Logit Models

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Contents

Chapter 1

Basics

1.1 Logit

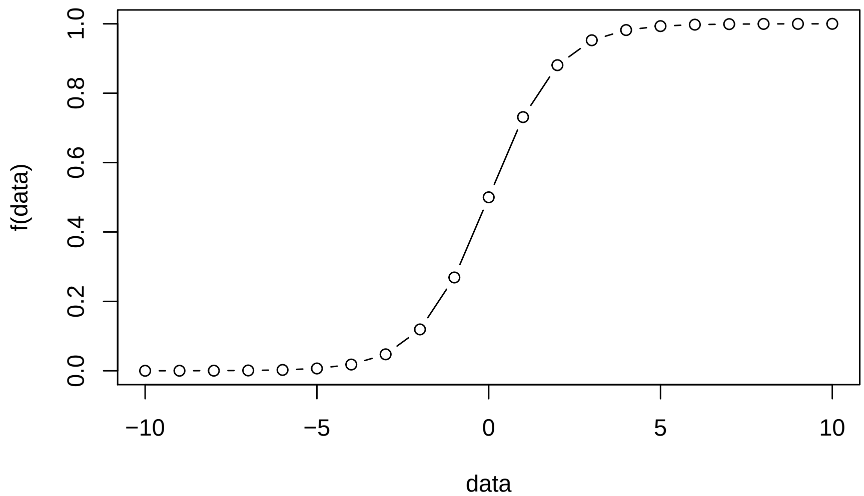
$$f(x) = log(\frac{p(y=1)}{1-p(y=1)})$$

The basic idea of logistic regression:

$$p(y=1) = \frac{1}{1+e^{-(\beta_0+\beta_1 x_1+...+\beta_n x_n)}} = \frac{e^{\beta_0+\beta_1 x_1+...+\beta_n x_n}}{1+e^{\beta_0+\beta_1 x_1+...+\beta_n x_n}}$$

Thus, $e^{\beta_0+\beta_1 x_1+...+\beta_n x_n}$ can be from $-\infty$ to $+\infty$, and $p(y=1)$ will be always within the range of $(0,1)$.

```
f<-function(x){exp(x)/(1+exp(x))}
data<-seq(-10,10,1)
plot(data,f(data),type = "b")
```



We can also write the function into another format as follows:

$$log \frac{p(y=1)}{1-p(y=1)} = \beta_0 + \beta_1 x_1 + ... + \beta_n x_n$$

Thus, we know that the regression coeficients of β_i actually change the "log-odds" of the event. Of course, note that the magnitude of β_i is dependent upon the units of x_i.

The following is an example testing whether that home teams are more likely to win in NFL games. The results show that the odd of winning is the same for both home and away teams.

```
mydata = read.csv(url('https://raw.githubusercontent.com/nfl-football-ops/Big-Data-Bowl
mydata$result_new<-ifelse(mydata$HomeScore>mydata$VisitorScore,1,0)
summary(mydata$result_new)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0000  0.0000  0.0000  0.4945  1.0000  1.0000
```

```
mylogit1 = glm(result_new~1, family=binomial, data=mydata)
summary(mylogit1)
```

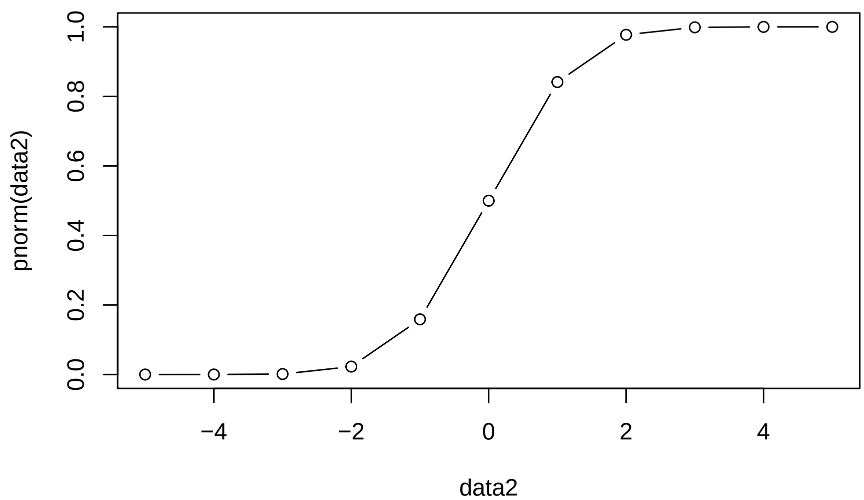
```
##
## Call:
```

```
## glm(formula = result_new ~ 1, family = binomial, data = mydata)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.168  -1.168  -1.168   1.187   1.187
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.02198    0.20967  -0.105    0.917
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 126.14  on 90  degrees of freedom
## Residual deviance: 126.14  on 90  degrees of freedom
## AIC: 128.14
##
## Number of Fisher Scoring iterations: 3
```

1.2 Probit

As noted above, logit $f(x) = log(\frac{p(y=1)}{1-p(y=1)})$ provides the resulting range of $(0, 1)$. Another way to provide the same rage is through the cdf of normal distribution.The following R code is used to illusrate this process.

```
data2<-seq(-5,5,1)
plot(data2,pnorm(data2),type = "b")
```



Thus, the cdf of normal distribution can be used to indicate the probability of $p(y = 1)$.

$$\Phi(\beta_0 + \beta_1 x_1 + ... + \beta_n x_n) = p(y = 1)$$

Similar to logit model, we can also write the inverse function of the cdf to get the function that can be from $-\infty$ to $+\infty$.

$$\beta_0 + \beta_1 x_1 + ... + \beta_n x_n = \Phi^{-1}(p(y = 1))$$

Thus, for example, if $X\beta$ = -2, based on $\Phi(\beta_0 + \beta_1 x_1 + ... + \beta_n x_n) = p(y = 1)$ we can get that the $p(y = 1) = 0.023$.

In contrast, if $X\beta = 3$, the $p(y = 1) = 0.999$.

```
pnorm(-2)
```

```
## [1] 0.02275013
```

```
pnorm(3)
```

```
## [1] 0.9986501
```

Let's assume that there is a latent variable called Y^* such that

$$Y^* = X\beta + \epsilon, \epsilon \sim N(0, \sigma^2)$$

You could think of Y^* as a kind of "proxy" between $X\beta + \epsilon$ and the observed $Y(1 or 0)$. Thus, we can get the following. Note that, it does not have to be zero, and can be any constant.

$$Y^* = \begin{cases} 0 & if \ y_i^* \leq 0 \\ 1 & if \ y_i^* > 0 \end{cases}$$

Thus,

$$y_i^* > 0 \Rightarrow \beta^{'} X_i + \epsilon_i > 0 \Rightarrow \epsilon_i > -\beta^{'} X_i$$

Thus, we can write it as follows. Note that $\frac{\epsilon_i}{\sigma} \sim N(0,1)$

$$p(y = 1|x_i) = p(y_i^* > 0|x_i) = p(\epsilon_i > -\beta^{'} X_i) = p(\frac{\epsilon_i}{\sigma} > \frac{-\beta^{'} X_i}{\sigma}) = \Phi(\frac{\beta^{'} X_i}{\sigma})$$

We thus can get:

$$p(y = 0|x_i) = 1 - \Phi(\frac{\beta^{'} X_i}{\sigma})$$

For $p(y = 1|x_i) = \Phi(\frac{\beta^{'} X_i}{\sigma})$, we can not really estimate both β and σ as they are in a ratio. We can assume $\sigma = 1$, then $\epsilon \sim N(0,1)$. We know y_i and x_i since we observe them. Thus, we can write it as follows.

$$p(y = 1|x_i) = \Phi(\beta^{'} X_i)$$

Chapter 2

MLE

2.1 Basic idea of MLE

Suppose that we flip a coin, $y_i = 0$ for tails and $y_i = 1$ for heads. If we get p heads from n trials, we can get the proportion of heads is p/n, which is the sample mean. If we do not do any further calculation, this is our best guess.

Suppose that the true proablity is ρ, then we can get:

$$\mathbf{L}(y_i) = \begin{cases} \rho \quad y_i = 1 \\ 1-\rho \quad y_i = 0 \end{cases}$$

Thus, we can also write it as follows.

$$\mathbf{L}(y_i) = \rho^{y_i}(1-\rho)^{1-y_i}$$

Thus, we can get:

$$\prod \mathbf{L}(y_i|\rho) = \rho^{\sum y_i}(1-\rho)^{\sum(1-y_i)}$$

Further, we can get a log-transformed format.

$$log(\prod \mathbf{L}(y_i|\rho)) = \sum y_i log\rho + \sum(1-y_i)log(1-\rho)$$

To maximize the log-function above, we can calculate the derivative with respect to ρ.

$$\frac{\partial log(\prod \mathbf{L}(y_i|\rho))}{\partial \rho} = \sum y_i \frac{1}{\rho} - \sum(1-y_i)\frac{1}{1-\rho}$$

Set the derivative to zero and solve for ρ, we can get

$$\sum y_i \frac{1}{\rho} - \sum (1-y_i)\frac{1}{1-\rho} = 0$$

$$\Rightarrow (1-\rho)\sum y_i - \rho \sum (1-y_i) = 0$$

$$\Rightarrow \sum y_i - \rho \sum y_i - n\rho + \rho \sum y_i = 0$$

$$\Rightarrow \sum y_i - n\rho = 0$$

$$\Rightarrow \rho = \frac{\sum y_i}{n} = \frac{p}{n}$$

Thus, we can see that the ρ maximizing the likelihood function is equal to the sample mean.

2.2 Coin flip example, probit, and logit

In the example above, we are not really trying to estimate a lot of regression coefficients. What we are doing actually is to calculate the sample mean, or intercept in the regresion sense. What does it mean? Let's use some data to explain it.

Suppose that we flip a coin 20 times and observe 8 heads. We can use the R's glm function to esimate the ρ. If the result is consistent with what we did above, we should observe that the *cdf* of the esimate of β_0 (i.e., intercept) should be equal to $8/20 = 0.4$.

2.2.1 Probit

```
coins<-c(rep(1,times=8),rep(0,times=12))
table(coins)
```

```
## coins
##  0  1
## 12  8
```

```
coins<-as.data.frame(coins)

probitresults <- glm(coins ~ 1, family = binomial(link = "probit"), data = coins)
probitresults
```

```
##
## Call:  glm(formula = coins ~ 1, family = binomial(link = "probit"),
##     data = coins)
##
## Coefficients:
## (Intercept)
##     -0.2533
##
## Degrees of Freedom: 19 Total (i.e. Null);  19 Residual
## Null Deviance:       26.92
## Residual Deviance: 26.92     AIC: 28.92
```

As we can see the intercept is -0.2533, and thus $\Phi(-0.2533471) = 0.4$

```
pnorm(probitresults$coefficients)
```

```
## (Intercept)
##         0.4
```

2.2.2 Logit

We can also use logit link to calculate the intercept as well. Recall that

$$p(y=1) = \frac{1}{1+e^{-(\beta_0+\beta_1 x_1+\ldots+\beta_n x_n)}} = \frac{e^{\beta_0+\beta_1 x_1+\ldots+\beta_n x_n}}{1+e^{\beta_0+\beta_1 x_1+\ldots+\beta_n x_n}}$$

Thus,

$$p(y=1) = \frac{e^{\beta_0}}{1+e^{\beta_0}}$$

```
logitresults <- glm(coins ~ 1, family = binomial(link = "logit"), data = coins)
logitresults$coefficients
```

```
## (Intercept)
##  -0.4054651
```

```
exp(logitresults$coefficients)/(1+exp(logitresults$coefficients))
```

```
## (Intercept)
##         0.4
```

2.3 Further on logit

The probablity of $y = 1$ is as follows:

$$p = p(y = 1) = \frac{1}{1 + e^{-(\beta_0+\beta_1 x_1+\ldots+\beta_n x_n)}} = \frac{e^{\beta_0+\beta_1 x_1+\ldots+\beta_n x_n}}{1 + e^{\beta_0+\beta_1 x_1+\ldots+\beta_n x_n}}$$

Thus, the likelihood function is as follows:

$$L = \prod p^{y_i}(1-p)^{1-y_i} = \prod (\frac{1}{1 + e^{-(\beta_0+\beta_1 x_1+\ldots+\beta_n x_n)}})^{y_i}(\frac{1}{1 + e^{\beta_0+\beta_1 x_1+\ldots+\beta_n x_n}})^{1-y_i}$$

$$= \prod (1 + e^{-(\beta_0+\beta_1 x_1+\ldots+\beta_n x_n)})^{-y_i}(1 + e^{\beta_0+\beta_1 x_1+\ldots+\beta_n x_n})^{-(1-y_i)}$$

Thus, the log-likelihood is as follows:

$$logL = \sum(-y_i \cdot log(1+e^{-(\beta_0+\beta_1 x_1+\ldots+\beta_n x_n)}) - (1-y_i) \cdot log(1+e^{\beta_0+\beta_1 x_1+\ldots+\beta_n x_n}))$$

Typically, optimisers minimize a function, so we use negative log-likelihood as minimising that is equivalent to maximising the log-likelihood or the likelihood itself.

```
#Source of R code: https://www.r-bloggers.com/logistic-regression/

mle.logreg = function(fmla, data)
{
  # Define the negative log likelihood function
  logl <- function(theta,x,y){
    y <- y
    x <- as.matrix(x)
    beta <- theta[1:ncol(x)]

    # Use the log-likelihood of the Bernouilli distribution, where p is
    # defined as the logistic transformation of a linear combination
    # of predictors, according to logit(p)=(x%*%beta)
    loglik <- sum(-y*log(1 + exp(-(x%*%beta))) - (1-y)*log(1 + exp(x%*%beta)))
    return(-loglik)
  }

  # Prepare the data
  outcome = rownames(attr(terms(fmla),"factors"))[1]
  dfrTmp = model.frame(data)
  x = as.matrix(model.matrix(fmla, data=dfrTmp))
```

```r
  y = as.numeric(as.matrix(data[,match(outcome,colnames(data))]))

  # Define initial values for the parameters
  theta.start = rep(0,(dim(x)[2]))
  names(theta.start) = colnames(x)

  # Calculate the maximum likelihood
  mle = optim(theta.start,logl,x=x,y=y, method = 'BFGS', hessian=T)
  out = list(beta=mle$par,vcov=solve(mle$hessian),ll=2*mle$value)
}
```

```r
mydata = read.csv(url('https://stats.idre.ucla.edu/stat/data/binary.csv'))
mylogit1 = glm(admit~gre+gpa+as.factor(rank), family=binomial, data=mydata)

mydata$rank = factor(mydata$rank) #Treat rank as a categorical variable
fmla = as.formula("admit~gre+gpa+rank") #Create model formula
mylogit2 = mle.logreg(fmla, mydata) #Estimate coefficients


 print(cbind(coef(mylogit1), mylogit2$beta))
```

```
##                           [,1]         [,2]
## (Intercept)      -3.989979073 -3.772676422
## gre               0.002264426  0.001375522
## gpa               0.804037549  0.898201239
## as.factor(rank)2 -0.675442928 -0.675543009
## as.factor(rank)3 -1.340203916 -1.356554831
## as.factor(rank)4 -1.551463677 -1.563396035
```

Chapter 3

Twitter Example

The following is part of my course project for Stat 536. It aims to replicate part of the findings from Barbera (2015) Birds of the Same Feather Tweet Together: Bayesian Ideal Point Estimation Using Twitter Data. Political Analysis 23 (1). Note that, the following model is much simpler than that in the original paper.

3.1 Model

Suppose that a Twitter user is presented with a choice between following or not following another target $j \in \{1, ..., m\}$. Let $y_j = 1$ if the user decides to follow j, and $y_j = 0$ otherwise.

$$y_j = \begin{cases} 1 & Following \\ 0 & NotFollowing \end{cases}$$

$$p(y_j = 1|\theta) = \frac{exp(-\theta_0|\theta_1 - x_j|^2)}{1 + exp(-\theta_0|\theta_1 - x_j|^2)}$$

We additionally know the priors of θ.

$$\theta_i \sim N(0, 10^2)(i = 0, 1)$$

The likelihood function is as follows.

$$L(Y|\theta) = \prod_{j=1}^{m} (\frac{exp(-\theta_0|\theta_1 - x_j|^2)}{1 + exp(-\theta_0|\theta_1 - x_j|^2)})^{y_j} (1 - \frac{exp(-\theta_0|\theta_1 - x_j|^2)}{1 + exp(-\theta_0|\theta_1 - x_j|^2)})^{(1-y_j)}$$

Thus, the posterior is as follows.

$$L(Y|\theta) \cdot N(\theta_0|0,10) \cdot N(\theta_1|0,10)$$

$$\propto \prod_{j=1}^{m} (\frac{exp(-\theta_0|\theta_1 - x_j|^2)}{1+exp(-\theta_0|\theta_1 - x_j|^2)})^{y_j}(1-\frac{exp(-\theta_0|\theta_1 - x_j|^2)}{1+exp(-\theta_0|\theta_1 - x_j|^2)})^{(1-y_j)} \cdot exp(-\frac{1}{2}(\frac{\theta_0}{10})^2) \cdot exp(-\frac{1}{2}(\frac{\theta_1}{10})^2)$$

3.2 Simulating Data of Senators on Twitter

Assume that we have 100 senators, 50 Democrats and 50 Republicans, who we know their ideology. Assume that Democrats have negative ideology scores to indicate that they are more liberal, whereas Republicans have positive scores to indicate that they are more conservative. The following is data simulation for senators.

```
# Republicans are more conservative, and they have positive numbers.
Republicans<-c()
Republicans<-rnorm(50,1,0.5)
No_Republicans<-rep(1:50,1)
Part_1<-cbind(No_Republicans,Republicans)

# Democrats are more liberal, and they have negative numbers.
Democrats<-c()
Democrats<-rnorm(50,-1,0.5)
No_Democrats<-rep(51:100,1)
Part_2<-cbind(No_Democrats,Democrats)
Data_Elites<-rbind(Part_1,Part_2)
Data_Elites<-as.data.frame(Data_Elites)
colnames(Data_Elites) <- c("Elite_No","Elite_ideology")

head(Data_Elites)
```

```
##   Elite_No Elite_ideology
## 1        1      1.0830563
## 2        2      0.9334548
## 3        3      0.8780085
## 4        4      1.1220610
## 5        5      0.7296087
## 6        6      0.3745218
```

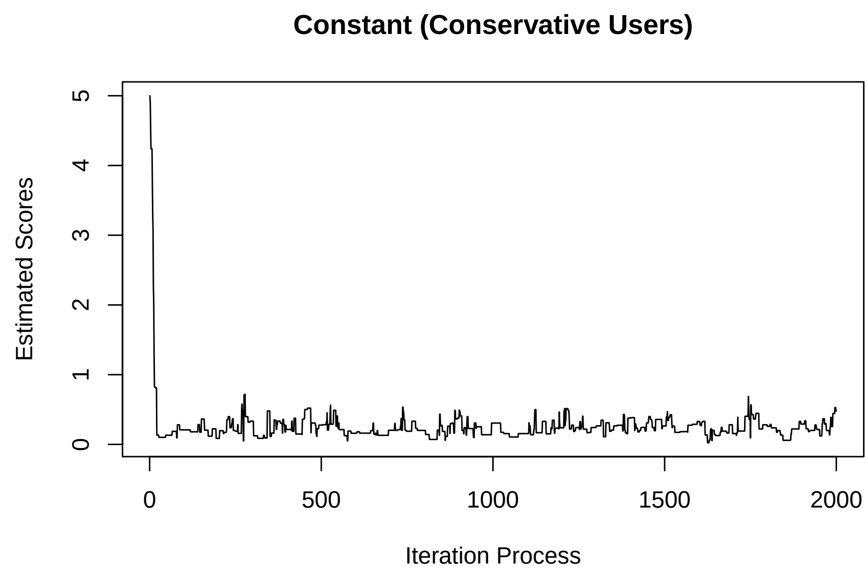
3.3 Simulating Data of Conservative Users on Twitter and Model Testing

Assume that we observe one Twitter user, who is more conservative. To simulate Twitter following data for this user, I assign this user to follow more Republican senators. Thus, if the Metropolis Hastings algorithm works as intended, we would expect to see a positive estimated value for their ideology. Importantly, as we can see in the histogram below, the estimated value indeed is positive, providing preliminary evidence for the statistical model and the algorithm. In addition, for the acceptance rate, we can see that the constant has a lower number than ideology, since we only accept a constant when it is positive.

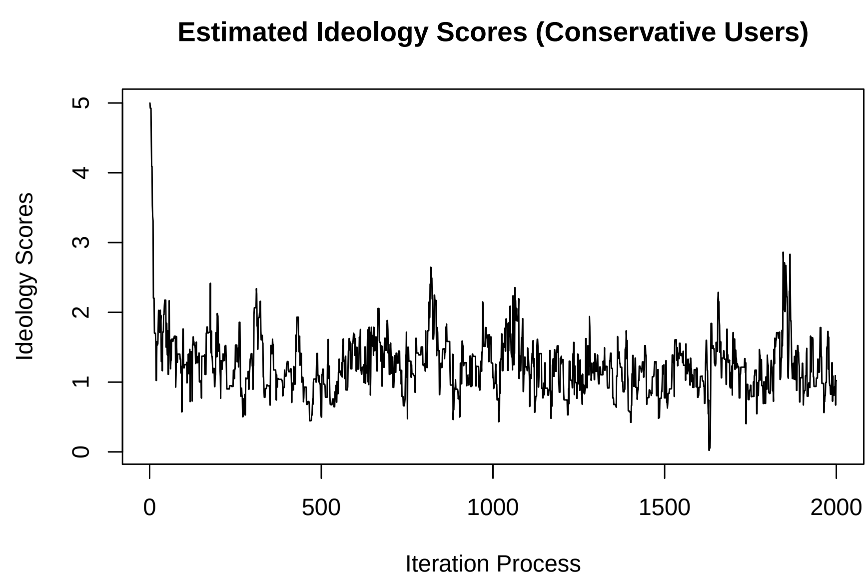
```
#This user approximately follows 45 Republican Senators and 10 Democrat Senators.
Data_user<-as.data.frame(matrix(c(ifelse(runif(50)<.1,0,1),ifelse(runif(50)<.8,0,1))), 100, 1)
colnames(Data_user)<-c("R_User")
Data_combined<-cbind(Data_Elites,Data_user)

X_data<-Data_combined$Elite_ideology
Y_data<-Data_combined$R_User

fit_C<-Bayes_logit(Y_data,X_data)
fit_C$acceptance_rate
```

```
## [1] 0.1740870 0.5127564
```

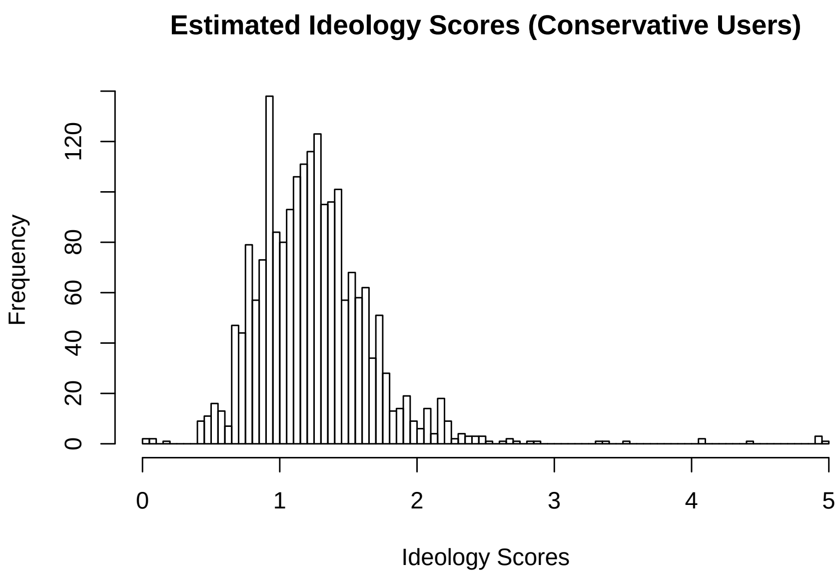
```
plot(fit_C$theta[,1],main="Constant (Conservative Users)",
     xlab="Iteration Process",ylab="Estimated Scores",type="l")
```




```
plot(fit_C$theta[,2],main="Estimated Ideology Scores (Conservative Users)",
     xlab="Iteration Process",ylab="Ideology Scores",type="l")
```



```
hist(fit_C$theta[,2],main="Estimated Ideology Scores (Conservative Users)",
     xlab="Ideology Scores",breaks = 100)
```



3.4 Simulating Data of Liberal Users on Twitter and Model Testing

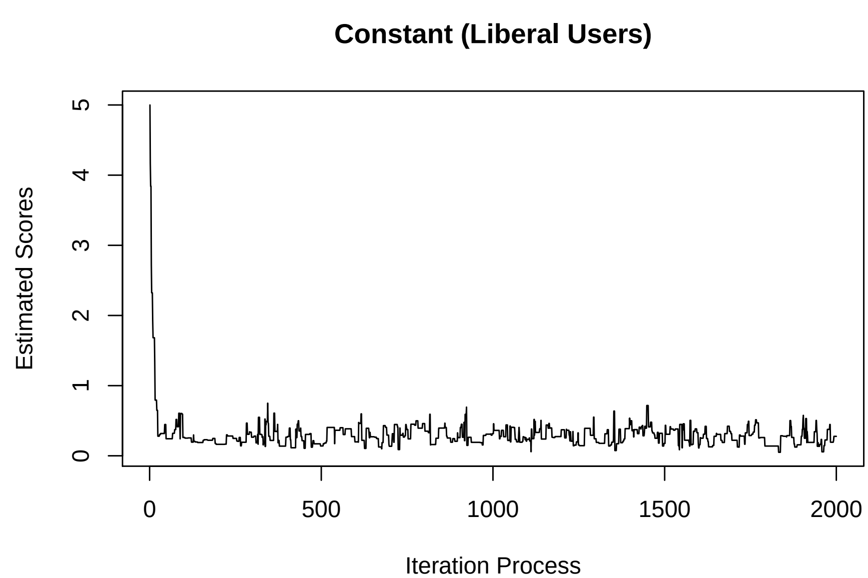
To further verify the Metropolis Hastings algorithm, I plan to test the opposite estimate. Specifically, assume that we observe another user, who is more liberal. To simulate Twitter following data for this user, I assign this user to follow more Democrat senators. In this case, we would expect to see a negative value for their estimated ideology. As we can see in the histogram shown below, as expected, the estimated value is negative, providing convergent evidence for the model and the algorithm.

```
#This user approximately follows 10 Republican Senators and 45 Democrat Senators.
Data_user<-as.data.frame(matrix(c(ifelse(runif(50)<.8,0,1),ifelse(runif(50)<.1,0,1))), 100, 1)
colnames(Data_user)<-c("L_User")
Data_combined<-cbind(Data_Elites,Data_user)

X_data<-Data_combined$Elite_ideology
Y_data<-Data_combined$L_User
```

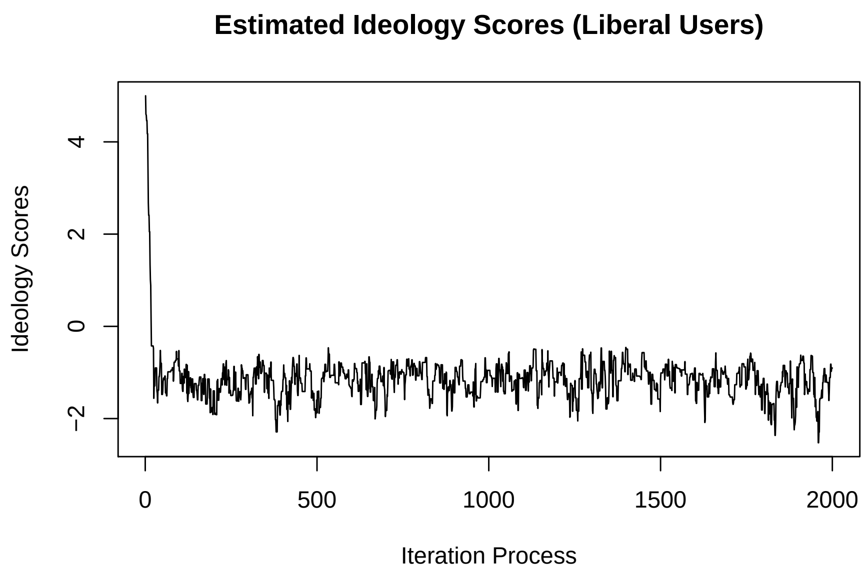
```
fit_L<-Bayes_logit(Y_data,X_data)
fit_L$acceptance_rate
```

```
## [1] 0.2021011 0.4917459
```

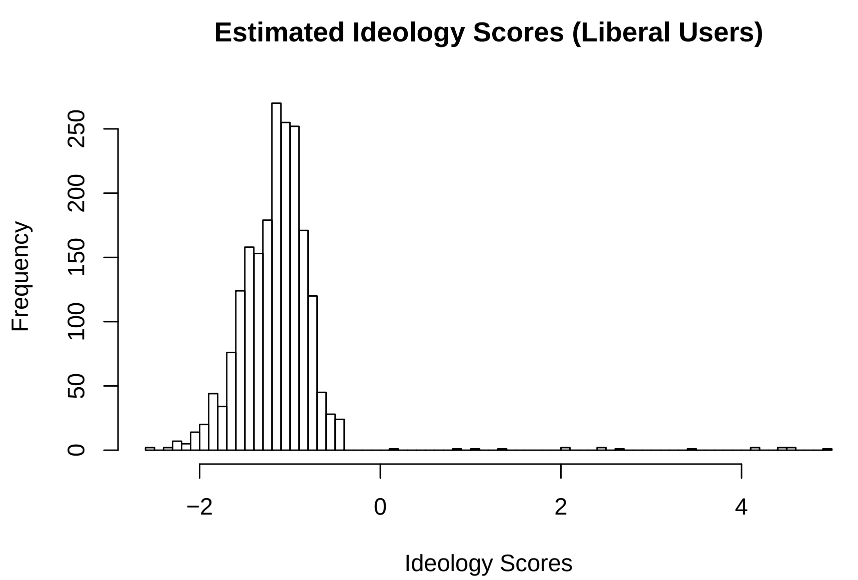
```
plot(fit_L$theta[,1],main="Constant (Liberal Users)",
     xlab="Iteration Process",ylab="Estimated Scores",type="l")
```




```
plot(fit_L$theta[,2],main="Estimated Ideology Scores (Liberal Users)",
     xlab="Iteration Process",ylab="Ideology Scores",type="l")
```




```r
hist(fit_L$theta[,2],main="Estimated Ideology Scores (Liberal Users)",
     xlab="Ideology Scores",breaks = 100)
```



Chapter 4

Linear Mixed Models

The following is a shortened version of Jonathan Rosenblatt's LMM tutorial. http://www.john-ros.com/Rcourse/lme.html.

In addition, another reference is from Douglas Bates's R package document. https://cran.r-project.org/web/packages/lme4/vignettes/lmer.pdf?fbclid=IwAR1nmmRP9A0BrhKdgBibNjM5acR_spTpXV8QlQGdmTWyQz3ZtV3LYn6kCbQ

Assume that y is a function of x and u, where x is the fixed effect and u is the random effect. Thus, we can get,

$$y|x, u = x'\beta + z'u + \epsilon$$

For random effect, one example can be that you want to test the treatment effect, and sample 8 observations from 4 groups. You measure before and after the treatment. In this case, x represents the treatment effect, whereas z represents the group effect (i.e., random effect). Note that, in this case, it reminds the paired t-test. Remember in SPSS, why do we do paired t-test? Typically, it is the case when we measure a subject (or, participant) twice. In this case, we can consider each participant as an unit of random effect (rather than as group in the last example.)

4.1 Calculate mean

The following code generates 4 numbers ($N(0, 10)$) for 4 groups. Then, replicate it within each group.That is, in the end, there are 8 observations.

Note that, in the following code, there are no "independent variables". Both the linear model and mixed model are actually just trying to calculate the mean. Note that lmer(y~1+1|groups) and lmer(y~1|groups) will generate the same results.

```
set.seed(123)
n.groups <- 4 # number of groups
n.repeats <- 2 # samples per group
#Generating index for observations belong to the same group
groups <- as.factor(rep(1:n.groups, each=n.repeats))
n <- length(groups)
#Generating 4 random numbers, assuming normal distribution
z0 <- rnorm(n.groups, 0, 10)
z <- z0[as.numeric(groups)] # generate and inspect random group effects
z
```

```
## [1] -5.6047565 -5.6047565 -2.3017749 -2.3017749 15.5870831 15.5870831  0.7050839
## [8]  0.7050839
```

```
epsilon <- rnorm(n,0,1) # generate measurement error
beta0 <- 2 # this is the actual parameter of interest! The global mean.
y <- beta0 + z + epsilon # sample from an LMM

# fit a linear model assuming independence
# i.e., assume that there is no "group things".
lm.5 <- lm(y~1)

# fit a mixed-model that deals with the group dependence
#install.packages("lme4")
library(lme4)
lme.5.a <- lmer(y~1+1|groups)
lme.5.b <- lmer(y~1|groups)
lm.5
```

```
##
## Call:
## lm(formula = y ~ 1)
##
## Coefficients:
## (Intercept)
##       4.283
```

```
lme.5.a
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: y ~ 1 + 1 | groups
## REML criterion at convergence: 36.1666
## Random effects:
##  Groups   Name        Std.Dev.
```

```
##  groups   (Intercept) 8.8521
##  Residual             0.8873
## Number of obs: 8, groups:  groups, 4
## Fixed Effects:
## (Intercept)
##       4.283
```

```
lme.5.b
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: y ~ 1 | groups
## REML criterion at convergence: 36.1666
## Random effects:
##  Groups   Name        Std.Dev.
##  groups   (Intercept) 8.8521
##  Residual             0.8873
## Number of obs: 8, groups:  groups, 4
## Fixed Effects:
## (Intercept)
##       4.283
```

4.2 Test the treatment effect

As we can see that, LLM and paired t-test generate the same t-value.

```
times<-rep(c(1,2),4) # first time and second time
times
```

```
## [1] 1 2 1 2 1 2 1 2
```

```
data_combined<-cbind(y,groups,times)
data_combined
```

```
##               y groups times
## [1,] -3.4754687      1     1
## [2,] -1.8896915      1     2
## [3,]  0.1591413      2     1
## [4,] -1.5668361      2     2
## [5,] 16.9002303      3     1
## [6,] 17.1414212      3     2
## [7,]  3.9291657      4     1
## [8,]  3.0648977      4     2
```

```r
lme_diff_times<- lmer(y~times+(1|groups))


t_results<-t.test(y~times, paired=TRUE)

lme_diff_times
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: y ~ times + (1 | groups)
## REML criterion at convergence: 35.0539
## Random effects:
##  Groups   Name        Std.Dev.
##  groups   (Intercept) 8.845
##  Residual             1.013
## Number of obs: 8, groups:  groups, 4
## Fixed Effects:
## (Intercept)        times
##      4.5691      -0.1908
```

```r
print("The following results are from paired t-test")
```

```
## [1] "The following results are from paired t-test"
```

```r
t_results$statistic
```

```
##         t
## 0.2664793
```

4.3 Another example

```r
data(Dyestuff, package='lme4')
attach(Dyestuff)
```

```
## The following objects are masked from Dyestuff (pos = 5):
##
##     Batch, Yield
```

```r
Dyestuff
```

```
##    Batch Yield
## 1      A  1545
## 2      A  1440
## 3      A  1440
## 4      A  1520
## 5      A  1580
## 6      B  1540
## 7      B  1555
## 8      B  1490
## 9      B  1560
## 10     B  1495
## 11     C  1595
## 12     C  1550
## 13     C  1605
## 14     C  1510
## 15     C  1560
## 16     D  1445
## 17     D  1440
## 18     D  1595
## 19     D  1465
## 20     D  1545
## 21     E  1595
## 22     E  1630
## 23     E  1515
## 24     E  1635
## 25     E  1625
## 26     F  1520
## 27     F  1455
## 28     F  1450
## 29     F  1480
## 30     F  1445
```

```r
lme_batch<- lmer( Yield ~ 1 + (1|Batch)  , Dyestuff )
summary(lme_batch)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Yield ~ 1 + (1 | Batch)
##    Data: Dyestuff
##
## REML criterion at convergence: 319.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4117 -0.7634  0.1418  0.7792  1.8296
##
```

```
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Batch    (Intercept) 1764     42.00
##  Residual             2451     49.51
## Number of obs: 30, groups:  Batch, 6
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  1527.50      19.38    78.8
```

4.4 Full LMM model

In the following, I used the data from the package of lme4. For Days + (1 | Subject), it only has random intercept; in contrast, Days + (Days| Subject) has both random intercept and random slope for Days. Note that, random effects do not generate specific slopes for each level of Days, but rather just a variance of all the slopes.

Therefore, we can see that "Days + (Days| Subject)" and "Days + (1+Days| Subject)" generate the same results. For more discussion, you can refer to the following link: https://www.jaredknowles.com/journal/2013/11/25/getting-started-with-mixed-effect-models-in-r

```
data(sleepstudy, package='lme4')
attach(sleepstudy)
```

```
## The following objects are masked from sleepstudy (pos = 5):
##
##     Days, Reaction, Subject
```

```
fm1 <- lmer(Reaction ~ Days + (1 | Subject), sleepstudy)
summary(fm1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Reaction ~ Days + (1 | Subject)
##    Data: sleepstudy
##
## REML criterion at convergence: 1786.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2257 -0.5529  0.0109  0.5188  4.2506
##
```

```
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Subject  (Intercept) 1378.2   37.12
##  Residual              960.5   30.99
## Number of obs: 180, groups:  Subject, 18
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept) 251.4051     9.7467   25.79
## Days         10.4673     0.8042   13.02
##
## Correlation of Fixed Effects:
##      (Intr)
## Days -0.371
```

```r
fm2<-lmer ( Reaction ~ Days + ( Days| Subject ) , data= sleepstudy )
summary(fm2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Reaction ~ Days + (Days | Subject)
##    Data: sleepstudy
##
## REML criterion at convergence: 1743.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.9536 -0.4634  0.0231  0.4633  5.1793
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  Subject  (Intercept) 611.90   24.737
##           Days         35.08    5.923   0.07
##  Residual             654.94   25.592
## Number of obs: 180, groups:  Subject, 18
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  251.405      6.824  36.843
## Days          10.467      1.546   6.771
##
## Correlation of Fixed Effects:
##      (Intr)
## Days -0.138
```

```
fm3<-lmer ( Reaction ~ Days + (1+Days| Subject ) , data= sleepstudy )
summary(fm3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Reaction ~ Days + (1 + Days | Subject)
##    Data: sleepstudy
##
## REML criterion at convergence: 1743.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.9536 -0.4634  0.0231  0.4633  5.1793
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  Subject  (Intercept) 611.90   24.737
##           Days         35.08    5.923   0.07
##  Residual             654.94   25.592
## Number of obs: 180, groups:  Subject, 18
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  251.405      6.824  36.843
## Days          10.467      1.546   6.771
##
## Correlation of Fixed Effects:
##      (Intr)
## Days -0.138
```

4.5 Serial correlations in time and space

The hierarchical model of $y|x, u = x'\beta + z'u + \epsilon$ can work well for correlations within blocks, but not for correlations in time as the correlations decay in time. The following uses nlme package to calculate time serial data.

```
library(nlme)
head(nlme::Ovary,n=50)
```

```
## Grouped Data: follicles ~ Time | Mare
##    Mare        Time follicles
## 1     1 -0.13636360        20
## 2     1 -0.09090910        15
## 3     1 -0.04545455        19
```

```
## 4      1  0.00000000         16
## 5      1  0.04545455         13
## 6      1  0.09090910         10
## 7      1  0.13636360         12
## 8      1  0.18181820         14
## 9      1  0.22727270         13
## 10     1  0.27272730         20
## 11     1  0.31818180         22
## 12     1  0.36363640         15
## 13     1  0.40909090         18
## 14     1  0.45454550         17
## 15     1  0.50000000         14
## 16     1  0.54545450         18
## 17     1  0.59090910         14
## 18     1  0.63636360         16
## 19     1  0.68181820         17
## 20     1  0.72727270         18
## 21     1  0.77272730         18
## 22     1  0.81818180         17
## 23     1  0.86363640         14
## 24     1  0.90909090         12
## 25     1  0.95454550         12
## 26     1  1.00000000         14
## 27     1  1.04545500         10
## 28     1  1.09090900         11
## 29     1  1.13636400         16
## 30     2 -0.15000000          6
## 31     2 -0.10000000          6
## 32     2 -0.05000000          8
## 33     2  0.00000000          7
## 34     2  0.05000000         16
## 35     2  0.10000000         10
## 36     2  0.15000000         13
## 37     2  0.20000000          9
## 38     2  0.25000000          7
## 39     2  0.30000000          6
## 40     2  0.35000000          8
## 41     2  0.40000000          8
## 42     2  0.45000000          6
## 43     2  0.50000000          8
## 44     2  0.55000000          7
## 45     2  0.60000000          9
## 46     2  0.65000000          6
## 47     2  0.70000000          4
## 48     2  0.75000000          5
## 49     2  0.80000000          8
```

```
## 50    2  0.85000000        11
```

```
fm1Ovar.lme <- nlme::lme(fixed=follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                   data = Ovary,
                   random = pdDiag(~sin(2*pi*Time)),
                   correlation=corAR1() )
summary(fm1Ovar.lme)
```

```
## Linear mixed-effects model fit by REML
##  Data: Ovary
##        AIC     BIC   logLik
##   1563.448 1589.49 -774.724
##
## Random effects:
##  Formula: ~sin(2 * pi * Time) | Mare
##  Structure: Diagonal
##         (Intercept) sin(2 * pi * Time) Residual
## StdDev:    2.858385           1.257977 3.507053
##
## Correlation Structure: AR(1)
##  Formula: ~1 | Mare
##  Parameter estimate(s):
##       Phi
## 0.5721866
## Fixed effects: follicles ~ sin(2 * pi * Time) + cos(2 * pi * Time)
##                        Value Std.Error  DF   t-value p-value
## (Intercept)        12.188089 0.9436602 295 12.915760  0.0000
## sin(2 * pi * Time) -2.985297 0.6055968 295 -4.929513  0.0000
## cos(2 * pi * Time) -0.877762 0.4777821 295 -1.837159  0.0672
##  Correlation:
##                    (Intr) s(*p*T
## sin(2 * pi * Time)  0.000
## cos(2 * pi * Time) -0.123  0.000
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.34910093 -0.58969626 -0.04577893  0.52931186  3.37167486
##
## Number of Observations: 308
## Number of Groups: 11
```

Chapter 5

Generalized Linear Mixed Models

5.1 Basics

The following is the note from Charle E. McCulloch's "Maximum likelihood algorithems for Generalized Linear Mixed Models"

5.2 Some References

http://www.biostat.umn.edu/~baolin/teaching/linmods/glmm.html

http://www.biostat.umn.edu/~baolin/teaching/probmods/GLMM_mcmc.html

https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html