

Section A: Data and Function information

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Contents

1	Preparation	2
2	Loading data and functions	2
3	Check data	2
4	Function:factor_analysis() was used for univariate Cox regression analysis.	2
5	Function:plot_KMCurve() was used for Kaplan-Meier analyses.	3
6	More details of function could be found in folder ‘/func’.	3

1 Preparation

2 Loading data and functions

This document presents R code for reproducing our major results as described in the paper. To start, first load the dependent packages, R functions needed for the analysis, and the data including patient clinical information and spatial organization features for the SYSUCC and BJCH samples.

```
load("./DataAndClinical.rdata")
source("./func/factor_analysis.R")
source("./func/plot_KMCurve.R")
source("./func/TableS3_Clinical_Associations.R")
source("./func/TableS4_PerasonCorrelation.R")
```

3 Check data

```
colnames(SYSUCC_data)

## [1] "Sample.ID" "os.time"
## [3] "os.event" "Age"
## [5] "Gender" "Primary_tumor_location"
## [7] "Pathological_Tstage" "Pathological_Nstage"
## [9] "Preoperative_chemotherapy" "Preoperative_CEA"
## [11] "Synchronous_liver_metastases" "Number_of_LM"
## [13] "Largest_diameter_of_CRLM" "Resection_margin"
## [15] "Concomitant_ablation" "CRS_score"
## [17] "CRS_group" "Adjuvant_chemotherapy"
## [19] "Distal_Stroma_ratio" "Distal_Debris_ratio"
## [21] "Distal_Lymphocyte_ratio" "Distal_Hepatocyte_ratio"
## [23] "Distal_Mucus_ratio" "Infiltrating_Stroma_ratio"
## [25] "Infiltrating_Debris_ratio" "Infiltrating_Lymphocyte_ratio"
## [27] "Infiltrating_Hepatocyte_ratio" "Infiltrating_Mucus_ratio"
## [29] "TUM_STR_interaction" "TUM_DEB_interaction"
## [31] "TUM_LYM_interaction" "TUM_HEP_interaction"
## [33] "TUM_MUC_interaction" "Overall_Stroma_ratio"
## [35] "Overall_Debris_ratio" "Overall_Lymphocyte_ratio"
## [37] "Overall_Hepatocyte_ratio" "Overall_Mucus_ratio"

all.equal(colnames(SYSUCC_data),colnames(BJCH_data))

## [1] TRUE
```

4 Function:factor_analysis() was used for univariate Cox regression analysis.

```
head(factor_analysis)

##
## 1 function (clin_factors, rfs, limit = NULL, string = F, ignore.mul.auto = T)
## 2 {
```

```
## 3     time <- rfs[, 1]
## 4     event <- rfs[, 2] == 1
## 5     if (!is.null(limit)) {
## 6         event[time > limit] <- F
```

5 Function: `plot_KMCurve()` was used for Kaplan-Meier analyses.

```
head(plot_KMCurve)
```

```
##
## 1 function (clinical, labels, limit = NULL, annot = NULL, color = NULL,
## 2     font = "Arial", xlab = "Follow up", ylab = "Survival Probability",
## 3     title = NULL, legend.pos = "top", palette = "jama_classic",
## 4     risk.table = T, risk.table.ratio = 0.4, anno.pos = "bottom",
## 5     anno.x.shift = 0.5)
## 6 {
```

6 More details of function could be found in folder ‘/func’.