

# Homework 9

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## Problem 1

```
knitr::include_graphics("q1.png")
```

$$h(x) = \frac{2x}{(1+x^2)^2}$$

$$H(x) = \int_0^x h(t) dt$$

$$= \ln(1+x^2)$$

$$S(x) = \text{Survival function}$$

$$= \exp\{-H(x)\}$$

$$= \frac{1}{1+x^2}$$

$$F(x) = \text{Cumulative Density Function}$$

$$= 1 - S(x)$$

$$= 1 - \frac{1}{1+x^2}$$

$$f(x) = \text{Probability Density Function}$$

$$= \frac{d}{dx} F(x)$$

$$= \frac{2x}{(1+x^2)^2}$$

## Problem 2

```
knitr::include_graphics("q2.png")
```

$t_i$	$n_i$	$d_i$	$C_i$	$\hat{\lambda}_i$	$\hat{S}(t)$	$\hat{H}(t) = -\log \hat{S}(t)$	$\hat{\tilde{H}}(t) = \sum d_i/n_i$
1	10	1	0	0.1	$1 \times (1 - 0.1) = 0.9$	0.045	0.1
2	9	2	0	0.22	$0.9 \times (1 - 0.22) = 0.7$	0.15	$0.1 + 0.22 = 0.32$
4	7	0	1	0	$0.7 \times (1 - 0) = 0.7$	0.15	0.32
5	6	0	1	0	$0.7 \times (1 - 0) = 0.7$	0.15	0.32
6	5	1	0	0.2	$0.7 \times (1 - 0.2) = 0.56$	0.25	0.52
7	4	0	1	0	$0.56 \times (1 - 0) = 0.56$	0.25	0.52
8	3	0	1	0	0.56	0.25	0.52
9	2	0	1	0	0.56	0.25	0.52
10	1	0	1	0	0.56	0.25	0.52

## Problem 3

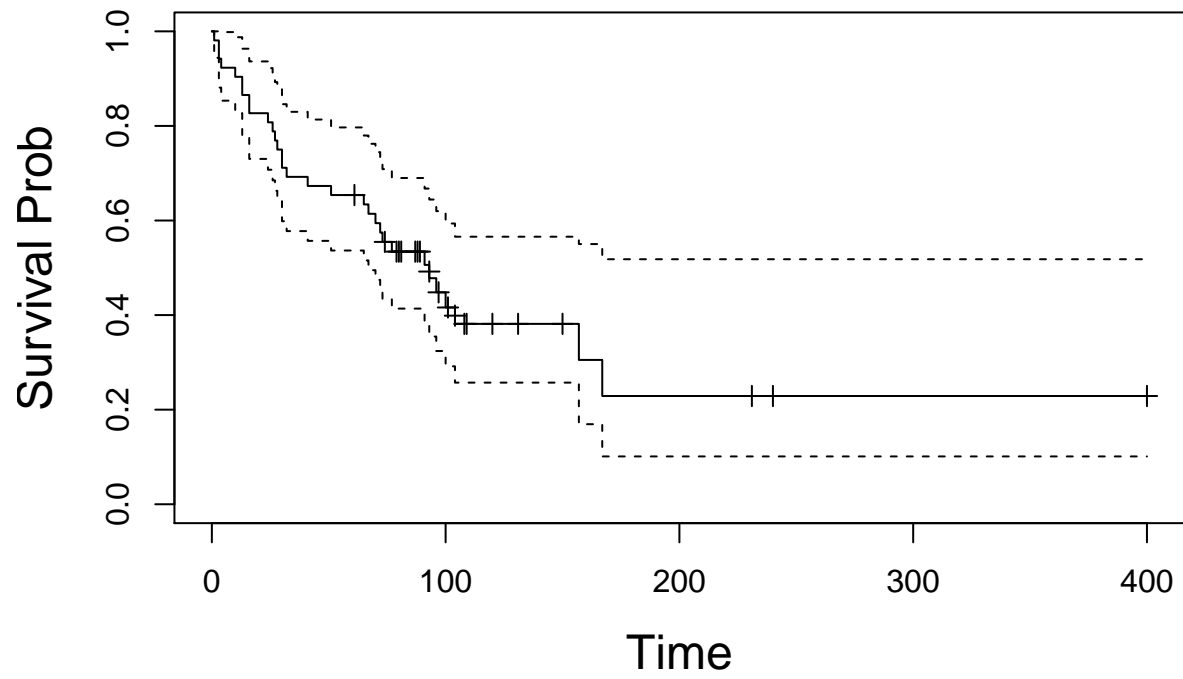
Use the tongue data in the R package KMsurv. For each tumor type (aneuploidy and diploid), plot the Kaplan-Meier curve of survival function and its pointwise 95% confidence intervals (using the log transformation). What are the estimated 1-year survival rate and 95% CI?

```
data("tongue")
tongue = tongue %>%
  as_tibble() %>%
  mutate(type = if_else(type == 1, "aneu", "di"))
```

### Aneuploid Plot

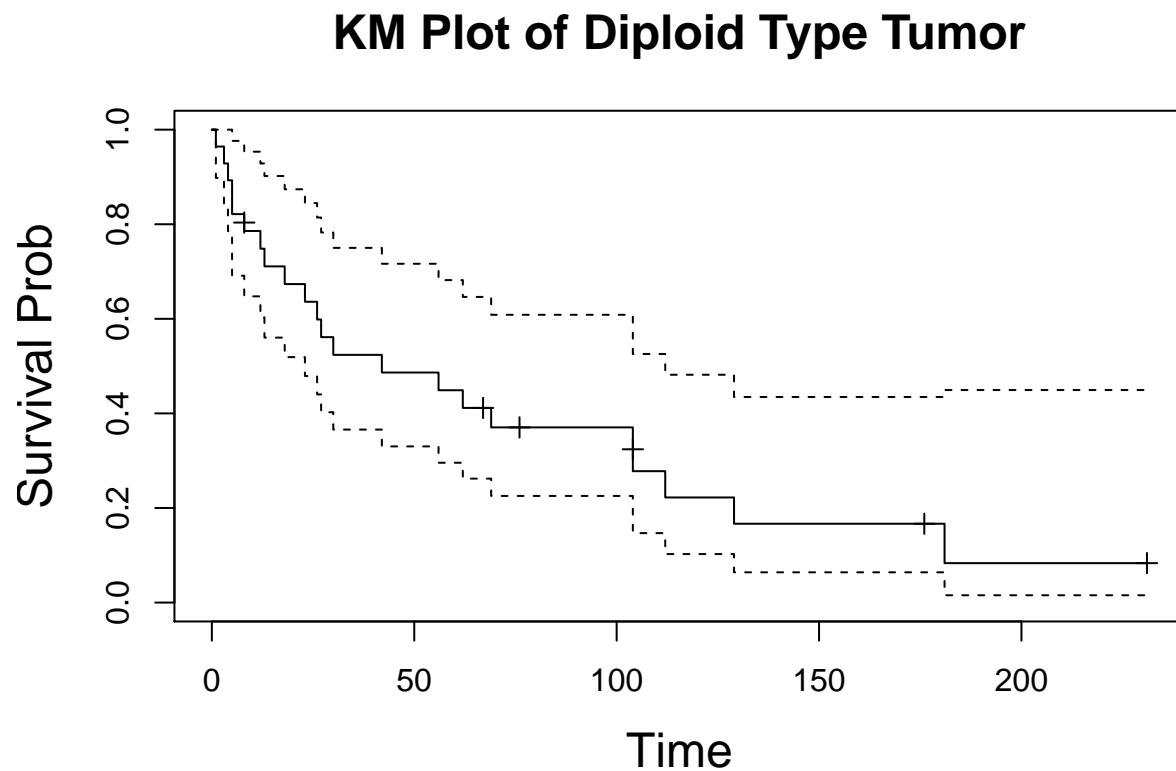
```
aneu.km = survfit(Surv(time, delta) ~ 1,
                  data = subset(tongue,
                                type == "aneu"),
                  conf.type = "log")
aneu.plot = plot(aneu.km,
                 conf.int = TRUE,
                 mark.time = TRUE,
                 xlab = "Time",
                 ylab = "Survival Prob",
                 main = "KM Plot of Aneuploid Type Tumor",
                 cex.lab = 1.5,
                 cex.main = 1.5)
```

**KM Plot of Aneuploid Type Tumor**



## Diploid Plot

```
di.km = survfit(Surv(time, delta) ~ 1,
                data = subset(tongue,
                              type == "di"),
                conf.type = "log")
di.plot = plot(di.km,
               conf.int = TRUE,
               mark.time = TRUE,
               xlab = "Time",
               ylab = "Survival Prob",
               main = "KM Plot of Diploid Type Tumor",
               cex.lab = 1.5,
               cex.main = 1.5)
```



## Prediction

```
tongue.km = survfit(Surv(time, delta) ~ type,
                    data = tongue)
tongue.summ = summary(tongue.km, time = 365/7)

ci = t(rbind(tongue.summ$surv, tongue.summ$lower, tongue.summ$upper))
rownames(ci) = c("aneuploid", "diploid")
colnames(ci) = c("estimate", "lower", "upper")
ci %>%
  knitr::kable()
```

	estimate	lower	upper
aneuploid	0.6538462	0.5365233	0.7968243
diploid	0.4863946	0.3302132	0.7164452