Annotate Peaks with peak2gene Element

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

Parameters in GUI

Parameter	Description	Default value
Genome file	Select a genome file (sqlite3 file) to search refGenes. (--genome).	hg19
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
Official gene symbols	Output official gene symbol instead of refseq name. (--symbol).	False
Distance	Set a number which unit is base. It will get the refGenes in n bases from peak center. (--distance).	3000

Parameters in Workflow File

Type: peak2gene-id

Parameter	Parameter in the GUI	Type
genome	**Genome file**	*string*
outpos	**Output file**	*string*
symbol	**Official gene symbols**	*boolean*
distance	**Distance**	*numeric*

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**	*ann-table-list*

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**	*ann-table-list*
Peak regions	**peak-annotation**	*ann-table-list*