survival_analysis_paperfig.Rmd

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get libraries & load data

```r
library(survival)
library(survminer)
## Loading required package: ggplot2
## Loading required package: ggpubr
## Loading required package: magrittr
library(ggplot2)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##     filter, lag
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

#load data
d1 = read.csv('/Users/kelly/cueexp/data/relapse_data/relapse_data_180516.csv')

#remove subjects without relapse data
d1 = d1[is.na(d1$relIn3Mos) == FALSE,]


#make relapse a factor
d1$relapse = as.factor(d1$relapse)
d1$relIn3Mos = as.factor(d1$relIn3Mos)
colnames(d1)[1] = 'subject'
d1$highlow <- factor(d1$nacc_drugs_beta > median(d1$nacc_drugs_beta), labels=c('high', 'low'), levels=c

#create survival variable
d1$nacc_drugs_beta <- as.numeric(d1$nacc_drugs_beta)

d2 <- select(d1, censored, obstime, nacc_drugs_beta, highlow) %>%
  filter(censored==0)

d1$survival <- with(d1, Surv(obstime, censored == 0))
d1$survival
##  [1] 204+  39    2  215   90+   0  102  213+   1  399  182+ 272  200+ 239
## [15] 111+  10   94+ 309  115   62   26   29   53  245  163+ 216+ 197+  64
## [29]  36    3  194+ 184+ 173+

d2$survival <- with(d2, Surv(obstime, censored == 0))
d2$survival
##  [1]  39    2  215    0  102    1  399  272  239   10  309  115   62   26
## [15]  29   53  245   64   36    3
```
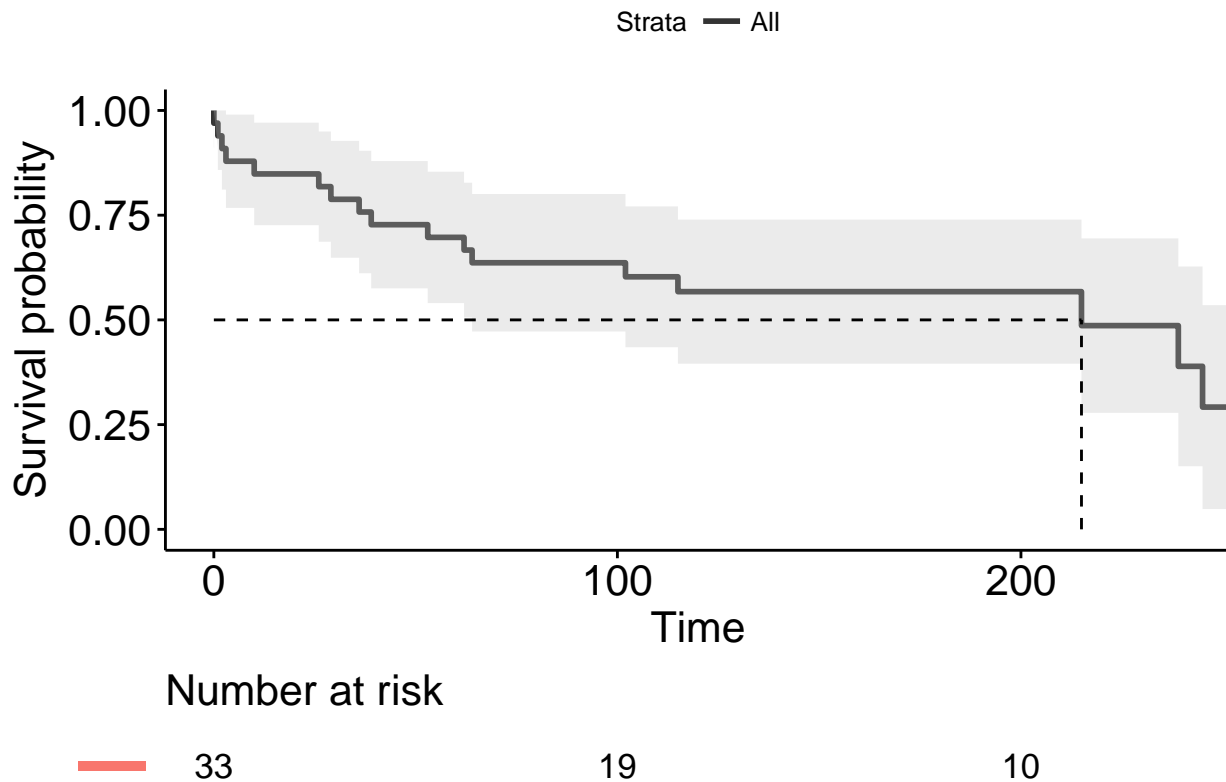
Kaplan-Meier survival plots

```r
# Figure 1 - all data
sfit_fig1 <- survfit(survival~1, type="kaplan-meier", conf.type="plain", data=d1)
#png(filename="KMcurve.png")
ggsurvplot(sfit_fig1,
           surv.median.line = "hv",
           pval=F,
           censor=F,
           conf.int=T,
           conf.int.style='ribbon',
         # xlim=c(0,320),
           xlim=c(0,240),
           risk.table = TRUE,
           tables.height = 0.2,
           tables.theme = theme_cleantable(),
    #        break.time.by = 30,
           risk.table.y.text = FALSE,
     #ggtheme = theme_survminer(),
           font.main = c(24, "plain","black"),
           font.x = c(16, "plain", "black"),
           font.y = c(16, "plain", "black"),
           font.tickslab = c(16, "plain", "black")) + scale_color_grey()
```



```r
# Figure 2 - median split based on NAcc responses to drugs
sfit_fig2 <- survfit(survival~highlow, data=d1,type="kaplan-meier", conf.type="plain")
```

```
ggsurvplot(sfit_fig2,
           surv.median.line = "none",
           pval=F,
           conf.int=T,
           conf.int.style='step',
           #palette = c("#E7B800","#2E9FDF"),
           legend.labs = c("High Cue Response","Low Cue Response"),
           xlim=c(0,240),
            #xlim=c(0,320),
           risk.table = TRUE,
           tables.height = 0.2,
           tables.theme = theme_cleantable(),
       #  break.time.by = 30,
           risk.table.y.text = FALSE,
       font.main = c(24, "plain","black"),
        font.x = c(16, "plain", "black"),
        font.y = c(16, "plain", "black"),
        font.tickslab = c(16, "plain", "black")) + scale_color_grey()
```
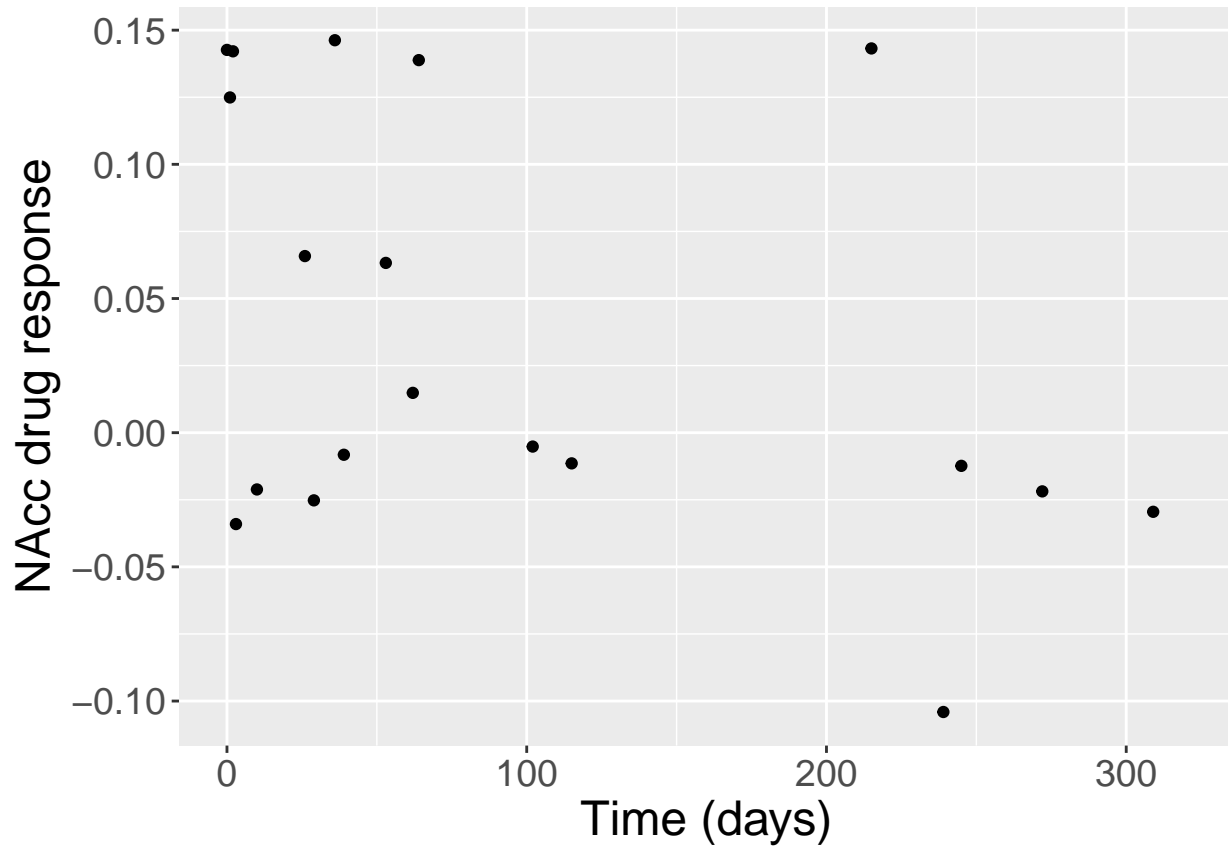

Strata ┼ High Cue Response ┼ Low Cue Response

Number at risk

16	6	2
17	13	8
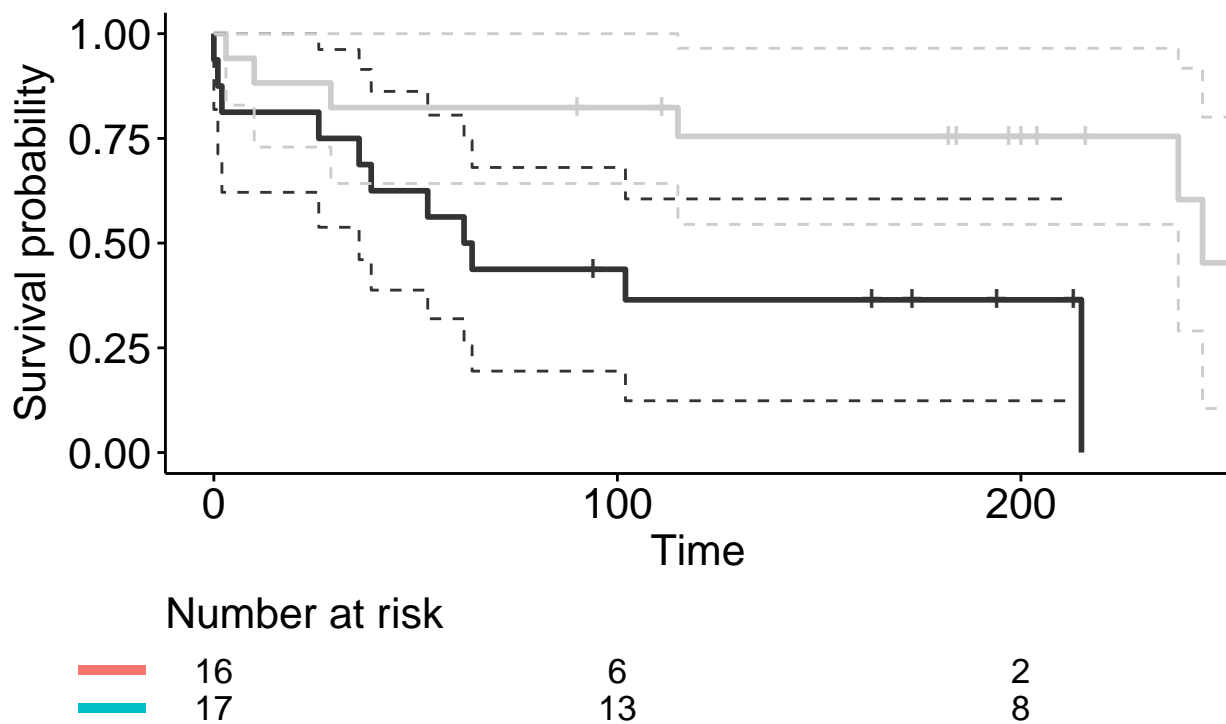
```
        #ggtheme = theme_survminer()) + scale_colour_grey()
```

scatter plot of days to relapse by nacc drug betas

```
# Figure 3
ggplot(data=d2, aes(x=obstime, y=nacc_drugs_beta)) +
```

```
geom_point() +
xlim(0,320) +
xlab("Time (days)") +
ylab("NAcc drug response") +
theme(text=element_text(size=18))
```


pairs plots

```
require(psych)
## Loading required package: psych
##
## Attaching package: 'psych'
## The following objects are masked from 'package:ggplot2':
##
##     %+%, alpha
dp = with(d1, data.frame(relapse, age, pa_drug, nacc_drugs_beta,nacc_food_beta))
pairs.panels(dp)
```