Cerberus annotation file specifications (Human)

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Software used

- cerberus (https://github.com/fairliereese/cerberus/releases/tag/v1) v1

Cerberus annotation object

After installing cerberus (from the above link), one can read in the annotation object using the following Python code

```
import cerberus
ca = cerberus.read(<cerberus annotation>.h5)
```

Fields of the CerberusAnnotation object

TSS / TES tables

Accessible using `ca.tss` and `ca.tes` respectively. These tables hold information of each TSS or TES region used to form the cerberus reference. File format roughly follows BED format with the following column specifications:

- Chromosome
- Start
- End
- Strand

- Name
    - Formed from the gene ID that the region is associated with and a number to make it unique. For example, ENSG00000000460_1 or ENSG00000000460_2
- source
    - Comma-separated list of sources that support the use of each region as a TSS or TES that were used as input into cerberus
- novelty
    - Novelty of region with respect to the sources used as references in the cerberus run. Will be either ‘Known’ or ‘Novel’
- gene_id
    - Gene ID that the region is associated with
- tss or tes
    - Number that is concatenated with gene_id to form the Name column

IC table

Accessible using `ca.ic`. This table holds information about each intron chain used to form the cerberus reference. File format is as follows:

- Chromosome
- Strand
- Coordinates
    - Hyphen-concatenated list of intron starts and end coordinates
    - Coordinates do NOT include the start of the first exon or end of the last exon
    - Monoexonic transcripts have a single hyphen as their coordinates
- Name
    - Formed from the gene ID that the IC is associated with and a number to make it unique. For example, ENSG00000000460_1 or ENSG00000000460_2
- source
    - Comma-separated list of sources that support the use of each IC that were used as input into cerberus
- novelty
    - Novelty of IC with respect to the sources used as references in the cerberus run. Will be one of the following: ‘Known’, ‘Unspliced’, ‘NNC’, ‘NIC’, ‘ISM’
    - Novelty categories based on terminology coined by SQANTI: https://github.com/ConesaLab/SQANTI
- gene_id
    - Gene ID that the IC is associated with
- ic
    - Number that is concatenated with gene_id to form the Name column

TSS / TES maps

Accessible using `ca.tss_map` or `ca.tes_map`. This table has information from the `cerberus agg_tss or agg_tes` run about which cerberus region each input region was assigned to. File format is as follows:

- Chromosome
- Start
- End
- Strand
- source
    - Name of the source that the input region came from
- Name
    - Name of the TSS or TES that the input region was assigned to. These regions are the ones named in `ca.tss` or `ca.tes`.

Transcript maps

Accessible using `ca.t_map`. This table has information from the `cerberus annotate_transcriptome` steps about which TSS, TES, and IC was assigned to each transcript from an input GTF. File format is as follows:

- original_transcript_id
    - Original ID of transcript used in input GTF
- ic
    - Number of IC used in this transcript
- ic_id
    - Name of IC used in this transcript, these names are in the `ca.ic.Name` column
- tss
    - Number of TSS used in this transcript
- tss_id
    - Name of TSS used in this transcript, these names are in the `ca.tss.Name` column
- tes
    - Number of TES used in this transcript
- tes_id
    - Name of TES used in this transcript, these names are in the `ca.tes.Name` column
- gene_id
    - Gene ID that input transcript is associated with
- gene_name
    - Name of gene that input transcript is associated with
- original_transcript_name
    - Original name of transcript used in input GTF
- transcript_triplet

    - Transcript triplet associated with this transcript based on the TSS, IC, and TES it was assigned
    - Formed as concatenation of other columns: [tss,ic,tes]
- transcript_id
    - New ID for transcript computed by cerberus based on the TSS, IC, and TES it was assigned
    - Formed as concatenation of other columns: gene_name[tss,ic,tes]
- transcript_name
    - New name for transcript computed by cerberus based on the TSS, IC, and TES it was assigned
    - Formed as concatenation of other columns: gene_id[tss,ic,tes]
- source
    - Nickname assigned to input GTF from which the input transcript was derived

Gene triplets

Accessible using `ca.triplets`. This table has information about the various gene triplets calculated for the ENCODE LR-RNA-seq project. File format is as follows:

- source
    - Name of the source used to compute the gene triplets
    - Can either be the name of a GTF that was annotated with `cerberus annotate_transcriptome` or another name that a different set of triplets was calculated from
        - Sources from annotated GTFs: lapa (representative of the ENCODE LR-RNA-seq dataset), v40, v29, GTEx
        - all: All isoforms annotated across all the sources
        - obs_det: All detected isoforms from the ENCODE LR-RNA-seq data (>=1 TPM in at least one library)
        - sample_det: Sample-level detected isoforms from the ENCODE LR-RNA-seq data (>= 1 TPM) in a given sample
        - sample_major: Sample-level major isoforms from the ENCODE LR-RNA-seq data. Major isoforms must be detected in the sample and together, are responsible for a cumulative 90% of the gene's expression in the given sample to be part of this set.
        - obs_major: The union of all major isoforms across every sample
        - obs_mm_det: All detected isoforms from the ENCODE LR-RNA-seq data (>= 1 TPM in at least one library) from libraries that roughly match the biosamples in the corresponding mouse LR-RNA-seq dataset
        - obs_mm_major: The union of major isoforms across the libraries that roughly match the biosamples in the corresponding mouse LR-RNA-seq dataset
- gid
    - Gene ID of gene triplet

- n_tss
    - Number of TSSs found for this gene triplet
- n_tes
    - Number of TESs found for this gene triplet
- n_ic
    - Number of ICs found for this gene triplet
- n_iso
    - Number of isoforms used to compute this gene triplet
- splicing_ratio
    - The splicing ratio (calculated as (2*n_ic)/(n_tss+n_tes))
- tss_ratio
    - The simplex coordinates for TSS usage calculated as n_tss/(n_tss+splicing_ratio+n_tes)
- spl_ratio
    - The simplex coordinates for TSS usage calculated as splicing_ratio/(n_tss+splicing_ratio+n_tes)
- tes_ratio
    - The simplex coordinates for TSS usage calculated as n_tes/(n_tss+splicing_ratio+n_tes)
- sector
    - The sector on the simplex that this gene falls in. One of ‘tss’, ‘splicing’, ‘tes’, ‘mixed’ or ‘simple’
- gname
    - Gene name of gene triplet
- sample
    - For the sample level triplets, the sample that the triplet was calculated in; otherwise NaN
- gene_tpm
    - For the sample level triplets, the TPM of the gene in the sample that the triplet was calculated in; otherwise NaN