

# 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

**License** MIT

**URL** <https://github.com/dwinter/mmod>

**Collate** 'diff\_stats.R' 'D\_Jost.R' 'Gst\_Hedrick.R' 'Gst\_Nei.R'  
'harmonic\_mean.R' 'jackknife\_pop.R' 'pairwise\_D.R'  
'pairwise\_Gst\_Hedrick.R' 'pairwise\_Gst\_Nei.R' 'help.R' 'diff\_test.R'

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`diff_stats`*Calculate differentiation statistics for a genind objects*

---

## Description

This function calculates three different statistics of differentiation for a genetic dataset. Nei's G<sub>st</sub>, Hedrick's G'<sub>st</sub> 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

Hedrick, PW. (2005), A Standardized Genetic Differentiation Measure. *Evolution* 59: 1633-1638.

Jost, L. (2008), G<sub>ST</sub> and its relatives do not measure differentiation. *Molecular Ecology*, 17: 4015-4026.

Nei M. (1973) Analysis of gene diversity in subdivided populations. *PNAS*: 3321-3323.

Nei M, Chesser RK. (1983). Estimation of fixation indices and gene diversities. *Annals of Human Genetics*. 47: 253-259.

## See Also

Other diffstat: [D\\_Jost](#), [Gst\\_Hedrick](#), [Gst\\_Nei](#)

## Examples

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

---

diff\_test*An exact test of population differentiation for Genind objects*

---

### Description

This function uses Fisher's exact test to determine if alleles in sub-populations are drawn randomly from a larger population (i.e. a significance test for allelic differentiation among sub-populations).

### 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 p-values for each locus in a dataset `_not_` estimates of effect size. Since most populations have some degree of population differentiation, very large samples are almost guaranteed to return significant results. Refer to estimates of D or G<sub>st</sub> to ascertain how meaningful such results might be.

### See Also

[fisher.test](#) which this function wraps

### Examples

```
data(nancycats)
diff_test(seploc(nancycats)[[2]], 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 averages 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.

**See Also**

Other D: [pairwise\\_D](#)

Other diffstat: [diff\\_stats](#), [Gst\\_Hedrick](#), [Gst\\_Nei](#)

**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)

## References

Hedrick, PW. (2005), A Standardized Genetic Differentiation Measure. *Evolution* 59: 1633-1638.

## See Also

Other diffstat: [diff\\_stats](#), [D\\_Jost](#), [Gst\\_Nei](#)

Other Hedrick: [pairwise\\_Gst\\_Hedrick](#)

## 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)

## References

Nei M. (1973) Analysis of gene diversity in subdivided populations. *PNAS*: 3321-3323.

Nei M, Chesser RK. (1983). Estimation of fixation indices and gene diversities. *Annals of Human Genetics*. 47: 253-259.

## See Also

Other diffstat: [diff\\_stats](#), [D\\_Jost](#), [Gst\\_Hedrick](#)

Other Nei: [pairwise\\_Gst\\_Nei](#)

## Examples

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

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harmonic_mean	<i>Harmonic mean</i>
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### Description

Calculate the harmonic mean of a numeric vector (will return NA if there are any negative numbers in the vector)

### Usage

```
harmonic_mean(x)
```

### Arguments

x	numeric vector
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### Examples

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

---

jackknife_populations	<i>Calculate differentiation stats for a jackknife sample of a Genind object</i>
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---

### Description

Makes a series of jackknife samples across populations from a Genind object and calculates differentiation stats for each sample.

### Usage

```
jackknife_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 jackknife replicates to run (default 1000)

## Examples

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

## End(Not run)
```

---

mmod

*Modern Measures of Divergence*


---

## Description

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

## Details

mmod is a package that brings two of these measures, Hedricks (2008)  $G_{ST}$  and Jost's (2008)  $D$  to R, along with an implementation of Nei's  $G_{ST}$  that uses nearly unbiased estimators for  $H_s$  and  $H_t$ , the two key parameters from which all these stats are calculated. All these functions work on `genind` objects from the library `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 populations in a `genind` object.

## Usage

```
pairwise_D(x)
```

## Arguments

`x` `genind` object (from package `adegenet`)

## References

Jost, L. (2008),  $G_{ST}$  and its relatives do not measure differentiation. *Molecular Ecology*, 17: 4015-4026.

**See Also**

Other D: [D\\_Jost](#)

Other pairwise: [pairwise\\_Gst\\_Hedrick](#), [pairwise\\_Gst\\_Nei](#)

**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 populations in a `genind` object.

**Usage**

```
pairwise_Gst_Hedrick(x)
```

**Arguments**

`x`                      `genind` object (from package `adegenet`)

**References**

Hedrick, PW. (2005), A Standardized Genetic Differentiation Measure. *Evolution* 59: 1633-1638.

**See Also**

Other Hedrick: [Gst\\_Hedrick](#)

Other pairwise: [pairwise\\_D](#), [pairwise\\_Gst\\_Nei](#)

**Examples**

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



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pairwise_Gst_Nei	<i>Calculates pairwise values of Nei's G<sub>st</sub></i>
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**Description**

This function calculates Nei's  $G_{st}$ , a measure of genetic differentiation, between all combinations of populations in a `genind` object.

**Usage**

```
pairwise_Gst_Nei(x)
```

**Arguments**

x	genind object (from package <code>adegenet</code> )
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**References**

Nei M. (1973) Analysis of gene diversity in subdivided populations. *PNAS*: 3321-3323.

Nei M, Chesser RK. (1983). Estimation of fixation indices and gene diversities. *Annals of Human Genetics*. 47: 253-259.

**See Also**

Other Nei: [Gst\\_Nei](#)

Other pairwise: [pairwise\\_D](#), [pairwise\\_Gst\\_Hedrick](#)

**Examples**

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

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