Package 'mmod'

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Title Modern measures of population divergence

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Depends R (>= 2.6.0), adegenet

ZipData no

Description mmod provides functions for measuring population divergence from genotypic data

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URL https://github.com/dwinter [update!]

Collate 'diff_stats.R' 'D_Jost.R' 'Gst_Hedrick.R' 'Gst_Nei.R'
'harmonic_mean.R' 'jacknife_pop.R' 'pairwise_D.R'
'pairwise_Gst_Hedrick.R' 'pairwise_Gst_Nei.R' 'help.R' 'diff_test.R'

R topics documented:

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diff_stats   *Calculate differentiation statistics for a genind objects*

Description

This function calculates three different statistics of differentiaion for a genetic dataset. Nei's Gst, Hedrick's G'st and Jost's D

Usage

```
diff_stats(x)
```

Arguments

x   genind object (from package adegenet)

Details

See individual functions D_Jost(), Gst_Hedrick() and Gst_Nei() for more details

References

Jost, L. (2008), GST and its relatives do not measure differentiation. Molecular Ecology, 17: 4015-4026.

Examples

```
data(nancycats)
diff_stats(nancycats)
```

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diff_test   *An exact test of population differntiation for Genind objects*

Description

This function performs and exact test of population differentiation based on allele frequencies in sub-population.

Usage

```
diff_test(x, sim = TRUE, nreps = 10000)
```

Arguments

x   genind object (from package adegenet)

sim   simulate p-value (required for all but the smallest datasets)

nreps   number of steps used to simulate p-value (default 1000)

Details

Note, this test returns a p-value _not_ an estimate of effect size. Since most populations have some degree of population differentiation, very large samples are almost guaranteed to return signifcant results. Refer to estimates of D or Gst to ascertain how meaningful such results might be.

Examples

```
data(nancycats)
diff_test(nancycats, nreps=100)
```

D_Jost   *Calculate Jost's D*

Description

This function calculates Jost's D from a genind object

Usage

```
D_Jost(x)
```

Arguments

x   genind object (from package adegenet)

Details

Takes a genind object with population information and calculates Jost's D Returns a list with values for each locus as well as two global estimates. 'global.het' uses the average haves of Hs and Ht across all loci while 'global.harm_mean' takes the harmonic mean of all loci.

Because estimators of Hs and Ht are used, its possible to have negative estimates of D. You should treat these as numbers close to zero.

References

Jost, L. (2008), GST and its relatives do not measure differentiation. Molecular Ecology, 17: 4015-4026.

Examples

```
data(nancycats)
D_Jost(nancycats)
```

Gst_Hedrick   *Calculate Nei's Gst using estimators for Hs and Ht*

Description

This function calculates Hedrick's G'st from a genind object

Usage

```
Gst_Hedrick(x)
```

Arguments

x   genind object (from package adegenet)

Details

Takes a genind object with population information and calculates Hedrick's G'st. This Returns a list with values for each locus as well as a global estimates

Because estimators of Hs and Ht are used, it's possible to have negative estimates of Gst. You should treat such results as zeros (or estimating a value close to zero, and getting it a little wrong)

Examples

```
data(nancycats)
Gst_Hedrick(nancycats)
```

Gst_Nei   *Calculate Nei's Gst using estimators for Hs and Ht*

Description

This function calculates Gst following Nei's method and using Nei and Chesser's estimators for Hs and Ht

Usage

```
Gst_Nei(x)
```

Arguments

x   genind object (from package adegenet)

Examples

```
data(nancycats)
Gst_Nei(nancycats)
```

`harmonic_mean`   *Harmonic mean*

Description

Calculate the harmonic mean of a numeric vector

Usage

```
harmonic_mean(x)
```

Arguments

x   numeric vector

Examples

```
data(nancycats)
pop.sizes <- table(pop(nancycats))
harmonic_mean(pop.sizes)
```

`jacknife_populations`
                    Calculate differentiation stats for a jacknife sample of a Genind opject

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Description

Makes a series of jacknife samples across populations from a Genind object

Usage

```
jacknife_populations(x, sample_frac = 0.5, nreps = 1000)
```

Arguments

x   genind object (from package adegenet)

sample_frac   fraction of pops to sample in each replication (default 0.5)

nreps   number of jacknife replicates to run (default 1000)

Examples

```
## Not run:
data(nancycats)
obs <- diff_stats(nancycats)
jn <- jacknife_populations(nancycats)
D_sampled <-jn[5,]
hist(D_sampled)
abline(h=obs$global)

## End(Not run)
```

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mmod   *Modern Measures of Divergence*

Description

Population geneticists have traditionally used Nei's Gst (often confusingly called Fst...) to measure divergence between populations. It turns out, Gst doesn't really measure divergence so, a set of new measures have been developed.

Details

mmod is a package that brings two of these mesures, Hedricks (2008) G'st and Jost's (2008) D to R, along wiht an implementation of Nei's Gst that uses nearly unbiased estimators for Hs and Ht, the two key paramaters from which all these stats are calculated. All these functions work on genind objects from the libary adegenet so data can be read in from standard genepop files.

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pairwise_D   *Calculates pairwise values of Jost's D*

Description

This function calculates Jost's D, a measure of genetic differentiation, between all combinations of populaitons in a genind object.

Usage

```
pairwise_D(x)
```

Arguments

x   genind object (from package adegenet)

Examples

```
data(nancycats)
pairwise_D(nancycats[1:26,])
```

```
pairwise_Gst_Hedrick
```
Calculates pairwise values of Hedrick's G'st

Description

This function calculates Hedrick's G'st, a measure of genetic differentiation, between all combinations of populaitons in a genind object.

Usage

```
pairwise_Gst_Hedrick(x)
```

Arguments

x   genind object (from package adegenet)

Examples

```
data(nancycats)
pairwise_Gst_Hedrick(nancycats[1:26,])
```

```
pairwise_Gst_Nei
```
Calculates pairwise values of Nei's Gst

Description

This function calculates Nei's Gst, a measure of genetic differentiation, between all combinations of populaitons in a genind object.

Usage

```
pairwise_Gst_Nei(x)
```

Arguments

x   genind object (from package adegenet)

Examples

```
data(nancycats)
pairwise_Gst_Nei(nancycats[1:26,])
```

Index