

Package ‘QHOT’

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Type Package

Title QTL Hotspot Detection

Version 0.1.0

Author ManHsia Yang

Maintainer ManHsia Yang <ymh@tari.gov.tw>

Description This function produces both the numerical and graphical summaries of the QTL hotspot detection in the genomes that are available on the worldwide web including the flanking markers of QTLs.

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

Repository CRAN

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QHOT	<i>QTL Hotspot Detection</i>
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Description

This function produces both the numerical and graphical summaries of the QTL hotspot detection in the genomes that are available on the worldwide web including the flanking markers of QTLs. Man-Hsia Yang, Dong-Hong Wu, Chen-Hung Kao. 2019. A Statistical Procedure for Genome-wide Detection of QTL Hotspots Using Public Databases with Application to Rice. G3-Genes Genom Genet DOI: 10.1534/g3.118.200922.

Usage

```
QHOT(DataQTL, DataCrop, ScanStep, NH, NP)
```

Arguments

DataQTL	a data-frame of values for QTL information including the trait names, which chromosomes localized, the left and right flanking marker positions of QTLs for the first to fourth columns, respectively.
DataCrop	a data-frame of values for chromosome information consisting of the names, center positions and lengths of chromosomes for the first to third columns, respectively.
ScanStep	a value for the length of every bin.
NH	a value for the number of spurious hotspots in the proposed method.
NP	a value for permutation times to calculate the threshold.

References

Man-Hsia Yang, Dong-Hong Wu, Chen-Hung Kao. 2019. A Statistical Procedure for Genome-wide Detection of QTL Hotspots Using Public Databases with Application to Rice. *G3-Genes Genom Genet* DOI: 10.1534/g3.118.200922.

Examples

```
Trait<-paste("t", sample(1:9, 100, replace=TRUE, prob=c(2, rep(1, 8)))/10), sep="")
chr<-1
L<-sample(seq(0, 90, by=10), 100, replace=TRUE, prob=c(0.5, 0.5, 5.5, rep(0.5, 7)))/10)
R<-L+sample(c(0.5, 1, 5, 10, 50), 100, replace=TRUE)
R[R>100]<-100
DataQTL.t<-data.frame(Trait, chr, L, R)
DataCrop.t<-data.frame(chr=1, center=75, length=100)
QHOT(DataQTL.t, DataCrop.t, ScanStep=0.5, NH=1, NP=1000)
```

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