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.

Run the command code “QHOT” in QHOT.RData to obtain the R codes of the function QHOT. Besides, QHOT.RData includes the information of rice application: DataQTL, DataCrop, NP=1000, NH=100and ScanStep=0.5. Run the command code ” QHOT (DataQTL, DataCrop, ScanStep=0.5,NH=100, NP=1000)” to obtain the results of rice real example presented in our study.

Usage

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

Arguments：

DataQTL a data-frame of values for QTL information including which chromosomes localized, trait names, flanking marker positions of QTLs, and the column names must be chr, Trait, L and R, respectively, or the function cannot work.

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.

Numerical Output：

Provide a list including the following information

1. The expected QTL frequency in every bin per chromosome.
2. The thresholds for proposed method and Q method.
3. The numbers of detected hotspots per chromosome for proposed method and Q method.

Graphical outputs：

Visualizing the summarized results including the expected QTL frequency of scan steps, the composition of QTLs for different traits in the detected hotspots.