TENET.AnnotationHub

May 20, 2026

`ENCODE_PLS_regions` *ENCODE PLS regions*

Description

A GRanges object containing regions of candidate cis-regulatory elements with promoter-like signatures as identified by the ENCODE SCREEN project. These consist of regions with high H3K4me3 and DNase signal, and located within 200 bp of a GENCODE transcription start site. **Citation:** ENCODE Project Consortium; Moore JE, Purcaro MJ, Pratt HE, et al. Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature. 2020 Jul;583(7818):699-710. doi: 10.1038/s41586-020-2493-4. Epub 2020 Jul 29. Erratum in: Nature. 2022 May;605(7909):E3. PMID: 32728249; PMCID: PMC7410828.

Usage

```
ENCODE_PLS_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 40,734 ranges and no metadata.

Source

https://screen.encodeproject.org

Examples

```
ENCODE_PLS_regions()
```

`ENCODE_dELS_regions` *ENCODE dELS regions*

Description

A GRanges object containing regions of candidate cis-regulatory elements with distal enhancer-like signatures as identified by the ENCODE SCREEN project. These consist of regions with high H3K27ac and DNase signal, but low H3K4me3 signal, and located more than 2kb from GENCODE transcription start sites. **Citation:** ENCODE Project Consortium; Moore JE, Purcaro MJ, Pratt HE, et al. Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature. 2020 Jul;583(7818):699-710. doi: 10.1038/s41586-020-2493-4. Epub 2020 Jul 29. Erratum in: Nature. 2022 May;605(7909):E3. PMID: 32728249; PMCID: PMC7410828.

Usage

```
ENCODE_dELS_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 786,756 ranges and no metadata.

Source

`https://screen.encodeproject.org`

Examples

```
ENCODE_dELS_regions()
```

`ENCODE_pELS_regions` *ENCODE pELS regions*

Description

A GRanges object containing regions of candidate cis-regulatory elements with proximal enhancer-like signatures as identified by the ENCODE SCREEN project. These consist of regions with high H3K27ac and DNase signal, but low H3K4me3 signal, and located 2kb or less from GENCODE transcription start sites. **Citation:** ENCODE Project Consortium; Moore JE, Purcaro MJ, Pratt HE, et al. Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature. 2020 Jul;583(7818):699-710. doi: 10.1038/s41586-020-2493-4. Epub 2020 Jul 29. Erratum in: Nature. 2022 May;605(7909):E3. PMID: 32728249; PMCID: PMC7410828.

Usage

```
ENCODE_pELS_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 171,292 ranges and no metadata.

Source

https://screen.encodeproject.org

Examples

```
ENCODE_pELS_regions()
```

`TENET_10_cancer_panel_enhancer_regions`

TENET 10 cancer panel enhancer regions

Description

A composite GRanges object containing regions of putative enhancer elements from 10 different cancer types (BRCA, BLCA, COAD, ESCA, HNSC, KIRP, LIHC, LUAD, LUSC, and THCA) primarily for use in the TENET Bioconductor package. This dataset is composed of H3K27ac and H3K4me1 peaks from ChIP-seq datasets collected from Cistrome.org and processed using the ENCODE pipelines. For additional information on component datasets, see the manifest file hosted at https://github.com/rhielab/TENET.AnnotationHub/blob/devel/data-raw/TENET_10_cancer_panel_enhancer_regions_manifest.tsv.

Usage

```
TENET_10_cancer_panel_enhancer_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 4,798,784 non-reduced ranges and metadata consisting of 1 variable. The peaks within each cancer type are reduced, but the final dataset with peaks across all 10 cancer types is not reduced.

`TYPE` (character) Lists which of the ten cancer types (BLCA, BRCA, COAD, ESCA, HNSC, KIRP, LIHC, LUAD, LUSC, or THCA) each region is relevant to

Examples

```
TENET_10_cancer_panel_enhancer_regions()
```

`TENET_10_cancer_panel_open_chromatin_regions`

TENET 10 cancer panel open chromatin regions

Description

A composite GRanges object containing regions of open chromatin from 10 different cancer types (BRCA, BLCA, COAD, ESCA, HNSC, KIRP, LIHC, LUAD, LUSC, and THCA) primarily for use in the TENET Bioconductor package. This dataset is composed of peaks from DNase I and ATAC-seq datasets collected from Cistrome.org and processed using the ENCODE guidelines, along with additional TCGA ATAC-seq peaks from cancer samples of these ten types. For additional information on component datasets, see the manifest file hosted at `https://github.com/rhielab/TENET.AnnotationHub/blob/devel/data-raw/TENET_10_cancer_panel_open_chromatin_regions_manifest.tsv`.

Usage

```
TENET_10_cancer_panel_open_chromatin_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 7,514,441 non-reduced ranges and metadata consisting of 1 variable. The peaks within each cancer type are reduced, but the final dataset with peaks across all 10 cancer types is not reduced.

`TYPE` (character) Lists which of the ten cancer types (BLCA, BRCA, COAD, ESCA, HNSC, KIRP, LIHC, LUAD, LUSC, or THCA) each region is relevant to

Examples

```
TENET_10_cancer_panel_open_chromatin_regions()
```

`TENET_10_cancer_panel_promoter_regions`

TENET 10 cancer panel promoter regions

Description

A composite GRanges object containing regions of putative promoter elements from 10 different cancer types (BRCA, BLCA, COAD, ESCA, HNSC, KIRP, LIHC, LUAD, LUSC, and THCA) primarily for use in the TENET Bioconductor package. This dataset is composed of H3K27me3 peaks from ChIP-seq datasets collected from Cistrome.org and processed using the ENCODE guidelines. For additional information on component datasets, see the manifest file hosted at `https://github.com/rhielab/TENET.AnnotationHub/blob/devel/data-raw/TENET_10_cancer_panel_promoter_regions_manifest.tsv`.

Usage

```
TENET_10_cancer_panel_promoter_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 2,627,647 non-reduced ranges and metadata consisting of 1 variable. The peaks within each cancer type are reduced, but the final dataset with peaks across all 10 cancer types is not reduced.

`TYPE` (character) Lists which of the ten cancer types (BLCA, BRCA, COAD, ESCA, HNSC, KIRP, LIHC, LUAD, LUSC, or THCA) each region is relevant to

Examples

```
TENET_10_cancer_panel_promoter_regions()
```

`TENET_consensus_enhancer_regions`

TENET consensus enhancer regions

Description

A composite GRanges object containing regions of putative enhancer elements from a variety of sources, primarily for use in the TENET Bioconductor package. This dataset is composed of regions of strong enhancers as annotated by the Roadmap Epigenomics ChromHMM expanded 18-state model based on 98 reference epigenomes, lifted over to the hg38 genome (the following 4 states represent strong enhancers: 7: Genic enhancer1, 8: Genic enhancer2, 9: Active Enhancer 1, and 10: Active Enhancer 2), as well as regions of human permissive enhancers identified by the FANTOM5 project in phase 1 and phase 2. For additional information on component datasets, see the manifest file hosted at `https://github.com/rhielab/TENET.AnnotationHub/blob/devel/data-raw/TENET_consensus_datasets_manifest.tsv`. **Citations:** Roadmap Epigenomics Consortium; Kundaje A, Meuleman W, Ernst J, et al. Integrative analysis of 111 reference human epigenomes. Nature. 2015 Feb 19;518(7539):317-30. doi: 10.1038/nature14248. PMID: 25693563; PMCID: PMC4530010. Lizio M, Harshbarger J, Shimoji H, et al. Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biol 16(1), 22 (2015). Abugessaisa I, Ramilowski JA, Lizio M, et al. FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. Nucleic Acids Res. 2021 Jan 8;49(D1):D892-D898. doi: 10.1093/nar/gkaa1054. PMID: 33211864; PMCID: PMC7779024.

Usage

```
TENET_consensus_enhancer_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 403,602 ranges and no metadata.

Source

`https://egg2.wustl.edu/roadmap/web_portal/chr_state_learning.html`
`https://fantom.gsc.riken.jp/5/data/`

Examples

```
TENET_consensus_enhancer_regions()
```

`TENET_consensus_open_chromatin_regions`

TENET consensus open chromatin regions

Description

A composite GRanges object containing regions of open chromatin from a variety of sources, primarily for use in the TENET Bioconductor package. This dataset is composed of DNase I hypersensitive regions from the master list compiled from 125 cell types by ENCODE, lifted over to the hg38 genome, along with TCGA ATAC-seq peaks from 410 cancer samples of 23 cancer types. For additional information on component datasets, see the manifest file hosted at `https://github.com/rhielab/TENET.AnnotationHub/blob/devel/data-raw/TENET_consensus_datasets_manifest.tsv`. **Citations:** ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. Nature. 2012 Sep 6;489(7414):57-74. doi: 10.1038/nature11247. PMID: 22955616; PMCID: PMC3439153. Thurman RE, Rynes E, Humbert R, et al. The accessible chromatin landscape of the human genome. Nature. 2012 Sep 6;489(7414):75-82. doi: 10.1038/nature11232. PMID: 22955617; PMCID: PMC3721348. Corces MR, Granja JM, Shams S, et al. The chromatin accessibility landscape of primary human cancers. Science. 2018 Oct 26;362(6413):eaav1898. doi: 10.1126/science.aav1898. PMID: 30361341; PMCID: PMC6408149.

Usage

```
TENET_consensus_open_chromatin_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 2,525,827 ranges and no metadata.

Source

`https://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeAwgDnaseMasterSites/`
`https://genome.ucsc.edu/cgi-bin/hgTrackUi?db=hg19&g=wgEncodeAwgDnaseMasterSites`
`https://gdc.cancer.gov/about-data/publications/ATACseq-AWG`

Examples

```
TENET_consensus_open_chromatin_regions()
```

`TENET_consensus_promoter_regions`

TENET consensus promoter regions

Description

A composite GRanges object containing regions of putative promoter elements from a variety of sources, primarily for use in the TENET Bioconductor package. This dataset is composed of regions flanking transcription start sites as annotated by the Roadmap Epigenomics ChromHMM expanded 18-state model based on 98 reference epigenomes, lifted over to the hg38 genome (the following 4 states represent regions flanking transcription start sites: 1: Active TSS, 2: Flanking TSS, 3: Flanking TSS Upstream, and 4: Flanking TSS Downstream). For additional information on component datasets, see the manifest file hosted at `https://github.com/rhielab/TENET.AnnotationHub/blob/devel/data-raw/TENET_consensus_datasets_manifest.tsv`. **Citation:** Roadmap Epigenomics Consortium; Kundaje A, Meuleman W, Ernst J, et al. Integrative analysis of 111 reference human epigenomes. Nature. 2015 Feb 19;518(7539):317-30. doi: 10.1038/nature14248. PMID: 25693563; PMCID: PMC4530010.

Usage

```
TENET_consensus_promoter_regions(metadata = FALSE)
```

Arguments

`metadata`	If TRUE, retrieve the AnnotationHub metadata instead of the object itself. Defaults to FALSE.

Value

A GRanges object with 361,315 ranges and no metadata.

Source

`https://egg2.wustl.edu/roadmap/web_portal/chr_state_learning.html`

Examples

```
TENET_consensus_promoter_regions()
```

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