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shRNAremoveOverlap, v9

Remove shRNAs overlapping in sequence > 3 basepairs from a gct data file

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Algorithm Version:

Introduction

shRNAremoveOverlap is a GenePattern module that removes shRNAs which overlap in sequence by greater than three basepairs from a GCT data file. Generally, it keeps shRNAs (rows) in a GCT data file, based on a user-defined list of shRNAs. The module outputs a new, smaller GCT file containing the dataset with any overlapping shRNAs removed (only keeps the shRNAs from the user-defined list).

Parameters

Name	Description
list *	The list of shRNAs that are not overlapping.
gct file *	The input gct data file.
mapping *	The shRNA to gene mapping file.
prefix *	The file name prefix.

* - required

Input Files

1. list
   - The list of shRNAs that are not overlapping. Each shRNA needs to be on a separate line of the file.
2. gct file
   - Data file containing shRNA data (GCT file format).
3. mapping file

  - The shRNA to gene mapping file.

Output Files

1. Data file with overlapping shRNAs removed   [prefix]_filtered2.rnai.gct
   - A GCT file containing the dataset with any overlapping shRNAs removed (only keeps the shRNAs from the user defined list).

Platform Dependencies

Task Type:
RNAi

CPU Type:
any

Operating System:
any

Language:
R

Version Comments

Version	Release Date	Description
9	2013-03-20	updated command line
8	2013-03-20	