Package 'dREG.HD'

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Title Refining dREG peaks by imputing DNase-I hypersensitivity site

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Depends
R (>= 2.14), bigWig (>= 0.2-9), e1071, rphast, dREG, graphics, snowfall, data.table, methods

LinkingTo

Suggests

Description This package is an analysis pipeline for refining dREG peaks

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Collate get_genomic_data.R dREG_HD_GPU_working.R

biocViews Sequencing, Analysis

LazyLoad yes

R topics documented:

dREG_HD	*Run dREG-HD*

Description

Run dREG-HD

Usage

```
dREG_HD(bed_path,
     bigwig_plus,
     bigwig_minus,
     chromInfo,
     model_path,
     ncores=4,
     use_rgtsvm = FALSE )
```

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Arguments

`bed_path`	path to the dREG peaks in bed format
`bigwig_plus`	the path the the plus strand of bigwig file
`bigwig_minus`	the path the the minus strand of bigwig file
`chromInfo`	the file specifies chromosome sizes
`model_path`	the path dREG-HD model
`ncores`	Number of CPU cores in parallel computing
`use_rgtsvm`	use GPU or not

Examples

```
bed_path <-system.file("extdata","k562.chr21.predictions.bed", package="dREG.HD")
bigwig_plus<-system.file("extdata","K562.chr21.plus.bw", package="dREG.HD")
bigwig_minus<-system.file("extdata","K562.chr21.minus.bw", package="dREG.HD")
chromInfo <-system.file("extdata","chromInfo.hg19", package="dREG.HD")
model_path <-system.file("extdata","dREG_HD.model.rdata", package="dREG.HD")


dREG_HD(bed_path= bed_path, bigwig_plus = bigwig_plus, bigwig_minus =bigwig_minus,chromInfo= chromInfo, mode
```

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