

DependencyBiomarkerDotplot Documentation

Description:

Creates a dotplot of Achilles gene dependency scores. The dots are colored based on the biomarker status of the cell line (i.e. mutation in gene or no mutation in gene). This module was created for use in the Broad Institute's Education Outreach high school computational curriculum.

Author:

Sara Howell (showell@broadinstitute.org)

Date:

7/2014

Summary:

DependencyBiomarkerDotplot is a GenePattern module that creates a dotplot for each user-inputted gene to help visually identify a possible gene dependency-biomarker pair. The user inputs a csv file containing Achilles gene level dependency data and a csv file containing biomarker data (i.e. mutation status). A pdf is created containing a dot plot for each gene of interest the user inputs. Each dot on the plot corresponds to one cell line and is colored based on the biomarker status of the gene in the cell line.

Input Parameters:

Name	Description
Achilles gene dependency scores data file	Format is a csv file, with cell lines in rows and genes in columns
Biomarker data file	Format is a csv file, with cell lines in rows and genes in columns
Genes #1-5	Please enter at least one and up to five genes of interest in the text boxes. The gene names should match exactly to the column names in the data files and are case-sensitive.

Output Files:

1. PDF containing a dotplot for each gene of interest.

DependencyBiomarkerPlot_*[Genes #1-5]*.pdf

Memory Requirements on GenePattern Server: 4G

Platform Dependencies

Module Type: RNAi
CPU type: any
OS: any
Language: R-2.15
R Packages Required: ggplot2_0.9.3.1