

Annotate Peaks with peak2gene Element

Gets refGenes near the ChIP regions identified by a peak-caller.

Element type: peak2gene-id

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Genome file	Select a genome file (sqlite3 file) to search refGenes. (--genome).	hg19	genome	<i>string</i>
Output file	Select which type of genes need to output. up for genes upstream to peak summit, down for genes downstream to peak summit, all for both up and down. (--op).	all	outpos	<i>string</i>
Official gene symbols	Output official gene symbol instead of refseq name. (--symbol).	False	symbol	<i>boolean</i>
Distance	Set a number which unit is base. It will get the refGenes in n bases from peak center. (--distance).	3000	distance	<i>numeric</i>

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Peak2gene data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Treatment features	_treat-ann	<i>ann-table-list</i>

And 1 *output port*:

Name in GUI: Peak2gene output data

Name in Workflow File: out-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Gene regions	gene-annotation	<i>ann-table-list</i>
Peak regions	peak-annotation	<i>ann-table-list</i>