

# 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** Rgtsvm

**Description** This package is an analysis pipeline for refining dREG peaks

**License** GPL-3

**Collate** get\_genomic\_data.R dREG\_HD\_GPU\_working.R

**biocViews** Sequencing, Analysis

**LazyLoad** yes

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dREG_HD	<i>Run dREG-HD</i>
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## Description

Run dREG-HD

## Usage

```
dREG_HD(bed_path,
        bigwig_plus,
        bigwig_minus,
        model,
        ncores=1,
        use_rgtsvm = FALSE )
```

**Arguments**

<code>bed_path</code>	path to the dREG peaks in bed format
<code>bigwig_plus</code>	the path the the plus strand of bigwig file
<code>bigwig_minus</code>	the path the the minus strand of bigwig file
<code>model</code>	the dREG-HD model trained by dREG-HD
<code>ncores</code>	Number of CPU cores in parallel computing
<code>use_rgtsvm</code>	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")
model_path <-system.file("extdata","dREG_HD.model.rdata", package="dREG.HD")
load(model_path)

dREG_HD(bed_path= bed_path, bigwig_plus = bigwig_plus, bigwig_minus =bigwig_minus, model=model)
```

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\*Topic **function**

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