Data for the HelloRanges Tutorial

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Package

HelloRangesData 1.38.0

Contents

1 Overview 2

1 Overview

In support of the tutorial vignette for the *HelloRanges* package, *HelloRangesData* provides an experimental dataset on DnaseI hypersensitivity [1], as well as several annotation tracks downloaded from the UCSC genome browser. The files were made available as part of the *bedtools* tutorial (http://quinlanlab.org/tutorials/bedtools/bedtools.html) by Aaron Quinlan.

The data are stored in files here:

```
> dir(system.file("extdata", package="HelloRangesData"))

 [1] "cpg.bed"
 [2] "exons.bed"
 [3] "fBrain-DS14718.hotspot.twopass.fdr0.05.merge.bed"
 [4] "fBrain-DS16302.hotspot.twopass.fdr0.05.merge.bed"
 [5] "fHeart-DS15643.hotspot.twopass.fdr0.05.merge.bed"
 [6] "fHeart-DS15839.hotspot.twopass.fdr0.05.merge.bed"
 [7] "fHeart-DS16621.hotspot.twopass.fdr0.05.merge.bed"
 [8] "fIntestine_Sm-DS16559.hotspot.twopass.fdr0.05.merge.bed"
 [9] "fIntestine_Sm-DS16712.hg19.hotspot.twopass.fdr0.05.merge.bed"
[10] "fIntestine_Sm-DS16822.hotspot.twopass.fdr0.05.merge.bed"
[11] "fIntestine_Sm-DS17808.hg19.hotspot.twopass.fdr0.05.merge.bed"
[12] "fIntestine_Sm-DS18495.hg19.hotspot.twopass.fdr0.05.merge.bed"
[13] "fKidney_renal_cortex_L-DS17550.hg19.hotspot.twopass.fdr0.05.merge.bed"
[14] "fLung_L-DS17154.hg19.hotspot.twopass.fdr0.05.merge.bed"
[15] "fLung_L-DS18421.hg19.hotspot.twopass.fdr0.05.merge.bed"
[16] "fLung_R-DS15632.hotspot.twopass.fdr0.05.merge.bed"
[17] "fMuscle_arm-DS19053.hg19.hotspot.twopass.fdr0.05.merge.bed"
[18] "fMuscle_back-DS18454.hg19.hotspot.twopass.fdr0.05.merge.bed"
[19] "fMuscle_leg-DS19115.hg19.hotspot.twopass.fdr0.05.merge.bed"
[20] "fMuscle_leg-DS19158.hg19.hotspot.twopass.fdr0.05.merge.bed"
[21] "fSkin_fibro_bicep_R-DS19745.hg19.hotspot.twopass.fdr0.05.merge.bed"
[22] "fStomach-DS17659.hg19.hotspot.twopass.fdr0.05.merge.bed"
[23] "gwas.bed"
[24] "hesc.chromHmm.bed"
[25] "hg19.genome"
```

There are 20 BED files from the DnaseI study, as well as BED files representing the CpG islands ('`cpg.bed`'), Refseq exons ('`exons.bed`'), disease-associated SNPs ('`gwas.bed`'), and functional annotations output by chromHMM given ENCODE human embrionic stem cell ChIP-seq data ('`hesc.chromHmm.bed`'). There is also a '`hg19.genome`' file indicating the chromosome lengths of the hg19 genome build.

Please see the *HelloRanges* vignette to learn how to work with these data with *Bioconductor*.

References

[1] Matthew T Maurano, Richard Humbert, Eric Rynes, Robert E Thurman, Eric Haugen, Hao Wang, Alex P Reynolds, Richard Sandstrom, Hongzhu Qu, Jennifer Brody, et al. Systematic localization of common disease-associated variation in regulatory dna. *Science*, 337(6099):1190–1195, 2012.