

2_Recreate

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Load Packages

Recreate Figure

```
# Run linear regression using GMR.Pre and Statins as predictors
fig_model <- lm(GMR.Post ~ GMR.Pre + Statins, data=df)
fig_model_summary <- as.data.frame(coef(summary(fig_model)))

kable(fig_model_summary)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	8.9140317	2.4254350	3.6752301	0.0002641
GMR.Pre	0.8709214	0.0322647	26.9930530	0.0000000
StatinsYes	0.1956456	1.6521118	0.1184215	0.9057827

```
# Create two lines with different intercepts for whether the person had Statins usage based off model
slope = fig_model_summary$Estimate[2]
yesStatins = fig_model_summary$Estimate[1] + fig_model_summary$Estimate[3]
noStatins = fig_model_summary$Estimate[1]
```

Now we continue to plotting the figure. We add two lines based off the linear regression model and see that they overlap just as in the figure in the paper.

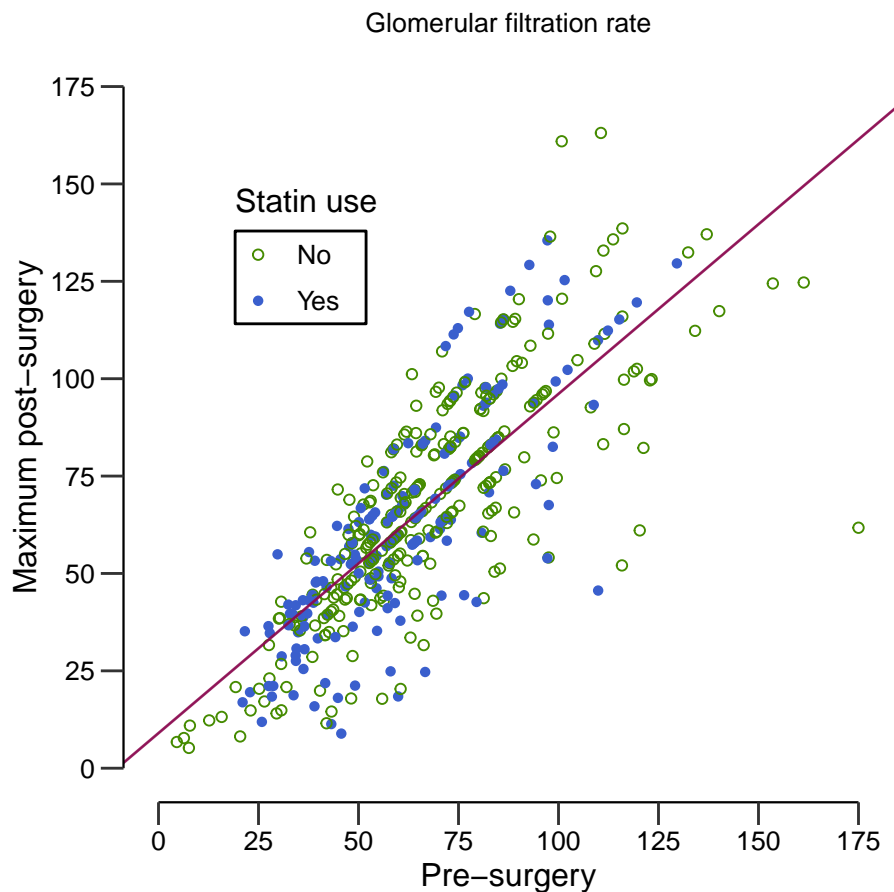
```
# handle the outlier point
df2 <- df %>% mutate(GMR.Pre = case_when(GMR.Pre < 175 ~ GMR.Pre,
                                           GMR.Pre >= 175 ~ 175))

ggplot(df2, aes(x=GMR.Pre, y=GMR.Post, color=Statins, shape=Statins), size = 10) +
  geom_point() +
  labs(y= "Maximum post-surgery",
       x = "Pre-surgery",
       title = "Glomerular filtration rate") +
  scale_color_manual(name = "Statin use",
                     labels= c('No', 'Yes'),
                     values=c('chartreuse4','royalblue3')) +
  scale_shape_manual(name = "Statin use",
                     labels= c('No', 'Yes'),
                     values = c(1, 16)) +
  scale_y_continuous(breaks = c(0, 25, 50, 75, 100, 125, 150, 175),
                     limits = c(0,175)) +
  scale_x_continuous(breaks = c(0, 25, 50, 75, 100, 125, 150, 175),
                     limits = c(0,175)) +
  geom_abline(intercept = noStatins, slope = slope, color = "deeppink4", size = 0.4, alpha = 0.8) +
  geom_abline(intercept = yesStatins, slope = slope, color = "deeppink4", size = 0.4, alpha = 0.8)
```

```

theme(plot.title = element_text(hjust = 0.5, size = 10),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      axis.line.x = element_line(colour = "black", size=0.4),
      axis.line.y = element_line(colour = "black", size=0.4),
      panel.background = element_blank(),
      legend.background = element_rect(fill = "white", colour = "black"),
      legend.position = c(0.23, 0.7),
      legend.key=element_blank(),
      legend.margin = margin(-0.6, -0.15, 0, 0, unit = "cm"),
      text = element_text(size = 12),
      axis.ticks.length = unit(0.3, "cm"),
      axis.text = element_text(size = 10),
      plot.margin = margin(15, 15, 15, 15),
      axis.text.x = element_text(colour="black", size = 10),
      axis.text.y = element_text(colour="black", size = 10),
      legend.text = element_text(colour="black", size = 10)) +
coord_capped_cart(bottom="both", left="both")

```



```

ggsave(file="figure1.png", width=5, height=5, dpi=600)

```

Recreate Table

```

table_model <- lm(GMR.Post ~
                  GMR.Pre +

```

```

Age +
Weight +
Female +
Diabetes +
CHF +
Pulm +
Renal.Insuff +
Acetylcystine +
Emergency +
HCT.Intraop +
TVol +
Crystalloid +
Colloid +
Statins, data=df)
table_model_summary <- as.data.frame(coef(summary(table_model)))

kable(table_model_summary)

```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	49.5329215	10.8538708	4.5636181	0.0000065
GMR.Pre	0.7900404	0.0360629	21.9072689	0.0000000
Age	-0.3519255	0.0803743	-4.3785812	0.0000149
Weight	-0.1396802	0.0545218	-2.5619134	0.0107351
Female	-2.8673563	2.0246314	-1.4162363	0.1573997
Diabetes	-1.4385025	2.3205095	-0.6199080	0.5356328
CHF	-7.7410629	2.8249597	-2.7402384	0.0063842
Pulm	-0.4472612	1.8308499	-0.2442915	0.8071166
Renal.Insuff	-10.2059416	3.3357918	-3.0595259	0.0023496
Acetylcystine	-1.0520022	2.5290975	-0.4159595	0.6776384
Emergency	-22.4239064	3.9298839	-5.7059971	0.0000000
HCT.Intraop	0.1534723	0.1471446	1.0430030	0.2975082
TVol	-0.0061549	0.0034991	-1.7589959	0.0792593
Crystalloid	0.0008111	0.0005167	1.5696867	0.1171924
Colloid	-0.0014597	0.0010926	-1.3359527	0.1822415
StatinsYes	0.0699882	1.6608099	0.0421410	0.9664050

First let's calculate the confidence interval and then scale the intervals and coefficient estimates using the "adjusted" proportions from the table.

```

# generate 95% confidence intervals
intervals <- confint(table_model)
colnames(intervals) <- c("lower", "upper")
intervals <- as.data.frame(intervals)

table_model_summary$lower <- intervals$lower
table_model_summary$upper <- intervals$upper

# adjust for proportions
adjust <- function(variable, factor, df){
  for (string in c("Estimate", "lower", "upper")){
    df[variable, string] <- factor * df[variable, string]
  }
  return(df)
}

```

```

table_model_summary <- adjust("GMR.Pre", 20, table_model_summary)
table_model_summary <- adjust("Age", 5, table_model_summary)
table_model_summary <- adjust("Weight", 10, table_model_summary)
table_model_summary <- adjust("HCT.Intraop", 5, table_model_summary)
table_model_summary <- adjust("TVol", 100, table_model_summary)
table_model_summary <- adjust("Crystalloid", 1000, table_model_summary)
table_model_summary <- adjust("Colloid", 500, table_model_summary)

```

Now that we have derived all the Adjusted estimates and their confidence intervals, lets create the variables to output in the final data frame.

```

# create the output CI variable
table_model_summary <- table_model_summary %>%
  mutate(outCI = paste(round(Estimate, digits=0), " (", round(lower, digits=0), ", ", round(upper, digits=0), ")"))

# only keep the rows to be displayed
table_model_summary <- table_model_summary[2:16, ]
table_model_summary <- table_model_summary[c("outCI", "Pr(>|t|)")]

# add in row and column names
rownames(table_model_summary) <- c("Preoperative eGFR (increase of 20 ml min-1 1.73 m-2)", "Patient age (increase of 5 years)", "Patient weight (increase of 10 kg)", "Patient hemoglobin (increase of 1 g/dl)", "Patient crystalloid (increase of 1000 ml)", "Patient colloid (increase of 500 ml)", "Patient TVol (increase of 100 ml)", "Patient HCT (increase of 5%)", "Patient GMR (increase of 20%)", "Patient Age", "Patient Weight", "Patient Hemoglobin", "Patient Crystalloid", "Patient Colloid", "Patient TVol", "Patient HCT")

super <- c("Preoperative eGFR (increase of 20 ml min-1 1.73 m-2)")
super2 <- c("Preoperative eGFR (increase of 20 ml min-1 1.73 m-2)", "Patient age (increase of 5 years)", "Patient weight (increase of 10 kg)", "Patient hemoglobin (increase of 1 g/dl)", "Patient crystalloid (increase of 1000 ml)", "Patient colloid (increase of 500 ml)", "Patient TVol (increase of 100 ml)", "Patient HCT (increase of 5%)", "Patient GMR (increase of 20%)", "Patient Age", "Patient Weight", "Patient Hemoglobin", "Patient Crystalloid", "Patient Colloid", "Patient TVol", "Patient HCT")

table_model_summary <- table_model_summary %>% mutate(rows = rownames(table_model_summary))

table_model_summary <- table_model_summary[c("rows", "outCI", "Pr(>|t|)")]

colnames(table_model_summary) <- c("Effect", "Adjusted* difference (95% CI) in mean postoperative eGFR", "P-value")

# create the formatted P-value column
table_model_summary <- table_model_summary %>%
  mutate(Pvalue = case_when(Pvalue < 0.001 ~ "<0.001",
                             Pvalue < 0.01 ~ paste(format(round(Pvalue, digits=3), nsmall=3), sep=""),
                             Pvalue < 1 ~ paste(format(round(Pvalue, digits=2), nsmall=2), sep="")))

```

Now let's make the table look nice! Note, much help with creating nice tables was taken from the code in: <https://towardsdatascience.com/create-latex-and-ms-word-tables-in-r-6ac919204247>.

```

table_model_summary$Effect <- super2

table_model_summary %>%
  kbl(caption = "Reproduction of Table 2",
      format="html",
      align="c",
      row.names = FALSE,
      col.names = c("Effect", "Adjusted* difference (95% CI) in mean postoperative eGFR", "P-value"),
      escape = FALSE) %>%
  kable_classic(full_width = F, html_font = "Helvetica")

```

Reproduction of Table 2

Effect

Adjusted* difference (95% CI) in mean postoperative eGFR
P-value
Preoperative eGFR (increase of 20 ml min⁻¹ 1.73 m⁻²)
16 (14, 17)
<0.001
Patient age (increase of 5 yr)
-2 (-3, -1)
<0.001
Weight (increase of 10 kg)
-1 (-2, 0)
0.01
Female gender (vs male)
-3 (-7, 1)
0.16
Diabetes (vs none)
-1 (-6, 3)
0.54
History of CHF (vs none)
-8 (-13, -2)
0.006
History of pulmonary disease (vs none)
0 (-4, 3)
0.81
History of chronic kidney disease (vs none)
-10 (-17, -4)
0.002
Use of acetylcysteine (vs none)
-1 (-6, 4)
0.68
Emergent case (vs scheduled)
-22 (-30, -15)
<0.001
Intraoperative haematocrit (increase of 0.05)
1 (-1, 2)
0.30
Total volume (increase of 0.1 litre kg⁻¹ h⁻²)

-1 (-1, 0)

0.08

Crystalloids (increase of 1 litre)

1 (0, 2)

0.12

Colloids (increase of 0.5 litre)

-1 (-2, 0)

0.18

Statin use (vs none)

0 (-3, 3)

0.97