.PAR Parameters

Name	Tool(s)	Long	Short	Value	Since	Description
~~COMPLETE3~~	asta	~~--cp3~~		~~Boolean~~	~~2.2~~	~~Require 3' complete transcripts~~ **DEPRECATED**, by (3.1) refactored to OUTOPTIONS.CP3
~~GENOME~~ CHR_SEQ	all	~~--genome~~ --chr	~~-g~~ -c	File	~~2.2~~ 3.1	Path to a folder with genomic sequences, one per chromosome (.FASTA format). The header tags of each chromosome have to coincide with the <seqname> field ($1) of the annotation (GTF file).
EVENTS	asta	--ev	-e	{ASE,ASI,DSP, VST}	3.1	Types of events that are considered: • ASE: external AS events • ASI: internal AS events • DSP: adDitional SPlicing events • VST: Variable SiTe events
EVENTS_ATR	asta	--ea	-a	{CP3,CSS,FLT, IOK,NMD,SEQ}	3.1	Event Attributes • CP3: predict 3'-complete • CSS: consider only introns with canonical splice sites • FLT: output flank type, 'constitutive' or 'alternative' • IOK: consider only introns that are acceptable considering basic splicing rules • NMD: predict NMD • SEQ: output splice site sequences of event flanks
EVENTS_DIMENSION	asta	 --ed	~~-k~~ -d	Integer	0.0 3.1	Dimension of the AS events to be extracted, Default is 2 (i.e. 'pairwise events'), and values < 2 stand for 'complete' events <TM>
EVENTS_FILE	asta	~~--out~~ --eo	-o	File|stdout	0.0 3.1	Keyword 'stdout' for writing results to the standard output stream, or a fully qualified path to the output file. The parameter is optional--if nothing is specified, the output will be written to a file '<input file>_astalavista.gtf.gz'.
EVENTS_OPT	asta	--ep	-p	{FLT,NMD,CP3}	3.1	Flags to control output options for events: • CP3: predict 3'-complete • CSS: consider canonical splice sites only • FLT: output flank type, i.e., 'constitutive' or 'alternative' site • IOK: acceptable introns • NMD: predict NMD • SEQ: output splice site sequences
EDGE_CONFIDENCE	asta	--ec		Integer	2.2	Level of confidence for edges (i.e., annotated transcription starts/poly-adenylation sites). The default is to trust no annotated edge and to extend overlapping first/last exons of a transcript to their most extreme position: • 0 if 'RefSeq' appears in the source field of the annotation • 1 if 'mRNA' appears in the source field of the annotation • 2 if 'EST' appears in the source field of the annotation • 3 if if none of the above applies All transcript edges of confidence level > edgeConfidence are extended in case the annotation shows another exon with the same adjacent splice site and an earlier/later start/end. **DEPRECATED**, to be refactored (soon)
~~FLANK_TYPE~~	asta	~~--flankType~~		~~Boolean~~	~~2.2~~	~~Output the type of the event flanks, i.e., 'constitutive' or 'alternative'.~~ **DEPRECATED**, by (3.1) refactored to OUTOPTIONS.FTY
GENE_ID	scorer	--gid	-g	File	3.1	Name and path of the GeneID parameter file with models for splice sites
HELP	all		-h	Boolean	3.0	Help on usage, list of parameters and corresponding descriptions
~~INPUT~~ **IN_FILE**	all	**--in**	**-i**	**File**	~~0.0~~ **3.1**	**Input file with reference annotation (.GTF format), MANDATORY**
INTRON_CONFIDENCE	asta	--ic		Integer	2.2	Level of intron confidence, below which introns are trusted without checks. The default is to trust all introns (i.e., ic= 255). Introns are assigned a confidency class: • 0 for 'RefSeq' appears in the source field of the annotation • 1 for 'mRNA' appears in the source field of the annotation • 2 for 'EST' appears in the source field of the annotation All introns in transcripts of confidence level > threshold are discarded. **DEPRECATED**, to be refactored (soon)

NMD	asta	--nmd			2.2	Check nonsense-mediated decay conditions. **DEPRECATED**, by (3.1) refactored to OUTOPTIONS.NMD
SITES	scorer	--ss	-s	{SSD,SSA,TSS, CLV,SST,SND, AUG,STP}	3.1	Types of sites that are output: • SSD: Splice Site Donor • SSA: Splice Site Acceptor • TSS: Transcription Start Site • CLV: Cleavage Site • SST: Soft Start (Unconfirmed 5'-end of transcribed sequence) • SND: Soft End (Unconfirmed 3'-end of transcribed sequence) • AUG: Start Codon • STP: Stop Codon
SITE_FILE	scorer	--so	-f	File|stdout	3.1	Keyword 'stdout' for writing results to the standard output stream, or a fully qualified path to the output file.
SITE_OPT	asta	--sp	-t	{SSS}	3.1	Flags to control optional output for sites: • SSS: Splice Site Score
SEQ_SITE	asta	--seqsite		Boolean	2.2	Output splice site sequences with events. **DEPRECATED**, by (3.1) refactored to EVENTS_ATR
TMP_DIR	all	--tmp		File	0.0	The temporary directory, reads the environment variable when set to 'null'.
VARIANT_ FILE	scorer	--vcf	v	File	3.1	Name and path of a file with the variant information (.VCF format)