

## P8131 HW9

### 3. Tongue data

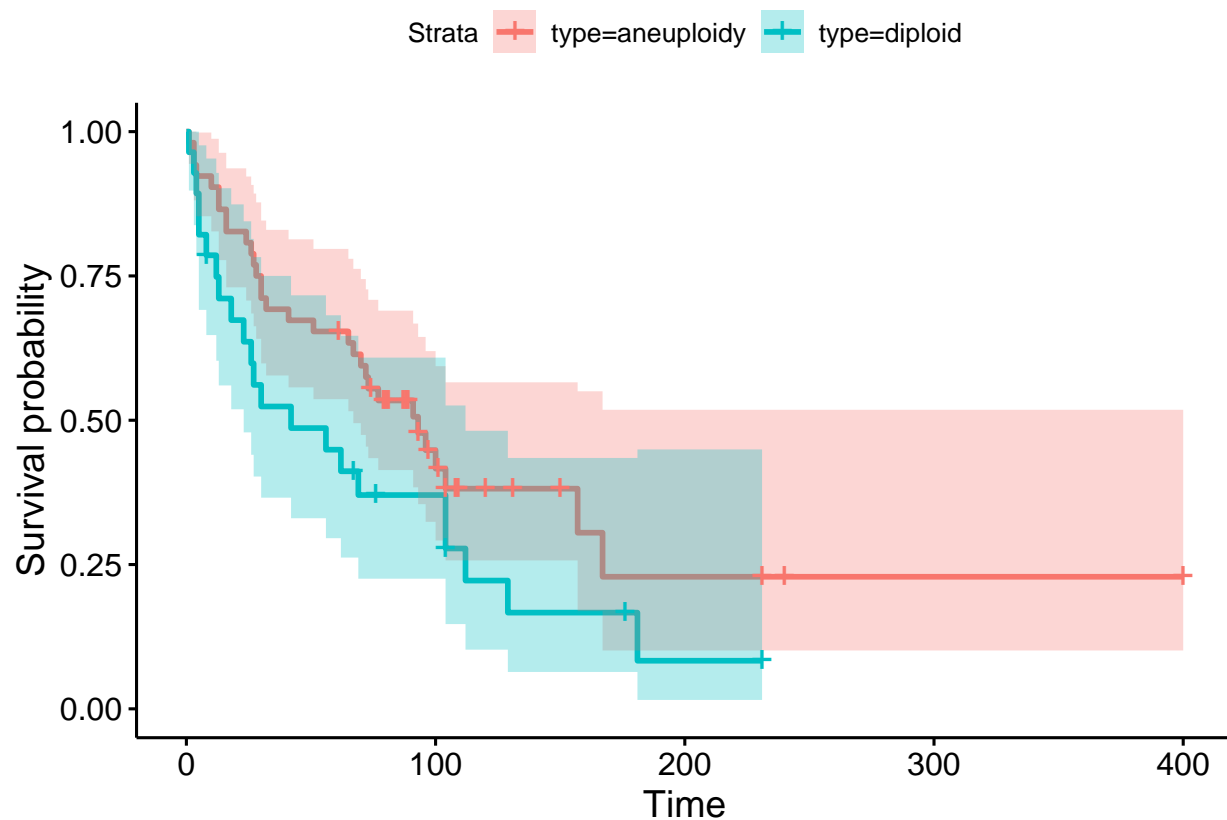
Tumor type: \* **type**: Tumor DNA profile (1=Aneuploid Tumor, 2=Diploid Tumor) \* **time**: Time to death or on-study time, weeks \* **delta** Death indicator (0: censored/alive, 1: observed/dead)

```
data(tongue)
tongue <- tongue %>%
  mutate(type = ifelse(type == 1, "aneuploidy", "diploid"))
Surv(tongue$time, tongue$delta, type='right') # 0: censored, 1: observed
```

```
## [1] 1 3 3 4 10 13 13 16 16 24 26 27 28 30 30 32 41 51 65
## [26] 93 96 100 104 157 167 61+ 74+ 79+ 80+ 81+ 87+ 87+ 88+ 89+ 93+ 97+ 101+ 104+
## [51] 240+ 400+ 1 3 4 5 5 8 12 13 18 23 26 27 30 42 56 62 69
## [76] 67+ 76+ 104+ 176+ 231+
```

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).

```
#survdif(Surv(time,cens)~treat, data=gehan) # log rank test
survival.fit <- survfit(Surv(time,delta)~type, data = tongue, conf.type='log')
ggsurvplot(survival.fit, conf.int=TRUE)
```



The estimated 1-year survival rate and 95% CI:

```
summary(survival.fit,time=c(365/7))
```

```
## Call: survfit(formula = Surv(time, delta) ~ type, data = tongue, conf.type = "log")
##
##           type=aneuploidy
##      time      n.risk  n.event  survival  std.err lower 95% CI upper 95% CI
##      52.143      34.000    18.000    0.654    0.066    0.537    0.797
##
##           type=diploid
##      time      n.risk  n.event  survival  std.err lower 95% CI upper 95% CI
##      52.1429     13.0000    14.0000    0.4864    0.0961    0.3302    0.7164
```

The estimated 1-year survival rate for patients with aneuploid tumor is about 0.654, with 95% CI [0.537,0.797], and the estimated 1-year survival rate for patients with diploid tumor is about 0.4864, with 95% CI [0.3302,0.7164].