

# Package ‘HelloRangesData’

December 19, 2024

**Type** Package

**Title** Data for the HelloRanges tutorial vignette

**Version** 1.33.0

**Author** Michael Lawrence

**Maintainer** Michael Lawrence <michafla@gene.com>

**Description** Provides the data that were used in the bedtools tutorial by Aaron Quinlan (<http://quinlanlab.org/tutorials/bedtools/bedtools.html>). Includes a subset of the DnaseI hypersensitivity data from ``Maurano et al. Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. Science. 2012. Vol. 337 no. 6099 pp. 1190-1195." The rest of the tracks were originally downloaded from the UCSC table browser. See the HelloRanges vignette for a port of the bedtools tutorial to R.

**License** GPL (>= 2)

**Suggests** BiocStyle

**biocViews** ExperimentData, SequencingData

**git\_url** <https://git.bioconductor.org/packages/HelloRangesData>

**git\_branch** devel

**git\_last\_commit** b837d27

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-12-19

## Contents