# Package 'dREG.HD'

October 19, 2016

**Version** 1.0.0

**Date** 2016-09-12

**Title** Refining dREG peaks by imputing DNase-I hypersensitivity site

**Author** Tinyi Chu, Charles G. Danko `<tc532@cornell.edu>`

**Maintainer** Tinyi Chu `<tc532@cornell.edu>`

**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

## R topics documented:

---

| dREG_HD | *Run dREG-HD* |
|---------|---------------|

---

## Description

Run dREG-HD

## Usage

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

**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` | the dREG-HD model trained by dREG-HD |
| `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")
load(model_path)

dREG_HD(bed_path= bed_path, bigwig_plus = bigwig_plus, bigwig_minus =bigwig_minus,chromIn
```

# Index