



## SurvivalDifference

**Description:** Tests for survival differences based on cls files  
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**Summary:** Once a genomics marker or predictive model for clinical outcome is built, the next step is to test whether it really predicts outcome of new cohorts, or whether it has better predictive ability compared to already known clinical markers/predictive models. "Survival analysis" modules perform such analyses seamlessly after clustering/marker gene/prediction analyses.

SurvivalDifference tests if there is a difference between two or more survival curves based on sample classes defined by genomic data. The log-rank test (Mantel-Haenszel test) and the generalized Wilcoxon test (Peto & Peto modification of the Gehan-Wilcoxon test) can be used [1-4]. These tests also can be performed only for sample classes of interest using the "subgroup" parameter.

### References:

1. Therneau TM. *Modeling Survival Data: Extending the Cox Model*. 2001, Springer, Berlin
2. Lumley T. *survival 2.20*, R package, <http://www.r-project.org/>
3. Venables WN, Ripley BD. *Survival Analysis in Modern Applied Statistics with S-PLUS*, 3<sup>rd</sup> Ed. 1999, Springer, New York.
4. Toyama N. *Survival analysis using R* in *The R Book*, Okada M, Ed. 2004, Kyuten-sha, Tokyo, p310-39

### Parameters:

Name	Description	Choices
input surv data file	Clinical data containing survival time and censor status -.txt Format shown below.	
input cls file	Class information file -.cls Specify either this file or the <i>cls.field</i> parameter.	
time field	Name of survival time field	Default: time
censor field	Name of censor field (event="1", no event="0")	Default: status
cls field	Name of class field in survival data file (optional) Specify either this value or the <i>input.cls.filename</i> parameter.	
test type	Type of test	log-rank test (default), generalized Wilcoxon test
subgroup	Subgroups (classes) to be compared (e.g. A, C as in 3 <sup>rd</sup> line of .cls file)	
output filename	Name of output file	Default: <output.filename>_SurvivalDifferenceTest.txt

# GenePattern

## Format for survival data input file:

<i>case id</i>	<i>&lt;cls.field&gt;</i>	<i>&lt;sensor.field&gt;</i>	<i>&lt;time.field&gt;</i>
<i>id1</i>	<i>class of case id1</i>	<i>event of case id1</i>	<i>event time of case id1</i>
<i>id2</i>	<i>class of case id2</i>	<i>event of case id2</i>	<i>event time of case id2</i>
<i>id3</i>	<i>class of case id3</i>	<i>event of case id3</i>	<i>event time of case id3</i>
<i>id4</i>	<i>class of case id4</i>	<i>event of case id4</i>	<i>event time of case id4</i>
...	...	...	...

The class labels are taken from either the .cls file or the <cls.field> column in the survival data input file (*input.cls.filename* or *cls.field* parameter, respectively). The <sensor.field> column contains either a 0 or 1 with event=1 or censor=0. The <time.field> is entered as a numeric value in survival data file.

### Example input files: [surv.txt](#), [surv.cls](#)

The example files contain mock data. To run an analysis using these files, enter “time” in the time field, and “censor” in the sensor field.

### Output Files:

1. <output.filename>\_SurvivalDifferenceTest.txt: summary of the results.

### Platform dependencies:

<b>Module type:</b>	Survival Analysis
<b>CPU type:</b>	any
<b>OS:</b>	any
<b>Language:</b>	R 2.5