

# Package ‘preciseTADhub’

July 10, 2025

**Type** Package

**Title** Pre-trained random forest models obtained using preciseTAD

**Version** 1.16.0

**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>

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**Author** Spiro Stilianoudakis [aut],  
           Mikhail Dozmorov [aut, cre]  
**Maintainer** Mikhail Dozmorov <mikhail.dozmorov@gmail.com>

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

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## 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)
```



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## \* **utilities**

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