Package: zalpha (via r-universe)

November 18, 2026

Type Package

Title Run a Suite of Selection Statistics

Version 0.3.0.9999

Author Clare Horscroft

Maintainer Clare Horscroft <chorscroft@aol.co.uk>

Description A suite of statistics for identifying areas of the genome under selective pressure. See Jacobs, Sluckin and Kivisild (2016) <doi:10.1534/genetics.115.185900>.

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Encoding UTF-8

Depends R (>= 2.10)

LazyData true

RoxygenNote 7.1.1

Suggests testthat (>= 2.1.0), knitr, rmarkdown, fitdistrplus

VignetteBuilder knitr

Repository https://chorscroft.r-universe.dev

Date/Publication 2021-12-02 10:27:24 UTC

RemoteUrl https://github.com/chorscroft/zalpha

RemoteRef HEAD

RemoteSha dd6fea5dca11e896cd464269728ed9ece489c1c4

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`create_LDprofile` *Creates an LD profile*

Description

An LD (linkage disequilibrium) profile is a look-up table containing the expected correlation between SNPs given the genetic distance between them. The use of an LD profile can increase the accuracy of results by taking into account the expected correlation between SNPs. This function aids the user in creating their own LD profile.

Usage

```
create_LDprofile(dist, x, bin_size, max_dist = NULL, beta_params = FALSE)
```

Arguments

`dist`	A numeric vector, or a list of numeric vectors, containing the genetic distance for each SNP.
`x`	A matrix of SNP values, or a list of matrices. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the `dist` vector. SNPs should all be biallelic.
`bin_size`	The size of each bin, in the same units as `dist`.
`max_dist`	Optional. The maximum genetic distance to be considered. If this is not supplied, it will default to the maximum distance in the `dist` vector.
`beta_params`	Optional. Beta parameters are calculated if this is set to TRUE. Default is FALSE.

Details

The input for `dist` and `x` can be lists. This allows multiple datasets to be used in the creation of the LD profile. For example, using all 22 autosomes from the human genome would involve 22 different distance vectors and SNP matrices. Both lists should be the same length and should correspond exactly to each other (i.e. the distances in each element of `dist` should go with the SNPs in the same element of x)

In the output, bins represent lower bounds. The first bin contains pairs where the genetic distance is greater than or equal to 0 and less than `bin_size`. The final bin contains pairs where the genetic distance is greater than or equal to `max_dist`-`bin_size` and less than `max_dist`. If the `max_dist` is not an increment of `bin_size`, it will be adjusted to the next highest increment. The final bin will be the bin that `max_dist` falls into. For example, if the `max_dist` is given as 4.5 and the `bin_size` is 1, the final bin will be 4. `max_dist` should be big enough to cover the genetic distances between pairs of SNPs within the window size given when the Z_α statistics are run. Any pairs with genetic distances bigger than `max_dist` will be assigned the values in the maximum bin of the LD profile.

By default, Beta parameters are not calculated. To fit a Beta distribution to the expected correlations, needed for the `Zalpha_BetaCDF` and `Zbeta_BetaCDF` statistics, `beta_params` should be set to TRUE and the package 'fitdistrplus' must be installed.

Ideally, an LD profile would be generated using data from a null population with no selection, For example by using a simulation if the other population parameters are known. However, often these are unknown or complex, so generating an LD profile using the same data as is being analysed is acceptable, as long as the bins are large enough.

Value

A data frame containing an LD profile that can be used by other statistics in this package.

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

`Zalpha_expected`, `Zalpha_rsq_over_expected`, `Zalpha_log_rsq_over_expected`, `Zalpha_Zscore`, `Zalpha_BetaCDF`, `Zbeta_expected`, `Zbeta_rsq_over_expected`, `Zbeta_log_rsq_over_expected`, `Zbeta_Zscore`, `Zbeta_BetaCDF`, `Zalpha_all`.

Examples

```
## load the snps example dataset
data(snps)
## Create an LD profile using this data
create_LDprofile(snps$cM_distances,as.matrix(snps[,3:12]),0.001)
## To get the Beta distribution parameter estimates, the fitdistrplus package is required
if (requireNamespace("fitdistrplus", quietly = TRUE)==TRUE) {
  create_LDprofile(snps$cM_distances,as.matrix(snps[,3:12]),0.001,beta_params=TRUE)
}
```

L_plus_R *Runs the L_plus_R function*

Description

Returns the $\binom{|L|}{2} + \binom{|R|}{2}$ value for each SNP location supplied to the function. `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`. For more information about the `L_plus_R` diversity statistic, please see Jacobs (2016).

Usage

```
L_plus_R(pos, ws, X = NULL)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the `L_plus_R` statistic will be calculated over. This should be on the same scale as the `pos` vector.
`X`	Optional. Specify a region of the chromosome to calculate `L_plus_R` for in the format `c(startposition, endposition)`. The start position and the end position should be within the extremes of the positions given in the `pos` vector. If not supplied, the function will calculate L_plus_R for every SNP in the `pos` vector.

Value

A list containing the SNP positions and the `L_plus_R` values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

Examples

```
## load the snps example dataset
data(snps)
## run L_plus_R over all the SNPs with a window size of 3000 bp
L_plus_R(snps$bp_positions,3000)
## only return results for SNPs between locations 600 and 1500 bp
L_plus_R(snps$bp_positions,3000,X=c(600,1500))
```

LDprofile *Dataset containing an example LD profile*

Description

A simulated LD profile, containing example LD statistics for genetic distances of 0 to 0.0049, in bins of size 0.0001.

Usage

```
data(LDprofile)
```

Format

A data frame with 50 rows and 5 variables:

bin the lower bound of each bin

rsq the expected r^2 value for a pair of SNPs, where the genetic distance between them falls in the given bin

sd the standard deviation of the expected r^2 value

Beta_a the first shape parameter for the Beta distribution fitted for this bin

Beta_b the second shape parameter for the Beta distribution fitted for this bin

LR *Runs the LR function*

Description

Returns the `|L||R|` value for each SNP location supplied to the function, where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`. For more information about the `|L||R|` diversity statistic, please see Jacobs (2016).

Usage

```
LR(pos, ws, X = NULL)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the `LR` statistic will be calculated over. This should be on the same scale as the `pos` vector.
`X`	Optional. Specify a region of the chromosome to calculate LR for in the format `c(startposition, endposition)`. The start position and the end position should be within the extremes of the positions given in the `pos` vector. If not supplied, the function will calculate LR for every SNP in the `pos` vector.

Value

A list containing the SNP positions and the LR values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

Examples

```
## load the snps example dataset
data(snps)
## run LR over all the SNPs with a window size of 3000 bp
LR(snps$bp_positions,3000)
## only return results for SNPs between locations 600 and 1500 bp
LR(snps$bp_positions,3000,X=c(600,1500))
```

---

snps *Dataset containing details on simulated SNPs*

Description

A dataset containing the positions, genetic distances and alleles for 20 SNPs, across 10 simulated chromosomes.

Usage

```
snps
```

Format

A data frame with 20 rows and 12 variables:

bp_positions location of the SNP on the chromosome e.g. in base pairs

cM_distances genetic distance of the SNP from the start of the chromosome e.g. in centimorgans

chrom_1 allele of the SNP on the first example chromosome

chrom_2 allele of the SNP on the second example chromosome

chrom_3 allele of the SNP on the third example chromosome

chrom_4 allele of the SNP on the fourth example chromosome

chrom_5 allele of the SNP on the fifth example chromosome

chrom_6 allele of the SNP on the sixth example chromosome

chrom_7 allele of the SNP on the seventh example chromosome

chrom_8 allele of the SNP on the eighth example chromosome

chrom_9 allele of the SNP on the ninth example chromosome

chrom_10 allele of the SNP on the tenth example chromosome

Examples

```
snps
```

`Zalpha` *Runs the Zalpha function*

Description

Returns a Z_α value for each SNP location supplied to the function. For more information about the Z_α statistic, please see Jacobs (2016). The Z_α statistic is defined as:

$$Z_\alpha = \frac{\binom{|L|}{2}^{-1} \sum_{i,j \in L} r^2_{i,j} + \binom{|R|}{2}^{-1} \sum_{i,j \in L} r^2_{i,j}}{2}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, and r^2 is equal to the squared correlation between a pair of SNPs

Usage

```
Zalpha(pos, ws, x, minRandL = 4, minRL = 25, X = NULL)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the Z_α statistic will be calculated over. This should be on the same scale as the `pos` vector.
`x`	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the `pos` vector. SNPs should all be biallelic.
`minRandL`	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
`minRL`	Minimum value for the product of the set sizes for R and L. Default is 25.
`X`	Optional. Specify a region of the chromosome to calculate Z_α for in the format `c(startposition, endposition)`. The start position and the end position should be within the extremes of the positions given in the `pos` vector. If not supplied, the function will calculate Z_α for every SNP in the `pos` vector.

Value

A list containing the SNP positions and the Z_α values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

Examples

```
## load the snps example dataset
data(snps)
## run Zalpha over all the SNPs with a window size of 3000 bp
Zalpha(snps$bp_positions,3000,as.matrix(snps[,3:12]))
## only return results for SNPs between locations 600 and 1500 bp
Zalpha(snps$bp_positions,3000,as.matrix(snps[,3:12]),X=c(600,1500))
```

`Zalpha_all` *Runs all the statistics in the zalpha package*

Description

Returns every statistic for each SNP location, given the appropriate parameters. See Details for more information.

Usage

```
Zalpha_all(
  pos,
  ws,
  x = NULL,
  dist = NULL,
  LDprofile_bins = NULL,
  LDprofile_rsq = NULL,
  LDprofile_sd = NULL,
  LDprofile_Beta_a = NULL,
  LDprofile_Beta_b = NULL,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the statistics will be calculated over. This should be on the same scale as the `pos` vector.
`x`	Optional. A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the `pos` vector. SNPs should all be biallelic.
`dist`	Optional. A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as `pos`.
`LDprofile_bins`	Optional. A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.

`LDprofile_rsq` Optional. A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.

`LDprofile_sd` Optional. A numeric vector containing the standard deviation of the r^2 values for the corresponding bin in the LD profile.

`LDprofile_Beta_a` Optional. A numeric vector containing the first estimated Beta parameter for the corresponding bin in the LD profile.

`LDprofile_Beta_b` Optional. A numeric vector containing the second estimated Beta parameter for the corresponding bin in the LD profile.

`minRandL` Minimum number of SNPs in each set R and L for the statistics to be calculated. L is the set of SNPs to the left of the target SNP and R to the right, within the given window size `ws`. Default is 4.

`minRL` Minimum value for the product of the set sizes for R and L. Default is 25.

`X` Optional. Specify a region of the chromosome to calculate the statistics for in the format `c(startposition, endposition)`. The start position and the end position should be within the extremes of the positions given in the `pos` vector. If not supplied, the function will calculate the statistics for every SNP in the `pos` vector.

Details

Not all statistics will be returned, depending on the parameters supplied to the function.
If `x` is not supplied, only `Zalpha_expected`, `Zbeta_expected`, `LR` and `L_plus_R` will be calculated.
For any of the statistics which use an expected r^2 value, the parameters `dist`, `LDprofile_bins` and `LDprofile_rsq` must be supplied. This includes the statistics: `Zalpha_expected`, `Zalpha_rsq_over_expected`, `Zalpha_log_rsq_over_expected`, `Zalpha_Zscore`, `Zalpha_BetaCDF`, `Zbeta_expected`, `Zbeta_rsq_over_expected`, `Zbeta_log_rsq_over_expected`, `Zbeta_Zscore` and `Zbeta_BetaCDF`.

- For `Zalpha_Zscore` and `Zbeta_Zscore` to be calculated, the parameter `LDprofile_sd` must also be supplied.
- For `Zalpha_BetaCDF` and `Zbeta_BetaCDF` to be calculated, the parameters `LDprofile_Beta_a` and `LDprofile_Beta_b` must also be supplied.

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the `create_LDprofile` function for more information on how to create an LD profile. For more information about the statistics, please see Jacobs (2016).

Value

A list containing the SNP positions and the statistics for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

Zalpha, Zalpha_expected, Zalpha_rsq_over_expected, Zalpha_log_rsq_over_expected, Zalpha_Zscore, Zalpha_BetaCDF, Zbeta, Zbeta_expected, Zbeta_rsq_over_expected, Zbeta_log_rsq_over_expected, Zbeta_Zscore, Zbeta_BetaCDF, LR, L_plus_R, create_LDprofile.

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zalpha_all over all the SNPs with a window size of 3000 bp
## will return all 15 statistics
Zalpha_all(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,LDprofile$sd,LDprofile$Beta_a,LDprofile$Beta_b)
## only return results for SNPs between locations 600 and 1500 bp
Zalpha_all(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,LDprofile$sd,LDprofile$Beta_a,LDprofile$Beta_b,X=c(600,1500))
## will only return statistics not requiring an LD profile
Zalpha_all(snps$bp_positions,3000,as.matrix(snps[,3:12]))
```

Zalpha_BetaCDF — *Runs the Zalpha function using a cumulative beta distribution function on the r-squared values for the region*

Description

Returns a $Z_\alpha^{BetaCDF}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_\alpha^{BetaCDF}$ statistic, please see Jacobs (2016). The $Z_\alpha^{BetaCDF}$ statistic is defined as:

$$Z_\alpha^{BetaCDF} = \frac{\binom{|L|}{2}^{-1} \sum_{i,j \in L} \frac{B(r^2_{i,j};a,b)}{B(a,b)} + \binom{|R|}{2}^{-1} \sum_{i,j \in R} \frac{B(r^2_{i,j};a,b)}{B(a,b)}}{2}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, and $\frac{B(r^2_{i,j};a,b)}{B(a,b)}$ is the cumulative distribution function for the Beta distribution given the estimated a and b parameters from the LD profile.

Usage

```
Zalpha_BetaCDF(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_Beta_a,
  LDprofile_Beta_b,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

pos	A numeric vector of SNP locations
ws	The window size which the $Z_{\alpha}^{BetaCDF}$ statistic will be calculated over. This should be on the same scale as the pos vector.
x	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the pos vector. SNPs should all be biallelic.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_Beta_a	A numeric vector containing the first estimated Beta parameter for the corresponding bin in the LD profile.
LDprofile_Beta_b	A numeric vector containing the second estimated Beta parameter for the corresponding bin in the LD profile.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate $Z_{\alpha}^{BetaCDF}$ for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate $Z_{\alpha}^{BetaCDF}$ for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of

distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the `create_LDprofile` function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_{\alpha}^{BetaCDF}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

`create_LDprofile`

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zalpha_BetaCDF over all the SNPs with a window size of 3000 bp
Zalpha_BetaCDF(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$Beta_a,LDprofile$Beta_b)
## only return results for SNPs between locations 600 and 1500 bp
Zalpha_BetaCDF(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$Beta_a,LDprofile$Beta_b,X=c(600,1500))
```

Zalpha_expected *Runs the Zalpha function on the expected r-squared values for the region*

Description

Returns a $Z_{\alpha}^{E[r^2]}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_{\alpha}^{E[r^2]}$ statistic, please see Jacobs (2016). The $Z_{\alpha}^{E[r^2]}$ statistic is defined as:

$$Z_{\alpha}^{E[r^2]} = \frac{\binom{|L|}{2}^{-1} \sum_{i,j \in L} E[r_{i,j}^2] + \binom{|R|}{2}^{-1} \sum_{i,j \in R} E[r_{i,j}^2]}{2}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, and $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile.

Usage

```
Zalpha_expected(
  pos,
  ws,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

pos	A numeric vector of SNP locations
ws	The window size which the $Z_\alpha^{E[r^2]}$ statistic will be calculated over. This should be on the same scale as the pos vector.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_rsq	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate $Z_\alpha^{E[r^2]}$ for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate $Z_\alpha^{E[r^2]}$ for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the create_LDprofile function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_\alpha^{E[r^2]}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

create_LDprofile

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zalpha_expected over all the SNPs with a window size of 3000 bp
Zalpha_expected(snps$bp_positions,3000,snps$cM_distances,LDprofile$bin,LDprofile$rsq)
## only return results for SNPs between locations 600 and 1500 bp
Zalpha_expected(snps$bp_positions,3000,snps$cM_distances,LDprofile$bin,LDprofile$rsq,X=c(600,1500))
```

Zalpha_log_rsq_over_expected

Runs the Zalpha function on the log of the r-squared values over the expected r-squared values for the region

---

Description

Returns a $Z_\alpha^{log_{10}(r^2/E[r^2])}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_\alpha^{log_{10}(r^2/E[r^2])}$ statistic, please see Jacobs (2016). The $Z_\alpha^{log_{10}(r^2/E[r^2])}$ statistic is defined as:

$$Z_\alpha^{log_{10}(r^2/E[r^2])} = \frac{\binom{|L|}{2}^{-1} \sum_{i,j \in L} log_{10}(r^2_{i,j}/E[r^2_{i,j}]) + \binom{|R|}{2}^{-1} \sum_{i,j \in R} log_{10}(r^2_{i,j}/E[r^2_{i,j}])}{2}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, and $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile.

Usage

```
Zalpha_log_rsq_over_expected(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  minRandL = 4,
```

```
  minRL = 25,
  X = NULL
)
```

Arguments

pos	A numeric vector of SNP locations
ws	The window size which the $Z_\alpha^{log_{10}(r^2/E[r^2])}$ statistic will be calculated over. This should be on the same scale as the pos vector.
x	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the pos vector. SNPs should all be biallelic.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_rsq	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate $Z_\alpha^{log_{10}(r^2/E[r^2])}$ for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate $Z_\alpha^{log_{10}(r^2/E[r^2])}$ for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the create_LDprofile function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_\alpha^{log_{10}(r^2/E[r^2])}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

create_LDprofile

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zalpha_log_rsq_over_expected over all the SNPs with a window size of 3000 bp
Zalpha_log_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq)
## only return results for SNPs between locations 600 and 1500 bp
Zalpha_log_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,X=c(600,1500))
```

`Zalpha_rsq_over_expected` *Runs the Zalpha function on the r-squared values over the expected r-squared values for the region*

Description

Returns a $Z_\alpha^{r^2/E[r^2]}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_\alpha^{r^2/E[r^2]}$ statistic, please see Jacobs (2016). The $Z_\alpha^{r^2/E[r^2]}$ statistic is defined as:

$$Z_\alpha^{r^2/E[r^2]} = \frac{\binom{|L|}{2}^{-1} \sum_{i,j \in L} r_{i,j}^2/E[r_{i,j}^2] + \binom{|R|}{2}^{-1} \sum_{i,j \in R} r_{i,j}^2/E[r_{i,j}^2]}{2}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, and $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile.

Usage

```
Zalpha_rsq_over_expected(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

pos	A numeric vector of SNP locations
ws	The window size which the $Z_\alpha^{r^2/E[r^2]}$ statistic will be calculated over. This should be on the same scale as the pos vector.
x	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the pos vector. SNPs should all be biallelic.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_rsq	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate $Z_\alpha^{r^2/E[r^2]}$ for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate $Z_\alpha^{r^2/E[r^2]}$ for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the create_LDprofile function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_\alpha^{r^2/E[r^2]}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

create_LDprofile

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zalpha_rsq_over_expected over all the SNPs with a window size of 3000 bp
Zalpha_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq)
## only return results for SNPs between locations 600 and 1500 bp
Zalpha_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,X=c(600,1500))
```

Zalpha_Zscore *Runs the Zalpha function using the Z score of the r-squared values for the region*

Description

Returns a Z_{α}^{Zscore} value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the Z_{α}^{Zscore} statistic, please see Jacobs (2016). The Z_{α}^{Zscore} statistic is defined as:

$$Z_{\alpha}^{Zscore} = \frac{\binom{|L|}{2}^{-1} \sum_{i,j \in L} \frac{r_{i,j}^2 - E[r_{i,j}^2]}{\sigma[r_{i,j}^2]} + \binom{|R|}{2}^{-1} \sum_{i,j \in R} \frac{r_{i,j}^2 - E[r_{i,j}^2]}{\sigma[r_{i,j}^2]}}{2}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile, and $\sigma[r^2]$ is the standard deviation.

Usage

```
Zalpha_Zscore(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  LDprofile_sd,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

pos	A numeric vector of SNP locations
ws	The window size which the Z_{α}^{Zscore} statistic will be calculated over. This should be on the same scale as the pos vector.
x	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the pos vector. SNPs should all be biallelic.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_rsq	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
LDprofile_sd	A numeric vector containing the standard deviation of the r^2 values for the corresponding bin in the LD profile.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate Z_{α}^{Zscore} for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate Z_{α}^{Zscore} for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the create_LDprofile function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the Z_{α}^{Zscore} values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

create_LDprofile

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zalpha_Zscore over all the SNPs with a window size of 3000 bp
Zalpha_Zscore(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,LDprofile$sd)
## only return results for SNPs between locations 600 and 1500 bp
Zalpha_Zscore(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,LDprofile$sd,X=c(600,1500))
```

Zbeta *Runs the Zbeta function*

Description

Returns a Z_β value for each SNP location supplied to the function. For more information about the Z_β statistic, please see Jacobs (2016). The Z_β statistic is defined as:

$$Z_\beta = \frac{\sum_{i \in L, j \in R} r^2_{i,j}}{|L||R|}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, and r^2 is equal to the squared correlation between a pair of SNPs

Usage

```
Zbeta(pos, ws, x, minRandL = 4, minRL = 25, X = NULL)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the Z_β statistic will be calculated over. This should be on the same scale as the `pos` vector.
`x`	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the `pos` vector. SNPs should all be biallelic.
`minRandL`	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
`minRL`	Minimum value for the product of the set sizes for R and L. Default is 25.
`X`	Optional. Specify a region of the chromosome to calculate Z_β for in the format `c(startposition, endposition)`. The start position and the end position should be within the extremes of the positions given in the `pos` vector. If not supplied, the function will calculate Z_β for every SNP in the `pos` vector.

Value

A list containing the SNP positions and the Z_β values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

Examples

```
## load the snps example dataset
data(snps)
## run Zbeta over all the SNPs with a window size of 3000 bp
Zbeta(snps$bp_positions,3000,as.matrix(snps[,3:12]))
## only return results for SNPs between locations 600 and 1500 bp
Zbeta(snps$bp_positions,3000,as.matrix(snps[,3:12]),X=c(600,1500))
```

`Zbeta_BetaCDF` *Runs the Zbeta function using a cumulative beta distribution function on the r-squared values for the region*

Description

Returns a $Z_\beta^{BetaCDF}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_\beta^{BetaCDF}$ statistic, please see Jacobs (2016). The $Z_\beta^{BetaCDF}$ statistic is defined as:

$$Z_\beta^{BetaCDF} = \frac{\sum_{i \in L, j \in R} \frac{B(r^2_{i,j};a,b)}{B(a,b)}}{|L||R|}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, and $\frac{B(r^2_{i,j};a,b)}{B(a,b)}$ is the cumulative distribution function for the Beta distribution given the estimated a and b parameters from the LD profile.

Usage

```
Zbeta_BetaCDF(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_Beta_a,
  LDprofile_Beta_b,
  minRandL = 4,
```

```
  minRL = 25,
  X = NULL
)
```

Arguments

pos	A numeric vector of SNP locations
ws	The window size which the $Z_{\beta}^{BetaCDF}$ statistic will be calculated over. This should be on the same scale as the pos vector.
x	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the pos vector. SNPs should all be biallelic.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_Beta_a	A numeric vector containing the first estimated Beta parameter for the corresponding bin in the LD profile.
LDprofile_Beta_b	A numeric vector containing the second estimated Beta parameter for the corresponding bin in the LD profile.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate $Z_{\beta}^{BetaCDF}$ for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate $Z_{\beta}^{BetaCDF}$ for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the create_LDprofile function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_{\beta}^{BetaCDF}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

create_LDprofile

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zbeta_BetaCDF over all the SNPs with a window size of 3000 bp
Zbeta_BetaCDF(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$Beta_a,LDprofile$Beta_b)
## only return results for SNPs between locations 600 and 1500 bp
Zbeta_BetaCDF(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$Beta_a,LDprofile$Beta_b,X=c(600,1500))
```

Zbeta_expected — *Runs the Zbeta function on the expected r-squared values for the region*

Description

Returns a $Z_\beta^{E[r^2]}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_\beta^{E[r^2]}$ statistic, please see Jacobs (2016). The $Z_\beta^{E[r^2]}$ statistic is defined as:

$$Z_\beta^{E[r^2]} = \frac{\sum_{i \in L, j \in R} E[r_{i,j}^2]}{|L||R|}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, and $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile.

Usage

```
Zbeta_expected(
  pos,
  ws,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  minRandL = 4,
```

```
  minRL = 25,
  X = NULL
)
```

Arguments

pos	A numeric vector of SNP locations
ws	The window size which the $Z_{\beta}^{E[r^2]}$ statistic will be calculated over. This should be on the same scale as the pos vector.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_rsq	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate $Z_{\beta}^{E[r^2]}$ for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate $Z_{\beta}^{E[r^2]}$ for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the create_LDprofile function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_{\beta}^{E[r^2]}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

create_LDprofile

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zbeta_expected over all the SNPs with a window size of 3000 bp
Zbeta_expected(snps$bp_positions,3000,snps$cM_distances,LDprofile$bin,LDprofile$rsq)
## only return results for SNPs between locations 600 and 1500 bp
Zbeta_expected(snps$bp_positions,3000,snps$cM_distances,LDprofile$bin,LDprofile$rsq,X=c(600,1500))
```

`Zbeta_log_rsq_over_expected` *Runs the Zbeta function on the log of the r-squared values over the expected r-squared values for the region*

Description

Returns a $Z_\beta^{log_{10}(r^2/E[r^2])}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_\beta^{log_{10}(r^2/E[r^2])}$ statistic, please see Jacobs (2016). The $Z_\beta^{log_{10}(r^2/E[r^2])}$ statistic is defined as:

$$Z_\beta^{log_{10}(r^2/E[r^2])} = \frac{\sum_{i \in L, j \in R} log_{10}(r^2_{i,j}/E[r^2_{i,j}])}{|L||R|}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, and $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile.

Usage

```
Zbeta_log_rsq_over_expected(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the $Z_\beta^{log_{10}(r^2/E[r^2])}$ statistic will be calculated over. This should be on the same scale as the `pos` vector.

x	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the pos vector. SNPs should all be biallelic.
dist	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as pos.
LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_rsq	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate $Z_\beta^{log_{10}(r^2/E[r^2])}$ for in the format c(startposition, endposition). The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate $Z_\beta^{log_{10}(r^2/E[r^2])}$ for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the create_LDprofile function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_\beta^{log_{10}(r^2/E[r^2])}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

create_LDprofile

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zbeta_log_rsq_over_expected over all the SNPs with a window size of 3000 bp
Zbeta_log_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
```

```
 LDprofile$bin,LDprofile$rsq)
## only return results for SNPs between locations 600 and 1500 bp
Zbeta_log_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,X=c(600,1500))
```

`Zbeta_rsq_over_expected` *Runs the Zbeta function on the r-squared values over the expected r-squared values for the region*

Description

Returns a $Z_\beta^{r^2/E[r^2]}$ value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the $Z_\beta^{r^2/E[r^2]}$ statistic, please see Jacobs (2016). The $Z_\beta^{r^2/E[r^2]}$ statistic is defined as:

$$Z_\beta^{r^2/E[r^2]} = \frac{\sum_{i \in L, j \in R} r_{i,j}^2 / E[r_{i,j}^2]}{|L||R|}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, and $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile.

Usage

```
Zbeta_rsq_over_expected(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the $Z_\beta^{r^2/E[r^2]}$ statistic will be calculated over. This should be on the same scale as the `pos` vector.
`x`	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the `pos` vector. SNPs should all be biallelic.

`dist`	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as `pos`.
`LDprofile_bins`	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
`LDprofile_rsq`	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
`minRandL`	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
`minRL`	Minimum value for the product of the set sizes for R and L. Default is 25.
`X`	Optional. Specify a region of the chromosome to calculate $Z_\beta^{r^2/E[r^2]}$ for in the format `c(startposition, endposition)`. The start position and the end position should be within the extremes of the positions given in the `pos` vector. If not supplied, the function will calculate $Z_\beta^{r^2/E[r^2]}$ for every SNP in the `pos` vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the `create_LDprofile` function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the $Z_\beta^{r^2/E[r^2]}$ values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

`create_LDprofile`

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zbeta_rsq_over_expected over all the SNPs with a window size of 3000 bp
Zbeta_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq)
## only return results for SNPs between locations 600 and 1500 bp
Zbeta_rsq_over_expected(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
```

```
LDprofile$bin,LDprofile$rsq,X=c(600,1500))
```

`Zbeta_Zscore` *Runs the Zbeta function using the Z score of the r-squared values for the region*

Description

Returns a Z_{β}^{Zscore} value for each SNP location supplied to the function, based on the expected r^2 values given an LD profile and genetic distances. For more information about the Z_{β}^{Zscore} statistic, please see Jacobs (2016). The Z_{β}^{Zscore} statistic is defined as:

$$Z_{\beta}^{Zscore} = \frac{\sum_{i \in L, j \in R} \frac{r_{i,j}^2 - E[r_{i,j}^2]}{\sigma[r_{i,j}^2]}}{|L||R|}$$

where `|L|` and `|R|` are the number of SNPs to the left and right of the current locus within the given window `ws`, r^2 is equal to the squared correlation between a pair of SNPs, $E[r^2]$ is equal to the expected squared correlation between a pair of SNPs, given an LD profile, and $\sigma[r^2]$ is the standard deviation.

Usage

```
Zbeta_Zscore(
  pos,
  ws,
  x,
  dist,
  LDprofile_bins,
  LDprofile_rsq,
  LDprofile_sd,
  minRandL = 4,
  minRL = 25,
  X = NULL
)
```

Arguments

`pos`	A numeric vector of SNP locations
`ws`	The window size which the Z_{β}^{Zscore} statistic will be calculated over. This should be on the same scale as the `pos` vector.
`x`	A matrix of SNP values. Columns represent chromosomes; rows are SNP locations. Hence, the number of rows should equal the length of the `pos` vector. SNPs should all be biallelic.
`dist`	A numeric vector of genetic distances (e.g. cM, LDU). This should be the same length as `pos`.

LDprofile_bins	A numeric vector containing the lower bound of the bins used in the LD profile. These should be of equal size.
LDprofile_rsq	A numeric vector containing the expected r^2 values for the corresponding bin in the LD profile. Must be between 0 and 1.
LDprofile_sd	A numeric vector containing the standard deviation of the r^2 values for the corresponding bin in the LD profile.
minRandL	Minimum number of SNPs in each set R and L for the statistic to be calculated. Default is 4.
minRL	Minimum value for the product of the set sizes for R and L. Default is 25.
X	Optional. Specify a region of the chromosome to calculate Z_β^{Zscore} for in the format `c(startposition, endposition)`. The start position and the end position should be within the extremes of the positions given in the pos vector. If not supplied, the function will calculate Z_β^{Zscore} for every SNP in the pos vector.

Details

The LD profile describes the expected correlation between SNPs at a given genetic distance, generated using simulations or real data. Care should be taken to utilise an LD profile that is representative of the population in question. The LD profile should consist of evenly sized bins of distances (for example 0.0001 cM per bin), where the value given is the (inclusive) lower bound of the bin. Ideally, an LD profile would be generated using data from a null population with no selection, however one can be generated using this data. See the `create_LDprofile` function for more information on how to create an LD profile.

Value

A list containing the SNP positions and the Z_β^{Zscore} values for those SNPs

References

Jacobs, G.S., T.J. Sluckin, and T. Kivisild, *Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps.* Genetics, 2016. **203**(4): p. 1807

See Also

`create_LDprofile`

Examples

```
## load the snps and LDprofile example datasets
data(snps)
data(LDprofile)
## run Zbeta_Zscore over all the SNPs with a window size of 3000 bp
Zbeta_Zscore(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,LDprofile$sd)
## only return results for SNPs between locations 600 and 1500 bp
Zbeta_Zscore(snps$bp_positions,3000,as.matrix(snps[,3:12]),snps$cM_distances,
 LDprofile$bin,LDprofile$rsq,LDprofile$sd,X=c(600,1500))
```

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