

# Package ‘HelloRangesData’

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**Type** Package

**Title** Data for the HelloRanges tutorial vignette

**Version** 1.29.0

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**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>

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