

# Survival Analysis

# Survival analysis

- ▶ So far, have seen:
  - ▶ response variable counted or measured (regression)
  - ▶ response variable categorized (logistic regression)
- ▶ But what if response is time until event (eg. time of survival after surgery)?
- ▶ Additional complication: event might not have happened at end of study (eg. patient still alive). But knowing that patient has “not died yet” presumably informative. Such data called *censored*.
- ▶ Enter *survival analysis*, in particular the “Cox proportional hazards model”.
- ▶ Explanatory variables in this context often called *covariates*.

# Packages

- ▶ Install packages `survival` and `survminer` if not done.

```
library(tidyverse)
library(survival)
library(survminer)
library(broom)
library(marginaleffects)
```

## Example: still dancing?

- ▶ 12 women who have just started taking dancing lessons are followed for up to a year, to see whether they are still taking dancing lessons, or have quit. The “event” here is “quit”.
- ▶ This might depend on:
  - ▶ a treatment (visit to a dance competition)
  - ▶ woman's age (at start of study).

# Data

| Months | Quit | Treatment | Age |
|--------|------|-----------|-----|
| 1      | 1    | 0         | 16  |
| 2      | 1    | 0         | 24  |
| 2      | 1    | 0         | 18  |
| 3      | 0    | 0         | 27  |
| 4      | 1    | 0         | 25  |
| 7      | 1    | 1         | 26  |
| 8      | 1    | 1         | 36  |
| 10     | 1    | 1         | 38  |
| 10     | 0    | 1         | 45  |
| 12     | 1    | 1         | 47  |

## About the data

- ▶ `months` and `quit` are kind of combined response:
  - ▶ `Months` is number of months a woman was actually observed dancing
  - ▶ `quit` is 1 if woman quit, 0 if still dancing at end of study.
- ▶ `Treatment` is 1 if woman went to dance competition, 0 otherwise.
- ▶ Fit model and see whether `Age` or `Treatment` have effect on survival.
- ▶ Want to do predictions for probabilities of still dancing as they depend on whatever is significant, and draw plot.

## Read data

► Column-aligned:

```
url <- "http://ritsokiguess.site/datafiles/dancing.txt"  
dance <- read_table(url)
```

# The data

```
dance
```

```
# A tibble: 12 x 4
```

|    | Months<br><dbl> | Quit<br><dbl> | Treatment<br><dbl> | Age<br><dbl> |
|----|-----------------|---------------|--------------------|--------------|
| 1  | 1               | 1             | 0                  | 16           |
| 2  | 2               | 1             | 0                  | 24           |
| 3  | 2               | 1             | 0                  | 18           |
| 4  | 3               | 0             | 0                  | 27           |
| 5  | 4               | 1             | 0                  | 25           |
| 6  | 5               | 1             | 0                  | 21           |
| 7  | 11              | 1             | 0                  | 55           |
| 8  | 7               | 1             | 1                  | 26           |
| 9  | 8               | 1             | 1                  | 36           |
| 10 | 10              | 1             | 1                  | 38           |
| 11 | 10              | 0             | 1                  | 45           |
| 12 | 12              | 1             | 1                  | 47           |



## Examine response and fit model

► Response variable:

```
dance %>% mutate(mth = Surv(Months, Quit)) -> dance  
dance
```

# A tibble: 12 x 5

|    | Months<br><dbl> | Quit<br><dbl> | Treatment<br><dbl> | Age<br><dbl> | mth<br><Surv> |
|----|-----------------|---------------|--------------------|--------------|---------------|
| 1  | 1               | 1             | 0                  | 16           | 1             |
| 2  | 2               | 1             | 0                  | 24           | 2             |
| 3  | 2               | 1             | 0                  | 18           | 2             |
| 4  | 3               | 0             | 0                  | 27           | 3+            |
| 5  | 4               | 1             | 0                  | 25           | 4             |
| 6  | 5               | 1             | 0                  | 21           | 5             |
| 7  | 11              | 1             | 0                  | 55           | 11            |
| 8  | 7               | 1             | 1                  | 26           | 7             |
| 9  | 8               | 1             | 1                  | 36           | 8             |
| 10 | 10              | 1             | 1                  | 38           | 10            |
| 11 | 10              | 0             | 1                  | 45           | 10+           |
| 12 | 12              | 1             | 1                  | 47           | 12            |

► Then fit model predicting mth from explanatories:

# Output looks a lot like regression

```
summary(dance.1)
```

Call:

```
coxph(formula = mth ~ Treatment + Age, data = dance)
```

n= 12, number of events= 10

|           | coef     | exp(coef) | se(coef) | z      | Pr(> z ) |
|-----------|----------|-----------|----------|--------|----------|
| Treatment | -4.44915 | 0.01169   | 2.60929  | -1.705 | 0.0882 . |
| Age       | -0.36619 | 0.69337   | 0.15381  | -2.381 | 0.0173 * |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|           | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-----------|-----------|------------|-----------|-----------|
| Treatment | 0.01169   | 85.554     | 7.026e-05 | 1.9444    |
| Age       | 0.69337   | 1.442      | 5.129e-01 | 0.9373    |

Concordance= 0.964 (se = 0.039 )

Likelihood ratio test= 21.68 on 2 df, p=2e-05

Wald test = 5.67 on 2 df, p=0.06

Score (logrank) test = 14.75 on 2 df, p=6e-04

# Conclusions

- ▶ Use  $\alpha = 0.10$  here since not much data.
- ▶ Three tests at bottom like global F-test. Consensus that something predicts survival time (whether or not dancer quit and how long it took).
- ▶ Age (definitely), Treatment (marginally) both predict survival time.

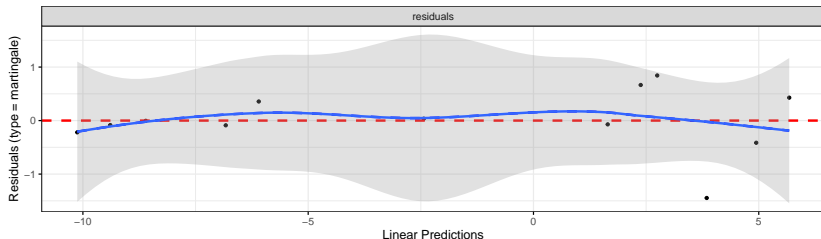
## Model checking

- ▶ With regression, usually plot residuals against fitted values.
- ▶ Not quite same here (nonlinear model), but “martingale residuals” should have no pattern vs. “linear predictor”.
- ▶ `ggcoxdiagnostics` from package `survminer` makes plot, to which we add `smooth`. If smooth trend more or less straight across, model OK.
- ▶ Martingale residuals can go very negative, so won't always look normal.

# Martingale residual plot for dance data

This looks good (with only 12 points):

```
ggcoxdiagnostics(dance.1) + geom_smooth(se = F)
```



## Predicted survival probs

- ▶ The function we use is called `survfit`, though actually works rather like `predict`.
- ▶ First create a data frame of values to predict from. We'll do all combos of ages 20 and 40, treatment and not, using `crossing` to get all the combos:

```
treatments <- c(0, 1)
ages <- c(20, 40)
dance.new <- crossing(Treatment = treatments, Age = ages)
dance.new
```

```
# A tibble: 4 x 2
  Treatment Age
  <dbl> <dbl>
1         0  20
2         0  40
3         1  20
4         1  40
```

# The predictions

One prediction *for each time* for each combo of age and treatment in `dance.new`:

```
s <- survfit(dance.1, newdata = dance.new, data = dance)
summary(s)
```

Call: `survfit(formula = dance.1, newdata = dance.new, data = dance)`

| time | n.risk | n.event | survival1 | survival2 | survival3 | survival4 |
|------|--------|---------|-----------|-----------|-----------|-----------|
| 1    | 12     | 1       | 8.76e-01  | 1.00e+00  | 9.98e-01  | 1.000     |
| 2    | 11     | 2       | 3.99e-01  | 9.99e-01  | 9.89e-01  | 1.000     |
| 4    | 8      | 1       | 1.24e-01  | 9.99e-01  | 9.76e-01  | 1.000     |
| 5    | 7      | 1       | 2.93e-02  | 9.98e-01  | 9.60e-01  | 1.000     |
| 7    | 6      | 1       | 2.96e-323 | 6.13e-01  | 1.70e-04  | 0.994     |
| 8    | 5      | 1       | 0.00e+00  | 2.99e-06  | 1.35e-98  | 0.862     |
| 10   | 4      | 1       | 0.00e+00  | 0.00e+00  | 0.00e+00  | 0.000     |
| 11   | 2      | 1       | 0.00e+00  | 0.00e+00  | 0.00e+00  | 0.000     |
| 12   | 1      | 1       | 0.00e+00  | 0.00e+00  | 0.00e+00  | 0.000     |

## Conclusions from predicted probs

- ▶ Older women more likely to be still dancing than younger women (compare “profiles” for same treatment group).
- ▶ Effect of treatment seems to be to increase prob of still dancing (compare “profiles” for same age for treatment group vs. not)
- ▶ Would be nice to see this on a graph. This is `ggsurvplot` from package `survminer`:

```
g <- ggsurvplot(s, conf.int = F)
```



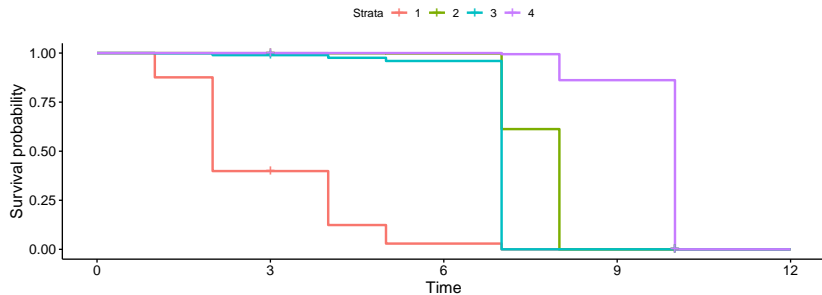
# “Strata” (groups)

► uses “strata” thus (dance.new):

```
# A tibble: 4 x 2
  Treatment Age
    <dbl> <dbl>
1         0  20
2         0  40
3         1  20
4         1  40
```

# Plotting survival probabilities

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# Discussion

- ▶ Survivor curve farther to the right is better (better chance of surviving longer).
- ▶ Best is age 40 with treatment, worst age 20 without.
- ▶ Appears to be:
  - ▶ age effect (40 better than 20)
  - ▶ treatment effect (treatment better than not)
  - ▶ In analysis, treatment effect only marginally significant.

## A more realistic example: lung cancer

- ▶ When you load in an R package, get data sets to illustrate functions in the package.
- ▶ One such is `lung`. Data set measuring survival in patients with advanced lung cancer.
- ▶ Along with survival time, number of “performance scores” included, measuring how well patients can perform daily activities.
- ▶ Sometimes high good, but sometimes bad!
- ▶ Variables below, from the data set help file (`?lung`).

# The variables

## Format

inst: Institution code  
time: Survival time in days  
status: censoring status 1=censored, 2=dead  
age: Age in years  
sex: Male=1 Female=2  
ph.ecog: ECOG performance score (0=good 5=dead)  
ph.karno: Karnofsky performance score (bad=0-good=100) rated by physician  
pat.karno: Karnofsky performance score as rated by patient  
meal.cal: Calories consumed at meals  
wt.loss: Weight loss in last six months

## Uh oh, missing values

```
lung %>% slice(1:16)
```

|    | inst | time | status | age | sex | ph.ecog | ph.karno | pat.karno | meal.cal | wt.loss |
|----|------|------|--------|-----|-----|---------|----------|-----------|----------|---------|
| 1  | 3    | 306  | 2      | 74  | 1   | 1       | 90       | 100       | 1175     | NA      |
| 2  | 3    | 455  | 2      | 68  | 1   | 0       | 90       | 90        | 1225     | 15      |
| 3  | 3    | 1010 | 1      | 56  | 1   | 0       | 90       | 90        | NA       | 15      |
| 4  | 5    | 210  | 2      | 57  | 1   | 1       | 90       | 60        | 1150     | 11      |
| 5  | 1    | 883  | 2      | 60  | 1   | 0       | 100      | 90        | NA       | 0       |
| 6  | 12   | 1022 | 1      | 74  | 1   | 1       | 50       | 80        | 513      | 0       |
| 7  | 7    | 310  | 2      | 68  | 2   | 2       | 70       | 60        | 384      | 10      |
| 8  | 11   | 361  | 2      | 71  | 2   | 2       | 60       | 80        | 538      | 1       |
| 9  | 1    | 218  | 2      | 53  | 1   | 1       | 70       | 80        | 825      | 16      |
| 10 | 7    | 166  | 2      | 61  | 1   | 2       | 70       | 70        | 271      | 34      |
| 11 | 6    | 170  | 2      | 57  | 1   | 1       | 80       | 80        | 1025     | 27      |
| 12 | 16   | 654  | 2      | 68  | 2   | 2       | 70       | 70        | NA       | 23      |
| 13 | 11   | 728  | 2      | 68  | 2   | 1       | 90       | 90        | NA       | 5       |
| 14 | 21   | 71   | 2      | 60  | 1   | NA      | 60       | 70        | 1225     | 32      |
| 15 | 12   | 567  | 2      | 57  | 1   | 1       | 80       | 70        | 2600     | 60      |
| 16 | 1    | 144  | 2      | 67  | 1   | 1       | 80       | 90        | NA       | 15      |

# A closer look

```
summary(lung)
```

| inst           | time            | status         | age            |
|----------------|-----------------|----------------|----------------|
| Min. : 1.00    | Min. : 5.0      | Min. :1.000    | Min. :39.00    |
| 1st Qu.: 3.00  | 1st Qu.: 166.8  | 1st Qu.:1.000  | 1st Qu.:56.00  |
| Median :11.00  | Median : 255.5  | Median :2.000  | Median :63.00  |
| Mean :11.09    | Mean : 305.2    | Mean :1.724    | Mean :62.45    |
| 3rd Qu.:16.00  | 3rd Qu.: 396.5  | 3rd Qu.:2.000  | 3rd Qu.:69.00  |
| Max. :33.00    | Max. :1022.0    | Max. :2.000    | Max. :82.00    |
| NA's :1        |                 |                |                |
| sex            | ph.ecog         | ph.karno       | pat.karno      |
| Min. :1.000    | Min. :0.0000    | Min. : 50.00   | Min. : 30.00   |
| 1st Qu.:1.000  | 1st Qu.:0.0000  | 1st Qu.: 75.00 | 1st Qu.: 70.00 |
| Median :1.000  | Median :1.0000  | Median : 80.00 | Median : 80.00 |
| Mean :1.395    | Mean :0.9515    | Mean : 81.94   | Mean : 79.96   |
| 3rd Qu.:2.000  | 3rd Qu.:1.0000  | 3rd Qu.: 90.00 | 3rd Qu.: 90.00 |
| Max. :2.000    | Max. :3.0000    | Max. :100.00   | Max. :100.00   |
|                | NA's :1         | NA's :1        | NA's :3        |
| meal.cal       | wt.loss         |                |                |
| Min. : 96.0    | Min. : -24.000  |                |                |
| 1st Qu.: 635.0 | 1st Qu.: 0.000  |                |                |
| Median : 975.0 | Median : 7.000  |                |                |
| Mean : 928.8   | Mean : 9.832    |                |                |
| 3rd Qu.:1150.0 | 3rd Qu.: 15.750 |                |                |
| Max. :2600.0   | Max. : 68.000   |                |                |
| NA's :47       | NA's :14        |                |                |

## Remove obs with *any* missing values

```
lung %>% drop_na() -> lung.complete  
lung.complete %>%  
  select(meal.cal:wt.loss) %>%  
  slice(1:10)
```

|    | meal.cal | wt.loss |
|----|----------|---------|
| 2  | 1225     | 15      |
| 4  | 1150     | 11      |
| 6  | 513      | 0       |
| 7  | 384      | 10      |
| 8  | 538      | 1       |
| 9  | 825      | 16      |
| 10 | 271      | 34      |
| 11 | 1025     | 27      |
| 15 | 2600     | 60      |
| 17 | 1150     | -5      |

Missing values seem to be gone.



# Check!

```
summary(lung.complete)
```

| inst     |        | time     |         | status   |        | age      |        |
|----------|--------|----------|---------|----------|--------|----------|--------|
| Min.     | : 1.00 | Min.     | : 5.0   | Min.     | :1.000 | Min.     | :39.00 |
| 1st Qu.: | 3.00   | 1st Qu.: | 174.5   | 1st Qu.: | 1.000  | 1st Qu.: | 57.00  |
| Median : | 11.00  | Median : | 268.0   | Median : | 2.000  | Median : | 64.00  |
| Mean     | :10.71 | Mean     | : 309.9 | Mean     | :1.719 | Mean     | :62.57 |
| 3rd Qu.: | 15.00  | 3rd Qu.: | 419.5   | 3rd Qu.: | 2.000  | 3rd Qu.: | 70.00  |
| Max.     | :32.00 | Max.     | :1022.0 | Max.     | :2.000 | Max.     | :82.00 |

| sex      |        | ph.ecog  |         | ph.karno |         | pat.karno |         |
|----------|--------|----------|---------|----------|---------|-----------|---------|
| Min.     | :1.000 | Min.     | :0.0000 | Min.     | : 50.00 | Min.      | : 30.00 |
| 1st Qu.: | 1.000  | 1st Qu.: | 0.0000  | 1st Qu.: | 70.00   | 1st Qu.:  | 70.00   |
| Median : | 1.000  | Median : | 1.0000  | Median : | 80.00   | Median :  | 80.00   |
| Mean     | :1.383 | Mean     | :0.9581 | Mean     | : 82.04 | Mean      | : 79.58 |
| 3rd Qu.: | 2.000  | 3rd Qu.: | 1.0000  | 3rd Qu.: | 90.00   | 3rd Qu.:  | 90.00   |
| Max.     | :2.000 | Max.     | :3.0000 | Max.     | :100.00 | Max.      | :100.00 |

| meal.cal |         | wt.loss  |          |
|----------|---------|----------|----------|
| Min.     | : 96.0  | Min.     | :-24.000 |
| 1st Qu.: | 619.0   | 1st Qu.: | 0.000    |
| Median : | 975.0   | Median : | 7.000    |
| Mean     | : 929.1 | Mean     | : 9.719  |
| 3rd Qu.: | 1162.5  | 3rd Qu.: | 15.000   |
| Max.     | :2600.0 | Max.     | : 68.000 |

No missing values left.

## Model 1: use everything except inst

```
names(lung.complete)
```

```
[1] "inst"      "time"      "status"    "age"       "sex"  
[6] "ph.ecog"   "ph.karno"  "pat.karno" "meal.cal"  "wt.loss"
```

► Event was death, goes with status of 2:

```
lung.complete %>%  
  mutate(resp = Surv(time, status == 2)) ->  
  lung.complete  
lung.1 <- coxph(resp ~ . - inst - time - status,  
  data = lung.complete  
)
```

“Dot” means “all the other variables”.

# summary of model 1

```
summary(lung.1)
```

Call:

```
coxph(formula = resp ~ . - inst - time - status, data = lung.complete)
```

n= 167, number of events= 120

|           | coef       | exp(coef) | se(coef)  | z      | Pr(> z )   |
|-----------|------------|-----------|-----------|--------|------------|
| age       | 1.080e-02  | 1.011e+00 | 1.160e-02 | 0.931  | 0.35168    |
| sex       | -5.536e-01 | 5.749e-01 | 2.016e-01 | -2.746 | 0.00603 ** |
| ph.ecog   | 7.395e-01  | 2.095e+00 | 2.250e-01 | 3.287  | 0.00101 ** |
| ph.karno  | 2.244e-02  | 1.023e+00 | 1.123e-02 | 1.998  | 0.04575 *  |
| pat.karno | -1.207e-02 | 9.880e-01 | 8.116e-03 | -1.488 | 0.13685    |
| meal.cal  | 2.835e-05  | 1.000e+00 | 2.594e-04 | 0.109  | 0.91298    |
| wt.loss   | -1.420e-02 | 9.859e-01 | 7.766e-03 | -1.828 | 0.06748 .  |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|           | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-----------|-----------|------------|-----------|-----------|
| age       | 1.0109    | 0.9893     | 0.9881    | 1.0341    |
| sex       | 0.5749    | 1.7395     | 0.3872    | 0.8534    |
| ph.ecog   | 2.0950    | 0.4773     | 1.3479    | 3.2560    |
| ph.karno  | 1.0227    | 0.9778     | 1.0004    | 1.0455    |
| pat.karno | 0.9880    | 1.0121     | 0.9724    | 1.0038    |
| meal.cal  | 1.0000    | 1.0000     | 0.9995    | 1.0005    |
| wt.loss   | 0.9859    | 1.0143     | 0.9710    | 1.0010    |

Concordance= 0.653 (se = 0.029 )

Likelihood ratio test= 28.16 on 7 df, p=2e-04

Wald test = 27.5 on 7 df, p=3e-04

Score (logrank) test = 28.31 on 7 df, p=2e-04

# Overall significance

The three tests of overall significance:

```
glance(lung.1) %>% select(starts_with("p.value"))
```

```
# A tibble: 1 x 4
```

|   | p.value.log | p.value.sc | p.value.wald | p.value.robust |
|---|-------------|------------|--------------|----------------|
|   | <dbl>       | <dbl>      | <dbl>        | <dbl>          |
| 1 | 0.000205    | 0.000193   | 0.000271     | NA             |

All strongly significant. *Something* predicts survival.

## Coefficients for model 1

```
tidy(lung.1) %>% select(term, p.value) %>% arrange(p.value)
```

```
# A tibble: 7 x 2
  term      p.value
  <chr>      <dbl>
1 ph.ecog  0.00101
2 sex      0.00603
3 ph.karno 0.0457
4 wt.loss  0.0675
5 pat.karno 0.137
6 age      0.352
7 meal.cal 0.913
```

- ▶ sex and ph.ecog definitely significant here
- ▶ age, pat.karno and meal.cal definitely not
- ▶ Take out definitely non-sig variables, and try again.

## Model 2

```
lung.2 <- update(lung.1, . ~ . - age - pat.karno - meal.cal)
tidy(lung.2) %>% select(term, p.value)
```

```
# A tibble: 4 x 2
  term      p.value
  <chr>    <dbl>
1 sex      0.00409
2 ph.ecog  0.000112
3 ph.karno 0.101
4 wt.loss  0.108
```

## Compare with first model:

```
anova(lung.2, lung.1)
```

Analysis of Deviance Table

Cox model: response is resp

Model 1: ~ sex + ph.ecog + ph.karno + wt.loss

Model 2: ~ (inst + time + status + age + sex + ph.ecog + p

|  | loglik | Chisq | Df | Pr(> Chi ) |
|--|--------|-------|----|------------|
|--|--------|-------|----|------------|

|   |         |  |  |  |
|---|---------|--|--|--|
| 1 | -495.67 |  |  |  |
|---|---------|--|--|--|

|   |         |       |   |       |
|---|---------|-------|---|-------|
| 2 | -494.03 | 3.269 | 3 | 0.352 |
|---|---------|-------|---|-------|

► No harm in taking out those variables.

## Model 3

Take out ph.karno and wt.loss as well.

```
lung.3 <- update(lung.2, . ~ . - ph.karno - wt.loss)
```

```
tidy(lung.3) %>% select(term, estimate, p.value)
```

```
# A tibble: 2 x 3
```

|   | term    | estimate | p.value  |
|---|---------|----------|----------|
|   | <chr>   | <dbl>    | <dbl>    |
| 1 | sex     | -0.510   | 0.00958  |
| 2 | ph.ecog | 0.483    | 0.000266 |



## Check whether that was OK

```
anova(lung.3, lung.2)
```

Analysis of Deviance Table

Cox model: response is resp

Model 1: ~ sex + ph.ecog

Model 2: ~ sex + ph.ecog + ph.karno + wt.loss

|  | loglik | Chisq | Df | Pr(> Chi ) |
|--|--------|-------|----|------------|
|--|--------|-------|----|------------|

|   |         |  |  |  |
|---|---------|--|--|--|
| 1 | -498.38 |  |  |  |
|---|---------|--|--|--|

|   |         |        |   |           |
|---|---------|--------|---|-----------|
| 2 | -495.67 | 5.4135 | 2 | 0.06675 . |
|---|---------|--------|---|-----------|

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

*Just OK.*

## Commentary

- ▶ OK (just) to take out those two covariates.
- ▶ Both remaining variables strongly significant.
- ▶ Nature of effect on survival time? Consider later.
- ▶ Picture?

# Plotting survival probabilities

- Create new data frame of values to predict for, then predict:

```
sexes <- c(1, 2)
ph.ecogs <- 0:3
lung.new <- datagrid(sex = sexes, ph.ecog = ph.ecogs, model = lung.3)
lung.new
```

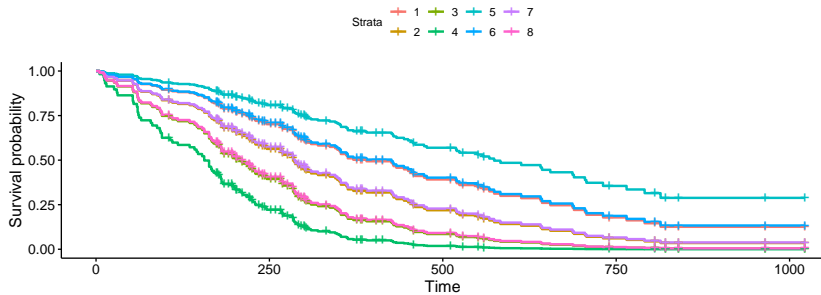
|   | sex | ph.ecog |
|---|-----|---------|
| 1 | 1   | 0       |
| 2 | 1   | 1       |
| 3 | 1   | 2       |
| 4 | 1   | 3       |
| 5 | 2   | 0       |
| 6 | 2   | 1       |
| 7 | 2   | 2       |
| 8 | 2   | 3       |

## Making the plot

```
s <- survfit(lung.3, newdata = lung.new, data = lung)
g <- ggsurvplot(s, conf.int = F)
```

# The plot

09



## Discussion of survival curves

- ▶ Best survival is teal-blue curve, stratum 5, females with `ph.ecog` score 0.
- ▶ Next best: blue, stratum 6, females with score 1, and red, stratum 1, males score 0.
- ▶ Worst: green, stratum 4, males score 3.
- ▶ For any given `ph.ecog` score, females have better predicted survival than males.
- ▶ For both genders, a lower score associated with better survival.

## The coefficients in model 3

```
tidy(lung.3) %>% select(term, estimate, p.value)
```

```
# A tibble: 2 x 3
```

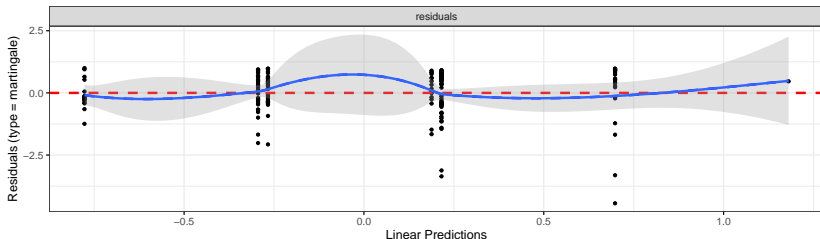
|   | term    | estimate | p.value  |
|---|---------|----------|----------|
|   | <chr>   | <dbl>    | <dbl>    |
| 1 | sex     | -0.510   | 0.00958  |
| 2 | ph.ecog | 0.483    | 0.000266 |

- ▶ sex coeff negative, so being higher sex value (female) goes with *less* hazard of dying.
- ▶ ph.ecog coeff positive, so higher ph.ecog score goes with *more* hazard of dying
- ▶ Two coeffs about same size, so being male rather than female corresponds to 1-point increase in ph.ecog score. Note how survival curves come in 3 pairs plus 2 odd.

# Martingale residuals for this model

No problems here:

```
ggcoxdiagnostics(lung.3) + geom_smooth(se = F)
```





## When the Cox model fails

- ▶ Invent some data where survival is best at middling age, and worse at high *and* low age:

```
age <- seq(20, 60, 5)
survtime <- c(10, 12, 11, 21, 15, 20, 8, 9, 11)
stat <- c(1, 1, 1, 1, 0, 1, 1, 1, 1)
d <- tibble(age, survtime, stat)
d %>% mutate(y = Surv(survtime, stat)) -> d
```

- ▶ Small survival time 15 in middle was actually censored, so would have been longer if observed.

# Fit Cox model

```
y.1 <- coxph(y ~ age, data = d)
summary(y.1)
```

Call:

```
coxph(formula = y ~ age, data = d)
```

n= 9, number of events= 8

|     | coef    | exp(coef) | se(coef) | z     | Pr(> z ) |
|-----|---------|-----------|----------|-------|----------|
| age | 0.01984 | 1.02003   | 0.03446  | 0.576 | 0.565    |

|     | exp(coef) | exp(-coef) | lower .95 | upper .95 |
|-----|-----------|------------|-----------|-----------|
| age | 1.02      | 0.9804     | 0.9534    | 1.091     |

Concordance= 0.545 (se = 0.105 )

Likelihood ratio test= 0.33 on 1 df, p=0.6

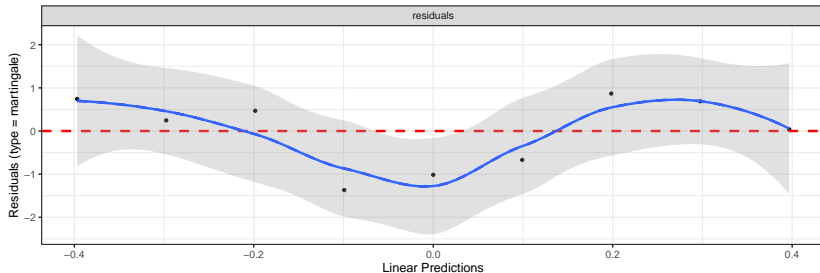
Wald test = 0.33 on 1 df, p=0.6

Score (logrank) test = 0.33 on 1 df, p=0.6

# Martingale residuals

Down-and-up indicates incorrect relationship between age and survival:

```
ggcoxdiagnostics(y.1) + geom_smooth(se = F)
```



## Attempt 2

Add squared term in age:

```
y.2 <- coxph(y ~ age + I(age^2), data = d)
tidy(y.2) %>% select(term, estimate, p.value)
```

```
# A tibble: 2 x 3
```

|   | term     | estimate | p.value |
|---|----------|----------|---------|
|   | <chr>    | <dbl>    | <dbl>   |
| 1 | age      | -0.380   | 0.116   |
| 2 | I(age^2) | 0.00483  | 0.0977  |

► (Marginally) helpful.

# Martingale residuals this time

Not great, but less problematic than before:

```
ggcoxdiagnostics(y.2) + geom_smooth(se = F)
```

