fitCons.UCSC.hg19

November 17, 2026

`fitCons.UCSC.hg19-package`
Annotation package for UCSC human fitCons scores of fitness consequence of functional annotations

---

Description

This annotation package stores fitCons scores from UCSC for the human genome (hg19), corresponding to fitness consequences of functional annotations. The data are stored in the form of `Rle` objects and are loaded automatically as an object of class `GScores`. The name of the exposed object matches the name of the package and part of the filename that contained the data imported into the package. The class definition and methods to access `GScores` objects are found in the `GenomicScores` software package.

Format

`fitCons.UCSC.hg19` GScores object containing fitCons conservation scores from UCSC for the human genome (hg19) c

Author(s)

R. Castelo

Source

Gulko B, Gronau I, Hubisz MJ, Siepel A. Probabilities of fitness consequences for point mutations across the human genome. Nat. Genet. 2015 Aug;47:276-83. (http://www.nature.com/ng/journal/v47/n3/full/ng.3196.htm

CSHL website of the Siepel Lab (URL: `http://http://siepellab.labsites.cshl.edu`) [March, 2018, accessed]

See Also

`GScores` `GenomicScores`

Examples

```
library(GenomicRanges)
library(fitCons.UCSC.hg19)

ls("package:fitCons.UCSC.hg19")

fitcons <- fitCons.UCSC.hg19
citation(fitcons)
gscores(fitcons, GRanges("chr7:117232380-117232384"))
```

Index

∗ **data**
fitCons.UCSC.hg19-package, 1
∗ **package**
fitCons.UCSC.hg19-package, 1

fitCons.UCSC.hg19, *1*
fitCons.UCSC.hg19
*(*fitCons.UCSC.hg19-package*)*, 1
fitCons.UCSC.hg19-package, 1

GenomicScores, *1*
GScores, *1*

Rle, *1*