Package 'BCRgt'

January 29, 2013

Title SNP array genotyping

Version 1.0

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Description Bayesian Cluster Regression based Genotyping algorithm for the samples with Copy Number Alterations

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biocViews SNP array, genotyping

LazyData yes

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Bcr.0 *Assign genotyping probabilities for individual SNP*

Description

Assign genotyping probabilities of each observation for AA, AB and BB genotypes.

Usage

Bcr.0 (T, kluster, pvar, pii, sdd, pBeta, Beta, x, y, n.n, p.conf)

Arguments

T a matrix that has a dimension of number of samples by numbers of SNPs genotyping

kluster number of clusters

pvar co-variance matrix for the prior distributions

pii initial probability of each cluster

sdd a vector of the random error terms for each cluster

pBeta a matrix of parameters of the prior distributions for slope and intercept for each cluster

Beta a matrix of estimated parameters for each cluster

x data matrix for A allele

y data matrix for B allele

n.n number of samples for genotyping

p.conf the confidence level for providing a genotyping call

Details

For " kluster ", " pvar ", " pii", “sdd”, “pBeta”, “Beta”

Data that are NA, Inf, NaN will not be allowed

Value

...

Bcr.y *Iteratively call each SNP*

Description

Find the most possible path of a HMM via viterbi algorithm

Usage

Bcr.y = function(state, M_A, M_B, nsnp, n.n, p.conf),

Arguments

state a matrix storing copy number information for all SNPs and samples

M_A matrix storing log-intensities of A alleles for all SNPs and samples

M_B matrix storing log-intensities of B alleles for all SNPs and samples

nsnp the index of a SNP on the array

n.n number of samples for genotyping

p.conf the confidence level for providing a genotyping call

Details

For "state", "M_A ", " M_B", “nsnp”, “n.n”
Data that are NA, Inf, NaN will not be allowed

Value

...

BCRgt *Perform BCRgt normalization*

Description

Main function for performing BCRgt genotyping

Usage

BCRgt (data.for.A, data.for.B, state.data, p.conf, nrows),

Arguments

data.for.A name of the data file for storing A allele log-intensities

data.for.B name of the data file for storing B allele log-intensities

state.data name of the file storing copy number information

p.conf the confidence level for providing a genotyping call

nrows number of SNPs to be genotyped

Details

For "data.for.A ", "data.for.B ",
Both files should be saved in .txt format, and look like the following:

GSM116887A	**GSM116888A**	**GSM116889A**	**GSM116890A**	**…**
9.93862292	9.19638788	9.36074519	8.09858448	…
…				

Note that each column represents a sample, and each row represents a SNP.
Rows should have been sorted by chromosome and physical location of all SNPs, in other words, the order of the SNPs is known, so that the genotype output file can be annotated later.

For "state.data"
The genotype files for the paired normal samples should be saved in .txt format, and should look like the following:

state.1	**state.2**	**state.3**	**state.4**	**state.5**	**state.6**	**...**
1	0	-1	-1	1	-1	...
2	0	-1	-1	1	-1	...
3	0	-1	-1	1	-1	...
...						

Note that rows should have been sorted by chromosome and physical location of all SNPs,

Value

...

Examples

data.for.A=paste("d:/example/ data.for.A.txt")

data.for.B=paste("d:/example/ data.for.B.txt")

state.data=paste("d:/example /copynumber.txt")

Genotype.matrix=BCRgt(data.for.A, data.for.B, state.data, nrows=3)