Package 'ebSNP'

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Type Package

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

Version 1.0

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Description Genotyping and SNP calling tool for single-sample next generation sequencing data analysis using an empirical Bayes method.

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`ebSNP-package` *Genotyping and SNP calling using single-sample next generation sequencing data*

Description

Genotyping and SNP calling for single-sample next generation sequencing using an empirical Bayes method

Details

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Author(s)

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References

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

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`ebSNP` *Genotype-call for single-sample next generation sequencing data using empirical Bayes method*

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)
```

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