu, C. H., Edwards, C., Fortin, M. J., ... & Selkoe, K. A. (2018). Diversity from genes to ecosystems: A unifying framework to study variation across biological metrics and scales. *Evolutionary Applications*. Chao, A., & Chiu, C. H. (2017). User's Guide for Online program iDIP (Information-based Diversity Partitioning).

See Also

IDIP

Examples

```
#assume we are working on a metacommunity contains 16 communities,  
#there are 4 aggregates in this metacommunity, and each aggregates  
#contains 7, 4,3,2 subaggregates or communities.The structure will be:  
str1=Str(nreg=4, r=c(7,4,3,2),n=16)
```

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