

Create CEAS Report Element

Provides summary statistics on ChIP enrichment in important genomic regions such as individual chromosomes, promoters, gene bodies or exons, and infers the genes most likely to be regulated by the binding factor under study.

Parameters in GUI

Parameter	Description	Default value
Output report file	Path to the report output file. Result for CEAS analysis.	
Output annotations file	Name of tab-delimited output text file, containing a row of annotations for every RefSeq gene. (file is not generated if no peak location data is supplied).	
Gene annotations table	Path to gene annotation table (e.g. a refGene table in sqlite3 db format (--gt)).	hg19
Span size	Span from TSS and TTS in the gene-centered annotation (base pairs). ChIP regions within this range from TSS and TTS are considered when calculating the coverage rates in promoter and downstream (--span).	3000
Wiggle profiling resolution	Wiggle profiling resolution. WARNING: Value smaller than the wig interval (resolution) may cause aliasing error. (--pf-res).	50
Promoter/downstream interval	Promoter/downstream intervals for ChIP region annotation are three values or a single value can be given. If a single value is given, it will be segmented into three equal fractions (e.g. 3000 is equivalent to 1000,2000,3000) (--rel-dist).	3000
BiPromoter ranges	Bidirectional-promoter sizes for ChIP region annotation. It's two values or a single value can be given. If a single value is given, it will be segmented into two equal fractions (e.g. 5000 is equivalent to 2500,5000) (--bisizes).	5000
Relative distance	Relative distance to TSS/TTS in WIGGLE file profiling (--rel-dist).	3000
Gene group files	Gene groups of particular interest in wig profiling. Each gene group file must have gene names in the 1st column. The file names are separated by commas (--gn-groups).	
Gene group names	Set this parameter empty for using default values. The names of the gene groups from "Gene group files" parameter. These names appear in the legends of the wig profiling plots. Values range: comma-separated list of strings. Default value: 'Group 1, Group 2,...Group n' (--gn-group-names).	

Parameters in Workflow File

Type: ceas-report

Parameter	Parameter in the GUI	Type
image-file	Output report file	<i>string</i>
anns-file	Output annotations file	<i>string</i>
anns-table	Gene annotations table	<i>string</i>
span	Span size	<i>numeric</i>
profiling-resolution	Wiggle profiling resolution	<i>numeric</i>
promoter-sizes	Promoter/downstream interval	<i>numeric</i>
promoter-bisizes	BiPromoter ranges	<i>string</i>
relative-distance	Relative distance	<i>string</i>
group-files	Gene group files	<i>string</i>
group-names	Gene group names	<i>string</i>

Input/Output Ports

The element has 1 *input port*:

Name in GUI: CEAS data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Enrichment signal	enrichment-signal	<i>ann-table-list</i>
Peak regions	peak-regions	<i>string</i>