

Appendix

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```
library(tidyverse)
library(survival)
library(survminer)
library(biostat3)
library(finalfit)
```

```
## Warning: package 'finalfit' was built under R version 4.2.3
```

```
library(dplyr)
library(kableExtra)
library(ggplot2)
library(ggpubr)
library(riskRegression)
library(regclass)
```

EDA

```
aids <- read.csv('data/AIDS_Clinical_Trials_Group175.csv')
aids <- aids%>%
  mutate(cid = as.factor(cid),

          trt = as.factor(trt), treat=as.factor(treat),

          hemo = as.factor(hemo),
          homo = as.factor(homo),
          drugs = as.factor(drugs),
          race = as.factor(race),
          gender = as.factor(gender),
          str2 = as.factor(str2),
          symptom = as.factor(symptom))
```

```
aids <- aids%>%
  mutate(cid=factor(cid,
    levels = c(0,1),
    labels = c("Censoring",
               "Failure")),
  treat=factor(treat,
    levels = c(0,1),
    labels = c("ZDV only",
```

```

        "Others")),
hemo=factor(hemo,
levels = c(0,1),
labels = c("No",
           "Yes")),
homo=factor(homo,
levels = c(0,1),
labels = c("No",
           "Yes")),
gender=factor(gender,
levels = c(0,1),
labels = c("Female",
           "Male")),
race=factor(race,
levels = c(0,1),
labels = c("White",
           "Non-white")),
drugs=factor(drugs,
levels = c(0,1),
labels = c("No",
           "Yes")),
symptom=factor(symptom,
levels = c(0,1),
labels = c("No",
           "Yes"))
)

```

sex age race hemo homo drug kanor symptom cd40

```

explanatory = c("age", "hemo", "homo", "race","gender","drugs","karnof","cd40","symptom","cd80","wtkg")
dependent = "treat"
baseline <- aids %>%
  mutate(
    cd80 = ff_label(cd80, "CD8 Count"),
    wtkg = ff_label(wtkg, "Weight"),
    gender = ff_label(gender, "Gender"),
    hemo = ff_label(hemo, "Hemophilia"),
    homo = ff_label(homo, "Homosexuality"),
    race = ff_label(race, "Race"),
    drugs = ff_label(drugs, "History of IV drug use "),
    karnof = ff_label(karnof, "Karnofsky score of 100"),
    cd40 = ff_label(cd40, "CD4 count"),
    age = ff_label(age, "Age"),
    symptom = ff_label(symptom, "Symptomatic infection"),
    treat = ff_label(treat, "Treatment")
  )%>%
  summary_factorlist(dependent, explanatory, column = TRUE, total_col = TRUE, col_totals_prefix = "N=", a
baseline

```

##	Dependent: Treatment	ZDV only	Others	Total
----	----------------------	----------	--------	-------

```
##           Age Mean (SD) 35.2 (8.9) 35.3 (8.7) 35.2 (8.7)
##           Hemophilia   No 490 (92.1) 1469 (91.4) 1959 (91.6)
##                               Yes 42 (7.9) 138 (8.6) 180 (8.4)
##           Homosexuality No 191 (35.9) 534 (33.2) 725 (33.9)
##                               Yes 341 (64.1) 1073 (66.8) 1414 (66.1)
##           Race         White 376 (70.7) 1146 (71.3) 1522 (71.2)
##                               Non-white 156 (29.3) 461 (28.7) 617 (28.8)
##           Gender       Female 100 (18.8) 268 (16.7) 368 (17.2)
##                               Male 432 (81.2) 1339 (83.3) 1771 (82.8)
## History of IV drug use No 469 (88.2) 1389 (86.4) 1858 (86.9)
##                               Yes 63 (11.8) 218 (13.6) 281 (13.1)
## Karnofsky score of 100 70 4 (0.8) 5 (0.3) 9 (0.4)
##                               80 17 (3.2) 63 (3.9) 80 (3.7)
##                               90 197 (37.0) 590 (36.7) 787 (36.8)
##                               100 314 (59.0) 949 (59.1) 1263 (59.0)
##           CD4 count Mean (SD) 353.2 (114.1) 349.6 (120.0) 350.5 (118.6)
## Symptomatic infection No 443 (83.3) 1326 (82.5) 1769 (82.7)
##                               Yes 89 (16.7) 281 (17.5) 370 (17.3)
##           CD8 Count Mean (SD) 987.2 (475.2) 986.4 (482.0) 986.6 (480.2)
##           Weight Mean (SD) 76.1 (13.2) 74.8 (13.3) 75.1 (13.3)
```

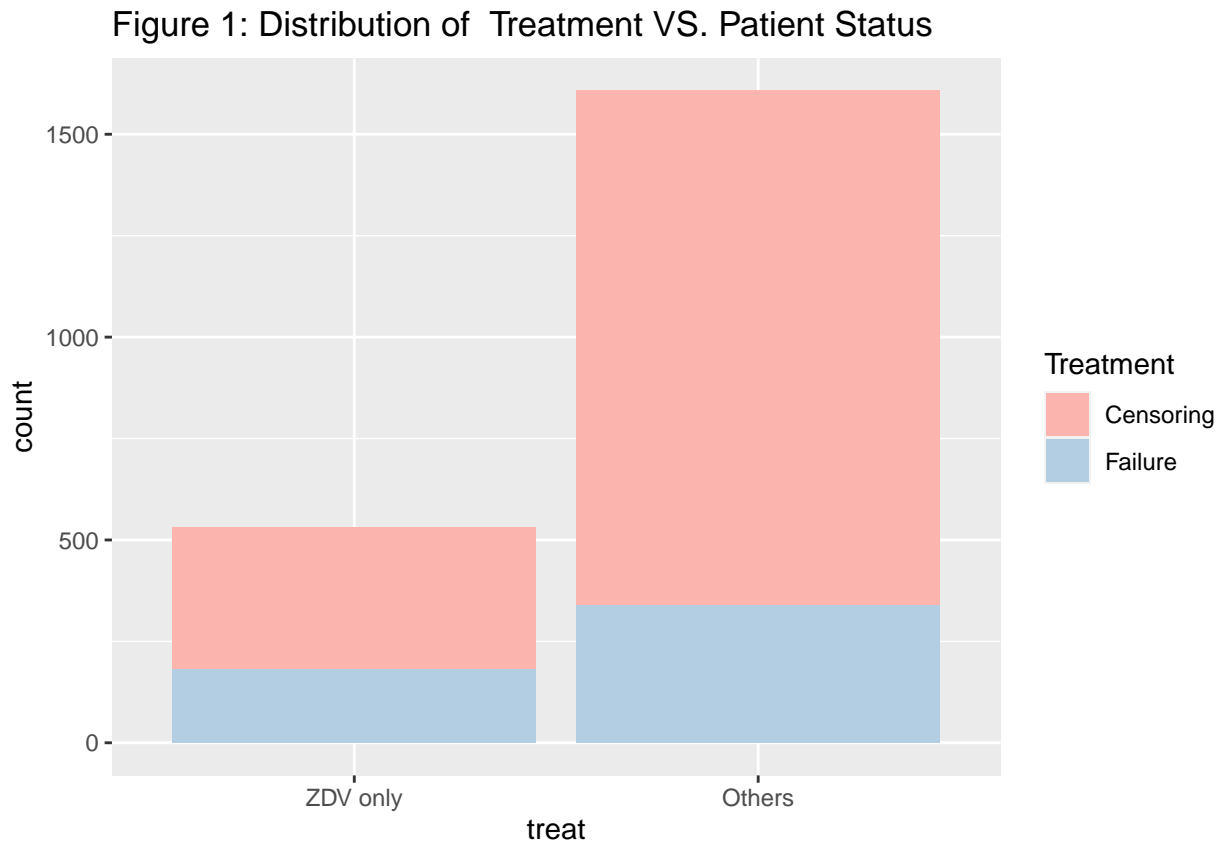
```
kable(baseline,caption = "Base-Line Characteristics of the Patients According to the Treatment Indicator")
```

Table 1: Base-Line Characteristics of the Patients According to the Treatment Indicator

Dependent: Treatment		ZDV only	Others	Total
Age	Mean (SD)	35.2 (8.9)	35.3 (8.7)	35.2 (8.7)
Hemophilia	No	490 (92.1)	1469 (91.4)	1959 (91.6)
	Yes	42 (7.9)	138 (8.6)	180 (8.4)
Homosexuality	No	191 (35.9)	534 (33.2)	725 (33.9)
	Yes	341 (64.1)	1073 (66.8)	1414 (66.1)
Race	White	376 (70.7)	1146 (71.3)	1522 (71.2)
	Non-white	156 (29.3)	461 (28.7)	617 (28.8)
Gender	Female	100 (18.8)	268 (16.7)	368 (17.2)
	Male	432 (81.2)	1339 (83.3)	1771 (82.8)
History of IV drug use	No	469 (88.2)	1389 (86.4)	1858 (86.9)
	Yes	63 (11.8)	218 (13.6)	281 (13.1)
Karnofsky score of 100	70	4 (0.8)	5 (0.3)	9 (0.4)
	80	17 (3.2)	63 (3.9)	80 (3.7)
	90	197 (37.0)	590 (36.7)	787 (36.8)
	100	314 (59.0)	949 (59.1)	1263 (59.0)
CD4 count	Mean (SD)	353.2 (114.1)	349.6 (120.0)	350.5 (118.6)
Symptomatic infection	No	443 (83.3)	1326 (82.5)	1769 (82.7)
	Yes	89 (16.7)	281 (17.5)	370 (17.3)
CD8 Count	Mean (SD)	987.2 (475.2)	986.4 (482.0)	986.6 (480.2)
Weight	Mean (SD)	76.1 (13.2)	74.8 (13.3)	75.1 (13.3)

```
ggplot(data=aids, aes(x=treat, fill=cid)) +
  geom_bar()+
  scale_fill_brewer(palette="Pastel1")+
  theme_minimal()
```

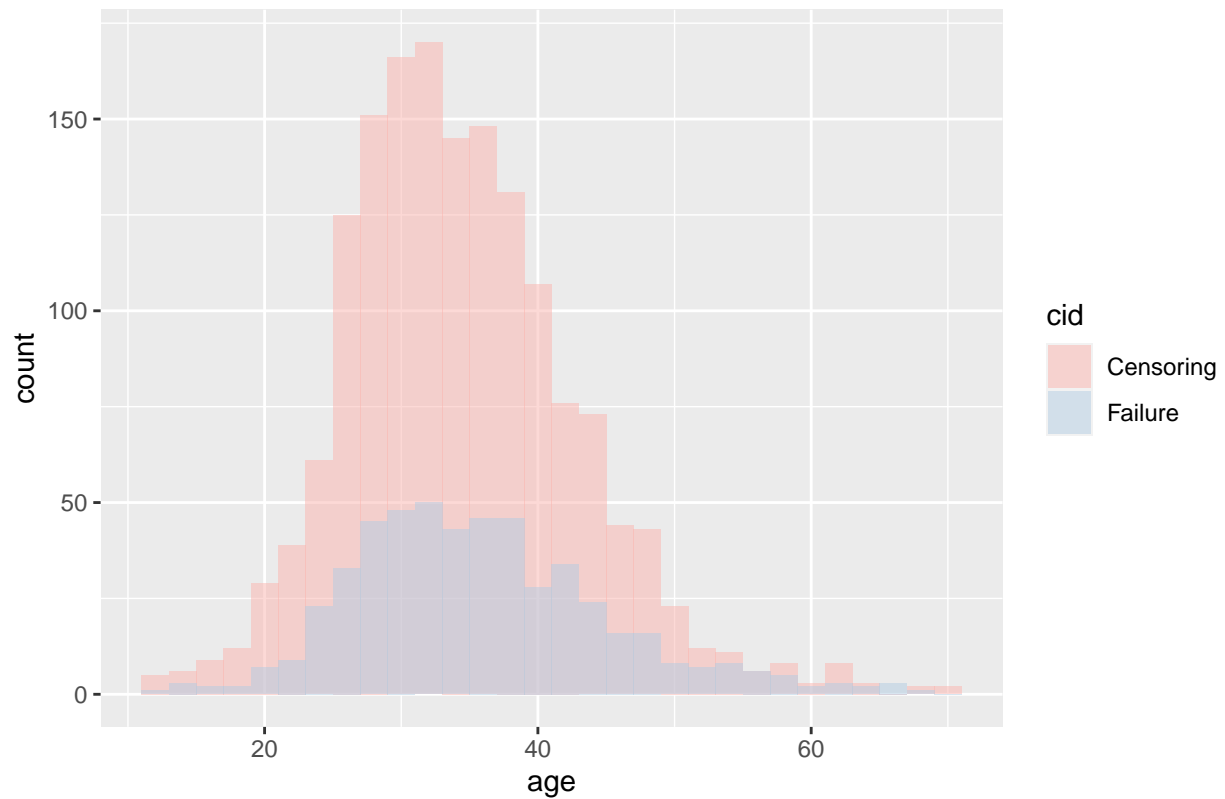
```
ggtitle("Figure 1: Distribution of Treatment VS. Patient Status")+
  guides(fill = guide_legend(title = "Treatment"))
```



```
ggplot(aids, aes(x=age, fill=cid)) +
  geom_histogram(alpha=0.5, position="identity")+
  scale_fill_brewer(palette = "Pastel1")+
  ggtitle("Figure 2: Distribution of Patient Age VS. Status")
```

'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.

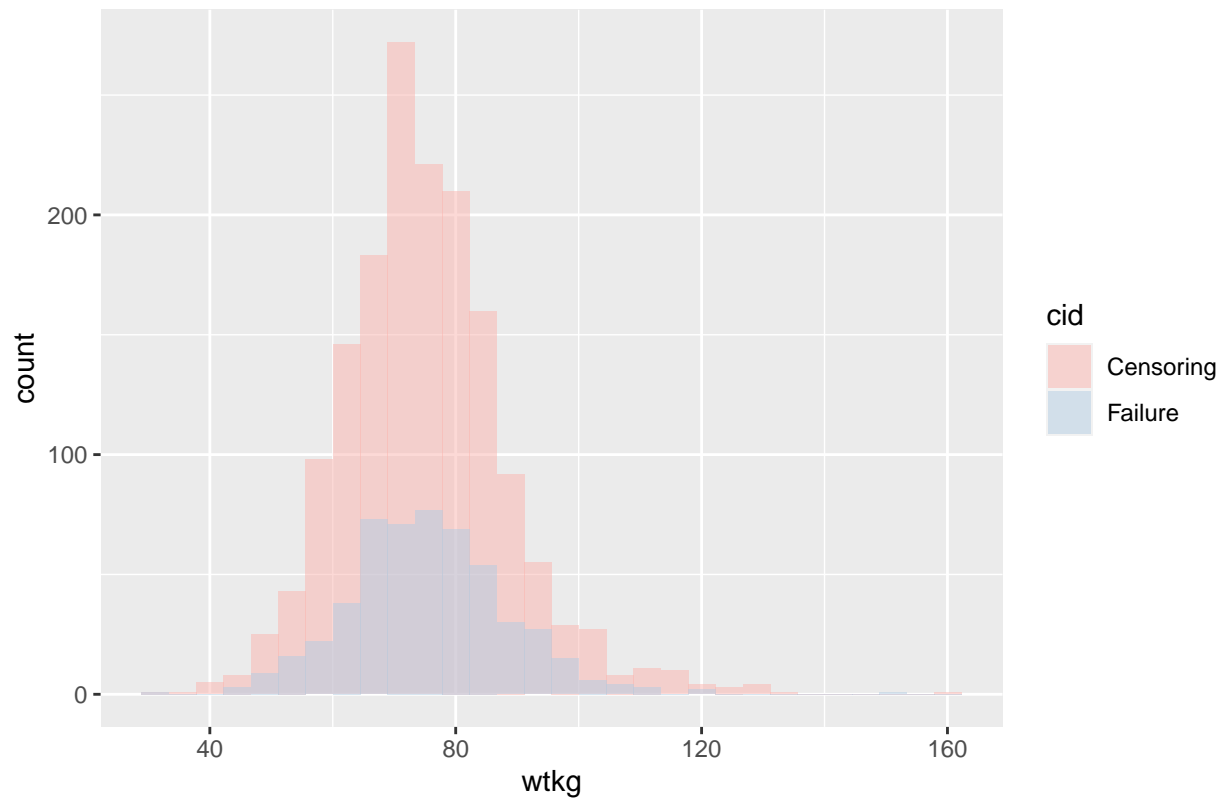
Figure 2: Distribution of Patient Age VS. Status



```
ggplot(aids, aes(x=wtkg, fill=cid)) +  
  geom_histogram(alpha=0.5, position="identity")+  
  scale_fill_brewer(palette = "Pastell")+  
  ggtitle("Figure 3: Distribution of Patient Weight VS. Status")
```

'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.

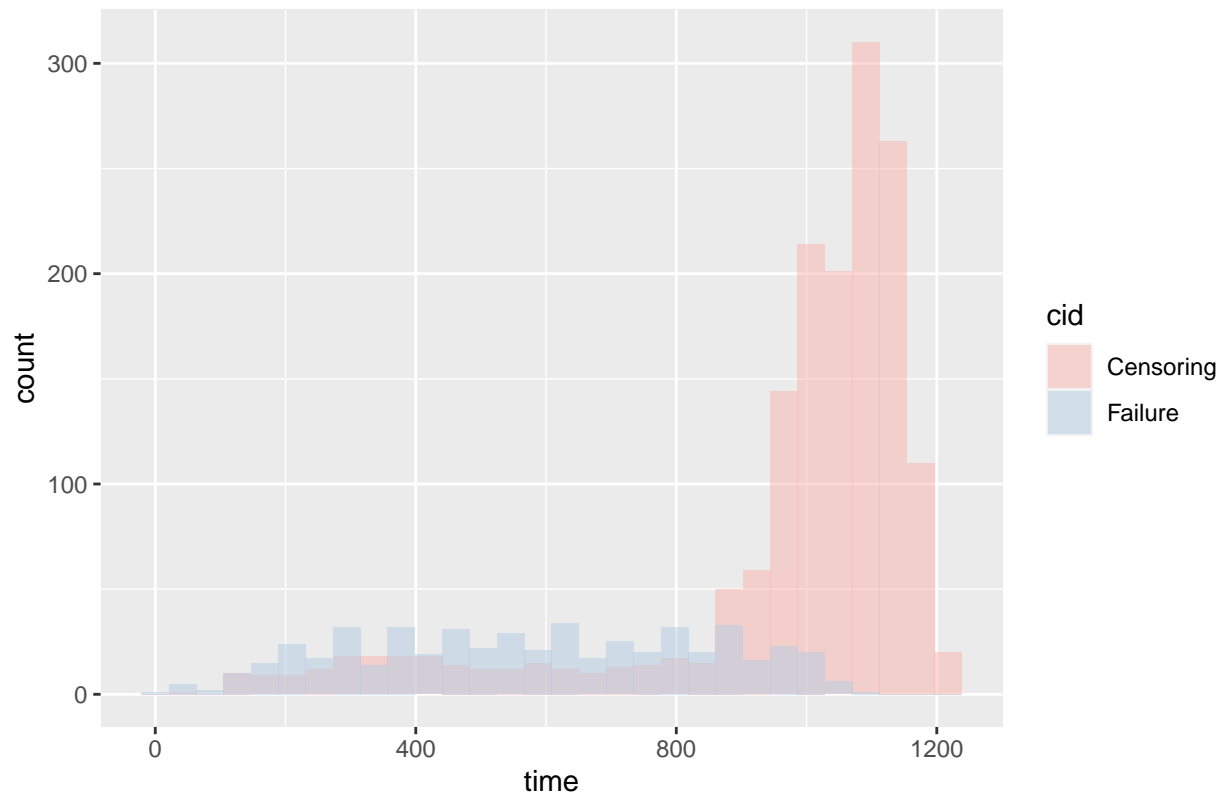
Figure 3: Distribution of Patient Weight VS. Status



```
ggplot(aids, aes(x=time, fill=cid)) +  
  geom_histogram(alpha=0.5, position="identity")+  
  scale_fill_brewer(palette = "Pastell")+  
  ggtitle("Figure 4: Distribution of Time to Failure or Censoring")
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

Figure 4: Distribution of Time to Failure or Censoring



```
p1 <- ggplot(aids,aes(x= treat, y=cd40,color=treat)) + geom_boxplot(show.legend = FALSE)+labs(x="")+scale_y_continuous(limits = c(0, 1000))
theme_minimal()

p2 <- ggplot(aids,aes(x= treat, y=cd420,color=treat)) + geom_boxplot(show.legend = FALSE)+labs(x="")+scale_y_continuous(limits = c(0, 1000))
theme_minimal()

p <- ggpubr::ggarrange(p1, p2, ncol=2,nrow = 1,common.legend = TRUE)
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_boxplot()').
```

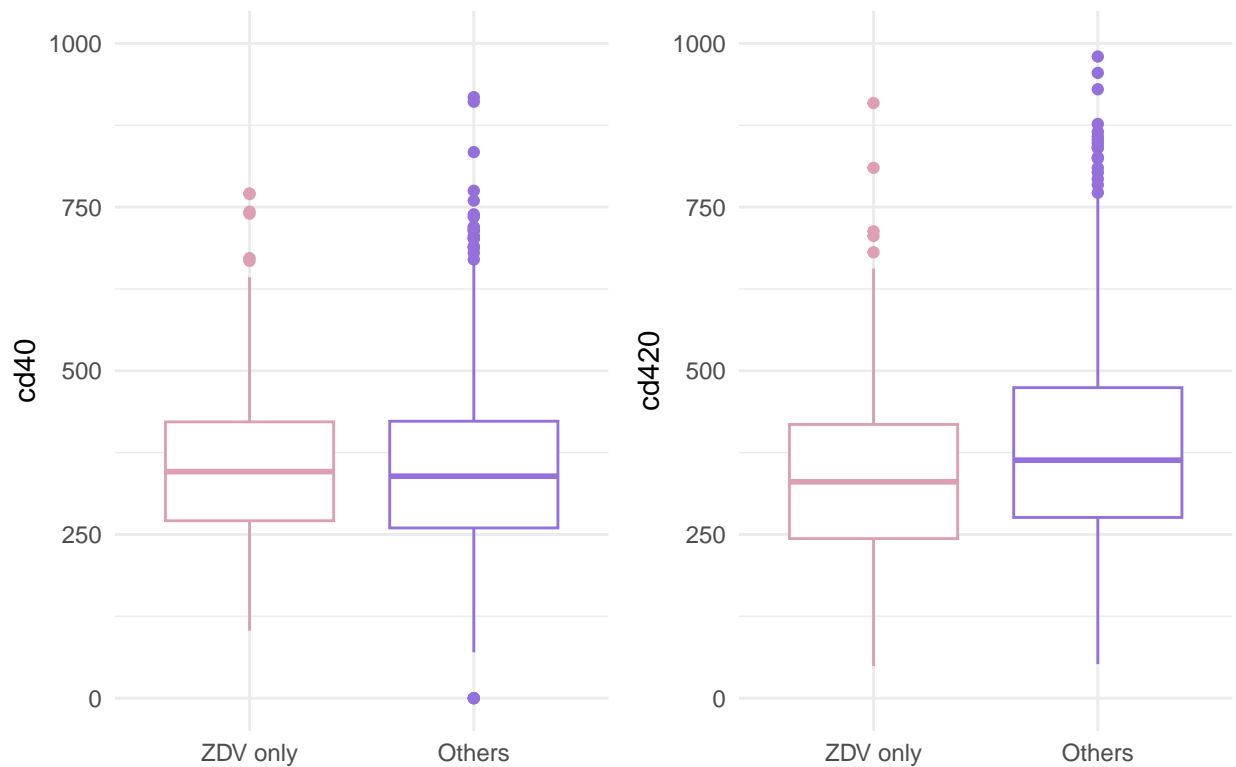
```
## Warning: Removed 3 rows containing non-finite values ('stat_boxplot()').
```

```
## Warning: Removed 1 rows containing non-finite values ('stat_boxplot()').
```

```
## Warning: Removed 3 rows containing non-finite values ('stat_boxplot()').
```

```
ggpubr::annotate_figure(p, top = ggpubr::text_grob("Figure 5: CD4 Count Change VS. Treatment Groups", c
```

Figure 5: CD4 Count Change VS. Treatment Groups



```
p3 <- ggplot(aids,aes(x= treat, y=cd80,color=treat)) + geom_boxplot(show.legend = FALSE)+labs(x="")+scale_y_continuous(limits = c(0, 4000))
theme_minimal()

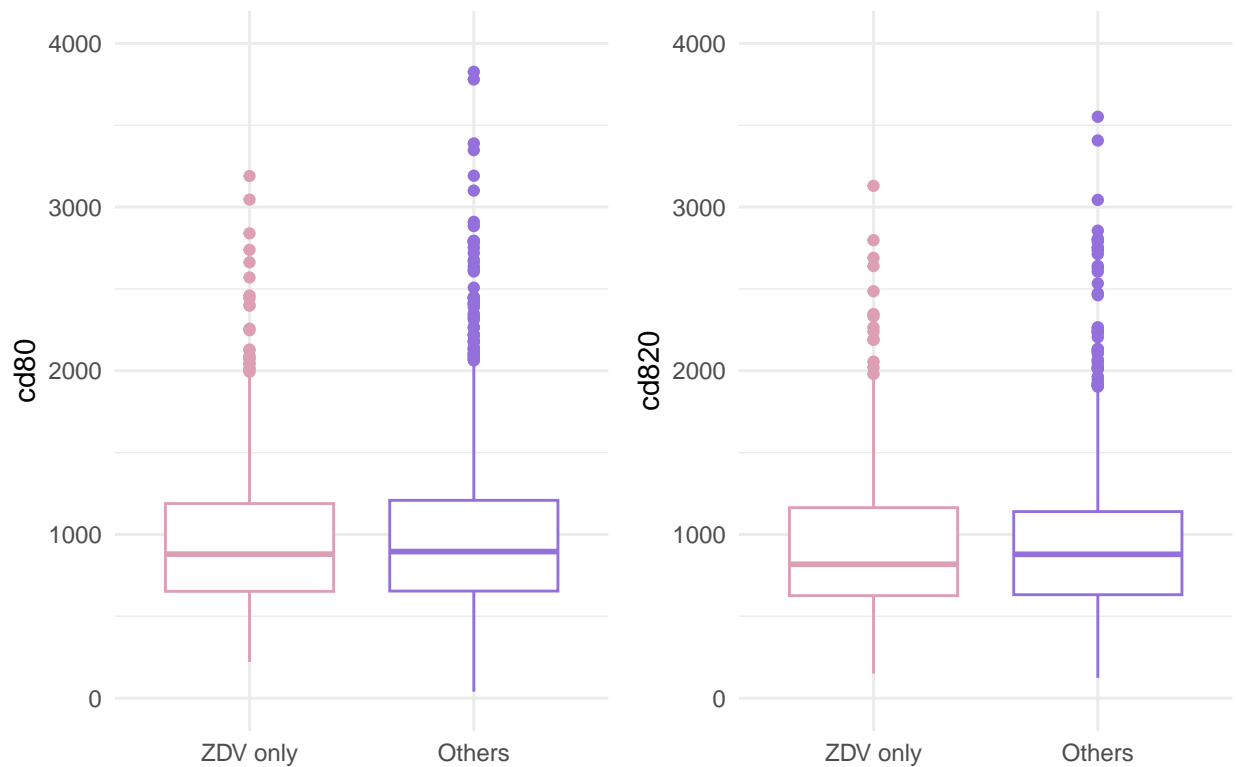
p4 <- ggplot(aids,aes(x= treat, y=cd820,color=treat)) + geom_boxplot(show.legend = FALSE)+labs(x="")+scale_y_continuous(limits = c(0, 4000))
theme_minimal()

p<- ggarrange(p3,p4,ncol=2,align = "hv",nrow = 1,common.legend = TRUE)
```

```
## Warning: Removed 2 rows containing non-finite values ('stat_boxplot()').
## Removed 2 rows containing non-finite values ('stat_boxplot()').
## Removed 2 rows containing non-finite values ('stat_boxplot()').
## Removed 2 rows containing non-finite values ('stat_boxplot()').
```

```
annotate_figure(p, top = text_grob("Figure 6: CD8 Count Change VS. Treatment Groups", color = "#0F2540"
```


Figure 6: CD8 Count Change VS. Treatment Groups



Non-parametric tests

```
aids <- read_csv("data/AIDS_Clinical_Trials_Group175.csv")
```

```
## New names:
## Rows: 2139 Columns: 25
## -- Column specification
## ----- Delimiter: "," dbl
## (25): ...1, time, trt, age, wtkg, hemo, homo, drugs, karnof, oprior, z30...
## i Use 'spec()' to retrieve the full column specification for this data. i
## Specify the column types or set 'show_col_types = FALSE' to quiet this message.
## * ' -> '...1'
```

```
aids %>% head()
```

```
## # A tibble: 6 x 25
##   ...1 time trt age wtkg hemo homo drugs karnof oprior z30 zprior
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1     0  948   2  48 89.8   0     0     0   100     0     0     1
## 2     1 1002   3  61 49.4   0     0     0    90     0     1     1
## 3     2  961   3  45 88.5   0     1     1    90     0     1     1
## 4     3 1166   3  47 85.3   0     1     0   100     0     1     1
```

```
## 5      4 1090      0   43 66.7      0      1      0    100      0      1      1
## 6      5 1181      1   46 88.9      0      1      1    100      0      1      1
## # i 13 more variables: preanti <dbl>, race <dbl>, gender <dbl>, str2 <dbl>,
## #   strat <dbl>, symptom <dbl>, treat <dbl>, offtrt <dbl>, cd40 <dbl>,
## #   cd420 <dbl>, cd80 <dbl>, cd820 <dbl>, cid <dbl>
```

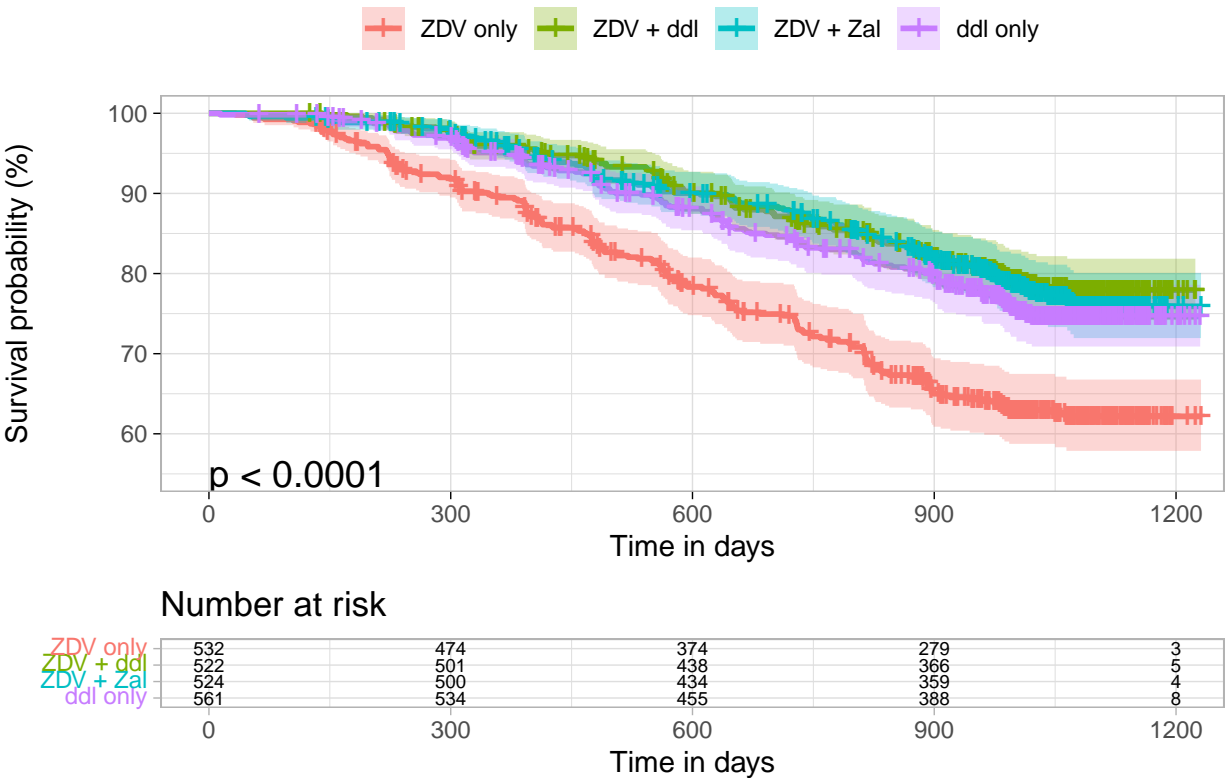
```
#KM estimate
```

```
km_fit_trt <- survfit(Surv(time, cid) ~ trt, data = aids)
pkm <- km_fit_trt %>% ggsurvplot(data = aids,
  fun = "pct", #can be replaced by cum hazard
  conf.int = TRUE,
  risk.table = TRUE,
  pval = TRUE,
  pval.coord = c(0,55),
  fontsize = 2.5,
  ggtheme = theme_light(),
  xlab = "Time in days",
  title = "Figure 4: Kaplan-Meier Survival Function Estimate",
  legend.title = "",
  legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zdl", "ddl only"),
  ylim = c(55, 100))

hkm <- km_fit_trt %>% ggsurvplot(data = aids,
  fun = "cumhaz", #can be replaced by cum hazard
  conf.int = TRUE,
  risk.table = TRUE,
  pval = TRUE,
  fontsize = 2.5,
  ggtheme = theme_light(),
  xlab = "Time in days",
  title = "Figure 5: Kaplan-Meier Cumulative Hazard Function",
  legend.title = "",
  legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zdl", "ddl only"))

pkm
```

Figure 4: Kaplan–Meier Survival Function Estimate

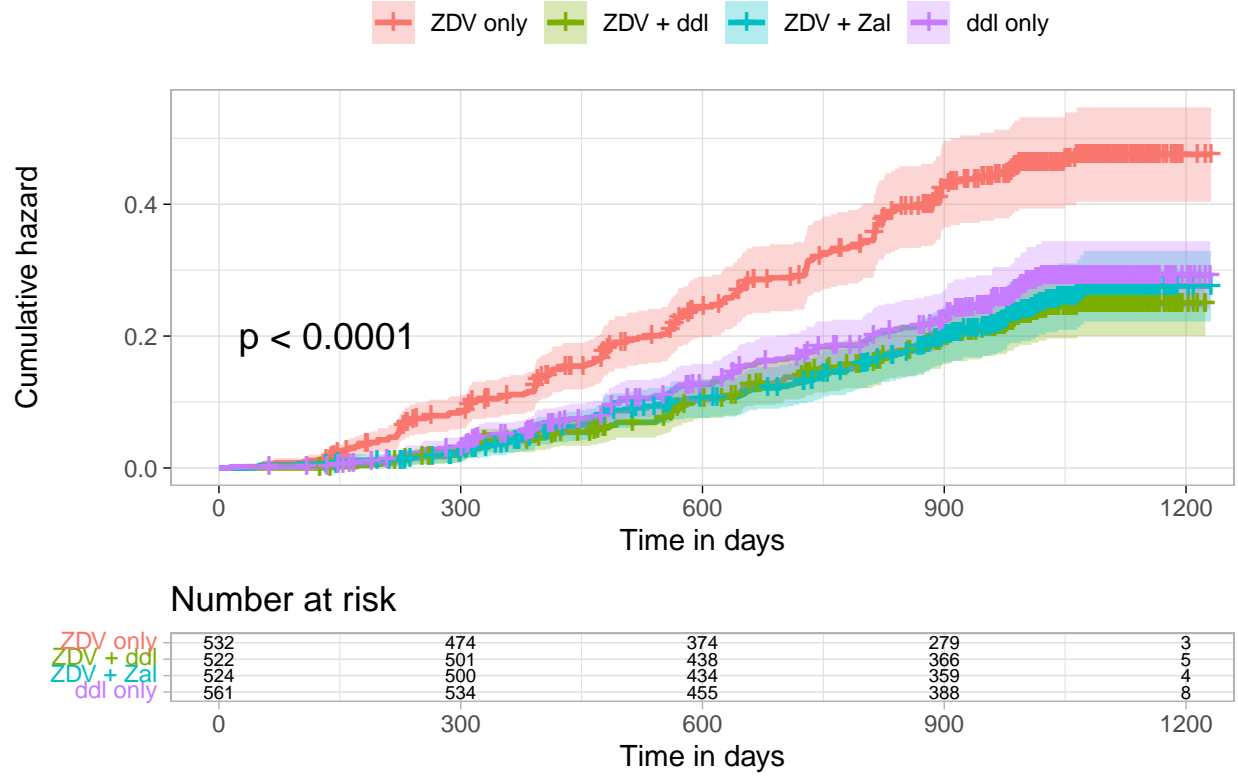


hkm

Table 2: t1

	10	15	20
trt=0	347	468	569
trt=1	626	822	986
trt=2	610	806	972
trt=3	537	672	898

Figure 5: Kaplan–Meier Cumulative Hazard Function



```
quantile(km_fit_trt, probs = c(0.1, 0.15, 0.2))$quantile %>% knitr::kable(caption = "t1")
```

Table 3: Quantile Survival Time (in days) by Treatments

Treatment	90 th	85 th	80 th
ZDV only	347 (284,406)	468 (394,557)	569 (484,649)
ZDV + ddl	626 (559,721)	822 (691,929)	986 (876,NA)
ZDV + Zai	610 (476,748)	806 (720,910)	972 (867,NA)
ddl only	537 (476,631)	672 (613,813)	898 (760,994)

```
survdif(Surv(time, cid) ~ trt, data = aids)
```

```
## Call:
```

```
## survdiff(formula = Surv(time, cid) ~ trt, data = aids)
```

```
##
##      N Observed Expected (O-E)^2/E (O-E)^2/V
## trt=0 532      181      116    37.030    47.67
## trt=1 522      103      134     6.988     9.40
## trt=2 524      109      132     4.158     5.58
## trt=3 561      128      139     0.933     1.27
##
##  Chisq= 49.2  on 3 degrees of freedom, p= 1e-10
```

```
aids %>%
  mutate(trt = case_when(trt == "0" ~ "ZDV only",
                        trt == "1" ~ "ZDV + ddl",
                        trt == "2" ~ "ZDV + Zal",
                        trt == "3" ~ "ddl only")) %>%
  pairwise_survdif(Surv(time, cid) ~ trt, data = ., p.adjust.method = "BH") %>%
  broom::tidy()
```

```
## # A tibble: 6 x 3
##   group1    group2      p.value
##   <chr>    <chr>    <dbl>
## 1 ZDV + ddl ddl only  0.278
## 2 ZDV + Zal ddl only  0.478
## 3 ZDV + Zal ZDV + ddl 0.636
## 4 ZDV only  ddl only  0.00000750
## 5 ZDV only  ZDV + ddl 0.0000000364
## 6 ZDV only  ZDV + Zal 0.000000242
```

Table 4: Pairwise Log-rank Tests by Treatments

group1	group2	P-value
ZDV + ddl	ddl only	0.2784441
ZDV + Zal	ddl only	0.4776330
ZDV + Zal	ZDV + ddl	0.6362565
ZDV only	ddl only	0.0000075***
ZDV only	ZDV + ddl	0.0000000***
ZDV only	ZDV + Zal	0.0000002***

KM curve for zdv history stratify

```
# non-ZDV treatment history
aids_non_zdv <- aids %>%
  filter(oprior == 1)

km_fit_trt1 <- survfit(Surv(time, cid) ~ trt, data = aids_non_zdv)
km_fit_trt1 %>% ggsurvplot(data = aids_non_zdv,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
```

```

ggtheme = theme_light(),
title = "Kaplan-Meier Estimate Without ZDV History",
legend.title = "",
legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zai", "ddl only"),
ylim = c(55, 100))

```

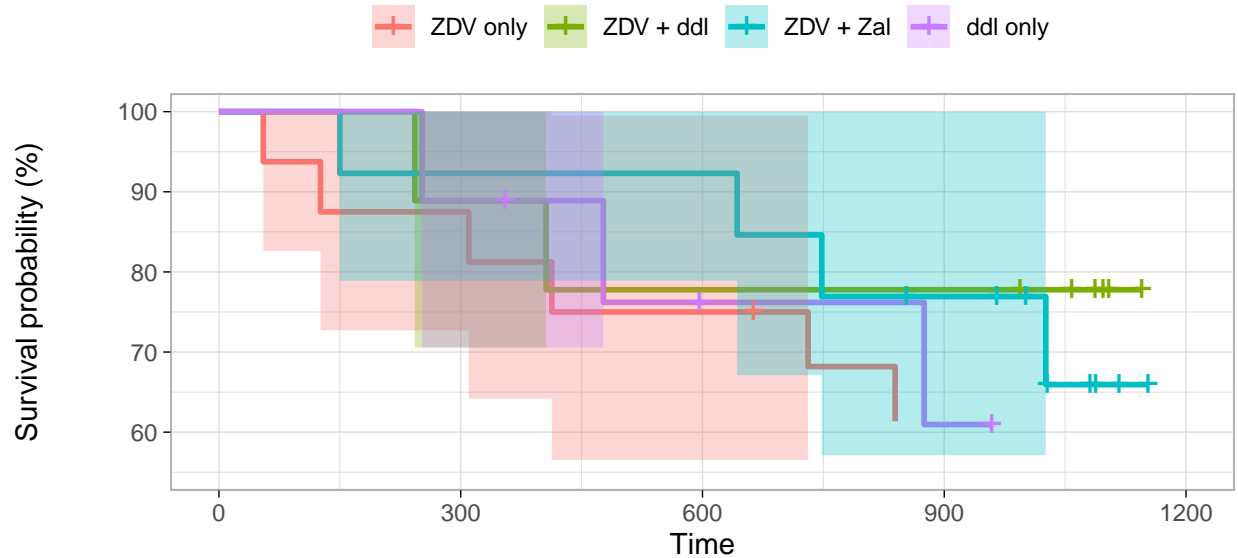
```
## Warning: Removed 12 rows containing missing values ('geom_step()').
```

```
## Warning: Removed 10 rows containing missing values ('geom_point()').
```

```
## Warning: Removed 12 rows containing missing values ('geom_step()').
```

```
## Warning: Removed 10 rows containing missing values ('geom_point()').
```

Kaplan-Meier Estimate Without ZDV History



Number at risk

ZDV only	16	14	12	9	0
ZDV + ddl	9	8	7	7	0
ZDV + Zai	13	12	12	9	0
ddl only	9	8	5	4	0
	0	300	600	900	1200

```
# ZDV in the 30 days prior to 175
```

```
aids_z30 = aids%>%
  filter(z30 == 1)
```

```

km_fit_trt2 <- survfit(Surv(time, cid) ~ trt, data = aids_z30)
km_fit_trt2 %>% ggsurvplot(data = aids_z30,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,

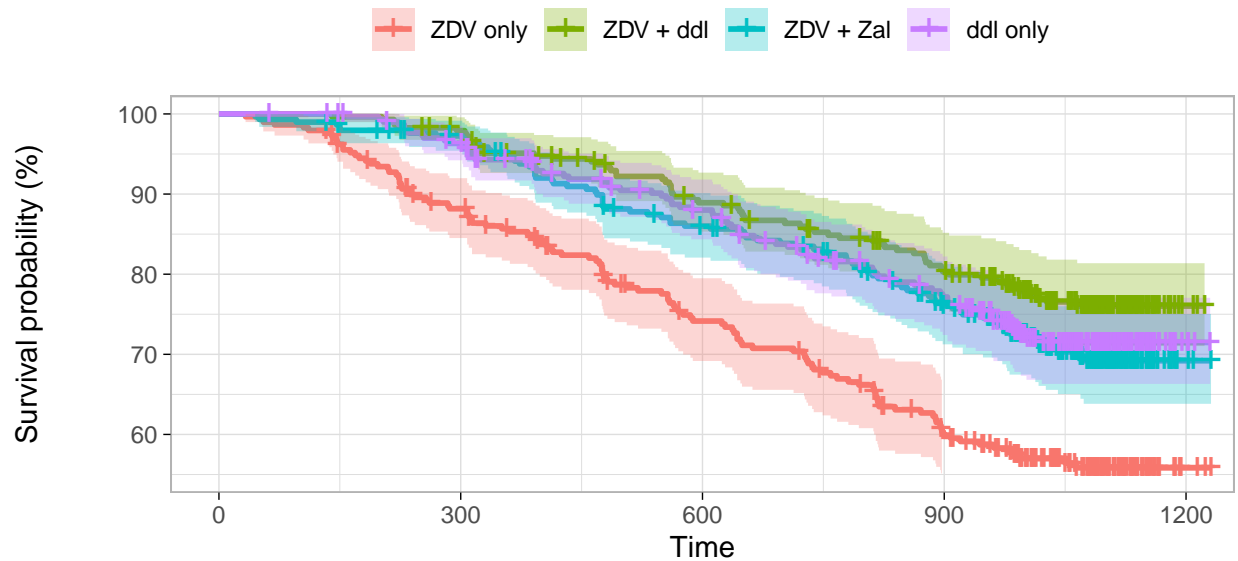
```

```

fontsize = 2,
ggtheme = theme_light(),
title = "Kaplan-Meier Estimate With ZDV 30 days prior",
legend.title = "",
legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zai", "ddl only"),
ylim = c(55, 100))

```

Kaplan-Meier Estimate With ZDV 30 days prior



Number at risk

ZDV only	291	248	196	151	3
ZDV + ddl	288	279	243	211	3
ZDV + Zai	294	279	240	200	4
ddl only	304	287	249	208	4
	0	300	600	900	1200

Time

```

# ZDV prior to 175
aids_zprior = aids%>%
  filter(zprior == 1)

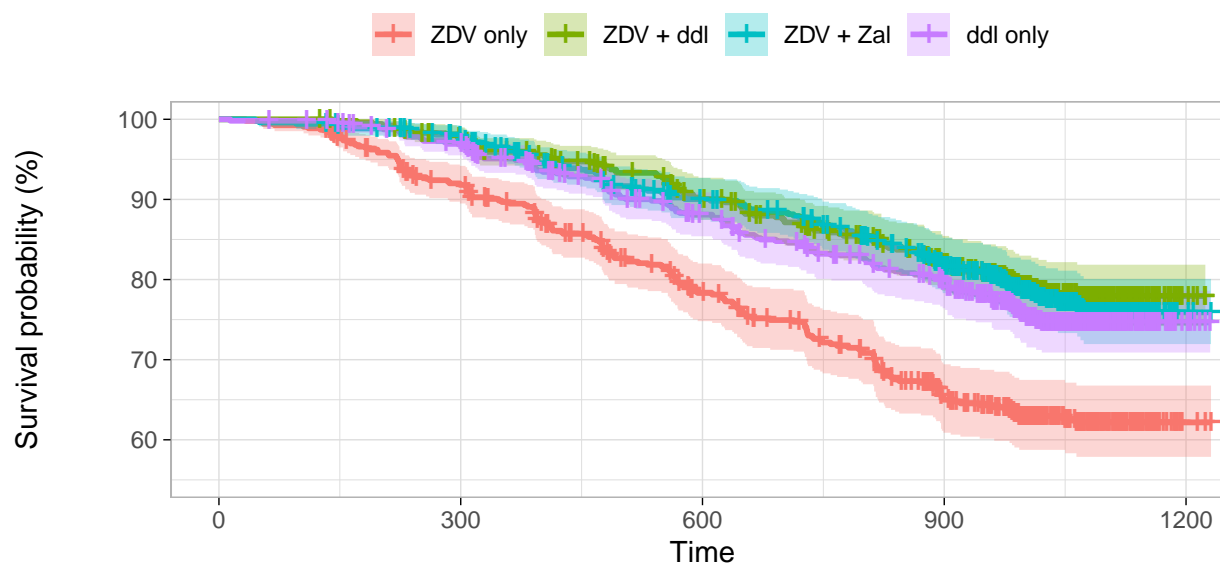
```

```

km_fit_trt3 <- survfit(Surv(time, cid) ~ trt, data = aids_zprior)
km_fit_trt3 %>% ggsurvplot(data = aids_zprior,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
  ggtheme = theme_light(),
  title = "Kaplan-Meier Estimate With ZDV 175 days prior to study",
  legend.title = "",
  legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zai", "ddl only"),
  ylim = c(55, 100))

```

Kaplan–Meier Estimate With ZDV 175 days prior to study



Number at risk

ZDV only	532	474	374	279	3
ZDV + ddl	522	501	438	366	5
ZDV + Zdl	524	500	434	359	4
ddl only	561	534	455	388	8
	0	300	600	900	1200

Time

```
survfit_result_zdv <- survfit(Surv(time, cid) ~ strata(oprior) + trt, data = aids)
survfit_result_zdv
```

```
## Call: survfit(formula = Surv(time, cid) ~ strata(oprior) + trt, data = aids)
##
##
##          n events median 0.95LCL 0.95UCL
## strata(oprior)=oprior=0, trt=0 516    174    NA      NA      NA
## strata(oprior)=oprior=0, trt=1 513    101    NA      NA      NA
## strata(oprior)=oprior=0, trt=2 511    105    NA      NA      NA
## strata(oprior)=oprior=0, trt=3 552    124    NA      NA      NA
## strata(oprior)=oprior=1, trt=0  16      7    NA     731     NA
## strata(oprior)=oprior=1, trt=1   9      2    NA      NA      NA
## strata(oprior)=oprior=1, trt=2  13      4    NA    1026     NA
## strata(oprior)=oprior=1, trt=3   9      4   994     875     NA
```

KM Curve for medical history stratify

```
# patient with drug used and has hemophilia
aids_hemo_drug = aids%>%
  filter(hemo==1)%>%
  filter(drugs ==1)
```



```
km_fit_trt4 <- survfit(Surv(time, cid) ~ trt, data = aids_hemo_drug)
km_fit_trt4 %>% ggsurvplot(data = aids_hemo_drug,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
  ggtheme = theme_light(),
  title = "Kaplan-Meier Estimate With Drugs and Hemophilia",
  legend.title = "",
  legend.labs = levels(aids$trt),
  ylim = c(55, 100))
```

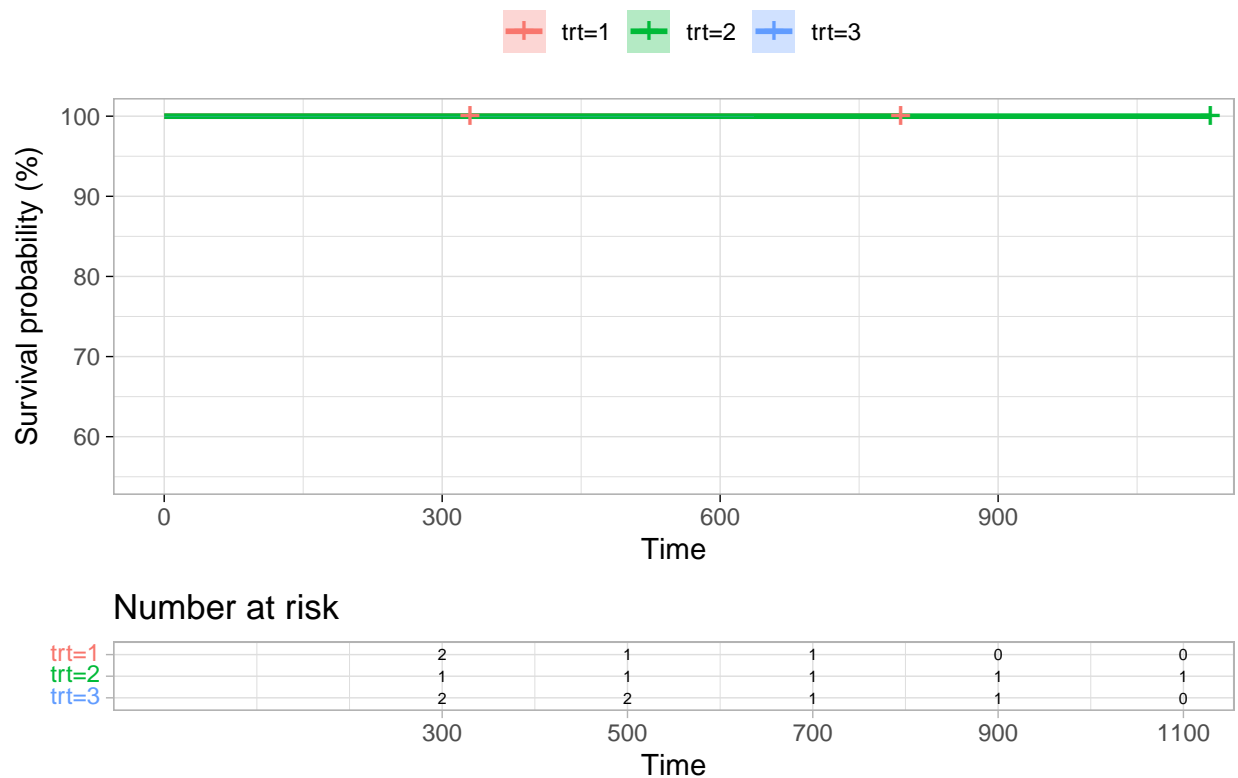
```
## Warning: Removed 2 rows containing missing values ('geom_step()').
```

```
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

```
## Warning: Removed 2 rows containing missing values ('geom_step()').
```

```
## Warning: Removed 1 rows containing missing values ('geom_point()').
```

Kaplan-Meier Estimate With Drugs and Hemophilia



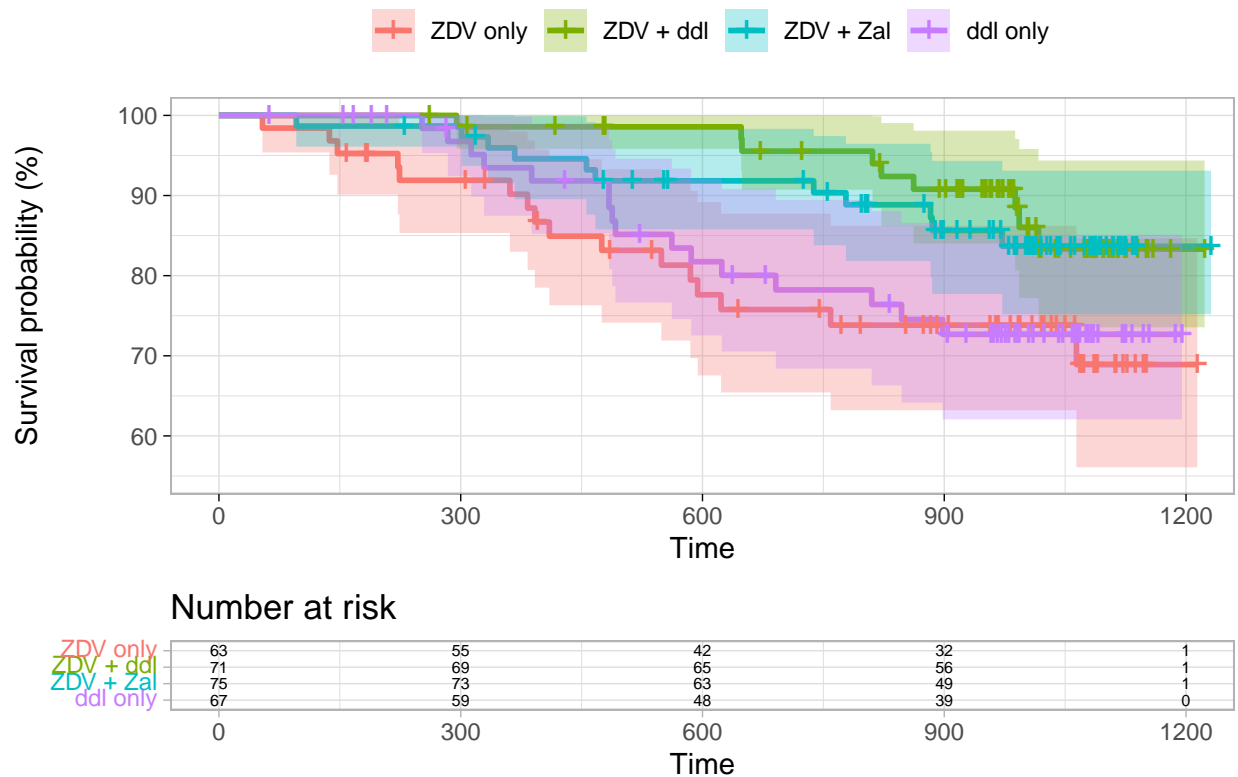
```
# patient with drug used and doesn't have hemophilia
aids_drug = aids%>%
  filter(hemo==0)%>%
  filter(drugs ==1)
```

```

km_fit_trt5 <- survfit(Surv(time, cid) ~ trt, data = aids_drug)
km_fit_trt5 %>% ggsurvplot(data = aids_drug,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
  ggtheme = theme_light(),
  title = "Group 2: Kaplan-Meier Estimate With Drug Used",
  legend.title = "",
  legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zai", "ddl only"),
  ylim = c(55, 100))

```

Group 2: Kaplan-Meier Estimate With Drug Used



```

# patient without drug used but has hemophilia
aids_hemo = aids%>%
  filter(hemo==1)%>%
  filter(drugs ==0)

```

```

km_fit_trt6 <- survfit(Surv(time, cid) ~ trt, data = aids_hemo)
km_fit_trt6 %>% ggsurvplot(data = aids_hemo,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
  ggtheme = theme_light(),
  title = "Group 3: Kaplan-Meier Estimate With Hemophilia",

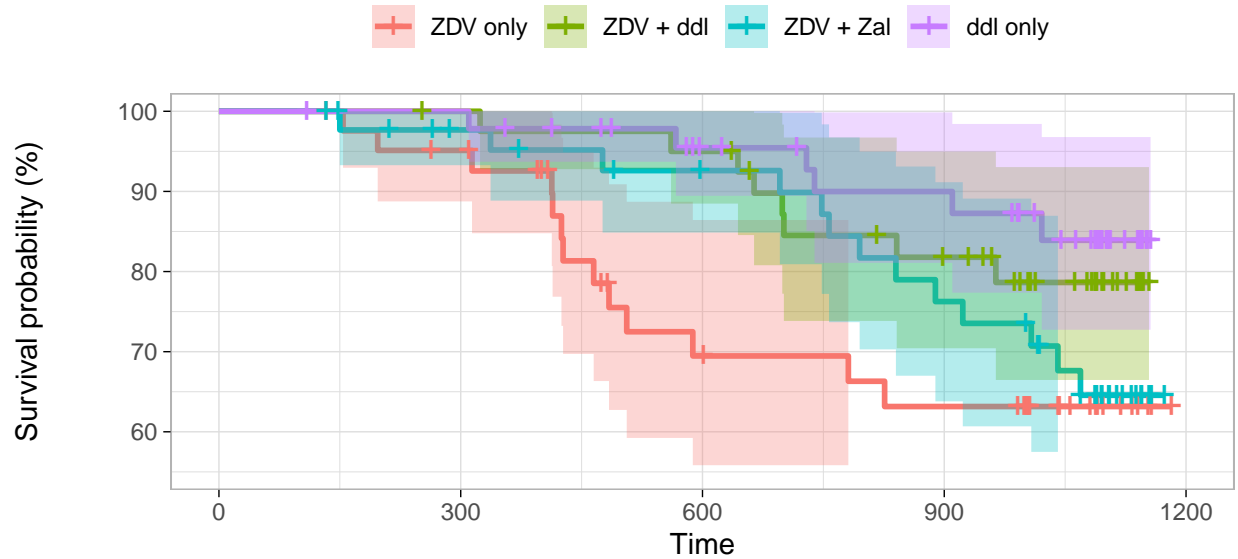
```

```

legend.title = "",
legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zdl", "ddl only"),
ylim = c(55, 100))

```

Group 3: Kaplan–Meier Estimate With Hemophilia



Number at risk

ZDV only	42	38	23	20	0
ZDV + ddl	41	40	38	29	0
ZDV + Zdl	45	39	34	28	0
ddl only	47	46	37	33	0
	0	300	600	900	1200

Time

```

# patient without drug used and doesn't have hemophilia
aids_nomedical = aids%>%
  filter(hemo==0)%>%
  filter(drugs ==0)

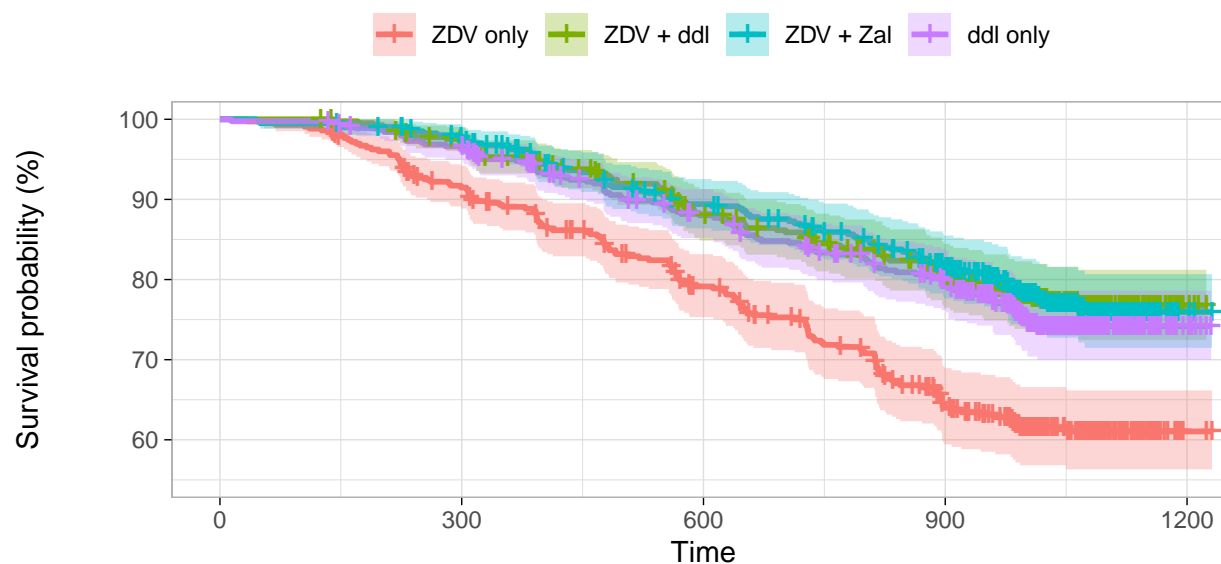
```

```

km_fit_trt7 <- survfit(Surv(time, cid) ~ trt, data = aids_nomedical)
km_fit_trt7 %>% ggsurvplot(data = aids_nomedical,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
  ggtheme = theme_light(),
  title = "Group 4:Kaplan-Meier Estimate Without medical history",
  legend.title = "",
  legend.labs = c("ZDV only", "ZDV + ddl", "ZDV + Zdl", "ddl only"),
  ylim = c(55, 100))

```

Group 4:Kaplan–Meier Estimate Without medical history



Number at risk

	0	300	600	900	1200
ZDV only	427	381	309	227	2
ZDV + ddl	408	390	334	281	4
ZDV + Zai	403	387	336	281	3
ddl only	445	427	368	315	8

Time

```
survfit_result_drug <- survfit(Surv(time, cid) ~ strata(drugs) + trt, data = aids)
survfit_result_drug
```

```
## Call: survfit(formula = Surv(time, cid) ~ strata(drugs) + trt, data = aids)
```

```
##
```

```
##              n events median 0.95LCL 0.95UCL
## strata(drugs)=drugs=0, trt=0 469    165    NA      NA      NA
## strata(drugs)=drugs=0, trt=1 449     94    NA      NA      NA
## strata(drugs)=drugs=0, trt=2 448     98    NA      NA      NA
## strata(drugs)=drugs=0, trt=3 492    111    NA      NA      NA
## strata(drugs)=drugs=1, trt=0  63     16    NA      NA      NA
## strata(drugs)=drugs=1, trt=1  73      9    NA      NA      NA
## strata(drugs)=drugs=1, trt=2  76     11    NA      NA      NA
## strata(drugs)=drugs=1, trt=3  69     17    NA      NA      NA
```

```
survfit_result_hemo <- survfit(Surv(time, cid) ~ strata(hemo) + trt, data = aids)
survfit_result_hemo
```

```
## Call: survfit(formula = Surv(time, cid) ~ strata(hemo) + trt, data = aids)
```

```
##
```

```
##              n events median 0.95LCL 0.95UCL
## strata(hemo)=hemo=0, trt=0 490    168    NA      NA      NA
## strata(hemo)=hemo=0, trt=1 479     95    NA      NA      NA
## strata(hemo)=hemo=0, trt=2 478     96    NA      NA      NA
## strata(hemo)=hemo=0, trt=3 512    121    NA      NA      NA
```

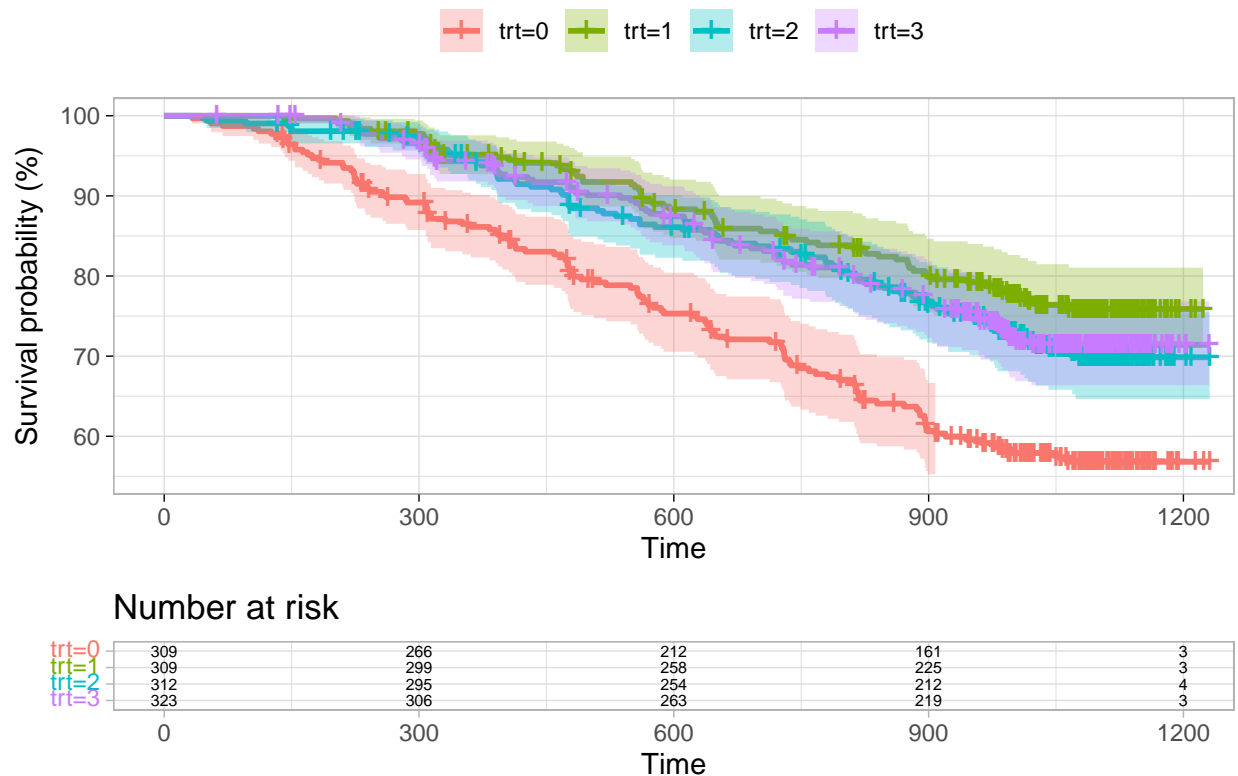
```
## strata(hemo)=hemo=1, trt=0 42      13      NA      826      NA
## strata(hemo)=hemo=1, trt=1 43       8      NA       NA      NA
## strata(hemo)=hemo=1, trt=2 46      13      NA       NA      NA
## strata(hemo)=hemo=1, trt=3 49       7      NA       NA      NA
```

KM curve for patient with or without azt therapy before

```
# patient with azt theory before
aids_azt_yes = aids%>%
  filter(str2==1)
```

```
km_fit_trt8 <- survfit(Surv(time, cid) ~ trt, data = aids_azt_yes)
km_fit_trt8 %>% ggsurvplot(data = aids_azt_yes,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
  ggtheme = theme_light(),
  title = "Kaplan-Meier Estimate Without medical history",
  legend.title = "",
  legend.labs = levels(aids$trt),
  ylim = c(55, 100))
```

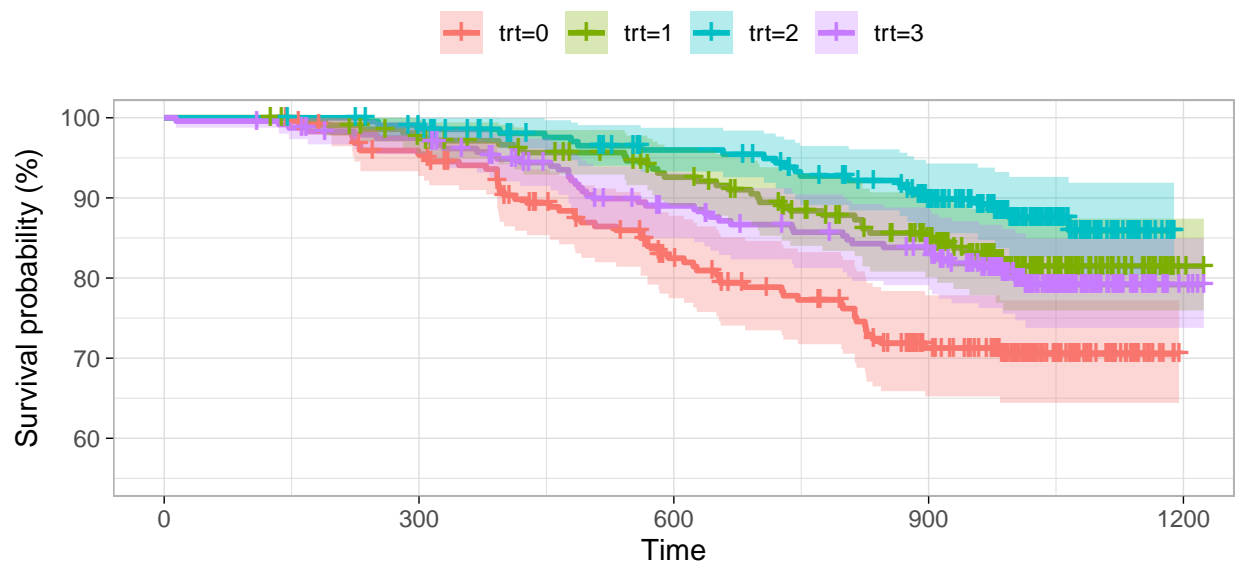
Kaplan-Meier Estimate Without medical history



```
# patient without azt therapy before
aids_azt_no <-
  aids %>%
  filter(str2==0)
```

```
km_fit_trt9 <- survfit(Surv(time, cid) ~ trt, data = aids_azt_no)
km_fit_trt9 %>% ggsurvplot(data = aids_azt_no,
  fun = "pct",
  conf.int = TRUE,
  risk.table = TRUE,
  fontsize = 2,
  ggtheme = theme_light(),
  title = "Kaplan-Meier Estimate Without medical history",
  legend.title = "",
  legend.labs = levels(aids$trt),
  ylim = c(55, 100))
```

Kaplan-Meier Estimate Without medical history



Number at risk

trt=0	223	208	162	118	0
trt=1	213	202	180	141	2
trt=2	212	205	180	147	0
trt=3	238	228	192	169	5
	0	300	600	900	1200
	Time				

```
survfit_result_azt <- survfit(Surv(time, cid) ~ strata(str2) + trt, data = aids)
survfit_result_azt
```

```
## Call: survfit(formula = Surv(time, cid) ~ strata(str2) + trt, data = aids)
##
##              n events median 0.95LCL 0.95UCL
## strata(str2)=str2=0, trt=0 223      59    NA      NA      NA
```

```
## strata(str2)=str2=0, trt=1 213      34      NA      NA      NA
## strata(str2)=str2=0, trt=2 212      23      NA      NA      NA
## strata(str2)=str2=0, trt=3 238      44      NA      NA      NA
## strata(str2)=str2=1, trt=0 309     122      NA      NA      NA
## strata(str2)=str2=1, trt=1 309      69      NA      NA      NA
## strata(str2)=str2=1, trt=2 312      86      NA      NA      NA
## strata(str2)=str2=1, trt=3 323      84      NA      NA      NA
```

Cox-PH model

```
aids = read_csv("data/AIDS_Clinical_Trials_Group175.csv") %>% mutate(trt = as.factor(trt),
                                                                    hemo = as.factor(hemo),
                                                                    homo = as.factor(homo),
                                                                    drugs = as.factor(drugs),
                                                                    race = as.factor(race),
                                                                    gender = as.factor(gender),
                                                                    str2 = as.factor(str2),
                                                                    symptom = as.factor(symptom)) %>%
```

```
## New names:
## Rows: 2139 Columns: 25
## -- Column specification
## ----- Delimiter: "," dbl
## (25): ...1, time, trt, age, wtkg, hemo, homo, drugs, karnof, oprior, z30...
## i Use 'spec()' to retrieve the full column specification for this data. i
## Specify the column types or set 'show_col_types = FALSE' to quiet this message.
## * ' -> '...1'
```

model selection *selection on personal information*

```
selectCox(Surv(time, cid) ~ trt + age + wtkg + homo + race + gender, data = aids, rule = "aic")
```

```
## $fit
## Cox Proportional Hazards Model
##
## rms::cph(formula = newform, data = data, x = TRUE, y = TRUE,
##           surv = TRUE)
##
##               Model Tests           Discrimination
##               Indexes
## Obs          2139    LR chi2      51.46    R2          0.024
## Events        521    d.f.          4    R2(4,2139)0.022
## Center -0.0148    Pr(> chi2) 0.0000    R2(4,521)0.087
##               Score chi2 56.26    Dxy          0.179
##               Pr(> chi2) 0.0000
##
##      Coef      S.E.   Wald Z Pr(>|Z|)
## trt=1 -0.7123 0.1235 -5.77  <0.0001
## trt=2 -0.6464 0.1213 -5.33  <0.0001
## trt=3 -0.5328 0.1155 -4.61  <0.0001
```

```
## age      0.0130 0.0049  2.66  0.0079
##
##
## $In
## [1] "trt" "age"
##
## $call
## selectCox(formula = Surv(time, cid) ~ trt + age + wtkg + homo +
##           race + gender, data = aids, rule = "aic")
##
## attr("class")
## [1] "selectCox"
```

\$In [1] "trt" "age"

selection on medical history/treatment history/lab results

```
selectCox(Surv(time, cid) ~ trt + hemo + drugs + karnof + str2 + symptom + cd40 + cd80, data = aids, rule = "aic")
```

```
## $fit
## Cox Proportional Hazards Model
##
## rms::cph(formula = newform, data = data, x = TRUE, y = TRUE,
##           surv = TRUE)
##
##
##               Model Tests      Discrimination
##               Indexes
## Obs          2139    LR chi2    228.09    R2          0.104
## Events        521    d.f.        9      R2(9,2139)0.097
## Center -3.6773    Pr(> chi2) 0.0000    R2(9,521)0.343
##               Score chi2 232.44    Dxy          0.393
##               Pr(> chi2) 0.0000
##
##               Coef    S.E.    Wald Z Pr(>|Z|)
## trt=1         -0.7949 0.1241  -6.41  <0.0001
## trt=2         -0.6685 0.1216  -5.50  <0.0001
## trt=3         -0.5744 0.1158  -4.96  <0.0001
## drugs=1       -0.3177 0.1460  -2.18  0.0295
## karnof        -0.0253 0.0069  -3.65  0.0003
## str2=1         0.3769 0.0956   3.94  <0.0001
## symptom=1     0.4061 0.1024   3.97  <0.0001
## cd40          -0.0042 0.0004  -9.30  <0.0001
## cd80           0.0005 0.0001   5.52  <0.0001
##
##
## $In
## [1] "trt"      "drugs"    "karnof"   "str2"     "symptom"  "cd40"     "cd80"
##
## $call
## selectCox(formula = Surv(time, cid) ~ trt + hemo + drugs + karnof +
##           str2 + symptom + cd40 + cd80, data = aids, rule = "aic")
##
## attr("class")
## [1] "selectCox"
```



```
$In [1] "trt" "drugs" "karnof" "str2" "symptom" "cd40" "cd80"
```

selection with interaction

```
selectCox(Surv(time, cid) ~ trt + drugs + karnof + str2 + symptom + cd40 + cd80 + age + age * drugs + a
```

```
## $fit
## Cox Proportional Hazards Model
##
## rms::cph(formula = newform, data = data, x = TRUE, y = TRUE,
##           surv = TRUE)
##
##               Model Tests           Discrimination
##               Indexes
## Obs          2139   LR chi2      231.48         R2          0.105
## Events        521   d.f.           11   R2(11,2139)0.098
## Center -3.289   Pr(> chi2) 0.0000   R2(11,521)0.345
##               Score chi2 235.70         Dxy          0.395
##               Pr(> chi2) 0.0000
##
##               Coef      S.E.    Wald Z Pr(>|Z|)
## trt=1          -0.7943 0.1241  -6.40  <0.0001
## trt=2          -0.6671 0.1216  -5.49  <0.0001
## trt=3          -0.5709 0.1159  -4.93  <0.0001
## karnof         -0.0248 0.0070  -3.56  0.0004
## str2=1          0.3731 0.0956   3.90  <0.0001
## symptom=1       0.4048 0.1023   3.96  <0.0001
## cd40           -0.0041 0.0004  -9.23  <0.0001
## cd80            0.0005 0.0001   5.44  <0.0001
## drugs=1         0.4399 0.8198   0.54  0.5916
## age            0.0093 0.0052   1.78  0.0759
## drugs=1 * age  -0.0206 0.0218  -0.95  0.3440
##
##
## $In
## [1] "trt"          "karnof"        "str2"          "symptom"       "cd40"
## [6] "cd80"          "drugs * age"
##
## $call
## selectCox(formula = Surv(time, cid) ~ trt + drugs + karnof +
##           str2 + symptom + cd40 + cd80 + age + age * drugs + age *
##           trt, data = aids, rule = "aic")
##
## attr(,"class")
## [1] "selectCox"
```

```
$In [1] "trt" "karnof" "str2" "symptom" "cd40" "cd80" "drugs * age"
```

final model

```
cox1 = coxph(Surv(time, cid) ~ trt + karnof + str2 + symptom + cd40 + cd80 + age * drugs, data = aids)
```

```
summary(cox1)
```

```
## Call:
## coxph(formula = Surv(time, cid) ~ trt + karnof + str2 + symptom +
##       cd40 + cd80 + age * drugs, data = aids)
##
## n= 2139, number of events= 521
##
##              coef exp(coef)    se(coef)      z Pr(>|z|)
## trt1          -7.943e-01  4.519e-01  1.241e-01 -6.401 1.54e-10 ***
## trt2          -6.671e-01  5.132e-01  1.216e-01 -5.487 4.09e-08 ***
## trt3          -5.709e-01  5.650e-01  1.159e-01 -4.927 8.34e-07 ***
## karnof        -2.478e-02  9.755e-01  6.971e-03 -3.555 0.000378 ***
## str21          3.731e-01  1.452e+00  9.563e-02  3.901 9.58e-05 ***
## symptom1       4.048e-01  1.499e+00  1.023e-01  3.956 7.63e-05 ***
## cd40          -4.108e-03  9.959e-01  4.451e-04 -9.228 < 2e-16 ***
## cd80           4.548e-04  1.000e+00  8.366e-05  5.436 5.45e-08 ***
## age           9.306e-03  1.009e+00  5.242e-03  1.775 0.075864 .
## drugs1         4.399e-01  1.553e+00  8.198e-01  0.537 0.591542
## age:drugs1    -2.061e-02  9.796e-01  2.178e-02 -0.946 0.343950
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##              exp(coef) exp(-coef) lower .95 upper .95
## trt1              0.4519    2.2129    0.3543    0.5763
## trt2              0.5132    1.9487    0.4044    0.6513
## trt3              0.5650    1.7698    0.4502    0.7091
## karnof            0.9755    1.0251    0.9623    0.9889
## str21             1.4522    0.6886    1.2040    1.7515
## symptom1          1.4990    0.6671    1.2266    1.8320
## cd40              0.9959    1.0041    0.9950    0.9968
## cd80              1.0005    0.9995    1.0003    1.0006
## age               1.0093    0.9907    0.9990    1.0198
## drugs1            1.5526    0.6441    0.3113    7.7419
## age:drugs1        0.9796    1.0208    0.9387    1.0223
##
## Concordance= 0.698 (se = 0.012 )
## Likelihood ratio test= 231.5 on 11 df,  p=<2e-16
## Wald test              = 229.8 on 11 df,  p=<2e-16
## Score (logrank) test = 235.7 on 11 df,  p=<2e-16
```

final model with age_group

```
aids = aids %>% mutate(age_group = as.factor(ifelse(age >= 11 & age <= 30, "11-30", ifelse(age >= 31 &
```

```
cox2 = coxph(Surv(time, cid) ~ trt + age_group + drugs + karnof + str2 + symptom + cd40 + cd80 + age_gr
```

```
summary(cox2)
```

```
## Call:
## coxph(formula = Surv(time, cid) ~ trt + age_group + drugs + karnof +
```

```
##      str2 + symptom + cd40 + cd80 + age_group * drugs, data = aids)
##
##      n= 2139, number of events= 521
##
##              coef exp(coef)    se(coef)      z Pr(>|z|)
## trt1          -8.001e-01  4.493e-01  1.242e-01 -6.441 1.18e-10 ***
## trt2          -6.658e-01  5.139e-01  1.216e-01 -5.473 4.43e-08 ***
## trt3          -5.673e-01  5.670e-01  1.160e-01 -4.891 1.00e-06 ***
## age_group31-50 -9.626e-02  9.082e-01  1.037e-01 -0.928 0.353341
## age_group51-70  3.464e-01  1.414e+00  1.901e-01  1.822 0.068462 .
## drugs1        -3.665e-01  6.932e-01  3.445e-01 -1.064 0.287443
## karnof         -2.381e-02  9.765e-01  7.007e-03 -3.398 0.000678 ***
## str21          3.772e-01  1.458e+00  9.591e-02  3.933 8.37e-05 ***
## symptom1       4.364e-01  1.547e+00  1.031e-01  4.233 2.31e-05 ***
## cd40           -4.186e-03  9.958e-01  4.476e-04 -9.353 < 2e-16 ***
## cd80           4.689e-04  1.000e+00  8.296e-05  5.652 1.58e-08 ***
## age_group31-50:drugs1 7.046e-02  1.073e+00  3.832e-01  0.184 0.854096
## age_group51-70:drugs1 4.513e-01  1.570e+00  6.976e-01  0.647 0.517674
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##              exp(coef) exp(-coef) lower .95 upper .95
## trt1              0.4493      2.2258      0.3522      0.5731
## trt2              0.5139      1.9460      0.4049      0.6522
## trt3              0.5670      1.7635      0.4517      0.7118
## age_group31-50    0.9082      1.1010      0.7412      1.1129
## age_group51-70    1.4139      0.7072      0.9741      2.0523
## drugs1            0.6932      1.4426      0.3529      1.3617
## karnof            0.9765      1.0241      0.9632      0.9900
## str21            1.4583      0.6858      1.2084      1.7598
## symptom1          1.5471      0.6464      1.2640      1.8935
## cd40              0.9958      1.0042      0.9949      0.9967
## cd80              1.0005      0.9995      1.0003      1.0006
## age_group31-50:drugs1 1.0730      0.9320      0.5063      2.2738
## age_group51-70:drugs1 1.5703      0.6368      0.4002      6.1623
##
## Concordance= 0.698 (se = 0.011 )
## Likelihood ratio test= 235.2 on 13 df,  p=<2e-16
## Wald test              = 233.4 on 13 df,  p=<2e-16
## Score (logrank) test = 239.7 on 13 df,  p=<2e-16
```

model checking *check multicollinearity*

```
VIF(cox2)
```

```
## Warning in VIF(cox2): No intercept: vifs may not be sensible.
```

```
##              GVIF Df GVIF^(1/(2*Df))
## trt          1.021160 3      1.003496
## age_group    1.221872 2      1.051372
## drugs        5.649854 1      2.376942
## karnof       1.065217 1      1.032094
## str2         1.018843 1      1.009378
```

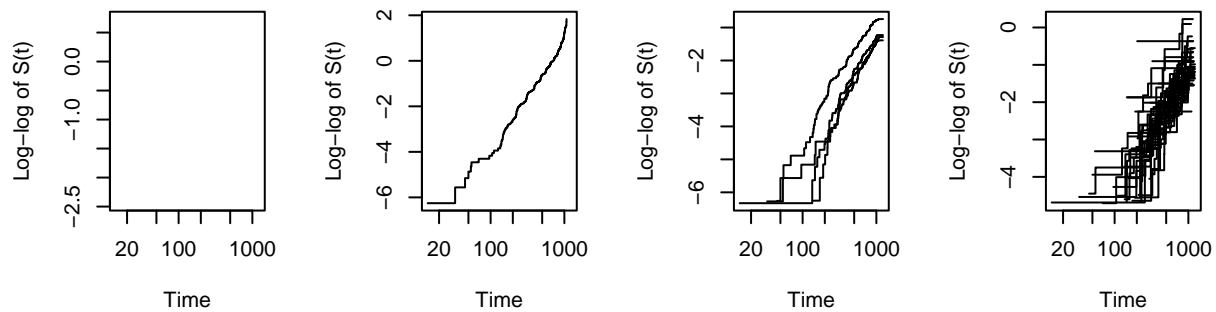
```
## symptom      1.062425  1      1.030740
## cd40         1.106090  1      1.051708
## cd80         1.074564  1      1.036612
## age_group:drugs 6.442779  2      1.593193
```

Plot log-log survival curve

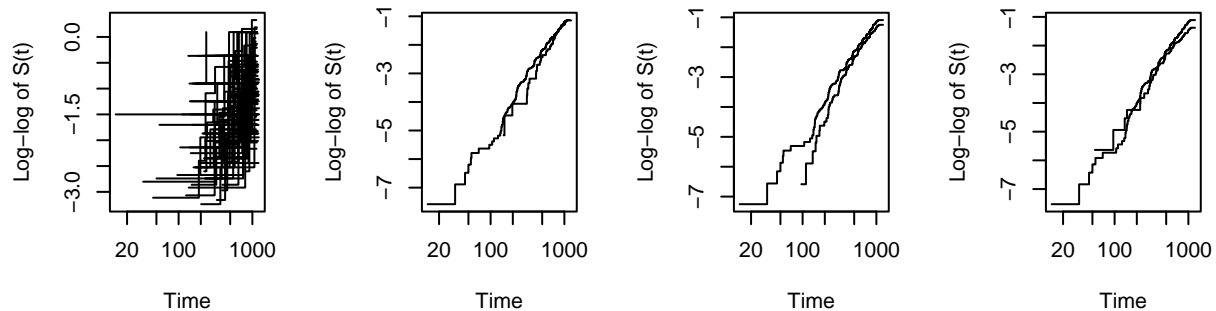
```
par(mfrow = c(2,4))
var_list = names(aids)

for (i in var_list) {
  plot(survfit(Surv(time, cid) ~ aids[[i]], data = aids),
       fun = 'cloglog',
       conf.int = FALSE,
       col = 1,
       lty = 1,
       xlab = "Time",
       ylab = "Log-log of S(t)",
       main = "Log-Log Survival Curves")
}
```

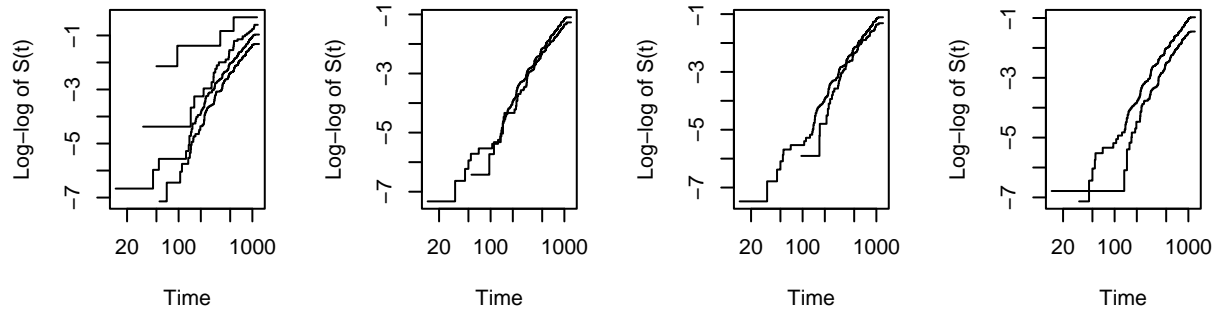
Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv



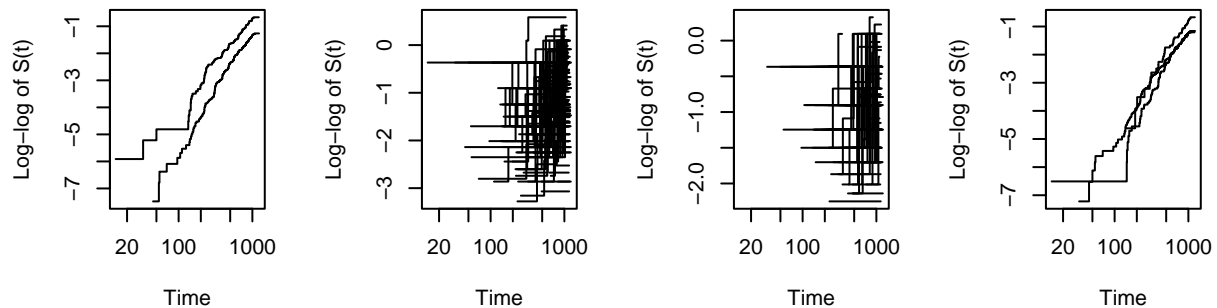
Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv



Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv



Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv Log-Log Survival Curv



Plot the observed and fitted

```
par(mfrow = c(1,1))

plot(survfit(Surv(time, cid) ~ 1, data = aids),
     conf.int = FALSE,
     col = 1,
     lty = 1,
     ylim = c(0.55,1),
     xlab = "Time",
     ylab = "Survival Probability",
     main = "Observed vs Fitted Survival Curves")

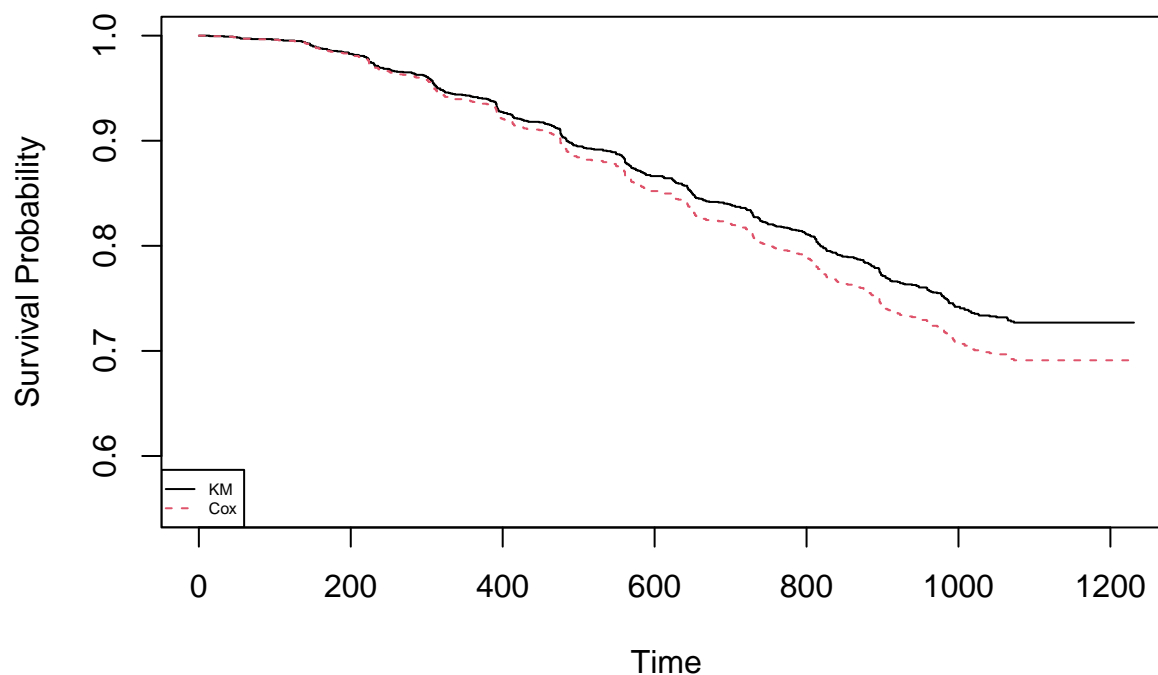
lines(survfit(cox2),
     conf.int = FALSE,
     col = 2,
     lty = 2,
     ylim = c(0.55,1))
```

```
## Warning in survfit.coxph(cox2): the model contains interactions; the default
## curve based on column means of the X matrix is almost certainly not useful.
## Consider adding a newdata argument.
```

```
legend("bottomleft",
     legend = c("KM", "Cox"),
```

```
col = 1:2,
lty = c(1, 2),
cex = 0.5,
merge = TRUE)
```

Observed vs Fitted Survival Curves



```
broom::tidy(cox2) %>%
  mutate(`exp(estimate)` = exp(estimate)) %>%
  relocate(`exp(estimate)`, .after = estimate) %>%
```

```
## # A tibble: 13 x 6
##   term                estimate `exp(estimate)` std.error statistic  p.value
##   <chr>                <dbl>         <dbl>    <dbl>    <dbl>    <dbl>
## 1 trt1                -0.800           0.449  0.124     -6.44 1.18e-10
## 2 trt2                -0.666           0.514  0.122     -5.47 4.43e- 8
## 3 trt3                -0.567           0.567  0.116     -4.89 1.00e- 6
## 4 age_group31-50      -0.0963          0.908  0.104     -0.928 3.53e- 1
## 5 age_group51-70       0.346           1.41   0.190       1.82 6.85e- 2
## 6 drugs1              -0.366           0.693  0.345     -1.06 2.87e- 1
## 7 karnof              -0.0238          0.976  0.00701    -3.40 6.78e- 4
## 8 str21               0.377           1.46   0.0959      3.93 8.37e- 5
## 9 symptom1            0.436           1.55   0.103       4.23 2.31e- 5
## 10 cd40               -0.00419          0.996  0.000448   -9.35 8.55e-21
## 11 cd80               0.000469          1.00   0.0000830    5.65 1.58e- 8
## 12 age_group31-50:drugs1 0.0705           1.07   0.383       0.184 8.54e- 1
## 13 age_group51-70:drugs1 0.451            1.57   0.698       0.647 5.18e- 1
```

```
#kable(caption = "Summary of Final Cox-PH model")
```

Table 5: Summary of Final Cox-PH model

term	estimate	exp(estimate)	std.error	statistic	p.value
trt1	-0.8001201	0.4492750	0.1242171	-6.4413036	<0.0000001
trt2	-0.6657643	0.5138806	0.1216476	-5.4728949	<0.0000001
trt3	-0.5673093	0.5670492	0.1159872	-4.8911374	0.0000010
age_group31-50	-0.0962569	0.9082307	0.1037108	-0.9281280	0.3533412
age_group51-70	0.3463719	1.4139283	0.1901102	1.8219527	0.0684622
drugs1	-0.3664675	0.6931787	0.3445059	-1.0637481	0.2874428
karnof	-0.0238122	0.9764691	0.0070067	-3.3984920	0.0006776
str21	0.3772408	1.4582554	0.0959051	3.9334819	0.0000837
symptom1	0.4363595	1.5470649	0.1030943	4.2326242	0.0000231
cd40	-0.0041861	0.9958226	0.0004476	-9.3526642	<0.0000001
cd80	0.0004689	1.0004690	0.0000830	5.6524859	<0.0000001
age_group31-50:drugs1	0.0704626	1.0730045	0.3831692	0.1838943	0.8540964
age_group51-70:drugs1	0.4512700	1.5703052	0.6975511	0.6469347	0.5176742