Package ‘ebSNP’

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Type Package
Title Genotyping and SNP calling using single-sample next generation sequencing data
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Author Na You
Maintainer Na You <youn@mail.sysu.edu.cn>
Description Genotyping and SNP calling tool for single-sample next generation sequencing data analysis using an empirical Bayes method.
License GPL-2
NeedsCompilation no
Repository CRAN
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R topics documented:

ebSNP-package ................................................................. 1
ebSNP ................................................................. 2

Index

Description

Genotyping and SNP calling using single-sample next generation sequencing data

Details
Author(s)

Na You
Maintainer: Na You <youn@mail.sysu.edu.cn>

References

Single-sample SNP Detection By Empirical Bayes Method Using Next Generation Sequencing Data

Description

Genotype-call tool for single-sample next generation sequencing data using empirical Bayes method.

Usage

ebSNP(dat, t1 = 0.5, t2 = 0.5, eps = 0.001, maxstep = 30)

Arguments

dat A data matrix with two rows, containing the number of major and minor alleles at each position. Each column corresponds to one position.
T1 Lower threshold for genotyping.
T2 Upper threshold for genotyping.
eps Stopping criteria of EM algorithm.
maxstep Maximum number of EM iterations.

Value

A list,
pi0.hat Estimate for pi0, the probability of a position bearing a homozygous genotype.
alpha.hat Estimate for alpha.
beta.hat Estimate for beta.
delta 1-g_i.
G Estimated genotypes.
Author(s)
Na You

References
Single-sample SNP Detection By Empirical Bayes Method Using Next Generation Sequencing Data

Examples

N <- 100
cvg <- 40
pi0 <- 0.95
a <- 1
b <- 10
pi1 <- 1-pi0
z <- rbinom(N,1,pi1)
n.homo <- N-sum(z)
p <- rep(0,N)
p[which(z==0)] <- rbeta(n.homo,a,b)
p[which(z==1)] <- 1/2
nc <- sapply(1-p,function(x) rbinom(1,cvg,x))
dat <- rbind(nc,cvg-nc)
ebSNP(dat)
ebSNP(dat,0.1,0.9)
Index

*Topic package
   ebSNP-package, 1

   ebSNP, 2
   ebSNP-package, 1