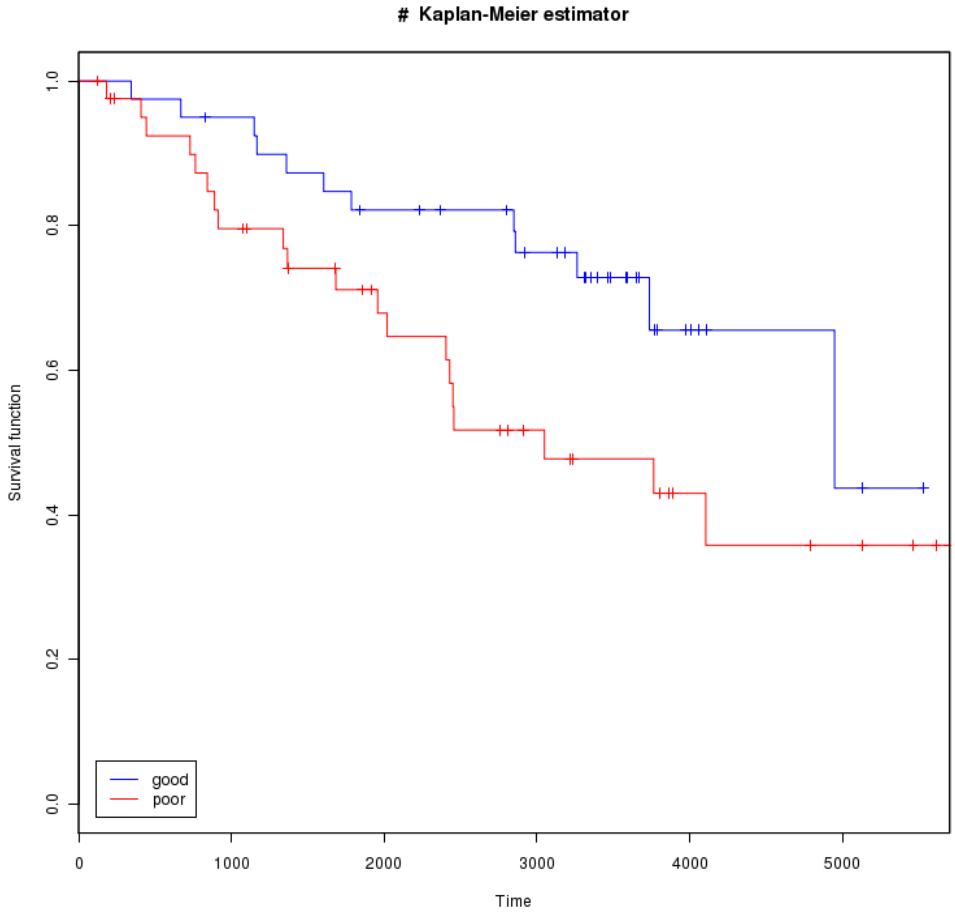
SurvivalCurve

Description: Draws survival curve based on cls file
Author: Yujin Hoshida (Broad Institute) gp-help@broadinstitute.org

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. SurvivalCurve generates survival curve for censored survival data [1-4]:



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*, 3rd 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

GenePattern

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 *cls.field* 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 *input.cls.filename* parameter.	
print fit results	whether to print survival fit results	no (default); yes: creates text output files as well as survival curve plot
line type color assign	assign line type/color automatically or manually	automatic (default); manual: uses parameter values to define line attributes
manual line type	line type(s) to use Ignored unless *line.type.color.assign* is manual.	1=solid, 2=dashed, 3=dotted, 4=dot-dashed
manual line color	line color(s) to use Ignored unless *line.type.color.assign* is manual.	e.g., black, blue, red, …
line width	line width	thin; thick; thickest
time conversion	survival time conversion	none (default); days to years; months to years
max time	maximum time (in original scale)	
surv function lower	lower limit of y axis range	Default: 0
surv function higher	upper limit of y axis range	Default: 1
curve type	type of survival curve	survival (default); event; cumulative hazard, complimentary log-log survival
show conf interval	show confidence interval?	yes (default) no
add legend	show legend?	yes (default); no
legend position	position of legend	left-bottom (default), left-top, right-bottom, right-top
output filename	name for output files	

Format for survival data input file:

case id	*<cls.field>*	*<censor.field>*	*<time.field>*
id1	*class of case id1*	*event of case id1*	*event time of case id1*
id2	*class of case id2*	*event of case id2*	*event time of case id2*
id3	*class of case id3*	*event of case id3*	*event time of case id3*
id4	*class of case id4*	*event of case id4*	*event time of case id4*
…	…	…	…

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 <censor.field> column contains either a 0 or 1 with event=1 or censor=0. The <time.field> is entered as a numeric value.

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 status field.

Output Files:

1. <output.filename>_SurvivalCurve.(png/pdf): Survival curve plot.
2. Text output of survival estimate (created if *print.fit.results* = yes):
   <output.filename>_FitSummary.txt,
   <output.filename_Table.txt

Platform dependencies:

Module type: Survival Analysis
CPU type: any
OS: any
Language: R 2.7

GenePattern Module Version Notes

Date	Version	Description
8/3/2012	v.3	SurvivalCurve v.3 modified to use R 2.7 and Cairo to output images in PNG format