This package includes three models for multi-task survival analysis.

The folder "data" includes the example data for usage. The data used for each task is stored in one single ".csv" file. Where each instance is represented as a row in file and the last two columns are survival\_times and censored\_indicators, respectively.

To wrong this code, the users should first run “multi\_cox\_prepare.m” to generate the training and testing file from the original files. The function has two input parameter, first denote the folder where all the data stored, and the second denotes the number of cross validation folders.

>> multi\_cox\_prepare '/data/Noname\_addone\_miRNA\_use/' 3

After running this function, we will have training and testing files for each cross validation.

Now we can run the experiment for three multi-task survival analysis models.

The “example\_cox\_CMTL.m” reforms to the Cluster Multi-task survival analysis models. This function have 6 arguments

* The Folder where the training and testing file stored
* Name of training file
* Name of testing file
* Number of searching parameter
* Number of clusters
* The rate of smallest search parameter compares to the largest one

\*\*\*run example of example\_cox\_CMTL.m

>> example\_cox\_CMTL 'Noname\_addone\_miRNA\_use/' 'train\_1' 'test\_1' 10 4 0.01

The “example\_cox\_L21.m” reforms to the L\_2,1 norm regularized Multi-task survival analysis models. This function has 6 arguments

* The Folder where the training and testing file stored
* Name of training file
* Name of testing file
* Number of searching parameter
* The rate of smallest search parameter compares to the largest one
* The scale of first searching point (usually set as 1)

\*\*\*run example of example\_cox\_CMTL.m

>> example\_cox\_L21 'Noname\_addone\_miRNA\_use/' 'train\_1' 'test\_1' 100 0.01 1

The “example\_cox\_Trace.m” reforms to the Trace norm regularized Multi-task survival analysis models. This function has 6 arguments

* The Folder where the training and testing file stored
* Name of training file
* Name of testing file
* Number of searching parameter
* The rate of smallest search parameter compares to the largest one
* The scale of first searching point (usually set as 1)

\*\*\*run example of example\_cox\_ Trace.m

>> example\_cox\_Trace 'Noname\_addone\_miRNA\_use/' 'train\_1' 'test\_1' 100 0.01 1