

# Package ‘statgenIBD’

September 14, 2021

**Type** Package

**Title** Calculation of IBD Probabilities

**Description** For biparental, three and four-way crosses Identity by Descent (IBD) probabilities can be calculated using Hidden Markov Models and inheritance vectors following Lander and Green (<<https://www.jstor.org/stable/29713>>) and Huang (<[doi:10.1073/pnas.1100465108](https://doi.org/10.1073/pnas.1100465108)>). One of a series of statistical genetic packages for streamlining the analysis of typical plant breeding experiments developed by Biometris.

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**License** GPL

**Encoding** UTF-8

**Depends** R (>= 3.6)

**Imports** ggplot2, Rcpp

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 7.1.2

**Suggests** rmarkdown, knitr, tinytest

**VignetteBuilder** knitr

**URL** <https://biometris.github.io/statgenIBD/index.html>,  
<https://github.com/Biometris/statgenIBD/>

**BugReports** <https://github.com/Biometris/statgenIBD/issues>

**NeedsCompilation** yes

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c.IBDprob	<i>Concatenate function for objects of class IBDprob</i>
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### Description

Concatenates objects of class IBDprob. All objects that are concatenated should have the same population type and the same map. The function is mainly meant for combining information for multiple crosses with overlapping parents.

### Usage

```
## S3 method for class 'IBDprob'
c(...)
```

### Arguments

... Objects of class IBDprob.

### Value

An object of class IBDprob containing data for all concatenated objects.

### Examples

```
## Compute IBD probabilities for AxB.
AB <- calcIBD(popType = "F4DH",
              markerFile = system.file("extdata/multipop", "AxB.txt",
                                       package = "statgenIBD"),
              mapFile = system.file("extdata/multipop", "mapfile.txt",
                                    package = "statgenIBD"))

## Compute IBD probabilities for Axc.
AC <- calcIBD(popType = "F4DH",
              markerFile = system.file("extdata/multipop", "AxC.txt",
                                       package = "statgenIBD"),
              mapFile = system.file("extdata/multipop", "mapfile.txt",
                                    package = "statgenIBD"))

## Combine results.
ABC <- c(AB, AC)
```

```
## Check summary.
summary(ABC)
```

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calcIBD	<i>Calculate IBD probabilities</i>
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## Description

Calculate IBD probabilities for different types of populations.

## Usage

```
calcIBD(
  popType,
  markerFile,
  mapFile,
  evalPos = NULL,
  evalDist = NULL,
  grid = TRUE,
  verbose = FALSE
)
```

## Arguments

popType	A character string indicating the type of population. One of DH, Fx, FxDH, BCx, BCxDH, BC1Sx, BC1SxDH, C3, C3DH, C3Sx, C3SxDH, C4, C4DH, C4Sx, C4SxDH (see Details).
markerFile	A character string indicating the location of the file with genotypic information for the population. The file should be in tab-delimited format with a header containing marker names.
mapFile	A character string indicating the location of the map file for the population. The file should be in tab-delimited format. It should consist of exactly three columns, marker, chromosome and position. There should be no header. The positions in the file should be in centimorgan.
evalPos	A data.frame with evaluation positions to which the calculations should be limited.
evalDist	An optional numerical value indicating the maximum distance for marker positions. Extra markers will be added based on the value of grid.
grid	Should the extra markers that are added to assure the a maximum distance of evalDist be on a grid (TRUE) or in between marker existing marker positions (FALSE).
verbose	Should messages indicating the progress of the process be printed?

## Details

IBD probabilities can be calculated for many different types of populations. In the following table all supported populations are listed. Note that the value of  $x$  in the population types is variable, with its maximum value depicted in the last column.

Population type	Cross	Description	max. x
DH	biparental	doubled haploid population	
Fx	biparental	Fx population (F1, followed by $x-1$ generations of selfing)	8
FxDH	biparental	Fx, followed by DH generation	8
BCx	biparental	backcross, second parent is recurrent parent	9
BCxDH	biparental	BCx, followed by DH generation	9
BC1Sx	biparental	BC1, followed by $x$ generations of selfing	7
BC1SxDH	biparental	BC1, followed by $x$ generations of selfing and DH	6
C3	three-way	three way cross: (AxB) x C	
C3DH	three-way	C3, followed by DH generation	
C3Sx	three-way	C3, followed by $x$ generations of selfing	7
C3SxDH	three-way	C3, followed by $x$ generations of selfing and DH generation	6
C4	four-way	four-way cross: (AxB) x (CxD)	
C4DH	four-way	C4, followed by DH generation	
C4Sx	four-way	C4, followed by $x$ generations of selfing	6
C4SxDH	four-way	C4, followed by $x$ generations of selfing and DH generation	6

## Value

An object of class IBDprob, a list with five elements,

**map** a data.frame with chromosome and position of the markers.

**markers** a 3-dimensional array of IBD probabilities with markers, genotypes and parents as array dimensions.

**parents** the parents.

**popType** the population type.

**multiCross** a logical value indicating if multiple crosses have been combined in the IBDprob object.

## Examples

```
## Compute IBD probabilities for Steptoe Morex.
SxMIBD <- calcIBD(popType = "DH",
  markerFile = system.file("extdata/SxM", "SxM_geno.txt",
    package = "statgenIBD"),
  mapFile = system.file("extdata/SxM", "SxM_map.txt",
    package = "statgenIBD"))

## Check summary.
summary(SxMIBD)

## Compute IBD probabilities for Steptoe Morex.
```

```
## Add extra evaluation positions in between existing marker positions
## to assure evaluation positions are at most 5 cM apart.
SxMIBD_Ext <- calcIBD(popType = "DH",
                     markerFile = system.file("extdata/SxM", "SxM_genos.txt",
                                               package = "statgenIBD"),
                     mapFile = system.file("extdata/SxM", "SxM_map.txt",
                                           package = "statgenIBD"),
                     evalDist = 5)

## Check summary.
summary(SxMIBD_Ext)
```

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<code>getProbs</code>	<i>Extract Probabilities for markers</i>
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## Description

Extract IBD probabilities for one or more markers from an object of class `IBDprob`.

## Usage

```
getProbs(IBDprob, markers, sumProbs = FALSE)
```

## Arguments

<code>IBDprob</code>	An object of class <code>IBDprob</code> .
<code>markers</code>	A character vector of markers that should be extracted.
<code>sumProbs</code>	Should the probabilities be summed per parent. If <code>TRUE</code> the probability for e.g. parent A in a cross with parent B will be calculated as $p_A + 0.5 * p_{AB}$ . If <code>FALSE</code> both $p_A$ and $p_{AB}$ will be output without further calculations.

## Value

A data.frame with IBD probabilities for the extracted markers in the column and genotypes in the rows.

## Examples

```
## Compute IBD probabilities for Steptoe Morex.
SxMIBD <- calcIBD(popType = "DH",
                 markerFile = system.file("extdata/SxM", "SxM_genos.txt",
                                           package = "statgenIBD"),
                 mapFile = system.file("extdata/SxM", "SxM_map.txt",
                                       package = "statgenIBD"))

## Get probabilities for a single marker.
probOne <- getProbs(IBDprob = SxMIBD,
                  markers = "plc")
```

```

head(probOne)

## Get probabilities for a multiple markers.
probMult <- getProbs(IBDprob = SxMIBD,
                    markers = c("plc", "tuba1"))
head(probMult)

```

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plot.IBDprob	<i>Plot function for objects of class IBDprob</i>
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### Description

Creates a plot for an object of class IBDprob.

### Usage

```

## S3 method for class 'IBDprob'
plot(x, ..., genotype, title = genotype, output = TRUE)

```

### Arguments

x	An object of class IBDprob.
...	Further arguments. Unused.
genotype	A character string indicating the genotype for which the plot should be made.
title	A character string, the title of the plot.
output	Should the plot be output to the current device? If FALSE, only a ggplot object is invisibly returned.

### Value

A ggplot object is invisibly returned.

### Examples

```

## Compute IBD probabilities for Steptoe Morex.
## Add extra evaluation positions in between exiting marker positions
## to assure evaluation positions are at most 2 cM apart.
SxMIBD_Ext <- calcIBD(popType = "DH",
                    markerFile = system.file("extdata/SxM", "SxM_geno.txt",
                                             package = "statgenIBD"),
                    mapFile = system.file("extdata/SxM", "SxM_map.txt",
                                           package = "statgenIBD"),
                    evalDist = 2)

## Plot results for genotype dh005.
plot(SxMIBD_Ext,
     genotype = "dh005")

```

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summary.IBDprob	<i>Summary function for objects of class IBDprob</i>
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### Description

Prints a short summary for objects of class IBDprob. The summary consists of the population type, number of evaluation points, number of individuals and names of the parents in the object.

### Usage

```
## S3 method for class 'IBDprob'  
summary(object, ...)
```

### Arguments

object	An object of class IBDprob.
...	Not used.

### Value

No return value, a summary is printed.

### Examples

```
## Compute IBD probabilities for Steptoe Morex.  
SxMIBD <- calcIBD(popType = "DH",  
                 markerFile = system.file("extdata/SxM", "SxM_geno.txt",  
                                           package = "statgenIBD"),  
                 mapFile = system.file("extdata/SxM", "SxM_map.txt",  
                                        package = "statgenIBD"))  
  
## Print summary  
summary(SxMIBD)
```

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writeFlapjack	<i>Write to Flapjack format</i>
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### Description

Export the results of an IBD calculation to Flapjack format so it can be visualized there.

**Usage**

```
writeFlapjack(  
  IBDprob,  
  outFileMap = "ibd_map.txt",  
  outFileGeno = "ibd_geno.txt"  
)
```

**Arguments**

IBDprob	An object of class IBDprob.
outFileMap	A character string, the full path to the output map file.
outFileGeno	A character string, the full path to the output genotype file.

**Value**

No output. Output files are written to a folder.

**Examples**

```
## Compute IBD probabilities for Steptoe Morex.  
SxMIBD <- calcIBD(popType = "DH",  
  markerFile = system.file("extdata/SxM", "SxM_geno.txt",  
    package = "statgenIBD"),  
  mapFile = system.file("extdata/SxM", "SxM_map.txt",  
    package = "statgenIBD"))  
  
## Write output in Flapjack format to temporary files.  
writeFlapjack(SxMIBD,  
  outFileMap = tempfile(fileext = ".txt"),  
  outFileGeno = tempfile(fileext = ".txt"))
```



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