# Package 'HelloRangesData'

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**Type** Package

**Title** Data for the HelloRanges tutorial vignette

**Version** 1.33.0

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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

**git_branch** devel

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