P8131 HW9

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```
Set output parameters
```

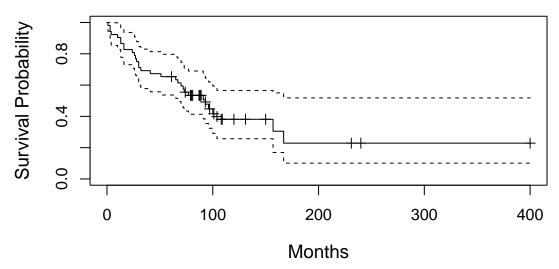
```
knitr::opts_chunk$set(
   fig.width = 6, fig.asp = .6, out.width = "90%"
)
```

Load package and data

```
library(survival)
data("tongue", package = "KMsurv") # type 1 = Aneuploid Tumor, type 2 = Diploid Tumor
# the follow code shows the right censored data
Surv(tongue$time, tongue$delta, type='right') # 0: censored, 1: observed death
```

Fit and plot a KM curve for the aneuploid tumor data

Aneuploid Tumor Survival Function KM curve



Obtain the survival rate at the 1 year mark with 95% CI

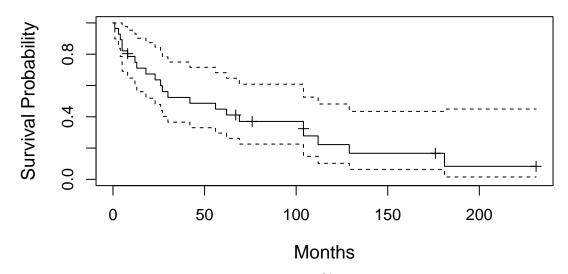
```
# time = 52 (52 weeks in a year); n.event: the cumulative number of deaths at the time point
surv_an = round(summary(km_an, time = 52)$surv, 3)
lcl_an = round(summary(km_an, time = 52)$lower, 3)
```

```
ucl_an = round(summary(km_an, time = 52)$upper, 3)
stat_an = rbind(c(surv_an, lcl_an, ucl_an))
colnames(stat_an) = c("Survival Rate", "CI Lower", "CI Upper")
knitr::kable(stat_an, "simple")
```

| Survival Rate | CI Lower | CI Upper |
|---------------|----------|----------|
| 0.654 | 0.537 | 0.797 |

Fit and plot a KM curve for the diploid tumor data

Diploid Tumor Survival Function KM curve



Obtain the survival rate at the 1 year mark with 95% CI

```
surv_di = round(summary(km_di, time = 52)$surv, 3)
lcl_di = round(summary(km_di, time = 52)$lower, 3)
ucl_di = round(summary(km_di, time = 52)$upper, 3)
stat_di = rbind(c(surv_di, lcl_di, ucl_di))
colnames(stat_di) = c("Survival Rate", "CI Lower", "CI Upper")
knitr::kable(stat_di, "simple")
```

| Survival Rate | CI Lower | CI Upper |
|---------------|----------|----------|
| 0.486 | 0.33 | 0.716 |