

Survival Analysis with R: Exercises

Exercise set 1

Take a look at the built in `colon` dataset. If you type `?colon` it'll ask you if you wanted help on the `colon` dataset from the `survival` package, or the `colon` operator. Click “Chemotherapy for Stage B/C colon cancer”, or be specific with `?survival::colon`. This dataset has survival and recurrence information on 929 people from a clinical trial on colon cancer chemotherapy. There are two rows per person, indicated by the event type (`etype`) variable – `etype=1` indicates that row corresponds to death; `etype=2` indicates recurrence.

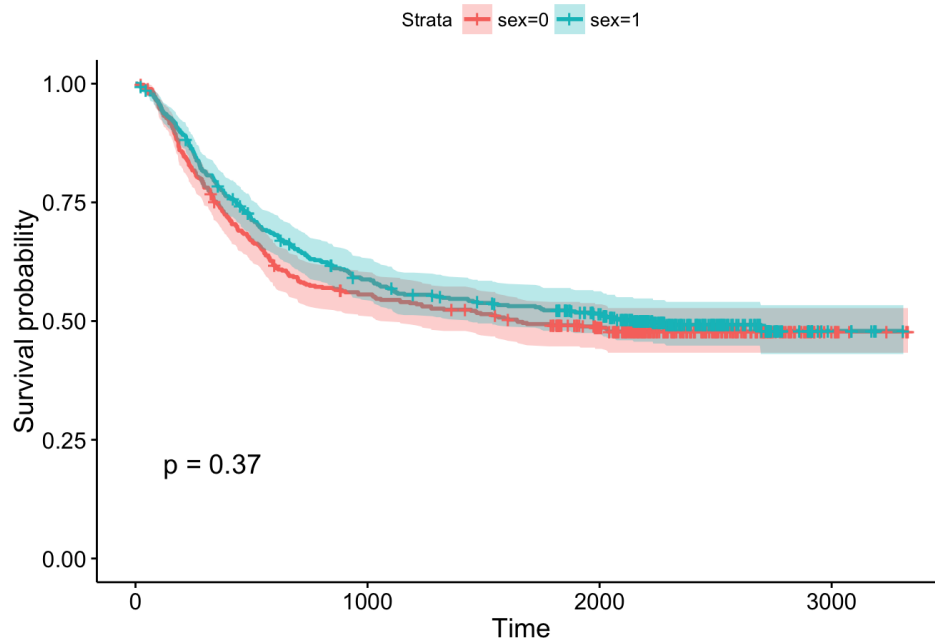
First, let's filter the data to only include the survival data, not the recurrence data. Let's call this new object `colondeath`. The `filter()` function is in the **dplyr** library, which you can get by running `library(dplyr)` or `library(tidyverse)`.

```
library(tidyverse)
colondeath <- filter(colon, etype==1)
head(colondeath)
```

1. Look at the help for `?colon` again. How are `sex` and `status` coded? How is this different from the `lung` data?
2. Using `survfit(Surv(..., ...), ~..., data=colondeath)`, create a survival curve separately for males versus females. Call the resulting object `sfit`. Run a `summary()` on this object, showing time points 0, 500, 1000, 1500, and 2000. Do males or females appear to fair better over this time period?

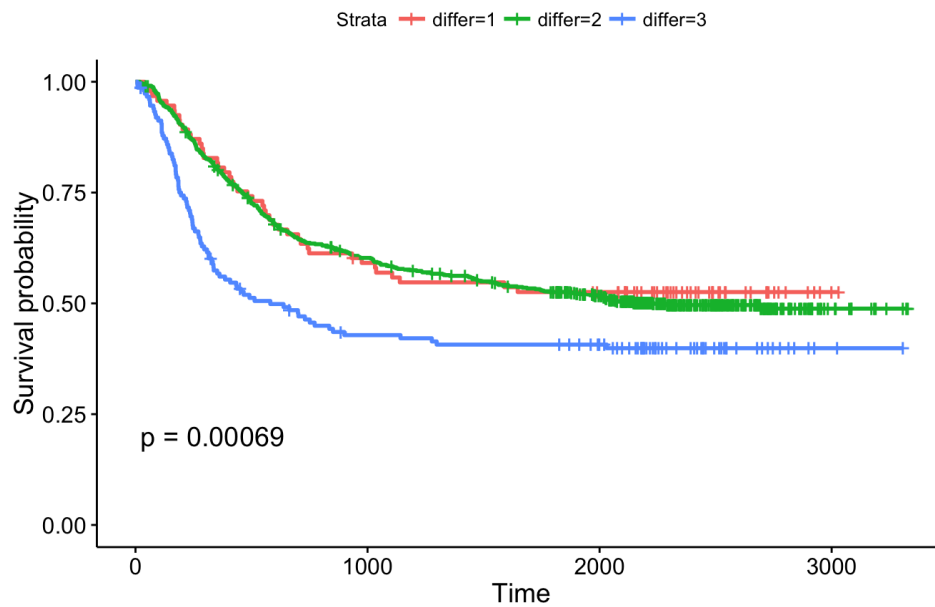
```
##                sex=0
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    0    445      0    1.000  0.0000      1.000      1.000
##   500    295    146    0.670  0.0224      0.627      0.715
##  1000    242     50    0.556  0.0237      0.512      0.604
##  1500    222     18    0.515  0.0238      0.470      0.564
##  2000    183     12    0.486  0.0239      0.442      0.535
##
##                sex=1
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    0    484      0    1.000  0.0000      1.000      1.000
##   500    338    138    0.713  0.0206      0.674      0.754
##  1000    274     59    0.588  0.0226      0.545      0.634
##  1500    246     23    0.538  0.0229      0.495      0.585
##  2000    211     10    0.516  0.0230      0.472      0.563
```

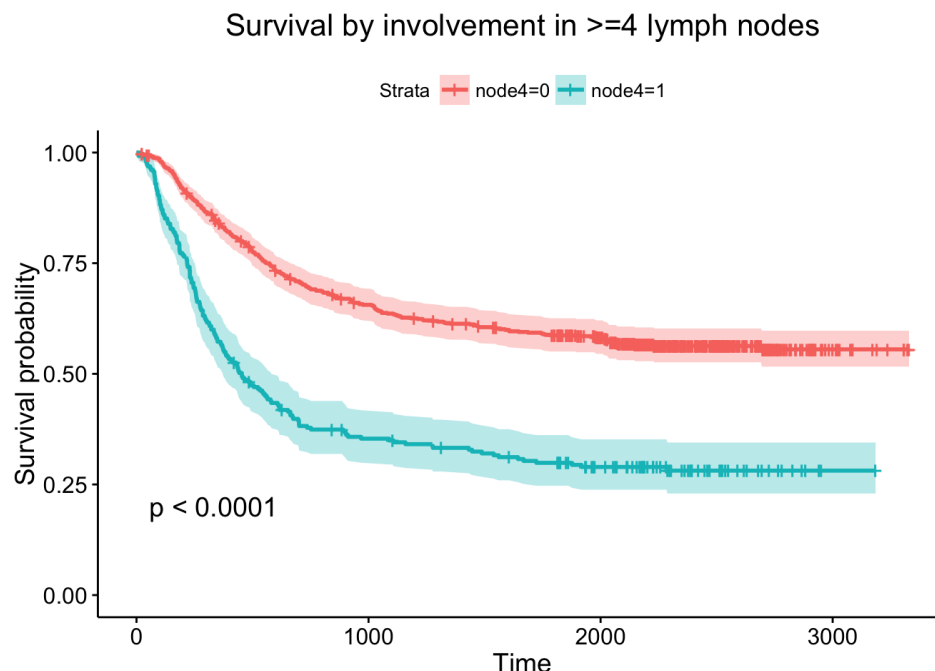
3. Using the `survminer` package, plot a Kaplan-Meier curve for this analysis with confidence intervals and showing the p-value. See `?ggsurvplot` for help. Is there a significant difference between males and females?



4. Create Kaplan-Meier plot stratifying by:
 - a. The extent of differentiation (well, moderate, poor), showing the p-value.
 - b. Whether or not there was detectable cancer in ≥ 4 lymph nodes, showing the p-value and confidence bands.

Survival by tumor differentiation





Exercise set 2

Let's go back to the `colon` cancer dataset. Remember, you created a `colondeath` object in the first exercise that only includes survival, not recurrence data points. See `?colon` for more information about this dataset.

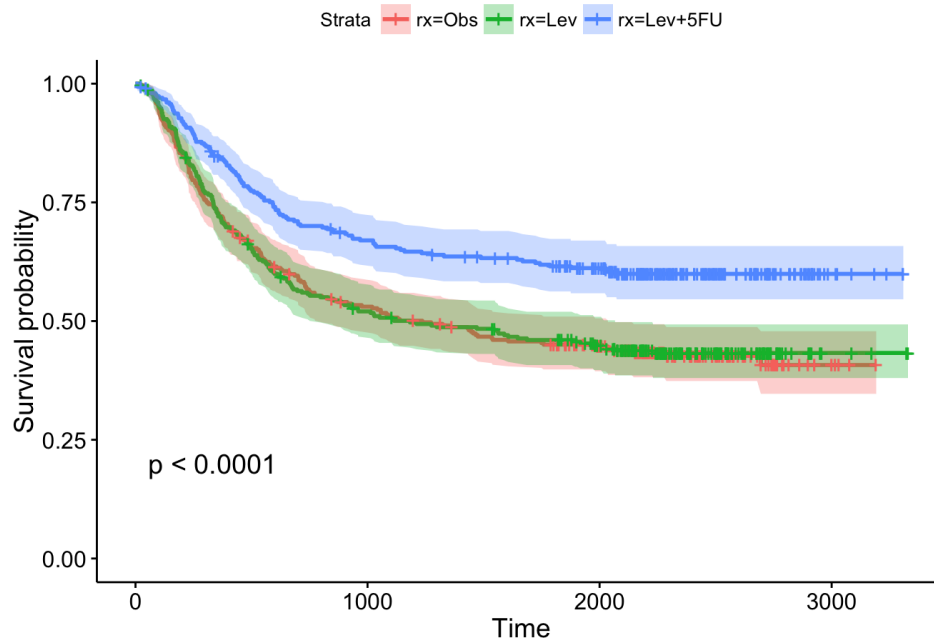
1. Take a look at `levels(colondeath$rx)`. This tells you that the `rx` variable is the type of treatment the patient was on, which is either nothing (coded `Obs`, short for Observation), Levamisole (coded `Lev`), or Levamisole + 5-fluorouracil (coded `Lev+5FU`). This is a factor variable coded with these levels, in that order. This means that `Obs` is treated as the baseline group, and other groups are dummy-coded to represent the respective group.

rx	Lev	Lev+5FU
Obs	0	0
Lev	1	0
Lev+5FU	0	1

2. Run a Cox proportional hazards regression model against this `rx` variable. How do you interpret the result? Which treatment seems to be significantly different from the control (Observation)?

```
##          coef exp(coef) se(coef)      z      p
## rxLev      -0.0151   0.9850  0.1071 -0.14   0.89
## rxLev+5FU -0.5121   0.5992  0.1186 -4.32 1.6e-05
##
## Likelihood ratio test=24.3 on 2 df, p=5.17e-06
## n= 929, number of events= 468
```

3. Show the results using a Kaplan-Meier plot, with confidence intervals and the p-value.



4. Fit another Cox regression model accounting for age, sex, and the number of nodes with detectable cancer. Notice the test statistic on the likelihood ratio test becomes much larger, and the overall model becomes more significant. What do you think accounted for this increase in our ability to model survival?

```
##          coef exp(coef) se(coef)      z      p
## rxLev      -0.06906   0.93327  0.10876 -0.64   0.53
## rxLev+5FU  -0.54193   0.58163  0.12056 -4.50  7e-06
## age        -0.00359   0.99642  0.00395 -0.91   0.36
## sex        -0.15147   0.85945  0.09420 -1.61   0.11
## nodes       0.08276   1.08628  0.00886  9.34 <2e-16
##
## Likelihood ratio test=90.3 on 5 df, p=0
## n= 911, number of events= 456
## (18 observations deleted due to missingness)
```

Exercise set 3

The “KIPAN” cohort (in `KIPAN.clinical`) is the pan-kidney cohort, consisting of KICH (chromaphobe renal cell carcinoma), KIRC (renal clear cell carcinoma), and KIPR (papillary cell carcinoma). The `KIPAN.clinical` has `KICH.clinical`, `KIRC.clinical`, and `KIPR.clinical` all combined.

1. Using `survivalTCGA()`, create a new object called `clinkid` using the `KIPAN.clinical` cohort. For the columns to extract, get both the disease code and the patient’s gender (`extract.cols=c("admin.disease_code", "patient.gender")`). The first few rows will look like this.

```
## times bcr_patient_barcode patient.vital_status admin.disease_code
## 1 1158 TCGA-KL-8323 1 kich
## 2 4311 TCGA-KL-8324 0 kich
## 3 725 TCGA-KL-8325 1 kich
## 4 3322 TCGA-KL-8326 0 kich
```

```
## 5 3553      TCGA-KL-8327      0      kich
## 6 3127      TCGA-KL-8328      0      kich
## patient.gender
## 1      female
## 2      female
## 3      female
## 4      male
## 5      female
## 6      male
```

2. The `xtabs()` command will produce tables of counts for categorical variables. Here's an example for how to use `xtabs()` for the built-in colon cancer dataset, which will tell you the number of samples split by sex and by treatment.

```
xtabs(~rx+sex, data=colon)
```

```
##          sex
## rx      0   1
## Obs    298 332
## Lev    266 354
## Lev+5FU 326 282
```

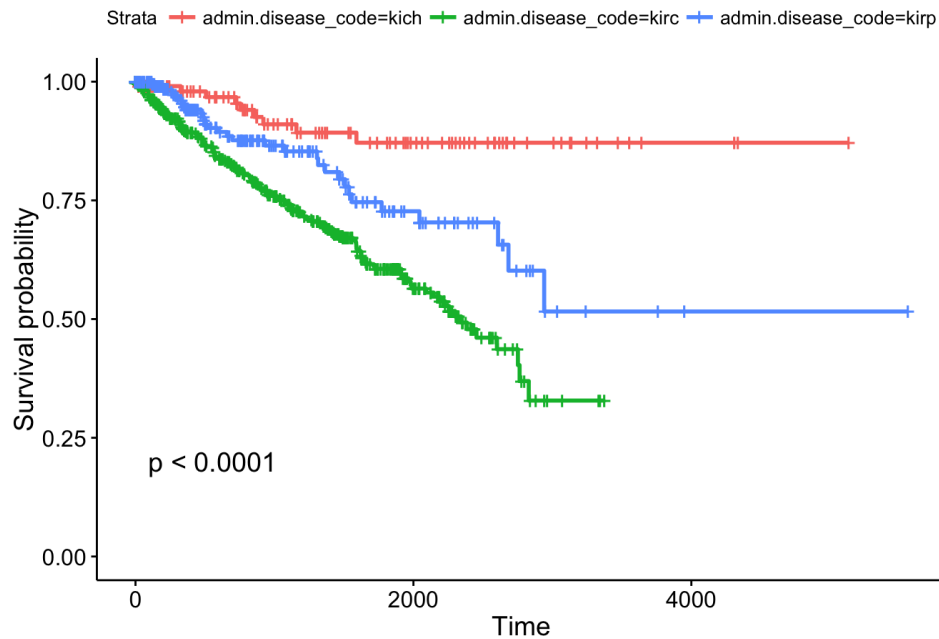
Use the same command to examine how many samples you have for each kidney sample type, separately by sex.

```
##          patient.gender
## admin.disease_code female male
##          kich      51   61
##          kirc     191  346
##          kirp      76  212
```

3. Run a Cox PH regression on the cancer type and gender. What's the effect of gender? Is it significant? How does survival differ by each type? Which has the worst prognosis?

```
##          coef exp(coef) se(coef)      z      p
## admin.disease_codekirc  1.5929   4.9179  0.3450  4.62 3.9e-06
## admin.disease_codekirp  0.9962   2.7080  0.3807  2.62 0.0089
## patient.gendermale    -0.0628   0.9391  0.1484 -0.42 0.6721
##
## Likelihood ratio test=39.4  on 3 df, p=1.4e-08
## n= 937, number of events= 203
```

4. Create survival curves for each different subtype.
 - a. Produce a Kaplan-Meier plot.
 - b. Show survival tables each year for the first 5 years.



```
## Call: survfit(formula = Surv(times, patient.vital_status) ~ admin.disease_code,
## data = clinkid)
```

```
##
##              admin.disease_code=kich
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    0    111      0   1.000  0.0000    1.000    1.000
##   365     86      2   0.980  0.0144    0.952    1.000
##   730     72      2   0.954  0.0226    0.911    0.999
##  1095     54      3   0.910  0.0329    0.848    0.977
##  1460     44      1   0.893  0.0366    0.824    0.967
##  1825     38      1   0.871  0.0415    0.794    0.957
##
##              admin.disease_code=kirc
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    0    536      0   1.000  0.0000    1.000    1.000
##   365    385     49   0.895  0.0142    0.868    0.924
##   730    313     32   0.816  0.0186    0.781    0.853
##  1095    250     26   0.744  0.0217    0.703    0.788
##  1460    181     20   0.678  0.0243    0.633    0.728
##  1825    112     16   0.606  0.0277    0.554    0.663
##
##              admin.disease_code=kirp
## time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    0    288      0   1.000  0.0000    1.000    1.000
##   365    145     10   0.941  0.0182    0.906    0.977
##   730    100      8   0.877  0.0278    0.824    0.933
##  1095     67      2   0.853  0.0316    0.793    0.917
##  1460     54      3   0.810  0.0388    0.737    0.889
##  1825     36      5   0.727  0.0495    0.636    0.831
```