

# Package ‘genepop’

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**Type** Package

**Title** Population Genetic Data Analysis Using Genepop

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**Description** Makes the Genepop software available in R. This software implements a mixture of traditional population genetic methods and some more focused developments: it computes exact tests for Hardy-Weinberg equilibrium, for population differentiation and for genotypic disequilibrium among pairs of loci; it computes estimates of F-statistics, null allele frequencies, allele size-based statistics for microsatellites, etc.; and it performs analyses of isolation by distance from pairwise comparisons of individuals or population samples.

**License** CeCILL-2

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<https://gitlab.mbb.univ-montp2.fr/francois/genepop>

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genepop-package

*Population genetic analyses using the Genepop software*

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## Description

A distribution of the Genepop software as an R package. The included C++ sources are suitable for compilation as a stand-alone executable. A shiny interface is also included. Genepop performs three main tasks: it computes **exact tests** for Hardy-Weinberg equilibrium ([test\\_HW](#)), for population differentiation ([test\\_diff](#)) and for genotypic disequilibrium among pairs of loci ([test\\_LD](#)); it computes **estimates** of F-statistics ([Fst](#)), null allele frequencies ([nulls](#)), allele size-based statistics for microsatellites, etc., and of number of immigrants by Barton & Slatkin's (1986) private allele method ([Nm\\_private](#)); It performs analyses of **isolation by distance** from pairwise comparisons of individuals or groups ([ibd](#)), including confidence intervals for "neighborhood size". It also provides various data [conversion](#) and [manipulation](#) utilities.

## Author(s)

R package originally developed by Jimmy Lopez and Khalid Belkhir from the C++ sources of the Genepop executable version 4.6 (2016; Rousset 2008).

## References

### Main reference for current maintained version of Genepop:

Rousset, F. (2008). Genepop'007: a complete reimplementation of the Genepop software for Windows and Linux. *Mol. Ecol. Res.* 8: 103-106.

Original Genepop publication:

Raymond, M. & Rousset, F., 1995b. GENEPOP Version 1.2: population genetics software for exact tests and ecumenicism. *J. Hered.* 86: 248-249.

Methods implemented in Genepop:

Barton, N. H. & Slatkin, M., 1986. A quasi-equilibrium theory of the distribution of rare alleles in a subdivided population. *Heredity* 56: 409-415.

Brookfield, J. F. Y., 1996. A simple new method for estimating null allele frequency from heterozygote deficiency. *Mol. Ecol.* 5: 453-455.

Goudet, J., Raymond, M., de Meeus, T. & Rousset, F., 1996. Testing differentiation in diploid populations. *Genetics* 144: 1931-1938.

Guo, S. W. & Thompson, E. A., 1992. Performing the exact test of Hardy-Weinberg proportion for multiple alleles. *Biometrics* 48: 361-372.

Kalinowski, S. T. & Taper, M. L., 2006. Maximum likelihood estimation of the frequency of null alleles at microsatellite loci. *Conserv. Genetics* 7:991-995.

Louis, E. J. & Dempster, E. R., 1987. An exact test for Hardy-Weinberg and multiple alleles. *Biometrics* 43: 805-811.

Mantel, N., 1967. The detection of disease clustering and a generalized regression approach. *Cancer Research* 27: 209-220.

Michalakis, Y. & Excoffier, L., 1996. A generic estimation of population subdivision using distances between alleles with special interest to microsatellite loci. *Genetics* 142: 1061-1064.

Raymond, M. & Rousset, F., 1995a. An exact test for population differentiation. *Evolution* 49: 1283-1286.

Robertson, A. & Hill, W. G., 1984. Deviations from Hardy-Weinberg proportions: sampling variances and use in estimation of inbreeding coefficients. *Genetics* 107: 703-718.

Rousset, F., 1996. Equilibrium values of measures of population subdivision for stepwise mutation processes. *Genetics* 142: 1357-1362.

Rousset, F., 1997. Genetic differentiation and estimation of gene flow from F-statistics under isolation by distance. *Genetics* 145: 1219-1228.

Rousset, F., 2000. Genetic differentiation between individuals. *J. Evol. Biol.* 13:58-62.

Rousset, F. & Raymond, M., 1995. Testing heterozygote excess and deficiency. *Genetics* 140: 1413-1419.

Watts, P. C., Rousset, F., Saccheri, I. J., Leblois, R., Kemp, S. J. & Thompson, D. J., 2007. Compatible genetic and ecological estimates of dispersal rates in insect (*Coenagrion mercuriale*: Odonata: Zygoptera) populations: analysis of 'neighbourhood size' using a more precise estimator. *Mol. Ecol.* 16: 737-751.

Weir, B. S., 1996. *Genetic Data Analysis II*. Sinauer, Sunderland, Mass.

Weir, B. S. & Cockerham, C. C., 1984. Estimating F-statistics for the analysis of population structure. *Evolution* 38: 1358-1370.

---

|            |                                        |
|------------|----------------------------------------|
| basic_info | <i>Allele and genotype frequencies</i> |
|------------|----------------------------------------|

---

### Description

Allele and genotype frequencies per locus and per sample. See [this section](#) of the Genepop executable documentation for more information on the statistical methods.

### Usage

```
basic_info(inputFile, outputFile = "", verbose = interactive())
```

### Arguments

|            |                                               |
|------------|-----------------------------------------------|
| inputFile  | The path of the input file, in Genepop format |
| outputFile | character: The path of the output file        |
| verbose    | logical: whether to print some information    |

### Value

The path of the output file is returned invisibly.

### Examples

```
locinfile <- genepopExample('sample.txt')
basic_info(locinfile, 'sample.txt.INF')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
```

---

|               |                                          |
|---------------|------------------------------------------|
| clean_workdir | <i>Removing files created by Genepop</i> |
|---------------|------------------------------------------|

---

### Description

This removes “temporary files” created by Genepop, but also output files, so it should be used only when one no longer needs the latter files. This function assumes that the input file name contains only alphanumeric, dot, or underscore characters.

### Usage

```
clean_workdir(
  otherfiles = NULL,
  path = ".",
  suffixes = c("GRA", "ISO", "MIG", "PRI", "DAT", "DG", "DIV", "D", "DIS", "FST", "NUL",
    "RHO", "2G2", "G", "GE", "GE2", "INF", "MSD", "TAB", "ST2"),
  in. = TRUE,
  cmdline = TRUE
)
```

**Arguments**

|            |                                                                                                                                                                                                              |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| otherfiles | Character vector(s): one or more names of files to be removed and not matched by the other arguments (such as the input file, or some output files not identified by their suffix, as shown in the Example). |
| path       | character vector: path from where files should be removed.                                                                                                                                                   |
| suffixes   | Character vector(s): suffixes of files to be removed (useful for output files with readily identifiable suffixes).                                                                                           |
| in.        | boolean: whether to remove the fichier.in file created by Genepop.                                                                                                                                           |
| cmdline    | boolean: whether to remove the cmdline.txt file created by Genepop.                                                                                                                                          |

**Examples**

```
# Removing files possibly written by other examples in the documentation:
clean_workdir(otherfiles=c("sample.txt", "Dsample.txt", "w2.txt",
"PEL1600withCoord.txt", "Rhesus.txt", "structest.txt"))
```

---

|                  |                                                 |
|------------------|-------------------------------------------------|
| Contingency-test | <i>Exact test on a single contingency table</i> |
|------------------|-------------------------------------------------|

---

**Description**

Performs an exact conditional contingency-table test. There are many other ways of doing this in R but this function replicates the functionality of earlier genepop code analysing a contingency table provided in a file with ad hoc format. See [this section](#) of the Genepop executable documentation for more information on the statistical methods.

**Usage**

```
struc(
  inputFile,
  settingsFile = "",
  dememorization = 10000,
  batches = 100,
  iterations = 5000,
  verbose = interactive()
)
```

**Arguments**

|                |                                                                                |
|----------------|--------------------------------------------------------------------------------|
| inputFile      | character: The path of the input file. This file should be in an ad hoc format |
| settingsFile   | character: The path of the settings file                                       |
| dememorization | integer: length of dememorization step of Markov chain algorithm               |
| batches        | integer: Number of batches                                                     |
| iterations     | integer: Iterations per batch                                                  |
| verbose        | logical: whether to print some information                                     |

**Value**

The path of the output file is returned invisibly.

**Examples**

```
locinfile <- genepopExample('structest.txt')
struc(locinfile)
if ( ! interactive()) clean_workdir(otherfiles='structest.txt')
```

---

|            |                         |
|------------|-------------------------|
| conversion | <i>File conversions</i> |
|------------|-------------------------|

---

**Description**

Converts input files from genepop format to some other formats (some maybe only of historical interest): Fstat, two Biosys formats. and linkdos. See [this section](#) of the Genepop executable documentation for more information on the statistical methods.

**Usage**

```
conversion(inputFile, format, outputFile = "", verbose = interactive())
```

**Arguments**

|            |                                                                              |
|------------|------------------------------------------------------------------------------|
| inputFile  | The path of the input file, in Genepop format                                |
| format     | Character string: must be one of 'Fstat', 'BiosysL', 'BiosysN', or 'Linkdos' |
| outputFile | character: The path of the output file                                       |
| verbose    | logical: whether to print some information                                   |

**Value**

The path of the output file is returned invisibly.

**Examples**

```
locinfile <- genepopExample('sample.txt')
conversion(locinfile, format='Fstat', 'sample.txt.DAT')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
```

---

|                 |                                                     |
|-----------------|-----------------------------------------------------|
| Differentiation | <i>Tests of genic and genotypic differentiation</i> |
|-----------------|-----------------------------------------------------|

---

**Description**

Exact conditional contingency-table tests for genic or genotypic differentiation. A single test for all populations, or distinct tests for all pairs of populations, may be computed. See [this section](#) of the Genepop executable documentation for more information on the statistical methods.

**Usage**

```
test_diff(
  inputFile,
  genic = TRUE,
  pairs = FALSE,
  outputFile = "",
  settingsFile = "",
  dememorization = 10000,
  batches = 100,
  iterations = 5000,
  verbose = interactive()
)
```

**Arguments**

|                |                                                                                                             |
|----------------|-------------------------------------------------------------------------------------------------------------|
| inputFile      | The path of the input file, in Genepop format                                                               |
| genic          | logical: whether to perform genic or genotypic tests                                                        |
| pairs          | logical: whether to test differentiation between all pairs of ppulation, or to perform a single global test |
| outputFile     | character: The path of the output file                                                                      |
| settingsFile   | character: The path of the settings file                                                                    |
| dememorization | integer: length of dememorization step of Markov chain algorithm                                            |
| batches        | integer: Number of batches                                                                                  |
| iterations     | integer: Iterations per batch                                                                               |
| verbose        | logical: whether to print some information                                                                  |

**Value**

The path of the output file is returned invisibly.

**Examples**

```
locinfile <- genepopExample('sample.txt')
test_diff(locinfile,outputFile='sample.txt.GE')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
```

Fst

*Fst (or rho\_ST) estimation***Description**

Evaluates Fst or related measures based on allele sizes, for all populations or for all pairs of populations. See [this section](#) of the Genepop executable documentation for more information on the statistical methods.

**Usage**

```
Fst(
  inputFile,
  sizes = FALSE,
  pairs = FALSE,
  outputFile = "",
  dataType = "Diploid",
  verbose = interactive()
)
```

**Arguments**

|            |                                                                                                                           |
|------------|---------------------------------------------------------------------------------------------------------------------------|
| inputFile  | The path of the input file, in Genepop format                                                                             |
| sizes      | logical: whether to estimate allele-size based statistics, or identity-based Fst                                          |
| pairs      | whether to estimate differentiation between all pairs of populations, or to compute a global estimate for all populations |
| outputFile | character: The path of the output file                                                                                    |
| dataType   | character: The haploid and diploid data                                                                                   |
| verbose    | logical: whether to print some information                                                                                |

**Value**

The path of the output file is returned invisibly.

**Examples**

```
locinfile <- genepopExample('sample.txt')
Fst(locinfile, outputFile= 'sample.txt.DIV')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
```

---

|            |                                             |
|------------|---------------------------------------------|
| genedivFis | <i>Gene diversities and Fis (or rho_IS)</i> |
|------------|---------------------------------------------|

---

## Description

Evaluates Fis and gene diversities, or related measures based on allele sizes. See [this section](#) of the Genepop executable documentation for more information on the identity-based statistical methods, and [this one](#) for allele-size based ones.

## Usage

```
genedivFis(  
  inputFile,  
  sizes = FALSE,  
  outputFile = "",  
  dataType = "Diploid",  
  verbose = interactive()  
)
```

## Arguments

|            |                                                                      |
|------------|----------------------------------------------------------------------|
| inputFile  | The path of the input file, in Genepop format                        |
| sizes      | logical: whether to compute statistics based on allele size, or not. |
| outputFile | character: The path of the output file                               |
| dataType   | character: The haploid and diploid data                              |
| verbose    | logical: whether to print some information                           |

## Value

The path of the output file is returned invisibly.

## Examples

```
locinfile <- genepopExample('sample.txt')  
genedivFis(locinfile,outputFile = 'sample.txt.DIV')  
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
```

---

|                |                                                                   |
|----------------|-------------------------------------------------------------------|
| genepopExample | <i>Copy an example file from the Genepop package distribution</i> |
|----------------|-------------------------------------------------------------------|

---

**Description**

This function is used to copy an example file to the user's directory. It should not be used when analysing one's own data!

**Usage**

```
genepopExample(filename)
```

**Arguments**

|          |                                                            |
|----------|------------------------------------------------------------|
| filename | The name of an example file from the Genepop distribution. |
|----------|------------------------------------------------------------|

**Value**

Returns the filename

---

|     |                                             |
|-----|---------------------------------------------|
| GUI | <i>Call an experimental GUI for Genepop</i> |
|-----|---------------------------------------------|

---

**Description**

Call an experimental GUI for Genepop

**Usage**

```
GUI()
```

**Value**

The return value of a 'shiny::runApp()' call.

Hardy-Weinberg

*Tests of Hardy-Weinberg genotypic proportions***Description**

Compute variants of the exact conditional test for Hardy-Weinberg genotypic proportions. The tests differ by their test statistics. `HWtable_analysis` handles a single table of genotype counts, and `test_HW` requires a standard genepop input file. See [this section](#) of the Genepop-executable documentation for more information on the statistical methods.

**Usage**

```
test_HW(
  inputFile,
  which = "Proba",
  outputFile = "",
  settingsFile = "",
  enumeration = FALSE,
  dememorization = 10000,
  batches = 20,
  iterations = 5000,
  verbose = interactive()
)

HWtable_analysis(
  inputFile,
  which = "Proba",
  settingsFile = "",
  enumeration = FALSE,
  dememorization = 10000,
  batches = 20,
  iterations = 5000,
  verbose = interactive()
)
```

**Arguments**

|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>inputFile</code> | character: The path of the input file. For <code>test_HW</code> , this file should be in Genepop format. For <code>HWtable_analysis</code> , it should be in ad hoc format illustrated by sample file <code>Rhesus.txt</code> used in the Examples section, and further detailed in <a href="#">this section</a> of the Genepop-executable documentation.                                                                                         |
| <code>which</code>     | character: 'Proba', 'excess', and 'deficit' to perform the probability test, score test for excess, and score tests for deficit, respectively, in each population and for each locus. <code>test_HW</code> additionally handles 'global excess' and 'global deficit' for global tests for all loci and/or all populations, and <code>HWtable_analysis</code> additionally handles 'Fis' to report basic information (allele frequencies and Fis). |

|                |                                                                                                |
|----------------|------------------------------------------------------------------------------------------------|
| outputFile     | character: The path of the output file                                                         |
| settingsFile   | character: The path of the settings file                                                       |
| enumeration    | logical: whether to compute the complete enumeration test for samples with less than 5 alleles |
| dememorization | integer: length of dememorization step of Markov chain algorithm                               |
| batches        | integer: Number of batches                                                                     |
| iterations     | integer: Iterations per batch                                                                  |
| verbose        | logical: whether to print some information                                                     |

### Value

The path of the output file is returned invisibly.

### Examples

```
locinfile <- genepopExample('sample.txt')
test_HW(locinfile, which='deficit', 'sample.txt.D')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
# Example in Guo & Thompson 1992 Table 5
locinfile <- genepopExample('Rhesus.txt')
outfile <- HWtable_analysis(locinfile,which='Proba',batches = 1000,iterations = 1000)
readLines(outfile)[21]
#clean_workdir(otherfiles='Rhesus.txt')
```

---

IBD

---

*Isolation by distance*


---

### Description

Estimates isolation by distance by regression of genetic distance to geographical distance. See [this section](#) of the Genepop executable documentation for more information on individual-based analyses and [this one](#) for group-based analyses.

### Usage

```
ibd(
  inputFile,
  outputFile = "",
  settingsFile = "",
  dataType = "Diploid",
  statistic = "F/(1-F)",
  geographicScale = "2D",
  CIconvergence = 0.95,
  testPoint = 0,
  minimalDistance = 1e-04,
  maximalDistance = 1e+09,
```

```

mantelPermutations = 1000,
mantelRankTest = FALSE,
bootstrapMethod = "ABC",
bootstrapNsim = 999,
verbose = interactive()
)

```

### Arguments

|                    |                                                                                                                                                                                                     |
|--------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| inputFile          | The path of the input file, in Genepop format                                                                                                                                                       |
| outputFile         | character: The path of the output file                                                                                                                                                              |
| settingsFile       | character: The path of the settings file                                                                                                                                                            |
| dataType           | character: 'haploid' or 'diploid'                                                                                                                                                                   |
| statistic          | character: The pairwise genetic distance, either 'a' or 'e' for diploid individual data, 'a-like' for haploid individual data, and 'F/(1-F)' or 'SingleGeneDiv' for group data (haploid or diploid) |
| geographicScale    | character: gives either the scale transformation 'Log' or 'Linear' for geographic distances, or the shape of the habitat '2D' or '1D'                                                               |
| CIcoverage         | numeric: The coverage probability of confidence intervals                                                                                                                                           |
| testPoint          | numeric: Given value of the slope to be tested                                                                                                                                                      |
| minimalDistance    | numeric: The minimal geographic distance                                                                                                                                                            |
| maximalDistance    | numeric: The maximal geographic distance                                                                                                                                                            |
| mantelPermutations | numeric: The number of permutations may be specified                                                                                                                                                |
| mantelRankTest     | logical: whether to use ranks in the Mantel test                                                                                                                                                    |
| bootstrapMethod    | character: which bootstrap method to use (one of "ABC", "BC" or "BCa").                                                                                                                             |
| bootstrapNsim      | integer: the number of bootstrap simulations to use (has no effect if method is "ABC").                                                                                                             |
| verbose            | logical: whether to print some information                                                                                                                                                          |

### Value

The path of the output file is returned invisibly.

### Examples

```

## Not run:
locinfile <- genepopExample('w2.txt')
outfile <- ibd(locinfile, 'w2.txt.IS0', geographicScale = 'Log', statistic='e')
if ( ! interactive()) clean_workdir(otherfiles='w2.txt')

locinfile <- genepopExample('PEL1600withCoord.txt')

```

```

outfile <- ibd(locinfile, 'PEL1600withCoord.ISO', statistic = 'SingleGeneDiv',
               geographicScale = '1D')
if ( ! interactive()) clean_workdir(otherfiles='PEL1600withCoord.txt')

## End(Not run)

```

---

Linkage

---

*Tables and exact test for genotypic linkage disequilibrium*


---

### Description

Exact test for each pair of loci in each population. See [this section](#) of the Genepop executable documentation for more information on the statistical methods.

### Usage

```

test_LD(
  inputFile,
  outputFile = "",
  settingsFile = "",
  dememorization = 10000,
  batches = 100,
  iterations = 5000,
  verbose = interactive()
)

write_LD_tables(inputFile, outputFile = "", verbose = interactive())

```

### Arguments

|                |                                                                  |
|----------------|------------------------------------------------------------------|
| inputFile      | The path of the input file, in Genepop format                    |
| outputFile     | character: The path of the output file                           |
| settingsFile   | character: The path of the settings file                         |
| dememorization | integer: length of dememorization step of Markov chain algorithm |
| batches        | integer: Number of batches                                       |
| iterations     | integer: Iterations per batch                                    |
| verbose        | logical: whether to print some information                       |

### Value

The path of the output file is returned invisibly.

## Examples

```
## Not run: # 'dontrun' only because a bit too slow for CRAN checks
locinfile <- genepopExample('sample.txt')
test_LD(locinfile, 'sample.txt.DIS')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')

## End(Not run)
locinfile <- genepopExample('sample.txt')
write_LD_tables(locinfile, 'sample.txt.TAB')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
```

---

manipulation

---

*Various data manipulation utilities*


---

## Description

Various procedures described in the linked sections of the Genepop executable documentation: [diploidize](#) haploid data, [relabel\\_alleles](#), [sample\\_haploid](#), and [pop\\_to\\_indiv](#). The latter procedure converts population samples (several individuals in each population) to individual data. The names given to the individuals in the new file created (names which are to be interpreted as coordinates in a spatial analysis) may be the population coordinates (given as the name of the last individual in the original data file), or each individual's coordinates (given as the name of each individual in the original data file).

## Usage

```
diploidize(inputFile, outputFile = "", verbose = interactive())

relabel_alleles(inputFile, outputFile = "", verbose = interactive())

pop_to_indiv(inputFile, coordinates, outputFile = "", verbose = interactive())

sample_haploid(inputFile, outputFile = "", verbose = interactive())
```

## Arguments

|             |                                                                                                                               |
|-------------|-------------------------------------------------------------------------------------------------------------------------------|
| inputFile   | The path of the input file, in Genepop format                                                                                 |
| outputFile  | character: The path of the output file                                                                                        |
| verbose     | logical: whether to print some information                                                                                    |
| coordinates | character: either 'population' (to use population coordinates) or any other character string (to use individual coordinates). |

## Examples

```
locinfile <- genepopExample('sample.txt')
outfile <- diploidize(inputFile = locinfile, outputFile="Dsample.txt")
if ( ! interactive()) clean_workdir(c("sample.txt", "Dsample.txt"))
```

---

|            |                              |
|------------|------------------------------|
| Nm_private | <i>Private allele method</i> |
|------------|------------------------------|

---

### Description

Estimation of Nm by private allele method of Slatkin and Barton. See [this section](#) of the Genepop executable documentation for more information on the statistical methods.

### Usage

```
Nm_private(
  inputFile,
  outputFile = "",
  dataType = "Diploid",
  verbose = interactive()
)
```

### Arguments

|            |                                               |
|------------|-----------------------------------------------|
| inputFile  | The path of the input file, in Genepop format |
| outputFile | character: The path of the output file        |
| dataType   | character: The haploid and diploid data       |
| verbose    | logical: whether to print some information    |

### Value

The path of the output file is returned invisibly.

### Examples

```
locinfile <- genepopExample('sample.txt')
Nm_private(locinfile, 'sample.txt.PRI')
if ( ! interactive()) clean_workdir(otherfiles='sample.txt')
```

---

|       |                                                                   |
|-------|-------------------------------------------------------------------|
| nulls | <i>Estimation of allele frequencies under genotyping failure.</i> |
|-------|-------------------------------------------------------------------|

---

### Description

Estimates allele frequencies (and failure rate if relevant) under different assumptions: maximum likelihood assuming that there is null allele (default method), maximum likelihood assuming that apparent nulls are technical failures independent of genotype ('ApparentNulls'), and Brookfield's (1996) estimator ('B96'). See [this section](#) of the Genepop executable documentation for more information on the statistical methods. Genepop takes the allele with the highest number for a given locus across all populations as the null allele. For example, if you have 4 alleles plus a null allele, a null homozygote individual should be indicated as e.g. 0505 or 9999 in the input file.

**Usage**

```

nulls(
  inputFile,
  outputFile = "",
  settingsFile = "",
  nullAlleleMethod = "",
  CIconvergence = 0.95,
  verbose = interactive()
)

```

**Arguments**

|                  |                                                                      |
|------------------|----------------------------------------------------------------------|
| inputFile        | The path of the input file, in Genepop format                        |
| outputFile       | character: The path of the output file                               |
| settingsFile     | character: The path of the settings file                             |
| nullAlleleMethod | character: 'ApparentNulls', 'B96' or anything else (default method). |
| CIconvergence    | numeric: The coverage probability of confidence interval             |
| verbose          | logical: whether to print some information                           |

**Value**

The path of the output file is returned invisibly.

---

|               |                                                  |
|---------------|--------------------------------------------------|
| setMantelSeed | <i>Set random generator seed for Mantel test</i> |
|---------------|--------------------------------------------------|

---

**Description**

Set random generator seed for Mantel test

**Usage**

```
setMantelSeed(seed)
```

**Arguments**

|      |                       |
|------|-----------------------|
| seed | integer: the new seed |
|------|-----------------------|

---

|               |                                                           |
|---------------|-----------------------------------------------------------|
| setRandomSeed | <i>Set random generator seed (except for Mantel test)</i> |
|---------------|-----------------------------------------------------------|

---

**Description**

Set random generator seed (except for Mantel test)

**Usage**

```
setRandomSeed(seed)
```

**Arguments**

|      |                       |
|------|-----------------------|
| seed | integer: the new seed |
|------|-----------------------|

---

|                 |                              |
|-----------------|------------------------------|
| set_restriction | <i>Programming utilities</i> |
|-----------------|------------------------------|

---

**Description**

getVersion returns the version number of the C++ code (the same number that identifies the C++ executable). set\_restriction(TRUE) sets the maximum number of populations and of loci to 300.

**Usage**

```
set_restriction(set = FALSE)
```

```
getVersion()
```

**Arguments**

|     |                                                                           |
|-----|---------------------------------------------------------------------------|
| set | logical: whether to set restrictions on number of populations and of loci |
|-----|---------------------------------------------------------------------------|

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