

CASAS: Cancer Survival Analysis Suite Tutorial

TAB 1. STANDARD SURVIVAL ANALYSIS

CASAS: Cancer Survival Analysis Suite **Standard Survival Analysis** Competing Risk Survival Analysis Landmark Survival Analysis Quantile Survival Analysis Optimal Cutoff Point Finder Grid for Summarized Significance Tutorial About Us

Read Me Univariate Survival Association (Cox Model) KM Analysis and Plot

NOTE1: In this tab, you are able to carry out standard survival analysis. On the left side panel, you have the options to upload data; select variables for univariate survival association analysis with cox proportional hazard model; meanwhile, select the variables for Kaplan Meier analysis; download the output table and plot accordingly.

NOTE2: To carry out univariate survival association analysis, it is based on cox proportional hazards model with entering one variable in the model each time. Select the variables of interest to generate the output table. You can choose the option to be "Yes" if you want to test the proportional hazard assumption.

NOTE3: To carry out Kaplan Meier Analysis, the variable of interest can be All Patients or a categorical variable. You also need to specify the time unit corresponding to the data in order for the plot to display correctly.

DATA FORMAT

1. Data should be input as a .txt or .xlsx or .csv file. The first row of the data file have information about the variables.
2. The remaining lines contain measurements one line per each subject/sample, described in the format below.
3. The first column of the file contains the survival time 'time' (column 1), survival status 'status' (column 2) followed by the other variables of interest.
a) Column_1: This should contain the survival time, for the user's reference.
b) Column_2: This should contain the Survival status, input as 'censored' vs 'dead'.
c) Remaining Columns: These columns should contain information with variables of interest, such as age, race, gender and patient id kept as reference.

Input your file
Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Variables for UVA
Select a Time Variable for Survival Analysis
time

Select a Censoring Variable for Survival Analysis
status

Select multiple Variables to Generate Univariate Survival Association Table
age sex

Test for Proportional Hazards Assumption:
☐ Yes
☒ No

Step 1:

Select the example dataset or upload your own.

To view example data and format, use download button to view .csv file.

Step 2:

The variables from the input file will be available as drop down for selection.

Choose appropriate survival time, censor status (0- Censor, 1- Event) variables from your uploaded dataset.

Step 3:

Enter variable(s) to generate the univariate analysis table to test association between variable and survival.

Optionally, user can test for Proportional Hazards assumption by selecting "yes". An additional column with the test p-value will be added to the results table.

Choose Variables for KM Analysis

Select a Categorical X-axis Variable as Cohort Group

sex

Select a Time Variable to Visualize KM Plot

time

Select a Censoring Variable to Visualize KM Plot

status

Time Unit:

- ☐ Years
☐ Months
☒ Days

Risk Table:

- ☒ Yes
☐ No

Step 4:

Choose appropriate categorical group, survival time, censor status (0- Censor, 1- Event) variables from your uploaded dataset to carry out Kaplan Meir analysis.

User can also select the appropriate time unit (Years, Months or Days). Days being the default.

Step 5:

User can opt to display the number at risk table under the KM curve in each categorical group.

Downloads

Type the file name you would like to save as

survivabletable

Download Survival Report

Type the file name you would like to save as

kmplot

Download KM Plot

Step 6:

User can download the results from the univariate analysis association for the variable(s) of his/her interest.

Step 7:

User can download the KM plot with or without the at risk table below as selected previously.

[Read Me](#) [Univariate Survival Association \(Cox Model\)](#) [KM Analysis and Plot](#)

Univariate Survival Association Analysis for Multiple Selected Variables

Show 10 entries

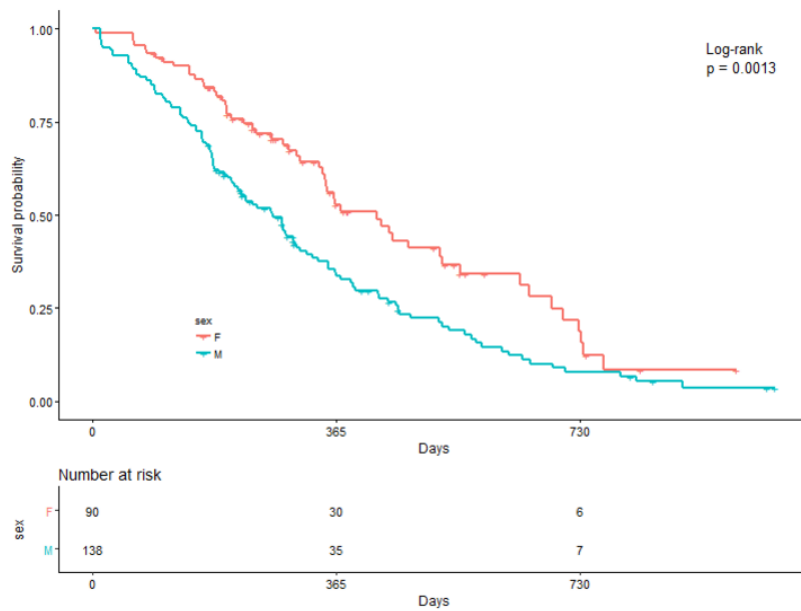
| Variable | Level | N | Hazard Ratio (95% CI) | Type 3 P-value | Log-rank P-value |
|----------|-------|-----|-----------------------|----------------|------------------|
| age | | 228 | 1.02 (1-1.04) | 0.0419 | - |
| sex | M | 138 | 1.7 (1.23-2.36) | 0.0015 | 0.0013 |
| | F | 90 | | | |

Showing 1 to 3 of 3 entries

Previous 1 Next

Univariate Survival Association analysis table is displayed for the single or multiple variables selected by the user. For example, here age and sex are being tested.

To Visualize the Kaplan Meier Plot:



KM plot stratified by the categorical variable sex. An at risk table is displayed under the KM plot. The time unit is days but can be changed using the options mentioned previously.

TAB 2. COMPETING RISK SURVIVAL ANALYSIS

CASAS: Cancer Survival Analysis Suite Standard Survival Analysis **Competing Risk Survival Analysis** Landmark Survival Analysis Quantile Survival Analysis Optimal Cutoff Point Finder Grid for Summarized Significance Tutorial About Us

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Variables for UVA

Select a Time Variable for Competing Risk Survival Analysis

ftime

Select a Censoring Variable for Competing Risk Survival Analysis

Status

Select multiple Variables to Generate Univariate Survival Association Table

Sex D Phase

Event Code:

☒ 1
☐ 2
☐ 0

Censor Code:

☐ 1
☐ 2
☒ 0

Read Me Univariate Survival Association (Fine and Gray Model) CIF Analysis and Plot

NOTE1: In this tab, you are able to carry out a competing risk survival analysis. The method is based on Fine and Gray's Model. On the left side panel, you have the options to upload data; select variables for univariate survival association analysis with Fine and Gray model; meanwhile, select the variables for cumulative incidence function analysis; download the output table and plot accordingly.

NOTE2: For UVA, choose variables of interest to enter the analysis. Meanwhile, you need to specify event code and censor code.

NOTE3: To generate a CIF plot and table, choose a categorical variable to compare or All Patient for overall. You can select the correct time unit based on the data. Also, you can choose to input time points of interest or not. Censor code is also need to be specified.

DATA FORMAT

1. Data should be input as a .txt or .xlsx or .csv file. The first row of the data file have information about the variables.

2. The remaining lines contain measurements one line per each subject/sample, described in the format below.

3. The first column contains survival time, the second column includes the survival status, followed by the other variables of interest.

a) Column_1: This should contain the Survival time, for the user's reference.

b) Column_2: This should contain the survival status, input as 0 for 'censored' vs 1 for 'dead'.

c) Remaining Columns: These columns should contain information with variables of interest, such as age, race, gender and patient id kept as reference.

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Variables for UVA

Select a Time Variable for Competing Risk Survival Analysis

ftime

Select a Censoring Variable for Competing Risk Survival Analysis

Status

Select multiple Variables to Generate Univariate Survival Association Table

Sex D Phase

Event Code:

☒ 1
☐ 2
☐ 0

Censor Code:

☐ 1
☐ 2
☒ 0

Step 1:

Select the example dataset or upload your own.

To view example data and format, use download button to view .csv file.

Step 2:

The variables from the input file will be available as drop down for selection.

Choose appropriate survival time, censor status (0/1/2) variables from your uploaded dataset.

For competing risk analysis, the user needs to select the code for the event and the censor. The third/last code would be the competing risk.

Step 3:

Enter variable(s) to generate the univariate analysis table to test association between variable and survival using Fine and Gray Model.

Choose Variables for CIF Analysis

Input Time Points:

☐ Yes

☒ No

Time Points Input

0, 10, 20, 30

Select a Categorical X-axis Variable as Cohort Group

Source

Select a Time Variable to Visualize CIF Plot

ftime

Select a Censoring Variable to Visualize CIF Plot

Status

Time Unit:

☐ Years

☒ Months

☐ Days

Event Code:

☒ 1

☐ 2

☐ 0

Censor Code:

☐ 1

☐ 2

☒ 0



Step 4:

Choose the time points at which CIF Estimate is to be reported. User can input time points of their choice or use the predefined time points at 0, 10, 20, 30 days.



Step 5:


Choose appropriate categorical group for stratifying the data, survival time, censor status (0- Censor, 1- Event, 2- Competing Risk) variables from your uploaded dataset to carry out CIF analysis. The user can select different status codes based on their data.

User can also select the appropriate time unit (Years, Months or Days). Days being the default.

Downloads

Type the file name you would like to save as

crrtable

 Download Competing Risk Report



Step 6:

User can download the results from the univariate analysis association for the variable(s) of his/her interest.

Type the file name you would like to save as

cifplot

 Download CIF Plot




Step 7:

User can download the CIF plot stratified by the categorical variable by event and competing risk. Gray's p-value is reported.

Type the file name you would like to save as

ciftable

 Download CIF Report



Step 8:

User can download the CIF result table for the time points of interest based on the strata.

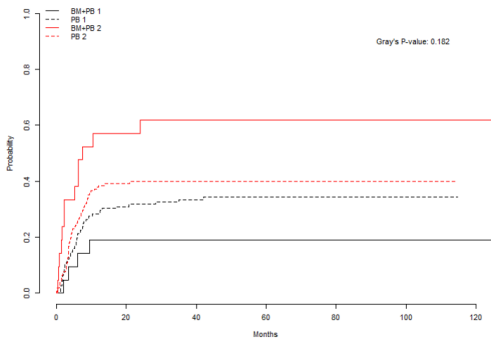
Univariate Competing Risk Survival Association Analysis for Multiple Selected Variables

Show 10 entries Search:

| Variable | Level | N | Hazard Ratio (95% CI) | Type 3 P-value | Gray's P-value |
|----------|---------|-----|-----------------------|----------------|----------------|
| Sex | M | 100 | 1.08 (0.64-1.84) | 0.77 | 0.7993 |
| | F | 77 | | | |
| D | AML | 104 | 0.64 (0.38-1.07) | 0.088 | 0.0907 |
| | ALL | 73 | | | |
| Phase | CR2 | 45 | 1.14 (0.48-2.74) | 0.77 | 0.199 |
| | CR3 | 12 | 1.38 (0.38-5.08) | 0.63 | |
| | Relapse | 73 | 3.04 (1.47-6.29) | 0.0027 | |
| | CR1 | 47 | | | |

Showing 1 to 8 of 8 entries Previous 1 Next

To Visualize the Cumulative Incidence Function Plot:



Show 100 entries Search:

| Source | Time (Months) | CIF Estimate (95% CI) |
|---------|---------------|------------------------|
| BM+PB 1 | 0 | 0 (NaN, NaN) |
| | 20 | 0.1905 (0.055, 0.3874) |
| | 40 | 0.1905 (0.055, 0.3874) |
| | 60 | 0.1905 (0.055, 0.3874) |
| | 80 | 0.1905 (0.055, 0.3874) |
| | 100 | 0.1905 (0.055, 0.3874) |
| | 120 | 0.1905 (0.055, 0.3874) |

Univariate Survival Association analysis table is displayed for the single or multiple variables selected by the user. For example, here association of Sex, Disease type and Phase of the disease are being tested.

CIF plot stratified by the categorical variable source and further by the event and the

CIF estimate table at 10, 20, 30 days (Time points) chosen by the user.

TAB 3. LANKMARK SURVIVAL ANALYSIS

CASAS: Cancer Survival Analysis Suite

Standard Survival Analysis

Competing Risk Survival Analysis

Landmark Survival Analysis

Quantile Survival Analysis

Optimal Cutoff Point Finder

Grid for Summarized Significance

Tutorial

About Us

Read Me

Landmark Survival Plot

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Variables for KM Analysis

Select a Categorical X-axis Variable as Cohort Group

sex

Select a Time Variable to Visualize CIF Plot

time

Select a Censoring Variable to Visualize CIF Plot

status

Input Time Point for Landmark Analysis

200

Time Unit:

Years

Months

Days

KM or CIF:

KM

CIF

NOTE1: In this tab, you are able to carry out landmark survival analysis. On the left side panel, you have the options to upload data; select variables for landmark analysis; you also need to specify the value for landmark analysis; download the output plot accordingly.

NOTE2: The analysis is based on the function from R package 'dynpred' to generate the landmark dataset.

NOTE3: You also need to specify the time unit corresponding to the data in order for the plot to display correctly. You can choose to get KM curves or CIF curves per research interest.

DATA FORMAT

1. Data should be input as a .txt or .xlsx or .csv file. The first row of the data file have information about the variables.

2. The remaining lines contain measurements one line per each subject/sample, described in the format below.

3. The first column of the file contains the survival time 'time' (column 1), survival status 'status' (column 2) followed by the other variables of interest.

a) Column_1. This should contain the survival time, for the user's reference.

b) Column_2. This should contain the Survival status, input as 'censored' vs 'dead'.

c) Remaining Columns. These columns should contain information with variables of interest, such as age, race, gender and patient id kept as reference.

Step 1:

Select the example dataset or upload your own.

To view example data and format, use download button to view .csv file.

Step 2:

The variables from the input file will be available as drop down for selection.

Choose appropriate Categorical group variable to stratify the data, survival time, censor status (0- Censor, 1- Event) variables from your uploaded dataset.


For Landmark analysis, additionally user needs to input the time point for landmark analysis. This should be in the same time unit as the survival time. Survival time unit also needs to be specified. By default, it is days.

Step 3:

Choose to display either a KM curve or a CIF curve for the landmark analysis. If user selects a KM curve option, a combined KM curve for overall survival until the landmark time followed by a landmark KM curve is generated with their respective p-values.

Downloads

Type the file name you would like to save as

 Download Landmark Plot



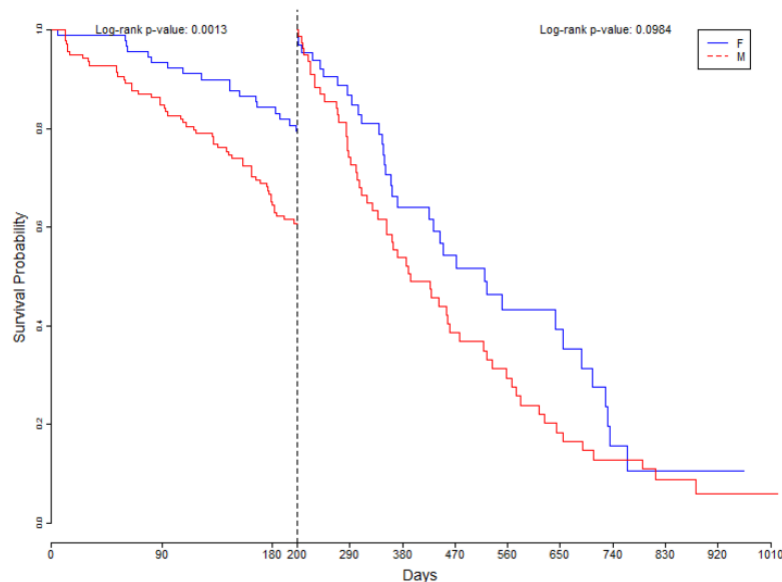
Step 4:

User can download the Landmark plot stratified by the categorical variable. Log rank p-values are also reported.

[Read Me](#)

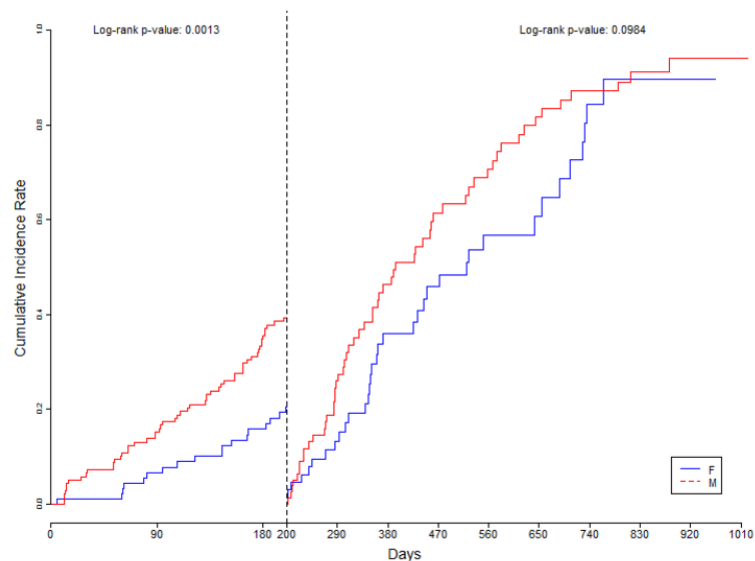
Landmark Survival Plot

To Visualize the Landmark Survival Plot:



A landmark analysis KM plot stratified by the categorical variable. Left side shows the overall survival curve and the right side represents the landmark survival plot.

To Visualize the Landmark Survival Plot:



Alternatively, a landmark analysis CIF plot stratified by the categorical variable.

KM or CIF:

☐ KM

☒ CIF

Left side shows the overall survival curve and the right side represents the landmark survival plot.

TAB 4. QUANTILE SURVIVAL ANALYSIS

CASAS: Cancer Survival Analysis Suite Standard Survival Analysis Competing Risk Survival Analysis Landmark Survival Analysis **Quantile Survival Analysis** Optimal Cutoff Point Finder Grid for Summarized Significance Tutorial About Us ▾

Read Me **Quantile Survival Plots and Output**

Input your file
Select an example ds or upload your own with 'Load my own'

Example ds File ▾

Download Example data

Choose Variable
Select Variable
log2_SAMHD1_Plus1 ▾

Choose Cutoff Point:

☐ Optimal Cutoff
☒ 25th Percentile
☐ 50th Percentile
☐ 75th Percentile

Choose Reference Level:

☒ Not Low
☐ Low

Run & generate a random numbers

Hit Run & Generate random number button above to display output on main panel.

NOTE1: In this tab, you are able to carry out quantile survival analysis. The quantile survival analysis in this shiny app is based on the method developed by Huang (2010 & 2016). For each quantile, the survival time difference will estimated with 95% CI. If it included 0, then that quantile is not significant. Otherwise, it is significant in that quantile.

NOTE2: On the left side panel, you have the options to upload data; select a continuous variable of interest to be dichotomized with optimal cutoff, 25 percentile, 50 percentile, 75 percentile; the option to choose reference level needs to be specified by the user with respect to interest; download the output table and plot accordingly.

NOTE3: Once you click the Run & Generate a random number button, the app will start to run the quantile survival analysis. You can then check the output plots and tables in the second subtab.

DATA FORMAT

1. Data should be input as a .txt or .xlsx or .csv file. The first row of the data file have information about the variables.
2. The remaining lines contain measurements one line per each subject/sample, described in the format below.
3. The first column of the file contains sample id, the second column includes the survival status 'os_censor' (column 2), survival time 'os_time' (column 3) followed by the other variables of interest.
 - a) Column_1: This should contain the Survival status, input as 0 for 'censored' vs 1 for 'dead'.
 - b) Column_2: This should contain the survival time, for the user's reference.
 - c) Remaining Columns: These columns should contain information with variables of interest, such as age, race, gender and patient id kept as reference.

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File ▾

Download Example data

Choose Variable

Select Variable

log2_SAMHD1_Plus1 ▾

Choose Cutoff Point:

- ☐ Optimal Cutoff
☒ 25th Percentile
☐ 50th Percentile
☐ 75th Percentile

Choose Reference Level:

- ☒ Not Low
☐ Low

Run & generate a random numbers

Hit Run & Generate random number button above to display output on main panel.

Step 1:

Select the example dataset or upload your own.

To view example data and format, use download button to view .csv file.

Step 2:

The variables from the input file will be available as drop down for selection.

Choose appropriate continuous variable (e.g. gene expression) you wish to stratify data. Based on your question of interest, user can choose the cut point to dichotomize the data (eg. Optimal cut-off using martingales residuals, based on the 25th, 50th or 75th percentile).

Accordingly, the reference category needs to be selected.


Step 3:

In order to run the analysis, user needs to hit 'Run & generate a random number'.

Downloads


Type the file name you would like to save as

QAplot

 Download Quantile Survival Plot


Type the file name you would like to save as

forestplot

 Download Forest Plot

Type the file name you would like to save as

Data for grid

 Download grid Data

Step 4:

User can download the Quantile Survival plot. This includes the overall KM analysis plot and the plot of mean survival differences between the two groups for each quantile.

Step 5:

User can download the Forest plot summar. This includes the overall KM analysis plot and the plot of mean survival differences between the two groups for each quantile.

Step 6:

If a user is interested in multiple genes (variables) in the same dataset or multiple datasets (for example, numerous cancer types), they can download the table of mean difference estimates for a comparative grid in tab 6.

Read Me

Quantile Survival Plots and Output

The three plots from left to right are as following:

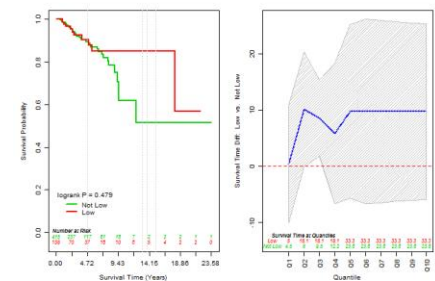
1. The first plot is KM plot with number at risk table for overall survival and log rank test p-value.
2. The second plot is the survival time difference with 95% CI between two dichotomized groups at 10 quantiles as Q1 to Q10 (defined as 10 percentile to 100 percentile by 10 percentile at mean survival time among all patients).
3. The third plot is the summary using forest plot for the survival time difference at 10 quantiles. The overall in forest plot corresponds to the transformed HR and 95% CI for overall survival (log(1/HR)). The transformed HR will be interpret as if 0 is included then it is not significant.

NOTE1: The first table contains hazard ratio and 95% CI with cox proportional hazard model for the overall survival with the variable of interest in the original scale.

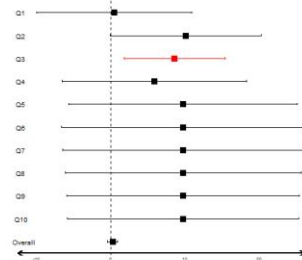
NOTE2: The second table 'Data for Forest Plot' contains information to generate the forest plot. For item 'overall', it shows the transformed HR and 95% CI. The last column in this table includes information of direction. It is also needed to generate a summarized Grid if you have multiple cancer types or subgroups.

NOTE3: To generate a summarized Grid if you have multiple cancer types or subgroups, you can download the data for Grid in the left side panel. You only need to keep the first two columns and transpose the data. Repeat this for different cancer types or subgroups and combine as a new datafile to generate a Grid in the tab: Grid for summarized significance'.

Quantile Survival Analysis Plots



Forest Plot for Survival Time Difference



Left to Right: Quantile Survival analysis plots stratified by the dichotomous groups, survival time difference with 95% CI between two dichotomized groups at 10 quantiles as Q1 to Q10 (defined as 10 percentile to 100 percentile by 10 percentile at mean survival time among all patients) based on method developed by Huang (2010 &2016). The third plot is the summary using forest plot for the survival time difference at 10 quantiles. The overall in forest plot corresponds to the transformed HR and 95% CI for overall survival (log(1/HR)). The transformed HR will be interpret as if 0 is included then it is not significant.

Univariate Cox Survival Analysis Table

Show 10 entries

Search:

| | Hazard Ratio | 95% CI Lower Limit | 95% CI Upper Limit | Z Score | P-value |
|---|--------------|--------------------|--------------------|---------|---------|
| 1 | 1.2757 | 0.399 | 1.5396 | -0.707 | 0.4796 |

Showing 1 to 1 of 1 entries

Previous1Next

Data for Forest Plot

Show entries

Search:

| | Quantiles | Mean Time Difference/Transformed Hazard Ratio(log(1/HR)) | CI Lower Limit | CI Upper Limit | Significance(0: Non-sig, 1:Not Low Better, 2:Low Better, 3:Non-estimable) |
|----|-----------|--|----------------|----------------|---|
| 1 | Q1 | 0.4466 | -10.0049 | 10.8981 | 0 |
| 2 | Q2 | 10.0677 | -0.1156 | 20.2911 | 0 |
| 3 | Q3 | 6.5808 | 1.7771 | 15.3945 | 2 |
| 4 | Q4 | 5.8548 | -6.6139 | 18.3235 | 0 |
| 5 | Q5 | 9.7315 | -5.7029 | 25.1689 | 0 |
| 6 | Q6 | 9.7315 | -6.6366 | 26.1028 | 0 |
| 7 | Q7 | 9.7315 | -6.4835 | 25.9468 | 0 |
| 8 | Q8 | 9.7315 | -6.1721 | 25.6351 | 0 |
| 9 | Q9 | 9.7315 | -5.9719 | 25.435 | 0 |
| 10 | Q10 | 9.7315 | -5.8856 | 25.3487 | 0 |
| 11 | Overall | 0.2435 | 0.9187 | -0.4316 | 0 |

Showing 1 to 11 of 11 entries

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Univariate Survival Association analysis table is displayed for the variable of interest.

Quantile wise mean survival time estimates with 95% CI limits with significance. This is useful for combining data from different cancer types or different variables (genes) in the same dataset.

TAB 5. OPTIMAL CUT-OFF FINDER

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Variable

Select Variable

log2_SAMHD1_Plus1

Downloads

Type the file name you would like to save as

MRplot

Download Martingale Residual Plot

Read Me **Optimal Cutoff Point Finder Output**

NOTE1: In this tab, you are able to search for optimal cutpoint for a continuous variable of interest. The method is based on Contal and O'Quigley (1999) and has also been implemented in SAS by Mandrekar et al. (2003).

NOTE2: In the output, a martingale residual plot is included. In the following table, you can find the cutpoint value of the variable and corresponding percentile.

DATA FORMAT

1. Data should be input as a .txt or .xlsx or .csv file. The first row of the data file have information about the variables.
2. The remaining lines contain measurements one line per each subject/sample, described in the format below.
3. The first column of the file contains sample id, the second column includes the survival status 'os_censor' (column 2), survival time 'os_time' (column 3) followed by the other variables of interest.
 - a) Column_1 This should contain the Survival status, input as 0 for 'censored' vs 1 for 'dead'.
 - b) Column_2 This should contain the survival time, for the user's reference.
 - c) Remaining Columns. These columns should contain information with variables of interest, such as age, race, gender and patient id kept as reference.

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Variable

Select Variable

log2_SAMHD1_Plus1

Downloads

Type the file name you would like to save as

MRplot

Download Martingale Residual Plot

Step 1:

Select the example dataset or upload your own.

To view example data and format, use download button to view .csv file.

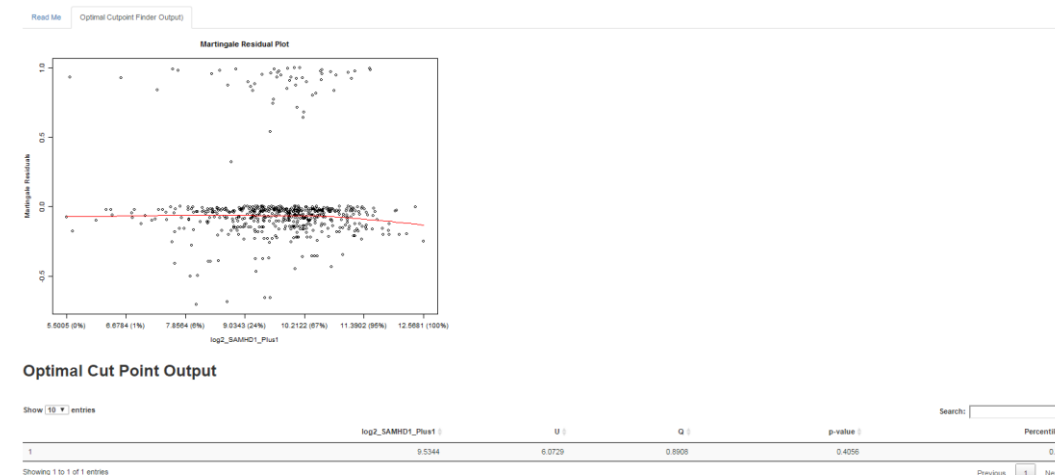
Step 2:

The variables from the input file will be available as drop down for selection.

Choose appropriate continuous variable (eg. gene expression) for which you wish to determine optimal cut – point based on Contal and O'Quigley (1999).

Step 3:

User can download the Martingale residual plot.



Martingale residual plot along with cut point value of the variable and corresponding percentile.

TAB 6. GRID FOR SUMMARIZED SIGNIFICANCE

Read Me

Summarized Significance Grid

NOTE1: In this tab, you are able to generate a grid if you have multiple cancer or groups of interest to run multiple quantile survival analysis separately.

NOTE2: On the left side panel, you have the options to upload data; select the reference level corresponding to the reference level chosen in quantile survival analysis; download the output plot accordingly.

NOTE3: To generate the input data, you can refer to the 'Quantile Survival Analysis' tab for more information.

DATA FORMAT

1. Data should be input as a .txt or .xlsx or .csv file. The first row of the data file have information about the variables.

2. The remaining lines contain measurements one line per each cancer type or subgroup, described in the format below:

3. The data is designed to have 13 columns.

a) Column_1. The column contains names of different cancer types or subgroups.

b) Column_13. This should contain the percentile for each cutpoint you used in quantile survival analysis.

c) Column_2 to Column 12. From 2nd to 12th column, the significance indications are included for 10 quantiles and overall.

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Reference Level:

Not Low

Low

Downloads

Type the file name you would like to save as

Grid

Download Grid Plot

Input your file

Select an example ds or upload your own with 'Load my own'

Example ds File

Download Example data

Choose Reference Level:

Not Low

Low

Downloads

Type the file name you would like to save as

Grid

Download Grid Plot

Read Me

Summarized Significance Grid

Step 1:

Select the example dataset or upload your own.

To view example data and format, use download button to view .csv file. This tab can combined results from various cancers of genes in the same cancer types.

Step 2:

Based on all the combined data, select the reference level. All data should have the same reference.

Step 3:

User can download the comparison grid to access the different cancers or genes within the same cancer type.

Summarized Significance conclusion over all cancer types

Color Key

Non-significant

Low Expression Better Survival

Not Low Expression Better Survival

Non-estimate

| Cancer Type | 01 | 02 | 03 | 04 | 05 | 06 | 07 | 08 | 09 | 010 |
|-------------|------|------|------|------|------|------|------|------|------|------|
| ACC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| BLCA | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| BRCA | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| CESC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| ESCA | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| GBM | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| GBMLGG | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| HNSC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| LIHC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| LUSC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| LUSC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| LIHC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| PAAD | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| PRAD | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| SARC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| SKCM | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| STAD | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| STES | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| THCA | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| THYM | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| UCEC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |
| UCEC | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue | Blue |

Comparison grid for various cancer types along with the percentiles used as cut-off in each case provided in the example data.