HW₆

```
library(plyr)
library(ggplot2)
```

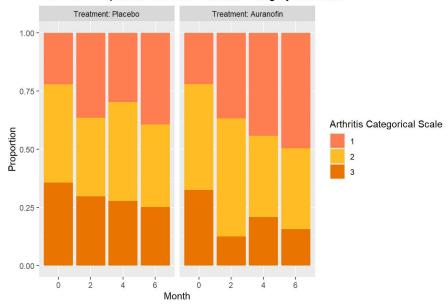
Section 1: Exploring Generalized Linear Mixed Effects Model (GLMM) Analysis

We will use data from a clinical trial comparing auranofin therapy (3 mg of oral gold, twice daily) and placebo for the treatment of rheumatoid arthritis (Bombardier et al., 1986). In this six-month, randomized, double-blind trial, 303 patients with classic or definite rheumatoid arthritis were randomized to one of the two treatment groups and followed over time. The outcome variable is a global impression scale (Arthritis Categorical Scale, ACS) measured at baseline (month 0), month 2, month 4, and month 6. This is a self- assessment of a patient's current arthritis, measured on a 5-level ordinal scale: (1) very good, (2) good, (3) fair, (4) poor, and (5) very poor. Baseline data on this outcome variable are available for 303 of the patients who participated in this trial; follow-up data at 6 months are available for 294 patients.

Data Preprocessing

Preliminary Analysis: Observed Proportions over Time

Observed Proportions of Each Outcome Category over Time



It appears that in the placebo group, ACS proportion for category 3 steadily declines over time. In the treatment group, the converse it true as proportion for category 3 increases following month 2. Also, the proportion of category 1 is higher in the treatment group compared to the control group accross different time points (except at baseline). At month 2, the category 2 proportion is substantially higher in treatment compared to control.

Equations for GLMM:

Let's write subject-specific equations for the GLMM, starting with thresholds, integrating covariates, beta coefficients, and random effects, and eventually converting equations to combined intercepts, factoring in each cumulative logit.

GLMM for the log-odds of a more favorable outcome with random slope and random intercept:

$$\begin{split} \operatorname{logit}\{E(Y_{ij} \leq c|b_i)\} &= \operatorname{log}\left\{\frac{Pr(Y_{ij} \leq c|b_i)}{Pr(Y_{ij} > c|b_i)}\right\} \\ &= a_c - (\beta_1 + \beta_2 \operatorname{Treatment}_i + \beta_3 \sqrt{\operatorname{Month}}_{ij} \\ &+ \beta_4 \operatorname{Treatment} * \sqrt{\operatorname{Month}}_{ij} + b_{1i} + b_{3i} \sqrt{\operatorname{Month}}_{ij}) \\ &= (a_c - \beta_1) + (\beta_2 \operatorname{Treatment}_i + \beta_3 \sqrt{\operatorname{Month}}_{ij} \\ &+ \beta_4 \operatorname{Treatment} * \sqrt{\operatorname{Month}}_{ij} + b_{1i} + b_{3i} \sqrt{\operatorname{Month}}_{ij}) \\ &= a_c^{\circ} - (\beta_2 \operatorname{Treatment}_i + \beta_3 \sqrt{\operatorname{Month}}_{ij} \\ &+ \beta_4 \operatorname{Treatment} * \sqrt{\operatorname{Month}}_{ij} + b_{1i} + b_{3i} \sqrt{\operatorname{Month}}_{ij}) \end{split}$$

$$b_i \sim ext{MVN}(0, G)$$
, where $G = egin{pmatrix} g_{11} & g_{12} \ g_{21} & g_{22} \end{pmatrix} = egin{pmatrix} \sigma_{b_{1i}}^2 & ext{Cov}(b_{1i}, b_{3i}) \ ext{Cov}(b_{1i}, b_{3i}) & \sigma_{b_{3i}}^2 \end{pmatrix}$

Incorporating Estimated Parameters:

We can transpose the equations using the estimated parameters extracted from the GLMM output, providing a nuanced understanding of the model's dynamics.

Cumulative Link Mixed Model fitted with the Laplace approximation

```
formula: as.factor(acs) ~ Treatment + SMONTH + TXSMTH + (SMONTH | ID)
data: df
```

```
link threshold nobs loaLik AIC
                                                       niter
                                                                     max.grad cond.H
  logit flexible 1194 -1115.48 2246.97 522(2625) 2.82e-04 8.3e+02
Random effects:
                            Variance Std.Dev. Corr
 Groups Name
 ID
           (Intercept) 2.55362 1.5980
            SMONTH
                            0.09292 0.3048
                                                     0.978
Number of groups: ID 303
Coefficients:
              Estimate Std. Error z value Pr(>IzI)
Treatment -0.1607 0.2919 -0.551 0.581969
                                0.1012 -3.870 0.000109 ***
SMONTH
               -0.3916
TXSMTH
                -0.3228
                                0.1416 -2.280 0.022632 *
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Threshold coefficients:
      Estimate Std. Error z value
112 -1.9178
                       0.2331 -8.227
                        0.2172 4.662
      1.0128
From R output: \hat{\sigma_{b_{1l}}^2}=2.55362; \hat{\sigma_{b_{2l}}^2}=0.09292 ; Corr(\hat{b_{1l}},b_{3l})=0.978
                                             \alpha_c^{\mathbb{O}} = \alpha_c^{\mathbb{O}} - \beta_1 : \alpha_c^{\mathbb{O}} \text{ is a combined new intercept, } \alpha_c^{\mathbb{O}} \text{ is a threshold, } \beta_1 \text{ is Intercept}
                                             lpha_1^{\mathbb{O}}=lpha_1-eta_1,lpha_1=0,lpha_1^{\mathbb{O}}=-1.9178, 	ext{ hence } \hat{eta}_1 	ext{ is } 1.9178
                                             \alpha_2^{\odot} = \alpha_2 - \beta_1, \hat{\alpha_2^{\odot}} = 1.0128, \text{ hence } \hat{\alpha_2} = 1.0128 + 1.9178 = 2.9306
Average of Subject-specific logit for a 'typical' subject, b_{1i}=0, b_{3i}=0
logit\{E(Y_{ij} \leq c|b_i)\} = a_c^{\circ} - (\beta_2 * \text{Treatment}_i + \beta_3 \sqrt{(\text{Month})_{ij}} + \beta_4 * \text{Treatment} * \sqrt{(\text{Month})_{ij}})
logit\{E(Y_{ij} \leq 1 | b_i = 0)\} = -1.9178 - (-0.1607 * \operatorname{Treatment}_i - 0.3916 \sqrt{(\operatorname{Month})}_{ii} - 0.3228 * \operatorname{Treatment} * \sqrt{(\operatorname{Month})}_{ii})
logit\{E(Y_{ij} \leq 2 | b_i = 0)\} = 1.0128 - (-0.1607*Treatment_i - 0.3916\sqrt{(Month)}_{ij} - 0.3228*Treatment* + \sqrt{(Month)}_{ii})
```

Random Effects Significance Test

A pivotal step involved testing the relevance of both random intercept and slope components within the model, we will examine the significance of each and decipher their implications on the overall model structure. We will compare the two models using liklihood ratio rest.

H_{0}: Variance of the random slope (b_{3i}) is zero H_{a}: Variance of the random slope (b_{3i}) is not zero

```
M1.2 <- clmm(as.factor(acs) ~ Treatment + SMONTH + TXSMTH + (1|ID),
data = df)

test.statistics <- -2*(M1.2$logLik-M1.1$logLik)
test.statistics

[1] 8.804148

p.value <- 0.5*(1-pchisq(test.statistics,1)) + 0.5*(1-pchisq(test.statistics,2))
```

```
[1] 0.007628685
```

p.value

With a p-value < than 0.05 and a test statistic of 8.804, we reject the null hypothesis. Thus, the model with random intercept and slopes is a better model based on the LRT.

The random effects can be interpreted as: - slope: heteogeneity among patients at baseline for change in log-odds of favorable response over time - intercept: heterogeneity among patients at baseline for log-odds of favorable response

Intervention Group Signifiance Test

With the optimal model, let's further examine the impact of intervention group on the subject-specific odds of a more favorable response over the study duration. We do this by formulating hypotheses, executing tests, and dissecting the results for insightful interpretation.

$$H_0:eta_4=0\ H_1:eta_4
eq 0$$

```
M1.3 <- clmm(as.factor(acs) ~ Treatment + SMONTH + (SMONTHID),
data = df)

test.statistics <- -2*(M1.3$logLik-M1.1$logLik)
test.statistics

[1] 5.22242

p.value <- 0.5*(1-pchisq(test.statistics,1)) + 0.5*(1-pchisq(test.statistics,2))
p.value
```

With a p-value < 0.05 and test statistic of 5.2242 for a liklihood ratio test, we reject the null hypothesis. We conclude that there is significant effect of intervention group on the change in subject-specific odds of a more favorable response over the duration of the study.

Interpreting Combined Intercepts

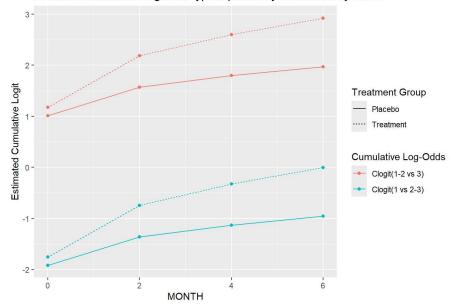
[1] 0.04787157

The first cumulative $logit\{Pr(Y_{ij} \leq 1)\}$ of a typical patient at baseline in the placebo group = $\hat{a_1^{\mathbb{C}}} = -1.9178$. The second second cumulative $logit\{Pr(Y_{ij} \leq 2)\}$ of a typical patient at baseline in the placebo group = $\hat{a_2^{\mathbb{C}}} = 1.0128$

Visualizing the Proportionality Assumption

```
#Output common intercepts for each logit:
alpha1_C<-M1.1$Theta[1]</pre>
alpha2_C<-M1.1$Theta[2]</pre>
Beta2<-M1.1$beta[1]</pre>
Beta3<-M1.1$beta[2]
Beta4<-M1.1$beta[3]
time < -c(0,2,4,6)
est.cum.logit<-data.frame(MONTH=rep(time,times=2),</pre>
                           SMONTH=rep(sqrt(time),times=2),
                           treatment=c(rep(0,times=4),rep(1,times=4)),
                           alpha12_C=c(rep(alpha1_C,times=8)),rep(alpha2_C,times=8)),
                           Clogit_type=c(rep("Clogit(1 vs 2-3)", times=8),
                                          rep("Clogit(1-2 vs 3)",times=8)))
est.cum.logit$TSMTH<-est.cum.logit$SMONTH*est.cum.logit$treatment</pre>
est.cum.logit$Clogit<-est.cum.logit$alpha12_C-(Beta2*est.cum.logit$treatment</pre>
                                                +Beta3*est.cum.logit$SMONTH
                                                +Beta4*est.cum.logit$TSMTH)
est.cum.logit$ctx <- factor(est.cum.logit$treatment,</pre>
                            levels=c(0,1),
                            labels=c("Placebo","Treatment"))
p2 \leftarrow ggplot(est.cum.logit, aes(x = MONTH,
             y = Clogit,
             group = interaction(ctx, Clogit_type)))
p2 + geom_line(aes(color = Clogit_type,linetype =ctx )) +
  geom_point((aes(color = Clogit_type))) +
labs(title = "Estimated cumulative logits for typical patient by treatement by month",
     y = "Estimated Cumulative Logit",
     color="Cumulative Log-Odds",
     linetype ="Treatment Group")
```

Estimated cumulative logits for typical patient by treatement by month

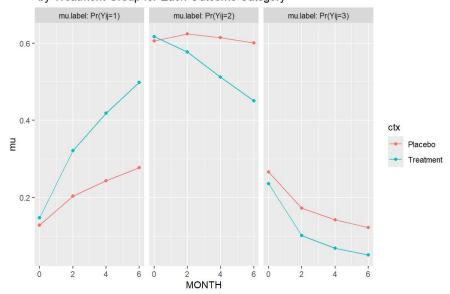


The slope of change in the cumulative log-odds for the favorable response is the same across (C-1) cumulative log-odds (logits). The log-odds are increasing proportionally across different cumulative logits, so that the ratios remain constant. The plot shows the predicted cumulative log-odds for the favorable response across time for two subject-specific ($b_{1i} = b_{3i} = 0$) log-odds.

Probability Estimation Plot

```
#Create a wide dataframe 'eta' from a long dataframe 'est.cum.logit'
eta1<-est.cum.logit[1:8,]</pre>
eta2<-est.cum.logit[9:16,]
eta<-eta1[,c("MONTH","SMONTH","treatment","alpha12_C","TSMTH","Clogit","ctx")]
names(eta)<-c("MONTH","SMONTH","treatment","alpha12_C","TSMTH","eta1","ctx")
eta$eta2 <- eta2$Clogit
eta$mu_1<-1/(1+exp(-eta$eta1))
eta$mu_2<-1/(1+exp(-eta$eta2))-1/(1+exp(-eta$eta1))
eta$mu_3<-1-1/(1+exp(-eta$eta2))
est.mu.data<-data.frame(MONTH=rep(eta$MONTH,times=3),
                     ctx=rep(eta$ctx,times=3),
                     mu=c(eta$mu_1,eta$mu_2,eta$mu_3),
                     mu.label=c(rep("Pr(Yij=1)",times=8),
                              rep("Pr(Yij=2)",times=8), rep("Pr(Yij=3)",times=8)))
for (i in 1:nrow(est.mu.data)) {
  est.mu.data$label[i]<-paste(as.character(est.mu.data$ctx[i]),</pre>
                              as.character(est.mu.data$mu.label[i]))
}
p5 <- ggplot(est.mu.data, aes(x=MONTH, y=mu, group=ctx))
p5 + facet_wrap(~mu.label, labeller=label_both) +
  geom_line(aes(color=ctx)) + geom_point(aes(color=ctx)) +
  labs(title="Predicted Probabilities for a Typical Subject over Time \n by Treatment Group for Each Outcome Category")
```

Predicted Probabilities for a Typical Subject over Time by Treatment Group for Each Outcome Category



For the Very Good category, probability of patients increased over time and the increase was sharper among the treatment group compared to the placebo. For the Good and Fair category, probability of patients decreased over time with a larger decrease in the treatment group compared to the placebo group. Compared to 1b, the proportion of patients in Very Good and Fair is higher across time. The direction of change (increase or decrease) is maintained, however it is much smoother in the predicted probabilities vs 1b.

Analyzing Subject-specific Odds Ratios

```
OR <- exp(sqrt(c(0,2,4,6))*-Beta4)

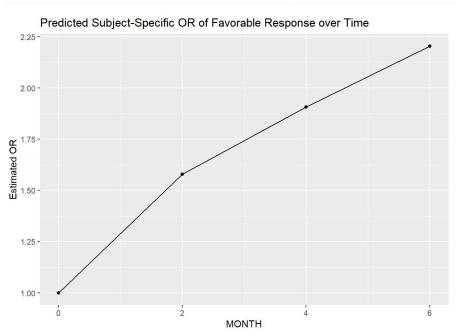
OR_DATA <- data.frame(MONTH=c(0,2,4,6), OR)

p4 <- ggplot(OR_DATA, aes(x=MONTH, y=OR))

p4 + geom_line() + geom_point()+

labs(title="Predicted Subject-Specific OR of Favorable Response over Time",

y="Estimated OR")
```



At 4 months, a patient assigned to treatment is approximately 2 times more likely to have a favorable response when compared to a similar patient treated with placebo.

Comparing with Reference Analysis

Compared to the "Applied Longitudinal Analysis, 2nd Edition" by Fitzmaurice, Laird, and Ware estimates, the estimated β 's for the random effects are about half in magnitude and the variance in double in magnitude. The dissimilarity likely arises from the fact that the book's model had 5 ordinal levels of ACS while ours had 3 ordinal levels. Even with a smaller level of granularity, the drug has significant effect in the change in subject-specific odds of a more favorable response over time. However, the effects are more pronounced and less variable when there are more ACS levels.

Section 2: Exploring Generalized Linear Mixed Effects Model for Nominal Response

Subject-specific Equations for GLMM:

Let's write out the subject-specific equations for the GLMM using covariates, beta coefficients, and random effects, considering "Poor or Very Poor" as the reference category.

Three-part MGLM specification for Nominal Outcome, $Y_{i,j}$

```
1. A distributional assumption of Y_{ij}|b_i \sim Multinomial(p_{ij}^{(1)}, p_{ij}^{(2)}, p_{ij}^{(3)}), where p_{ij}^{(c)} = \mu_{ij}^{*(c)} = E(Y_{ij} = c|b_i^{(c)}) = Pr(Y_{ij} = c|b_i^{(c)}); 
2. \eta_{ij}^{*(c)} = X_{ij}\beta^{(c)} + Z_{ij}b_i^{(c)}; 
3. g(\mu_{ij}^{*(c)}) = logit\{Pr(Y_{ij} = c|b_i^{(c)})\} = log\{\frac{Pr(Y_{ij} = c|b_i^{(c)})}{Pr(Y_{ij} = C|b_i^{(c)})}\}
```

Baseline category logit with "Poor or Very Poor" (3) as the reference, we have 2 generalized logits:

$$log\{\frac{Pr(Y_{ij}=c|b_{i}^{(c)})}{Pr(Y_{ij}=3|b_{i}^{(c)})}\} = \beta_{1}^{(c)} + \beta_{2}^{(c)} * \text{Treatment}_{i} + \beta_{3}^{(c)} * \sqrt{(\text{Month})}_{ij} + \beta_{4}^{(c)} * \text{Treatment} * \sqrt{(\text{Month})}_{ij} + b_{1i}^{(c)}, c = 1, 2$$

$$b_{1i}^{(c)} \sim N(0, \sigma_{b_{i}^{(c)}}^{2})$$

Interpretation of Random Effects

```
library(mclogit)
library(memisc)
dfacs2[dfacs==1]<-3
df$acs2[df$acs==2]<-2
df$acs2\Gammadf$acs==3\Gamma<-1
df$acsn <- factor(df$acs)
df$acsn2 <- factor(df$acs2)
df$id <- factor(df$ID)</pre>
M2.1 <- mblogit(formula = acsn2 ~ Treatment + SMONTH + TXSMTH,
               random=~1lid, catCov = "free", data=df,
               control = mmclogit.control(epsilon=1e-08, maxit = 25,
                                            trace=TRUE, trace.inner=FALSE,
                                            avoid.increase=FALSE.
                                            break.on.increase=FALSE,
                                            break.on.infinite=FALSE.
                                            break.on.negative=FALSE
               )
```

```
Iteration 1 - deviance = 2354.677 - criterion = 0.794223
Iteration 2 - deviance = 2344.297 - criterion = 0.03072274
Iteration 3 - deviance = 2331.546 - criterion = 6.921906e-05
Iteration 4 - deviance = 2331.038 - criterion = 1.273286e-09
converged
summary(M2.1)
```

```
Call:
mblogit(formula = acsn2 ~ Treatment + SMONTH + TXSMTH, data = df,
    random = ~1 I id, catCov = "free", control = mmclogit.control(epsilon = 1e-08,
    maxit = 25, trace = TRUE, trace.inner = FALSE, avoid.increase = FALSE,
    break.on.increase = FALSE, break.on.infinite = FALSE,
    break.on.negative = FALSE))
```

```
Equation for 2 vs 1:
                       Estimate Std. Error z value Pr(>IzI)
(Intercept) 0.1547 0.2078 0.744 0.457
Treatment 0.3334 0.2938 1.135 0.256
SMONTH
                             0.1023 0.1115 0.917
                                                                                              0.359
TXSMTH
                            0.0941 0.1631 0.577
                                                                                        0.564
Equation for 3 vs 1:
                      Estimate Std. Error z value Pr(>IzI)
Treatment 0.08273 0.36795 0.225 0.82211
SMONTH 0.41872 0.12976 3.227 0.00125 **
TXSMTH
                       0.35545 0.18914 1.879 0.06020 .
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
(Co-)Variances:
Grouping level: id
       Estimate
                                          Std.Err.
2~1 1.2206
                                          0.04749
3~1 0.3608 2.0948 0.12543 0.21400
Approximate residual deviance: 2331
Number of Fisher scoring iterations: 4
Number of observations
   Groups by id: 303
   Individual observations: 1194
 mtable(M2.1)
Calls:
M2.1: mblogit(formula = acsn2 ~ Treatment + SMONTH + TXSMTH, data = df,
        random = ~1 I id, catCov = "free", control = mmclogit.control(epsilon = 1e-08,
                 maxit = 25, trace = TRUE, trace.inner = FALSE, avoid.increase = FALSE,
                 break.on.increase = FALSE, break.on.infinite = FALSE,
                 break.on.negative = FALSE))
                                                    2/1 3/1
_____
   (Intercept)
                                                   0.155 -0.650*
                                                  (0.208) (0.258)
                                                   0.333 0.083
   Treatment
                                                 (0.294) (0.368)
                                                 0.102 0.419**
   SMONTH
                                                  (0.111) (0.130)
   TXSMTH
                                                    0.094 0.355
                                                  (0.163) (0.189)
   2/1 x VCov(~1,~1) 1.221 0.361
                                             (0.047) (0.125)
   3/1 x VCov(~1,~1) 0.361 2.095
                                                  (0.125) (0.214)
    Groups by id 303
                          2331.0
   Deviance
   Ν
    Significance: *** = p < 0.001;
                                  ** = p < 0.01;
                                   * = p < 0.05
  1. \  \, \text{Equation for Fair vs Poor: } \\ log\{\frac{Pr(Y_{ij}=2|b_i^{(c)})}{Pr(Y_{ij}=3|b_i^{(c)})}\} = -0.65045 + 0.08273 * \\ \text{Treatment}_i + 0.41872\sqrt{(\text{Month})}_{ij} + 0.35545 * \\ \text{Treatment} * \sqrt{(\text{Month})}_{ij} + b_{1i}^{(c)} + 0.08273 * \\ \text{Treatment}_i + 0.41872\sqrt{(\text{Month})}_{ij} + 0.35545 * \\ \text{Treatment}_i + 0.41872\sqrt{(\text{Month})}_{ij} + 0.41872\sqrt{(\text{Month})}_{ij} + 0.41872\sqrt{(\text{Month})}_{ij} + 0.41872\sqrt{(\text{Month})}_{ij} + 0.41872\sqrt{(\text{Month})}_
       where b_{1i}^{(c)} \sim N(0, 2.0948)
  2. Equation for Good or Very Good vs Poor:
      log\{\frac{Pr(Y_{ij}=1|b_i^{(c)})}{Pr(Y_{ii}=3|b_i^{(c)})}\} = 0.1547 + 0.3334* \text{Treatment}_i + 0.1023\sqrt{(\text{Month})}_{ij} + 0.0941* \text{Treatment}* \sqrt{(\text{Month})}_{ij} + b_{1i}^{(c)} \text{ where } b_{1i}^{(c)} \sim N(0, 1.2206)
```

Intervention Group Effect Test

```
Using a Wald Test: H_0:eta_{{\scriptscriptstyle A}}^{(1)}=0 H_a:eta_{{\scriptscriptstyle A}}^{(1)}
eq 0
```

- 1. Fair vs Poor: With a z-value of 0.577 and p-value > 0.05 (0.564), we fail to reject the null hypothesis. This means that there is not a significant effect of intervention group on the change in subject-specific odds of a more favorable response over the duration of the study.
- 2. Good or Very Good vs Poor: With a z-value of 1.879 and p-value > 0.05 (0.06), we fail to reject the null hypothesis. This means that there is not a significant effect of intervention group on the change in subject-specific odds of a more favorable response over the duration of the study.

Interpretation of Intercepts

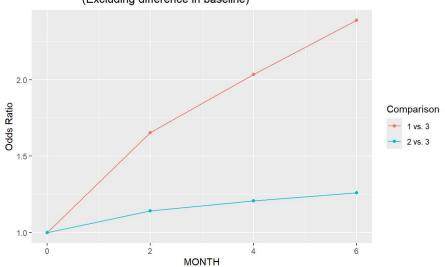
- 1. The log-odds of the Fair category relative to the Poor category is estimated to change by $\widehat{\beta_1^{(2)}} = -0.65045$ for an individual with propensity to respond higher relative to the baseline category.
- 2. The log-odds of the Good or Very Good category relative to the Fair category is estimated to change by $\widehat{\beta_1^{(1)}} = 0.1547$ for an individual with propensity to respond higher relative to the baseline category.

The interpretations are different from Section 1 because Section 1 looks at the cumulative logits and is not specific to which C-1 logit is being looked at while 3iii looks at logit specific to each C-1.

Odds Ratios Plot

```
MONTH < -rep(c(0,2,4,6),2)
SM=sart(MONTH)
Numerator=c(rep(1,4),rep(2,4))
Beta4_hat<-c(rep(0.35545,4),rep(0.094,4))
OR_data<-cbind(Numerator, MONTH,SM,Beta4_hat)</pre>
rownames(OR_data) <- 1:8</pre>
OR_data <- as.data.frame(apply(OR_data[ , 1:4], 2, as.numeric))</pre>
OR_data$OR <- exp(OR_data$SM*OR_data$Beta4_hat)</pre>
#Create a factor variable for Comparison
OR_data$Comparison <- factor(OR_data$Numerator,</pre>
                               levels=c(1,2),
                               labels=c("1 vs. 3","2 vs. 3"))
p2 <- ggplot(OR_data, aes(x=MONTH, y=OR, group=Comparison))</pre>
p2 + geom_line(aes(color=Comparison)) + geom_point(aes(color=Comparison)) +
  labs(title="Estimated Subject-Specific
               Baseline Odds Ratios over Time: \nDrug vs Placebo
               (Excluding difference in baseline)", y="0dds Ratio")
```

Estimated Subject-Specific
Baseline Odds Ratios over Time:
Drug vs Placebo
(Excluding difference in baseline)



At 4 months, a patient assigned to the treatment is approximately 1.2 times more likely to feel Fair vs. Poor compared to a similar patient treated with placebo. At 4 months, a patient assigned to the treatment is approximately 2 times more likely to feel Very Good or Good vs. Poor compared to a similar patient treated with placebo.

Probability Estimation Equations

Let's write equations for estimating probabilities of each level of the nominal response for a typical subject. To understand the numerical workings, we can calculate the probability of a "Fair" response at 6 months for a treatment group patient with a specific random intercept.

$$log\{\frac{Pr(Y_{ij}=c|b_i^{(c)})}{Pr(Y_{ij}=3|b_i^{(c)})}\} = \beta_1^{(c)} + \beta_2^{(c)} * \text{Treatment}_i + \beta_3^{(c)} * \sqrt{(\text{Month})}_{ij} + \beta_4^{(c)} * \text{Treatment} * \sqrt{(\text{Month})}_{ij} + b_{1i}^{(c)}, c = 1, 2$$

 $\text{For Fair vs Poor: } log\{\frac{Pr(Y_{ij}=c|b^{(c)})}{Pr(Y_{ij}=3|b^{(c)})}\} = \beta_1^{(c)} + \beta_2^{(c)} * \text{Treatment}_i + \beta_3^{(c)} * \sqrt{(\text{Month})}_{ij} + \beta_4^{(c)} * \text{Treatment} * \sqrt{(\text{Month})}_{ij} + b_{1i}^{(c)}$

$$Pr(Y_{ij}=c|b_i) = exp(eta_1^{(c)}+eta_2^{(c)}* ext{Treatment}_i+eta_3^{(c)}*\sqrt{(ext{Month})}_{ij}$$

$$+\beta_4^{(c)}*\text{Treatment}*\sqrt{(\text{Month})}_{ij} + b_{1i}^{(c)})*Pr(Y_{ij} = 3|b_i)$$

$$= exp(0.1547 + 0.3334 \text{Treatment}_i + 0.1023 * \sqrt{(\text{Month})}_{ij} + 0.0941 \text{Treatment} * \sqrt{(\text{Month})}_{ij}$$

For Good or Very Good vs Poor:

$$log\{\frac{Pr(Y_{ij}=c|b_{i}^{(c)})}{Pr(Y_{ij}=3|b_{i}^{(c)})}\} = \beta_{1}^{(c)} + \beta_{2}^{(c)} * \text{Treatment}_{i} + \beta_{3}^{(c)} * \sqrt{(\text{Month})}_{ij} + \beta_{4}^{(c)} * \text{Treatment} * \sqrt{(\text{Month})}_{ij} + b_{1i}^{(c)}$$

$$Pr(Y_{ij} = c|b_i) = exp(eta_1^{(c)} + eta_2^{(c)} * \operatorname{Treatment}_i + eta_3^{(c)} * \sqrt{(\operatorname{Month})}_i$$

$$+\beta_4^{(c)}* \operatorname{Treatment}*\sqrt{(\operatorname{Month})}_{ij} + b_{1i}^{(c)}) * Pr(Y_{ij} = 3|b_i)$$

$$= exp(-0.65045 + 0.08273 \text{Treatment}_i + 0.41872 * \sqrt{(\text{Month})}_{ij} + 0.35545 \text{Treatment} * \sqrt{(\text{Month})$$

Given
$$Pr(Y_{ij}=3|b_i)=1-Pr(Y_{ij}=1|b_i)-Pr(Y_{ij}=2|b_i)$$
, we can derive $Pr(Y_{ij}=3|b_i)=\frac{1}{1+exp(\eta_{ij}^{(1)^*}+b_{1i})+exp(\eta_{ij}^{(2)^*}+b_{1i})}$. Thus, $Pr(Y_{ij}=1|b_i)=\frac{exp(\eta_{ij}^{(1)^*}+b_{1i})}{1+exp(\eta_{ij}^{(1)^*}+b_{1i})+exp(\eta_{ij}^{(2)^*}+b_{1i})}$ and $Pr(Y_{ij}=2|b_i)=\frac{exp(\eta_{ij}^{(2)^*}+b_{1i})}{1+exp(\eta_{ij}^{(1)^*}+b_{1i})+exp(\eta_{ij}^{(2)^*}+b_{1i})}$.

Using this, we can get the probability of probability of having "Fair" response at 6 months of follow up for a patient randomized to the treatment group with a random intercept $b_i = -0.17$:

$$Pr(Y_{ij} = 2|b_i = -0.17) = \frac{exp(0.1547 + 0.3334 + 0.1023(\sqrt{6}) + 0.0941(\sqrt{6}) - 0.17)}{1 + exp(-0.65045 + 0.08273 + 0.41872(\sqrt{6}) + 0.35545(\sqrt{6}) - 0.17) + exp(0.1547 + 0.3334 + 0.1023(\sqrt{6}) + 0.0941(\sqrt{6}) - 0.17)} = \frac{2.223716}{1 + 3.185475 + 2.223716} = 0.3469574$$