

# CH1

2023-06-03

## 패키지

```
library(tidyverse)
library(survival)
library(survminer)
library(ggsci)
library(ggsignif)
library(gtsummary)
library(forestmodel)
```

## 테이블 만들기

```
dt1<-read_csv("C:\\Users\\phl02\\Desktop\\P\\bio\\ch1\\Ch1_table1.csv")

dt1 %>%
  select(-id, -hcc_yr, -m6_alb) %>%
  tbl_summary(by=LC,missing='no') %>%
  add_p() %>%
  add_overall() %>%
  modify_spanning_header( c('stat_1','stat_2')~'**Liver Function**')
```

Characteristic	Overall, N = 1,000	Cirrhosis, N = 526	No cirrhosis, N = 474	p-value
Sex				0.038
F	317 (32%)	182 (35%)	135 (28%)	
M	683 (68%)	344 (65%)	339 (72%)	
Age	47 (40, 53)	50 (44, 55)	43 (35, 49)	<0.001
ALT	107 (61, 203)	86 (49, 155)	134 (86, 258)	<0.001
Bilirubin	1.20 (0.90, 1.60)	1.30 (1.10, 1.80)	1.10 (0.90, 1.38)	<0.001
PT	1.09 (1.03, 1.18)	1.14 (1.06, 1.27)	1.05 (1.01, 1.10)	<0.001
Creatinine	0.90 (0.70, 1.00)	0.90 (0.70, 0.90)	0.90 (0.80, 1.00)	0.002
Platelet	149 (104, 186)	109 (81, 145)	182 (157, 210)	<0.001
Albumin	3.80 (3.50, 4.10)	3.70 (3.20, 4.10)	4.00 (3.70, 4.13)	<0.001
HBeAg				<0.001
Negative	351 (35%)	214 (41%)	137 (29%)	
Positive	641 (65%)	307 (59%)	334 (71%)	
HCC	151 (15%)	135 (26%)	16 (3.4%)	<0.001

## Multivariable analysis table

```
dt2<-read_csv("C:\\Users\\phl02\\Desktop\\P\\bio\\ch1\\Ch1_multi.csv")

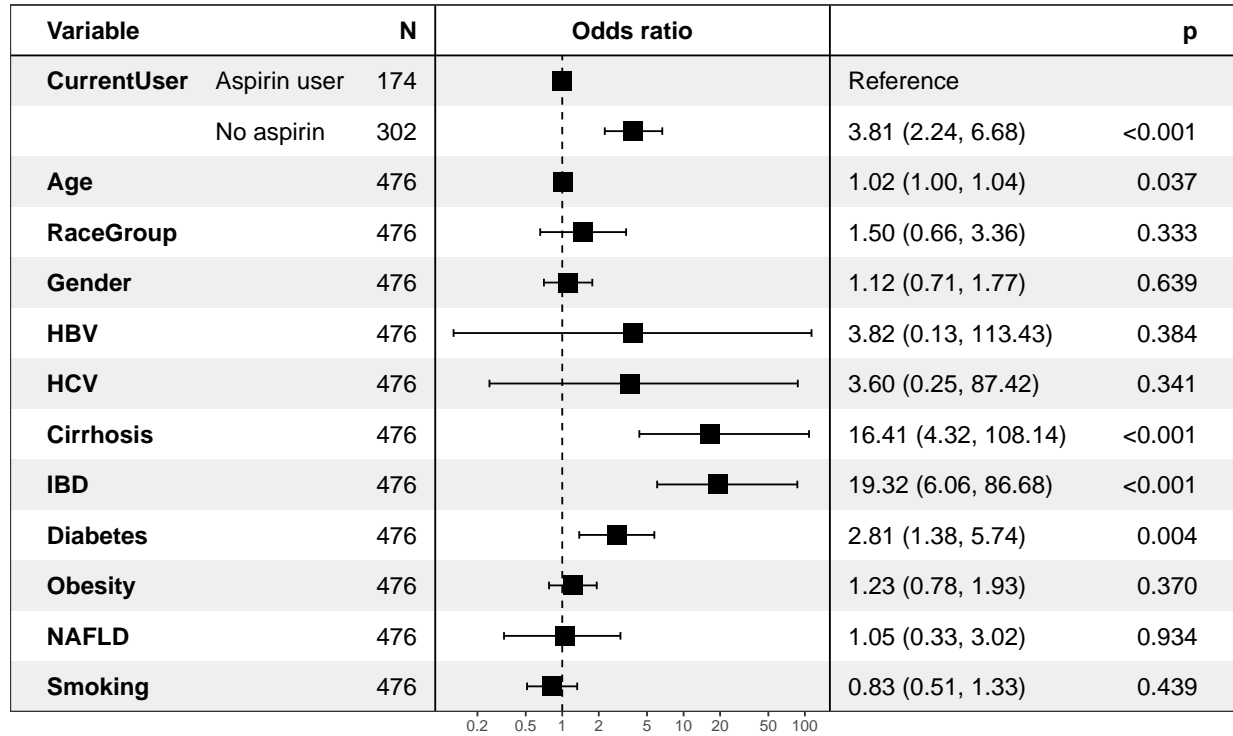
fit.multi <- glm(Group~CurrentUser+Age+RaceGroup+Gender+
                 HBV+HCV+Cirrhosis+IBD+Diabetes+Obesity+
                 NAFLD+Smoking,
                 family=binomial, data=dt2)

tbl_regression(fit.multi, exponentiate = T) %>%
  bold_labels() %>%
  bold_p()
```

Characteristic	OR	95% CI	p-value
<b>CurrentUser</b>			
Aspirin user	—	—	
No aspirin	3.81	2.24, 6.68	<0.001
<b>Age</b>	1.02	1.00, 1.04	<b>0.037</b>
<b>RaceGroup</b>	1.50	0.66, 3.36	0.3
<b>Gender</b>	1.12	0.71, 1.77	0.6
<b>HBV</b>	3.82	0.13, 113	0.4
<b>HCV</b>	3.60	0.25, 87.4	0.3
<b>Cirrhosis</b>	16.4	4.32, 108	<0.001
<b>IBD</b>	19.3	6.06, 86.7	<0.001
<b>Diabetes</b>	2.81	1.38, 5.74	<b>0.004</b>
<b>Obesity</b>	1.23	0.78, 1.93	0.4
<b>NAFLD</b>	1.05	0.33, 3.02	>0.9
<b>Smoking</b>	0.83	0.51, 1.33	0.4

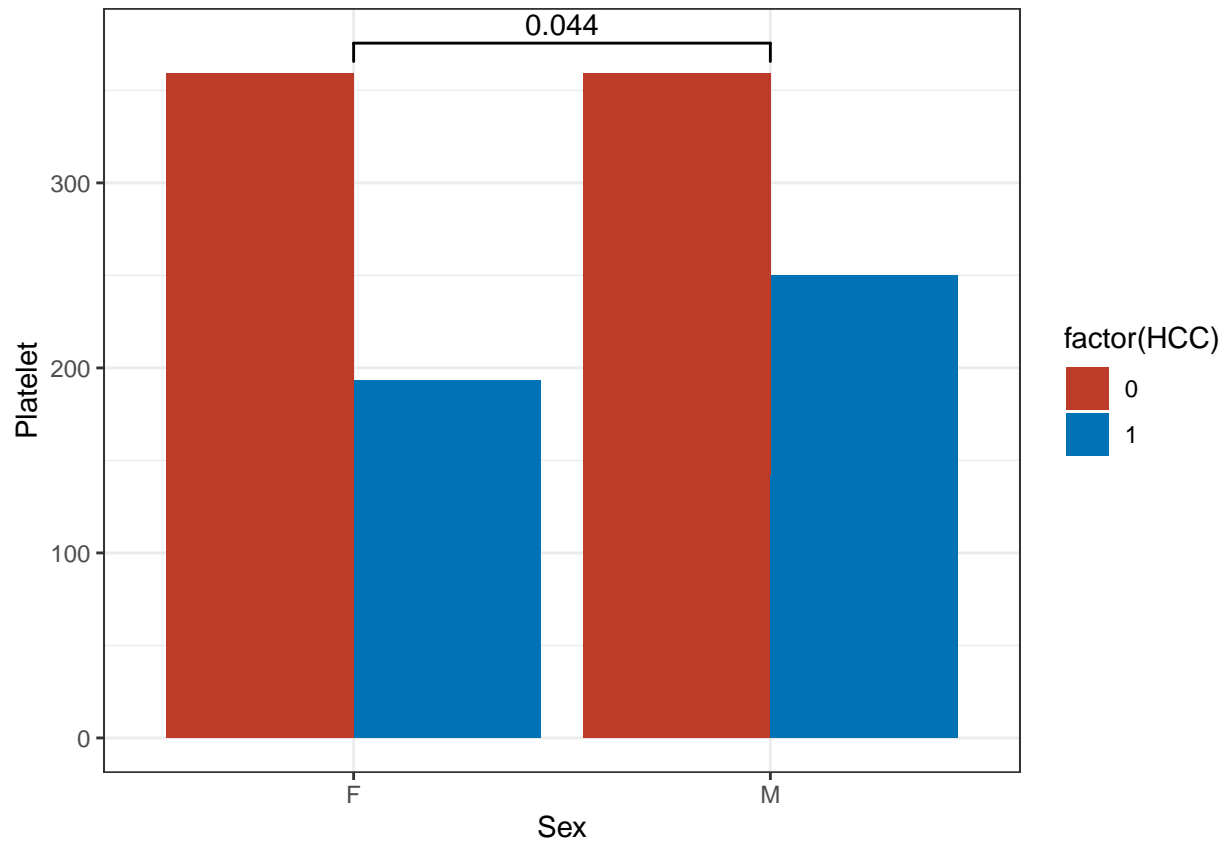
## Forest plot

```
forest_model(fit.multi)
```



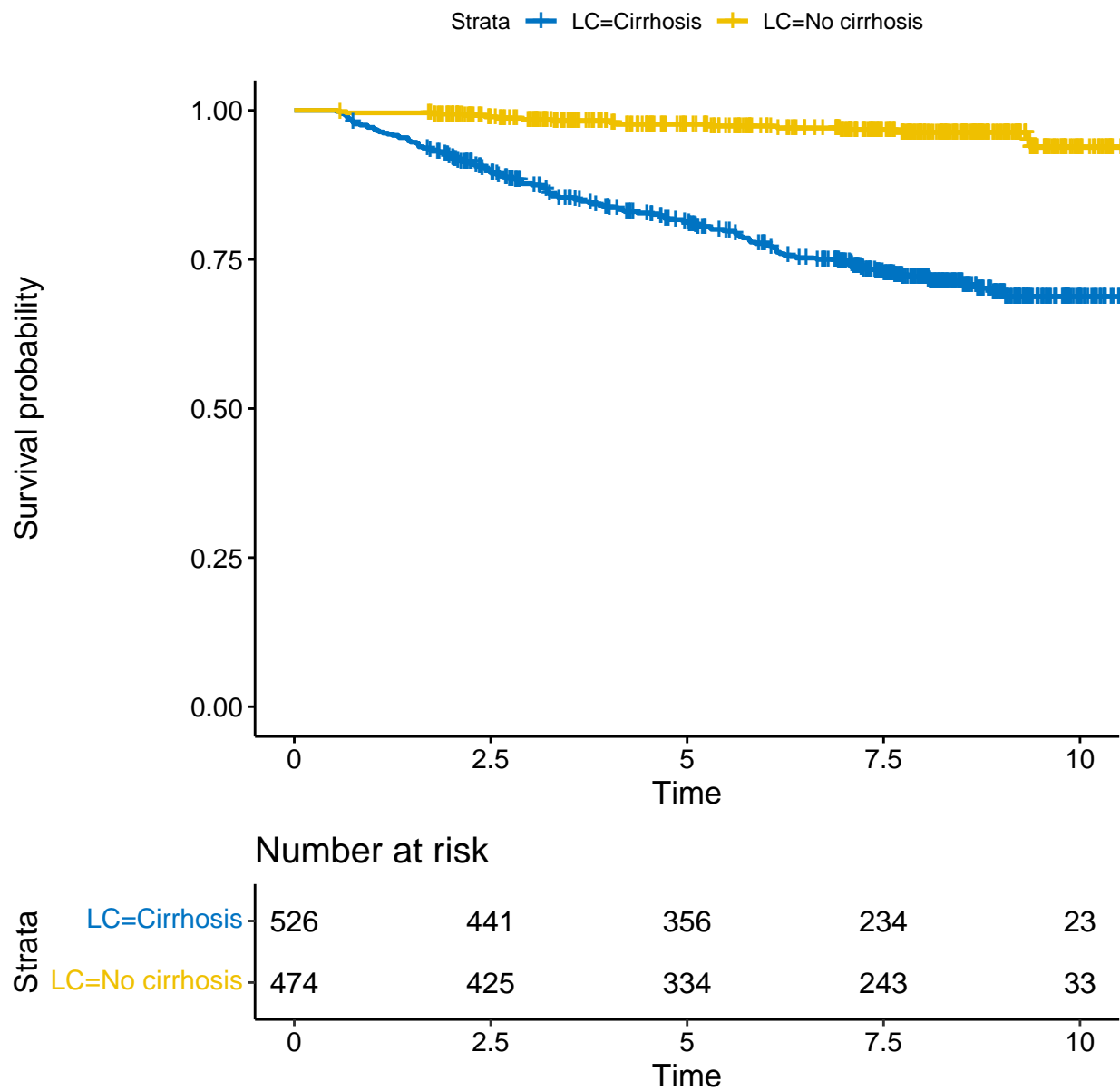
## NEJM bar 그래프

```
ggplot(dt1,aes(x= Sex, y=Platelet, fill=factor(HCC)))+  
  geom_bar(stat='identity', position='dodge')+  
  theme_bw()+  
  scale_fill_nejm()+  
  geom_signif(comparisons = list(c('F','M')))
```



## JCO KM 그래프

```
km1<-survfit(Surv(hcc_yr, HCC)~LC, data=dt1)
ggsurvplot(km1,palette = 'jco',risk.table = T)
```



## Waterfall 그래프

```
dt1 %>%  
  filter(id<=30) %>%  
  select(id,Sex,Albumin,m6_alb) %>%  
  mutate(delta_alb=Albumin-m6_alb) %>%  
  ggbarplot(x='id', y='delta_alb',  
            fill='Sex',  
            sort.val='desc',  
            sort.by.groups = FALSE)
```

