3.1 - Tool ASTA (AS Event Retriever)

Description

The AStalavista tool asta extracts all alternative splicing (AS) events from a given genomic annotation of exon-intron gene coordinates. By comparing all given transcripts, AStalavista detects the variations in their splicing structure and identify all AS events (like exon skipping, alternate donor, etc) by assigning to each of them an AS code. You can use AStalavista for any genome by providing your own annotation set, the identifier of your gene(s) of interest, or analyze the AS landscape of reference annotation datasets like Gencode, RefSeq, Ensembl, FlyBase,...The output is provided in a specific GTF format.

References

- Foissac S, Sammeth M (2007) *ASTALAVISTA: dynamic and flexible analysis of alternative splicing events in custom gene datasets.* Nucleic Acids Research 35 (Web Server issue): W297-299
- Sammeth M, Foissac S, Guigó R (2008) *A general definition and nomenclature for alternative splicing events.* PLoS Computational Biology 4(8): e1000147 doi:10.1371/journal.pcbi.1000147
- Sammeth M (2009) *Complete alternative splicing events are bubbles in splicing graphs.* Journal of Computational Biology 16: 1117-1140

Examples

Pairwise AS event extraction from a transcriptome

```
astalavista -t asta -i <annotation.gtf>
```

where <annotation.gtf> is an annotation in GTF format. The output file (also a GTF format for AS events) is written to the same folder as the input, and can be redirected by the command line flag "–eo". For more information, cf. the Section Parameters.

Complete AS events

```
astalavista -t asta -i <annotation.gtf> -d 0
```

The command retrieves events in their complete resolution according to the provided transcriptome annotation <annotation.gtf>: events with two, three, four, etc. alternate variants are output together instead of breaking them down to pairwise events.

Including events linked to alternative transcription initiation and alternative poly-adenylation, cleavage and 3'-end formation

```
astalavista -t asta -i <annotation.gtf> -e [ASE,ASI]
```

The command line flag "-e" specifies the types of events that are collected: ASE are "external" AS events that include splicing variations linked to alternative transcription start and polyA/cleavage sites, ASI are "internal" AS events that are delimited by common splice sites at both ends. More information about different event type options can be found in the Section Parameters.

Outputting splice site sequences

```
astalavista -t asta -i <annotation.gtf> -c <genome-folder> -a [SEQ]
```

Output splice sites with their flanking splice site sequences. ⚠️ Note that for obtaining sequences, FASTA files with the genomic sequence are required (e. g. chr1.fasta, chr2.fasta, scaffoldXYZ.fasta, ...).