



## PrognosticGene

**Description:** Evaluate clinical outcome association of a gene

**Author:** Kensuke Kojima, Yujin Hoshida (Icahn School of Medicine at Mount Sinai, yujin.hoshida@mssm.edu)

### Summary

This module evaluates association of a gene of interest with clinical outcome (time-to-event outcome) based on user-defined cut-off of expression level of the gene (using percentile or standard deviation).

### Parameters

Name	Description
Gene of interest	Gene name or Probe ID of interest in first column of input.exp.file.
input exp filename	Gene expression data (.gct)
input outcome filename	Clinical outcome data (time and censor variables). 1st column should be sample names in the same order with .gct file (tab-delimited .txt).
output name	Prefix for output files.
cutoff percentile	Cut-off to group samples (percentile). If "0", cutoff.sd is used. Default: 0
cutoff sd	Cut-off to group samples (mean + standard deviation). If "0", cutoff.percentile is used. Default: 0
time field	Name of survival time variable (time to event)



sensor field	Name of sensor variable (0:ensor, 1:event)
curve type	Type of survival curve ("event" or "survival")

### Input Files

1. input exp filename (.gct)  
Normalized gene expression dataset in GenePattern GCT file format.
2. input outcome filename (.txt)  
Clinical dataset including time-to-event variable and censoring information. Tab-delimited text.

### Output Files

1. Bar graph of gene expression (.png)
2. Kaplan-Meier curve (.png)
3. Summary of log-rank test (.txt)
4. Summary data table (clinical data, expression data, class information) (.txt)

### Example Data

[provide example data, including input files and parameter settings; this could be links to example data files on a server or FTP site somewhere]

### Platform Dependencies

<b>Module type:</b>	Module
<b>CPU type:</b>	Any
<b>OS:</b>	Any
<b>Language:</b>	R