

Code Appendix

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```
library(tidyverse)
```

```
## -- Attaching packages -----  
## v ggplot2 3.2.1      v purrr   0.3.2  
## v tibble  2.1.3      v dplyr  0.8.3  
## v tidyr   1.0.0      v stringr 1.4.0  
## v readr   1.3.1      v forcats 0.4.0  
  
## -- Conflicts -----  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()    masks stats::lag()
```

```
library(geepack)
```

Read data

```
alc_dat <- readxl::read_xls("./data/ALCDEP.xls")  
  
alc_dat <- janitor::clean_names(alc_dat) %>%  
  mutate(treatment = factor(treatment)) %>%  
  mutate(gender = factor(gender, levels = c(0,1), labels = c("Male", "Female")))  
  
alc_dat_long <- alc_dat %>%  
  pivot_longer(nd0:nd60, names_to = "days", values_to = "drinks", names_prefix = "nd")
```

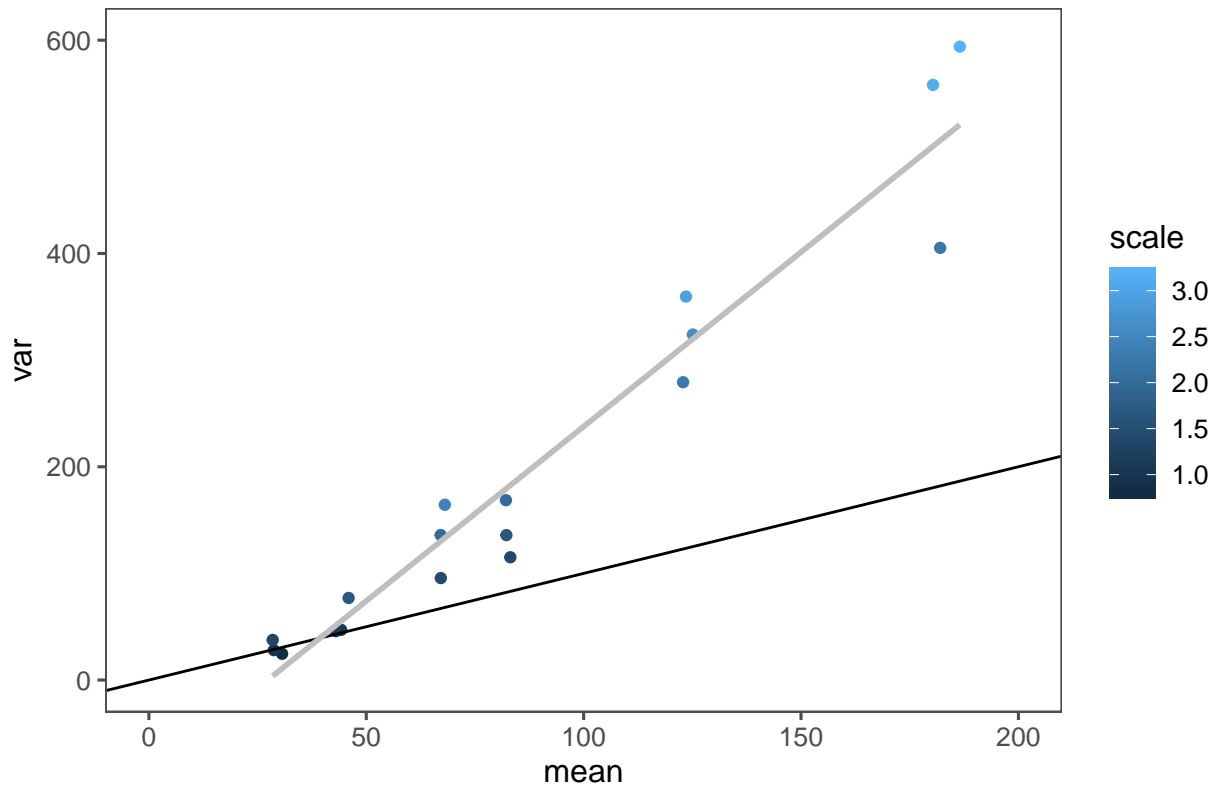
Explore outcome distribution

```
summary(alc_dat_long$drinks)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   
##    16.00  47.00   79.00   92.01 127.00  252.00
```

```
alc_dat_long %>%
  group_by(gender, days, treatment) %>%
  summarize(mean = mean(drinks),
            var = var(drinks),
            scale = var/mean) %>%
  ggplot(aes(x = mean, y = var, color = scale)) + geom_point() + geom_abline(intercept = 0, slope = 1)
```

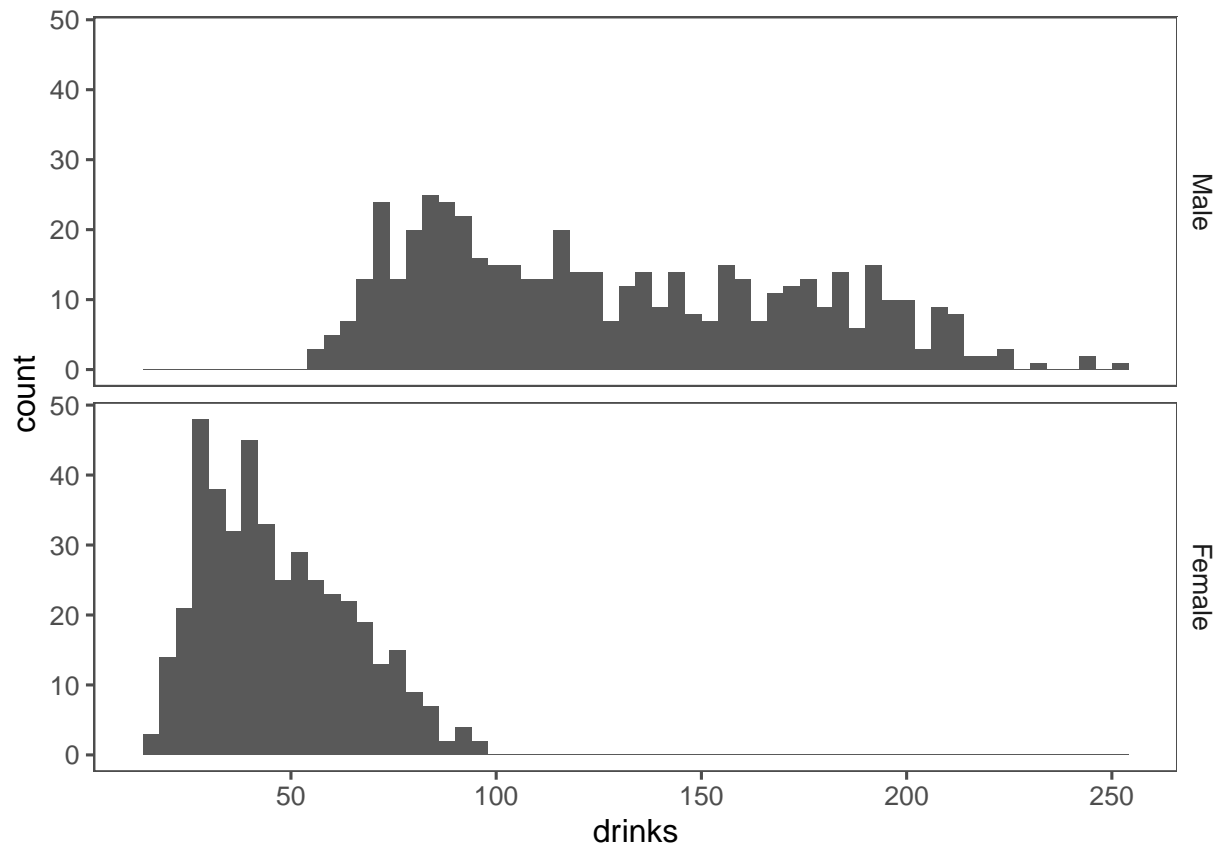
Potential overdispersion in Poisson outcome



#still some overdispersion if poisson in the gender x treatment x time model; maybe need negative binom

#normal approximation?

```
alc_dat_long %>%
  ggplot(aes(x = drinks)) + geom_histogram(bins = 60) + ggthemes::theme_few() + facet_grid(c("gender"))
```

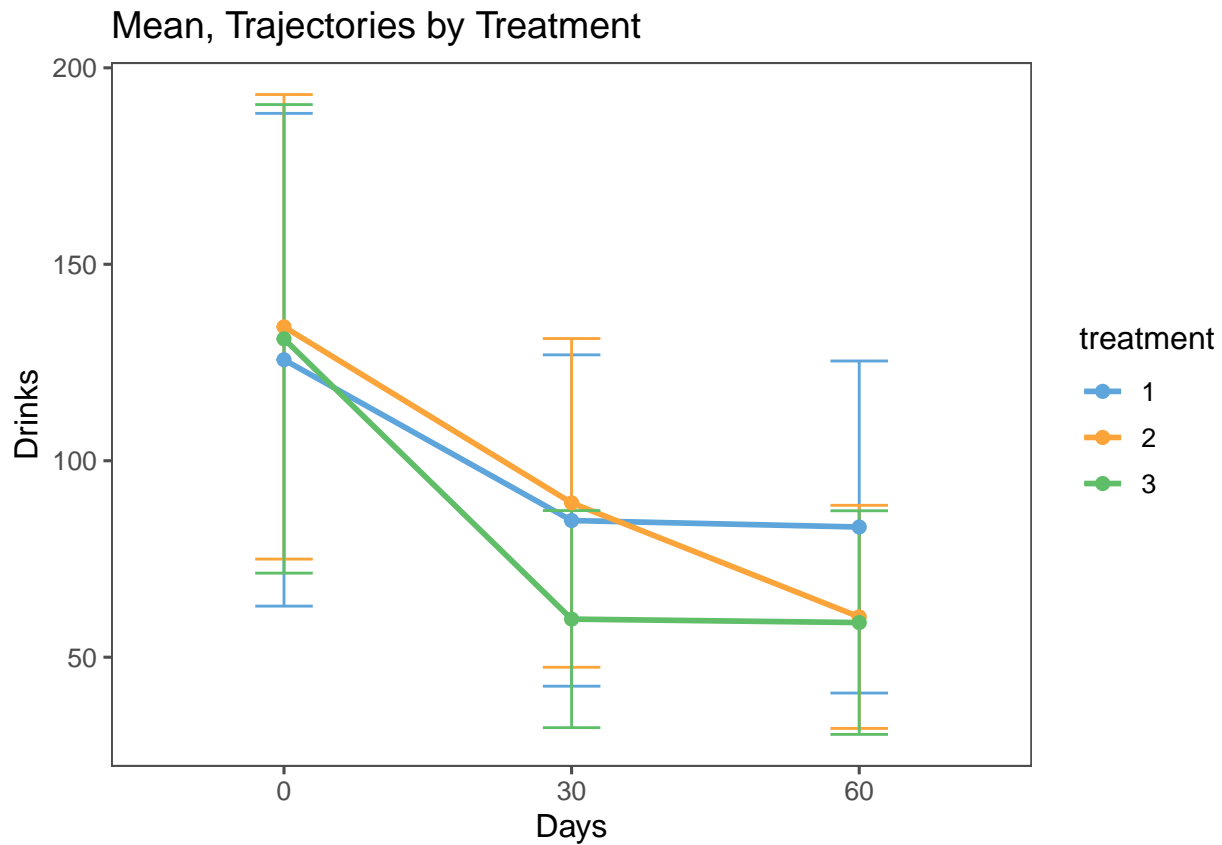


#clearly not a normal distribution, clearly poisson

Choose a poisson-distributed outcome and check diagnostics for overdispersion.

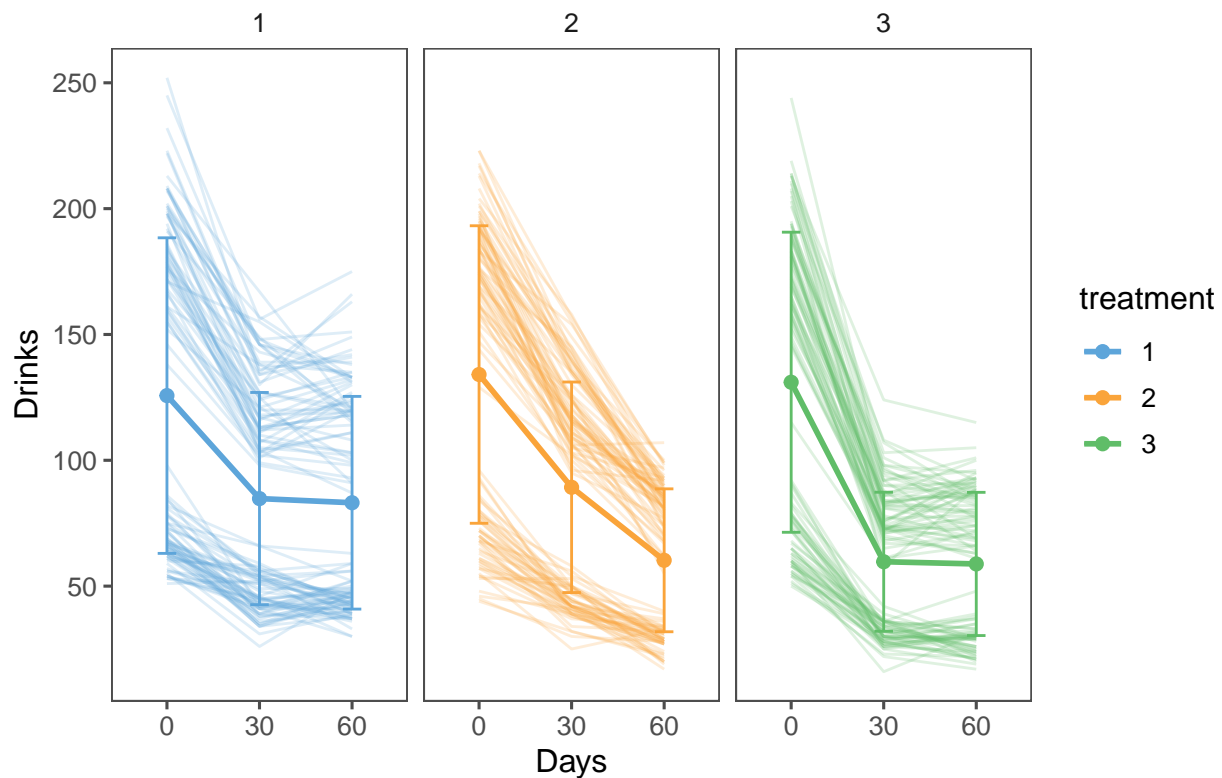
Exploratory Mean and Trajectory Plots

```
alc_dat_long %>%
  group_by(treatment, days) %>%
  summarize(mean_drinks = mean(drinks),
            upper = mean_drinks + sd(drinks),
            lower = mean_drinks - sd(drinks)) %>%
  ggplot(aes(x = days, color = treatment)) +
  geom_line(aes(y = mean_drinks, group = treatment), size = 1) +
  geom_errorbar(aes(ymin = lower, ymax = upper, group = treatment), width = 0.2) +
  geom_point(aes(y = mean_drinks), size = 2) +
  ggthemes::theme_few() + ggthemes::scale_color_few() + labs(title = "Mean, Trajectories by Treatment", y = "Mean Drinks")
```



```
alc_dat_long %>%
  group_by(treatment, days) %>%
  summarize(mean_drinks = mean(drinks),
            upper = mean_drinks + sd(drinks),
            lower = mean_drinks - sd(drinks)) %>%
  ggplot(aes(x = days, color = treatment)) +
  geom_line(aes(y = mean_drinks, group = treatment), size = 1) +
  geom_errorbar(aes(ymin = lower, ymax = upper, group = treatment), width = 0.2) +
  geom_point(aes(y = mean_drinks), size = 2) +
  geom_line(data = alc_dat_long, aes(x = days, y = drinks, group = sid), alpha = 0.2) +
  ggthemes::theme_few() + ggthemes::scale_color_few() + facet_grid(~treatment) + labs(title = "Raw Traj")
```

Raw Trajectories

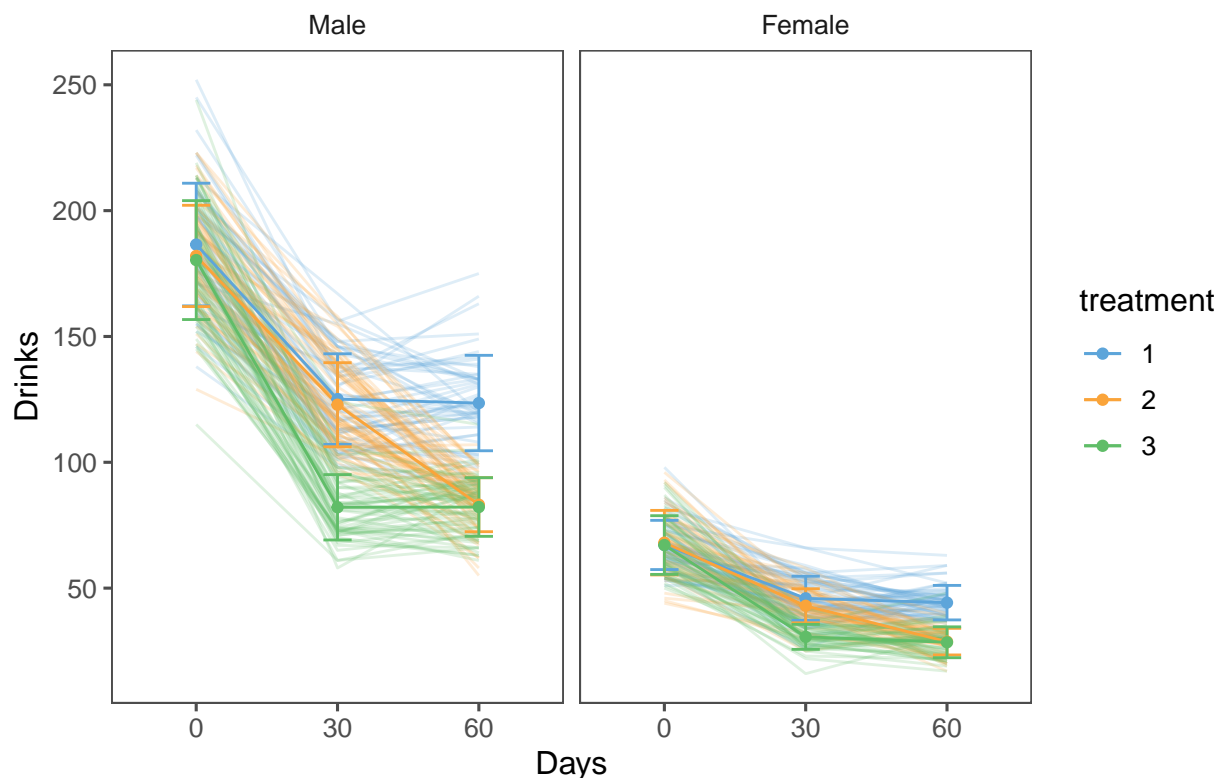


There are clearly two groups of patients in all groups, with a wide berth between the groups: those whose baseline number of alcoholic drinks in the past 30 days is less than 100 (~3 drinks/day) and those who are closer to 150 in the past 30 days (5 drinks a day).

Perhaps this could be a gender effect:

```
alc_dat_long %>%
  group_by(treatment, days, gender) %>%
  summarize(mean_drinks = mean(drinks),
            upper = mean_drinks + sd(drinks),
            lower = mean_drinks - sd(drinks)) %>%
  ggplot(aes(x = days, color = treatment)) +
  geom_line(data = alc_dat_long, aes(x = days, y = drinks, group = sid), alpha = 0.2) +
  geom_line(aes(y = mean_drinks, group = treatment)) +
  geom_errorbar(aes(ymin = lower, ymax = upper, group = treatment), width = 0.2) +
  geom_point(aes(y = mean_drinks)) +
  ggthemes::theme_few() + ggthemes::scale_color_few() + facet_grid(~gender) + labs(title = "Raw Trajectories")
```

Raw Trajectories



It is, in fact, a gender effect, and variance shrinks a great deal when the outcome is stratified on gender. Luckily, there does not seem to be heterogeneity of treatment effect by gender; the treatment trajectories look the same, but scaled to the respective within-gender mean.

Now, let's look at faceting on relapsers vs. no relapsers:

```
library(janitor)

##
## Attaching package: 'janitor'
## The following objects are masked from 'package:stats':
##
##   chisq.test, fisher.test

alc_dat %>%
  tabyl(treatment, relapse) %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting(digits = 2) %>%
  adorn_ns() %>%
  knitr::kable(caption = "Contingency table of Relapse by Treatment")
```

Table 1: Contingency table of Relapse by Treatment

treatment	0	1
1	17.92% (19)	82.08% (87)
2	54.21% (58)	45.79% (49)
3	86.14% (87)	13.86% (14)

```

alc_dat %>%
  tabyl(treatment, relapse) %>%
  chisq.test()

##
## Pearson's Chi-squared test
##
## data: .
## X-squared = 96.71, df = 2, p-value < 2.2e-16
#significant differences. pairwise:

alc_dat %>%
  filter(treatment %in% 1:2) %>%
  mutate(treatment = forcats::fct_drop(treatment)) %>%
  tabyl(treatment, relapse) %>%
  chisq.test(.)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: .
## X-squared = 28.815, df = 1, p-value = 7.962e-08

alc_dat %>%
  filter(treatment %in% c(1,3)) %>%
  mutate(treatment = forcats::fct_drop(treatment)) %>%
  tabyl(treatment, relapse) %>%
  chisq.test(.)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: .
## X-squared = 93.61, df = 1, p-value < 2.2e-16

alc_dat %>%
  filter(treatment %in% 2:3) %>%
  mutate(treatment = forcats::fct_drop(treatment)) %>%
  tabyl(treatment, relapse) %>%
  chisq.test(.)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: .
## X-squared = 23.603, df = 1, p-value = 1.184e-06
#all pairwise differences are highly significant

alc_dat_grouped <- alc_dat %>%
  mutate(treatment = forcats::fct_relevel(treatment, "3")) %>%
  group_by(treatment, gender) %>%
  count(relapse) %>%
  pivot_wider(names_from = relapse, values_from = n, names_prefix = "relapse_")

```

```
response_table = cbind(alc_dat_grouped$relapse_1, alc_dat_grouped$relapse_0)
treatment <- alc_dat_grouped$treatment
glm_relapse_ref <- glm(response_table ~ treatment , family = binomial)

broom::tidy(glm_relapse_ref, exponentiate = TRUE, conf.int = TRUE) %>%
  dplyr::select(term, estimate, std.error, conf.low, conf.high) %>%
  knitr::kable(caption = "Logistic Regression of Treatment on 6-month Relapse")
```

Table 2: Logistic Regression of Treatment on 6-month Relapse

term	estimate	std.error	conf.low	conf.high
(Intercept)	0.1609195	0.2879632	0.0876527	0.2734223
treatment1	28.4548872	0.3834692	13.8353111	62.5513004
treatment2	5.2500000	0.3472353	2.7182467	10.6829755

```
broom::glance(glm_relapse_ref) %>%
  summarize(test = 1 - pchisq(deviance, df.residual)) #acceptable
```

```
## # A tibble: 1 x 1
##   test
##   <dbl>
## 1 0.863
```

```
anova(glm_relapse_ref, test = "Chisq") #significant
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: response_table
##
## Terms added sequentially (first to last)
##
##
##           Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                5    106.856
## treatment  2    106.11          3    0.745 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

GEE models

Exploratory Correlation Plots

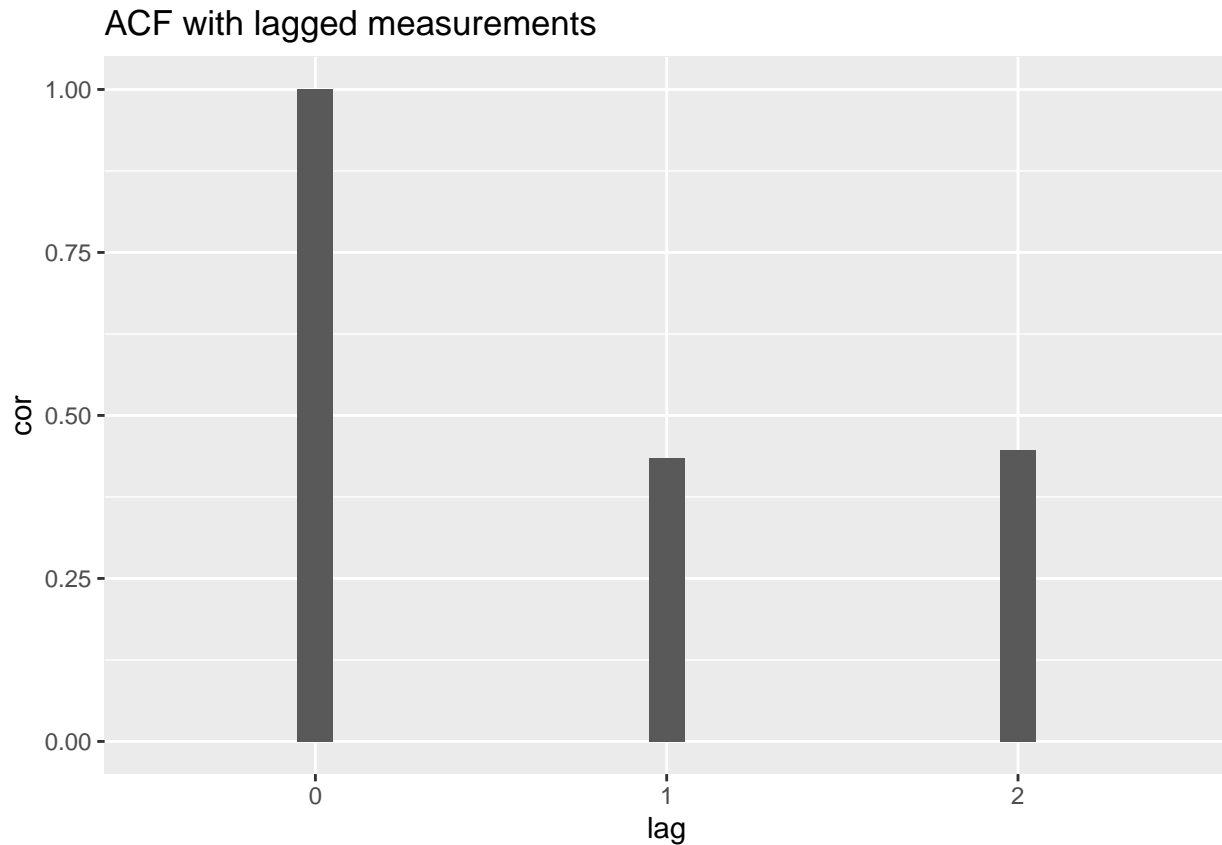
```
sat_mod <- glm(drinks ~ gender + treatment*days, family = "poisson", data = alc_dat_long) #super satura
alc_dat_long %>%
  modelr::add_residuals(sat_mod) %>%
  dplyr::select(sid, days, treatment, gender, resid) %>%
  mutate(days = as.numeric(days)) %>%
  group_by(sid) %>%
  mutate(lag_1 = lag(resid, 1),
```



```

lag_2 = lag(resid, 2)) %>%
ungroup() %>% group_by(gender, treatment) %>%
summarize(cor_0 = cor(resid, resid, use = "pairwise.complete.obs"),
          cor_1 = cor(resid, lag_1, use = "pairwise.complete.obs"),
          cor_2 = cor(resid, lag_2, use = "pairwise.complete.obs")) %>% ungroup() %>%
summarize(cor_0 = mean(cor_0), cor_1 = mean(cor_1), cor_2 = mean(cor_2)) %>%
pivot_longer(c("cor_0", "cor_1", "cor_2"), names_to = "lag", values_to = "cor", names_prefix = "cor_")
ggplot(aes(x = lag, y = cor)) +
geom_col(width = 0.1) +
labs(title = "ACF with lagged measurements")

```



Fit GEE models

```

pois_gee <- geeglm(drinks ~ treatment*days + gender,
                  family = poisson,
                  data = alc_dat_long,
                  id = sid,
                  corstr = "exchangeable")

summary(pois_gee)

```

```

##
## Call:
## geeglm(formula = drinks ~ treatment * days + gender, family = poisson,

```

```
##      data = alc_dat_long, id = sid, corstr = "exchangeable")
##
## Coefficients:
##              Estimate Std.err      Wald Pr(>|W|)
## (Intercept)      5.22505  0.01566 1.114e+05  <2e-16 ***
## treatment2      -0.01568  0.01905  6.780e-01    0.410
## treatment3      -0.02564  0.02039  1.581e+00    0.209
## days30          -0.39386  0.01425  7.642e+02  <2e-16 ***
## days60          -0.41353  0.01253  1.089e+03  <2e-16 ***
## genderFemale    -1.00888  0.01448  4.856e+03  <2e-16 ***
## treatment2:days30 -0.01293  0.01901  4.620e-01    0.497
## treatment3:days30 -0.39227  0.02087  3.534e+02  <2e-16 ***
## treatment2:days60 -0.38624  0.01892  4.165e+02  <2e-16 ***
## treatment3:days60 -0.38748  0.01928  4.038e+02  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Estimated Scale Parameters:
##              Estimate Std.err
## (Intercept)      1.901  0.1121
##
## Correlation: Structure = exchangeable Link = identity
##
## Estimated Correlation Parameters:
##              Estimate Std.err
## alpha      0.4603  0.03397
## Number of clusters: 314 Maximum cluster size: 3
pois_gee_int <- geeglm(drinks ~ treatment*days + treatment*gender,
  family = poisson,
  data = alc_dat_long,
  id = sid,
  corstr = "ar1")
summary(pois_gee_int) #ns

##
## Call:
## geeglm(formula = drinks ~ treatment * days + treatment * gender,
##       family = poisson, data = alc_dat_long, id = sid, corstr = "ar1")
##
## Coefficients:
##              Estimate Std.err      Wald Pr(>|W|)
## (Intercept)      5.2287  0.0178 85835.74  <2e-16 ***
## treatment2      -0.0197  0.0225    0.76    0.38
## treatment3      -0.0298  0.0247    1.47    0.23
## days30          -0.3939  0.0142  764.23  <2e-16 ***
## days60          -0.4135  0.0125 1089.27  <2e-16 ***
## genderFemale    -1.0222  0.0235 1884.16  <2e-16 ***
## treatment2:days30 -0.0129  0.0190    0.46    0.50
## treatment3:days30 -0.3923  0.0209  353.36  <2e-16 ***
## treatment2:days60 -0.3862  0.0189  416.54  <2e-16 ***
## treatment3:days60 -0.3875  0.0193  403.80  <2e-16 ***
## treatment2:genderFemale  0.0150  0.0351    0.18    0.67
## treatment3:genderFemale  0.0159  0.0370    0.18    0.67
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Estimated Scale Parameters:
##           Estimate Std.err
## (Intercept)      1.9    0.112
##
## Correlation: Structure = ar1 Link = identity
##
## Estimated Correlation Parameters:
##           Estimate Std.err
## alpha      0.549    0.033
## Number of clusters: 314 Maximum cluster size: 3

pois_gee_intd <- geeglm(drinks ~ treatment*days + days*gender,
  family = poisson,
  data = alc_dat_long,
  id = sid,
  corstr = "ar1")

broom::tidy(pois_gee_intd, exponentiate = TRUE, conf.int = TRUE) #significant effect for day 60 but very

## # A tibble: 12 x 7
##   term                estimate std.error statistic p.value conf.low conf.high
##   <chr>                <dbl>    <dbl>    <dbl>   <dbl>   <dbl>   <dbl>
## 1 (Intercept)         185.      0.0158  1.09e+5    0      180.    191.
## 2 treatment2           0.985    0.0191  6.17e-1  0.432    0.949    1.02
## 3 treatment3           0.975    0.0204  1.51e+0  0.219    0.937    1.02
## 4 days30              0.677    0.0150  6.72e+2    0      0.658    0.698
## 5 days60              0.670    0.0136  8.62e+2    0      0.652    0.688
## 6 genderFemale        0.368    0.0172  3.38e+3    0      0.356    0.381
## 7 treatment2:days~    0.986    0.0190  5.39e-1  0.463    0.950    1.02
## 8 treatment3:days~    0.675    0.0209  3.53e+2    0      0.648    0.703
## 9 treatment2:days~    0.677    0.0189  4.24e+2    0      0.653    0.703
## 10 treatment3:days~   0.677    0.0193  4.08e+2    0      0.652    0.703
## 11 days30:genderFe~    0.984    0.0199  6.55e-1  0.418    0.947    1.02
## 12 days60:genderFe~    0.953    0.0197  5.84e+0  0.0156   0.917    0.991

anova(pois_gee, pois_gee_int)

## Analysis of 'Wald statistic' Table
##
## Model 1 drinks ~ treatment * days + treatment * gender
## Model 2 drinks ~ treatment * days + gender
##   Df    X2 P(>|Chi|)
## 1  2 0.257    0.88

anova(pois_gee, pois_gee_intd)

## Analysis of 'Wald statistic' Table
##
## Model 1 drinks ~ treatment * days + days * gender
## Model 2 drinks ~ treatment * days + gender
##   Df    X2 P(>|Chi|)
## 1  2 5.86    0.053 .
```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##Trajectories##
#get contrast of treatment 3 days 60 to treatment 3 days 30
#get contrast of treatment 1 days 60 to treatment 1 days 30
#get contrast of treatment 3 days 60 to treatment 3 days 30

## Treatment effect ##
#get contrast of treatment 3 days 60 to treatment 2 days 60
#get contrast of treatment 3 days 60 to treatment 2 days 20

colnames(pois_gee$geese$vbeta) = names(coef(pois_gee))
rownames(pois_gee$geese$vbeta) = names(coef(pois_gee))
var_b0 = pois_gee$geese$vbeta["(Intercept)","(Intercept)"]
var_b1 = pois_gee$geese$vbeta["treatment2","treatment2"]
var_b2 = pois_gee$geese$vbeta["(Intercept)","(Intercept)"]
var_b3 = pois_gee$geese$vbeta["(Intercept)","(Intercept)"]
var_b4 = pois_gee$geese$vbeta["(Intercept)","(Intercept)"]

var_b6 = pois_gee$geese$vbeta["genderFemale","genderFemale"]
cov_b0b6 = pois_gee$geese$vbeta["genderFemale","(Intercept)"]
women_count_baseline = exp(coef(pois_gee)["(Intercept)"] + coef(pois_gee)["genderFemale"])
women_var_baseline = var_b0 + var_b6 + 2*cov_b0b6
women_ci_baseline = c(exp(coef(pois_gee)["(Intercept)"] + coef(pois_gee)["genderFemale"] - qchisq(0.975, 1)*sqrt(women_var_baseline),
exp(coef(pois_gee)["(Intercept)"] + coef(pois_gee)["genderFemale"] + qchisq(0.975, 1)*sqrt(women_var_baseline)))

var_b4 = pois_gee$geese$vbeta["days30","days30"]
var_b5 = pois_gee$geese$vbeta["days60","days60"]
cov_b4b5 = pois_gee$geese$vbeta["days30","days60"]
d30_to_d60_rr = exp(coef(pois_gee)["days60"] - coef(pois_gee)["days30"])
d30_d60_var = var_b4 + var_b5 - 2*cov_b4b5
d30_to_d60_ci = c(exp(coef(pois_gee)["days60"] - coef(pois_gee)["days30"] - qchisq(0.975, 1)*sqrt(d30_d60_var)),
exp(coef(pois_gee)["days60"] - coef(pois_gee)["days30"] + qchisq(0.975, 1)*sqrt(d30_d60_var)))

#treatment 2 to treatment 1
var_trt2 = pois_gee$geese$vbeta["treatment2","treatment2"]
var_trt2d30 = pois_gee$geese$vbeta["treatment2:days30","treatment2:days30"]
cov_day30trt2 = pois_gee$geese$vbeta["treatment2:days30","treatment2"]
trt2day30totrt1day30_rr = exp(coef(pois_gee)["treatment2"] + coef(pois_gee)["treatment2:days30"])
trt2day30totrt1day30_var = var_trt2 + var_trt2d30 - 2*cov_day30trt2
trt2day30totrt1day30_ci = c(exp(log(trt2day30totrt1day30_rr) - qchisq(0.975, 1)*sqrt(trt2day30totrt1day30_var)),
exp(log(trt2day30totrt1day30_rr) + qchisq(0.975, 1)*sqrt(trt2day30totrt1day30_var)))

var_trt2d60 = pois_gee$geese$vbeta["treatment2:days60","treatment2:days60"]
cov_day60trt2 = pois_gee$geese$vbeta["treatment2:days60","treatment2"]
trt2day60totrt1day60_rr = exp(coef(pois_gee)["treatment2"] + coef(pois_gee)["treatment2:days60"])
trt2day60totrt1day60_var = var_trt2 + var_trt2d60 + 2*cov_day60trt2
trt2day60totrt1day60_ci = c(exp(log(trt2day60totrt1day60_rr) - qchisq(0.975, 1)*sqrt(trt2day60totrt1day60_var)),
exp(log(trt2day60totrt1day60_rr) + qchisq(0.975, 1)*sqrt(trt2day60totrt1day60_var)))

cov_day60day30trt2 = pois_gee$geese$vbeta["treatment2:days60","treatment2:days30"]
trt2trt1_day60today30_r_rr = exp(coef(pois_gee)["treatment2:days60"] - coef(pois_gee)["treatment2:days30"])
trt2trt1_day60today30_r_var = var_trt2d30 + var_trt2d60 - 2*cov_day60day30trt2
trt2trt1_day60today30_r_ci = c(exp(log(trt2trt1_day60today30_r_rr) - qchisq(0.975, 1)*sqrt(trt2trt1_day60today30_r_var)),
exp(log(trt2trt1_day60today30_r_rr) + qchisq(0.975, 1)*sqrt(trt2trt1_day60today30_r_var)))

#treatment 3 to treatment 1
var_trt3 = pois_gee$geese$vbeta["treatment3","treatment3"]

```

```

var_trt3d30 = pois_gee$geese$vbeta["treatment3:days30", "treatment3:days30"]
cov_day30trt3 = pois_gee$geese$vbeta["treatment3:days30", "treatment3"]
trt3day30totrt1day30_rr = exp(coef(pois_gee)["treatment3"] + coef(pois_gee)["treatment3:days30"])
trt3day30totrt1day30_var = var_trt3 + var_trt3d30 - 2*cov_day30trt3
trt3day30totrt1day30_ci = c(exp(log(trt3day30totrt1day30_rr) - qchisq(0.975, 1)*sqrt(trt3day30totrt1day30_var)),
                             exp(log(trt3day30totrt1day30_rr) + qchisq(0.975, 1)*sqrt(trt3day30totrt1day30_var)))

var_trt3d60 = pois_gee$geese$vbeta["treatment3:days60", "treatment3:days60"]
cov_day60trt3 = pois_gee$geese$vbeta["treatment3:days60", "treatment3"]
trt3day60totrt1day60_rr = exp(coef(pois_gee)["treatment3"] + coef(pois_gee)["treatment3:days60"])
trt3day60totrt1day60_var = var_trt3 + var_trt3d60 + 2*cov_day60trt3
trt3day60totrt1day60_ci = c(exp(log(trt3day60totrt1day60_rr) - qchisq(0.975, 1)*sqrt(trt3day60totrt1day60_var)),
                             exp(log(trt3day60totrt1day60_rr) + qchisq(0.975, 1)*sqrt(trt3day60totrt1day60_var)))

cov_day60day30trt3 = pois_gee$geese$vbeta["treatment3:days60", "treatment3:days30"]
trt3trt1_day60today30_r_rr = exp(coef(pois_gee)["treatment3:days60"] - coef(pois_gee)["treatment3:days30"])
trt3trt1_day60today30_r_var = var_trt3d30 + var_trt3d60 - 2*cov_day60day30trt3
trt3trt1_day60today30_r_ci = c(exp(log(trt3trt1_day60today30_r_rr) - qchisq(0.975, 1)*sqrt(trt3trt1_day60today30_r_var)),
                             exp(log(trt3trt1_day60today30_r_rr) + qchisq(0.975, 1)*sqrt(trt3trt1_day60today30_r_var)))

#treatment 3 to treatment 2
cov_day30trt3trt2 = pois_gee$geese$vbeta["treatment3:days30", "treatment2"]
cov_day30trt3day30trt2 = pois_gee$geese$vbeta["treatment3:days30", "treatment2:days30"]
cov_trt3day30trt2 = pois_gee$geese$vbeta["treatment3", "treatment2:days30"]
cov_trt3trt2 = pois_gee$geese$vbeta["treatment3", "treatment2"]
trt3day30totrt2day30_rr = exp(coef(pois_gee)["treatment3"] + coef(pois_gee)["treatment3:days30"] -
                              coef(pois_gee)["treatment2"] - coef(pois_gee)["treatment2:days30"])
trt3day30totrt2day30_var = var_trt3 + var_trt3d30 + var_trt2 + var_trt2d30 + 2*cov_day30trt3 + 2*cov_day30trt2
trt3day30totrt2day30_ci = c(exp(log(trt3day30totrt2day30_rr) - qchisq(0.975, 1)*sqrt(trt3day30totrt2day30_var)),
                              exp(log(trt3day30totrt2day30_rr) + qchisq(0.975, 1)*sqrt(trt3day30totrt2day30_var)))

cov_day60trt3trt2 = pois_gee$geese$vbeta["treatment3:days60", "treatment2"]
cov_day60trt3day60trt2 = pois_gee$geese$vbeta["treatment3:days60", "treatment2:days60"]
cov_trt3day60trt2 = pois_gee$geese$vbeta["treatment3", "treatment2:days60"]
cov_trt3trt2 = pois_gee$geese$vbeta["treatment3", "treatment2"]
trt3day60totrt2day60_rr = exp(coef(pois_gee)["treatment3"] + coef(pois_gee)["treatment3:days60"] -
                              coef(pois_gee)["treatment2"] - coef(pois_gee)["treatment2:days60"])
trt3day60totrt2day60_var = var_trt3 + var_trt3d30 + var_trt2 + var_trt2d30 + 2*cov_day30trt3 + 2*cov_day60trt3
trt3day60totrt2day60_ci = c(exp(log(trt3day60totrt2day60_rr) - qchisq(0.975, 1)*sqrt(trt3day60totrt2day60_var)),
                              exp(log(trt3day60totrt2day60_rr) + qchisq(0.975, 1)*sqrt(trt3day60totrt2day60_var)))

broom::tidy(pois_gee, exponentiate = TRUE, conf.int = TRUE) %>%
  dplyr::select(term, estimate, std.error, conf.low, conf.high) %>%
  knitr::kable(caption = "Ratio of expected counts from Poisson GEE model (Exchangeable covariance)")

```

Table 3: Ratio of expected counts from Poisson GEE model (Exchangeable covariance)

term	estimate	std.error	conf.low	conf.high
(Intercept)	185.870	0.016	180.253	191.662
treatment2	0.984	0.019	0.948	1.022
treatment3	0.975	0.020	0.937	1.014
days30	0.674	0.014	0.656	0.694
days60	0.661	0.013	0.645	0.678
genderFemale	0.365	0.014	0.354	0.375

term	estimate	std.error	conf.low	conf.high
treatment2:days30	0.987	0.019	0.951	1.025
treatment3:days30	0.676	0.021	0.648	0.704
treatment2:days60	0.680	0.019	0.655	0.705
treatment3:days60	0.679	0.019	0.654	0.705