Package 'preciseTADhub'

March 11, 2025

Type Package

Title Pre-trained random forest models obtained using preciseTAD

Version 1.15.0

Description An experimentdata package to supplement the preciseTAD package containing pre-trained models and the variable importances of each genomic annotation used to build the model parsed into list objects and available in ExperimentHub. In total, preciseTADhub provides access to n=84 random forest classification models optimized to predict TAD/chromatin loop boundary regions and stored as .RDS files. The value, n, comes from the fact that we considered l=2 cell lines {GM12878, K562}, g=2 ground truth boundaries {Arrowhead, Peakachu}, and c=21 autosomal chromosomes {CHR1, CHR2, ..., CHR22} (omitting CHR9). Furthermore, each object is itself a two-item list containing: (1) the model object, and (2) the variable importances for CTCF, RAD21, SMC3, and ZNF143 used to predict boundary regions. Each model is trained via a ``holdout'' strategy, in which data from chromosomes {CHR1, CHR2, ..., CHRi-1, CHRi+1, ..., CHR22} were used to build the model and the ith chromosome was reserved for testing. See https://doi.org/10.1101/2020.09.03.282186 for more detail on the model building strategy.

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Depends R (>= 4.1)

Encoding UTF-8

LazyData true

Suggests knitr, rmarkdown, markdown, BiocStyle, preciseTAD

Imports ExperimentHub

VignetteBuilder knitr

biocViews ExperimentData, PackageTypeData, ExperimentHub, Genome

NeedsCompilation no

RoxygenNote 7.1.1

BugReports https://github.com/dozmorovlab/preciseTADhub/issues

URL https://github.com/dozmorovlab/preciseTADhub

git_url https://git.bioconductor.org/packages/preciseTADhub

git_branch devel

git_last_commit 25e0ff0

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-03-11

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Contents

`preciseTADhub-package` *Pre-trained models obtained using preciseTAD as* `list` *objects.*

Description

preciseTADhub is package that give users access to pre-trained random forest models that can be leveraged to predict TAD and/or chromatin loop boundaries using the preciseTAD R package. These data have been parsed into `list` objects and RDS files and are available in `ExperimentHub`.

Details

See the vignette for examples of using these data in predicting precise boundary location at base-level resolution.

browseVignettes("preciseTADhub")

Details of how these data were created are in the scripts/ directory of the source package.

Examples

```
## Not run:
library(ExperimentHub)
eh <- ExperimentHub()
myfiles <- query(eh, "preciseTADhub")
CHR1_GM12878_5kb_Arrowhead <- myfiles[[1]]

## End(Not run)
```

readEH *A wrapper function for efficiently reading in user-specified random forest models generated by* preciseTAD::TADrandomForest*, built on cell-line specific CTCF, RAD21, SMC3, and ZNF143 ChIP-seq peak regions.*

Description

A wrapper function for efficiently reading in user-specified random forest models generated by preciseTAD::TADrandomForest, built on cell-line specific CTCF, RAD21, SMC3, and ZNF143 ChIP-seq peak regions.

Usage

```
readEH(chr, cl, gt, source)
```

Arguments

chr	Which chromosome was used as the holdout during the training process. That is, all other chromosomes were combined when building the random forest.
cl	The cell line that was used (either "GM12878" or "K562")
gt	The ground-truth TAD or chromatin loop boundaries used to construct the binary response vector (either "Arrowhead" or "Peakachu".
source	The source of the files stored on ExperimentHub using query(hub, "package_name").

Value

A trained model object from caret

Examples

```
# Suppose we want to read in the model that was built using CHR1-CHR21,
# on GM12878, using Arrowhead defined TAD boundaries at 5kb resolution.

#Initialize ExperimentHub
library(ExperimentHub)
hub <- ExperimentHub()
query(hub, "preciseTADhub")
myfiles <- query(hub, "preciseTADhub")

CHR22_GM12878_5kb_Arrowhead <- readEH(chr = "CHR22",
                                      cl = "GM12878",
                                      gt = "Arrowhead",
                                      source = myfiles)
```

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