Lab 8

Jun Rao

10/21/2019

```
#-------------------------------------
#-------------------------------------
# Import/Load the rstan library:
library(tidyverse)
library(rstan)
library(loo)
rstan_options(auto_write = TRUE)
options(mc.cores = parallel::detectCores())
#-------------------------------------
#-------------------------------------
```

Random effects & Simpson's paradox

In this assignment, we will learn an important lesson about why accounting for group-level differences is essential in your analyses. I have provided you with a data set () that has one outcome variable, one input variable, and one group-level identifier. Note that the input variable has been centered and scaled for you.

Your tasks (35 points)

1.Import your data into R.

```
# Read in the .CSV file:
df = read_csv("lab8_data.csv")

#observations
n_sample = nrow(df)

#number of groups
n_group = length(unique(df$group_idx))

#y
y = df$y_obs

#x
x = df$x_scaled

#group_idx
group_idx = df$group_idx
```

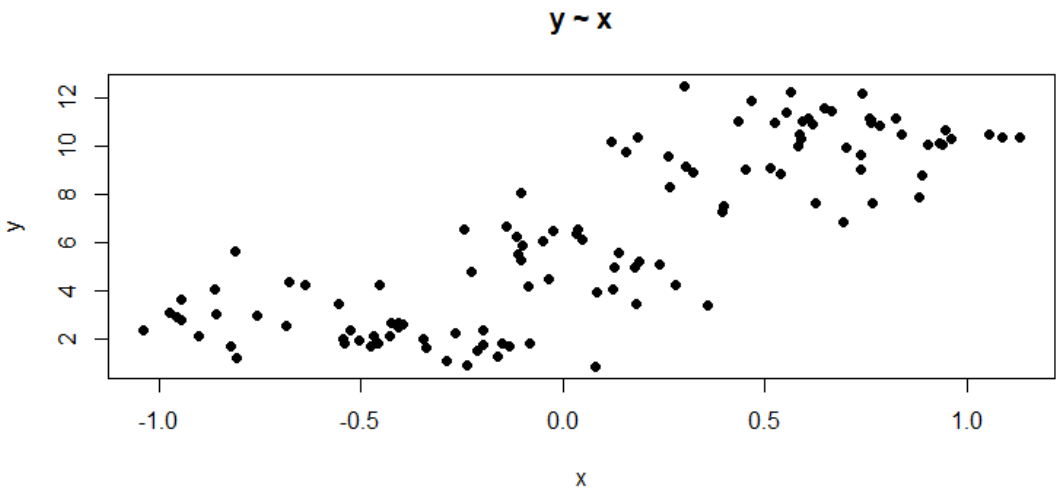
```
head(df)
```

```
## # A tibble: 6 x 3
##   y_obs x_scaled group_idx
##   <dbl>    <dbl>     <dbl>
## 1  1.78   -0.540         1
## 2  2.09   -0.901         1
## 3  2.33   -1.04          1
## 4  1.21   -0.807         1
## 5  2.88   -0.957         1
## 6  2.96   -0.756         1
```

2.Create two scatterplots (5 points):

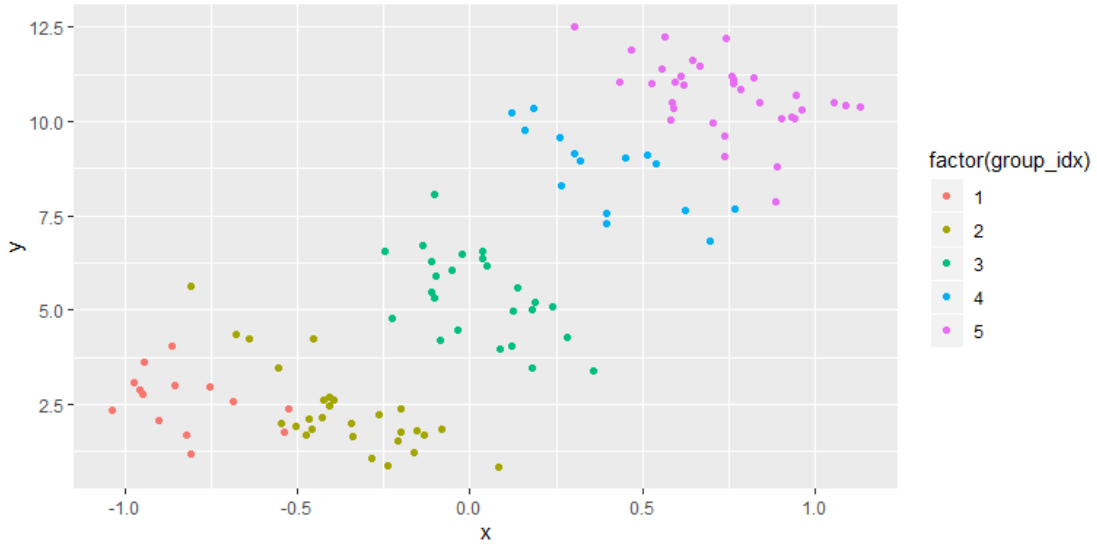
(a) A scatterplot with distinction between groups

```
plot(x, y, main="y ~ x",xlab="x", ylab="y", pch=19)
```



(b) A scatterplot with data from specific groups that are clearly distinct

```
ggplot(df, aes(x , y , color = factor(group_idx))) +
  geom_point(shape = 19)
```



3.Fit a linear regression with complete pooling (i.e., no distinction between groups). Write a brief interpretation about the linear relationship between the input and the outcome variable. In other words, interpret the slope parameter. (10 points)

```
stan_data_1 = list(n_sample = n_sample,
                   x_vec = x,
                   y_vec = y)

params_monitor = c("beta", "alpha", "sigma_resid", "log_lik")

test_fit_1 = stan(file = "LinReg.stan",
                  data = stan_data_1,
                  pars = params_monitor,
                  chains = 1, # How many chains to run
                  iter = 10, # How many iterations per chain
                  algorithm="NUTS")

##
## SAMPLING FOR MODEL 'LinReg' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would tak
e 0 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: WARNING: No variance estimation is
## Chain 1:          performed for num_warmup < 20
## Chain 1:
## Chain 1: Iteration: 1 / 10 [ 10%]  (Warmup)
## Chain 1: Iteration: 2 / 10 [ 20%]  (Warmup)
## Chain 1: Iteration: 3 / 10 [ 30%]  (Warmup)
## Chain 1: Iteration: 4 / 10 [ 40%]  (Warmup)
```

```
## Chain 1: Iteration: 5 / 10 [ 50%]  (Warmup)
## Chain 1: Iteration: 6 / 10 [ 60%]  (Sampling)
## Chain 1: Iteration: 7 / 10 [ 70%]  (Sampling)
## Chain 1: Iteration: 8 / 10 [ 80%]  (Sampling)
## Chain 1: Iteration: 9 / 10 [ 90%]  (Sampling)
## Chain 1: Iteration: 10 / 10 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 0.001 seconds (Warm-up)
## Chain 1:                0 seconds (Sampling)
## Chain 1:                0.001 seconds (Total)
## Chain 1:
```

```
## Now we will run our full model:
# How many samples do we want of each parameter, from each chain?
n_mc_samples = 1000
# How much burn-in?
n_burn = 500
# How much thinning? (take the ith value of the chain)
n_thin = 3
# Total iterations needed:
n_iter_total = (n_mc_samples * n_thin) + n_burn
model_fit_1 =
 stan(fit = test_fit_1, # So it knows we're already compiled
      file = "LinReg.stan",
      data = stan_data_1,
      pars = params_monitor,
      chains = 3,
      warmup = n_burn,
      thin = n_thin,
      iter = n_iter_total,
       algorithm="NUTS")
model_out_1 = rstan::extract(model_fit_1)
str(model_out_1)
```

```
## List of 5
##  $ beta       : num [1:3000(1d)] 5.16 4.36 5.25 5.28 5.21 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
##  $ alpha      : num [1:3000(1d)] 6.04 5.79 5.87 5.62 5.39 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
##  $ sigma_resid: num [1:3000(1d)] 2.34 2.33 2.12 1.92 2.09 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
##  $ log_lik    : num [1:3000, 1:117] -1.97 -2.02 -1.85 -1.7 -1.73 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ iterations: NULL
##   .. ..$           : NULL
##  $ lp__       : num [1:3000(1d)] -265 -267 -263 -265 -266 ...
```

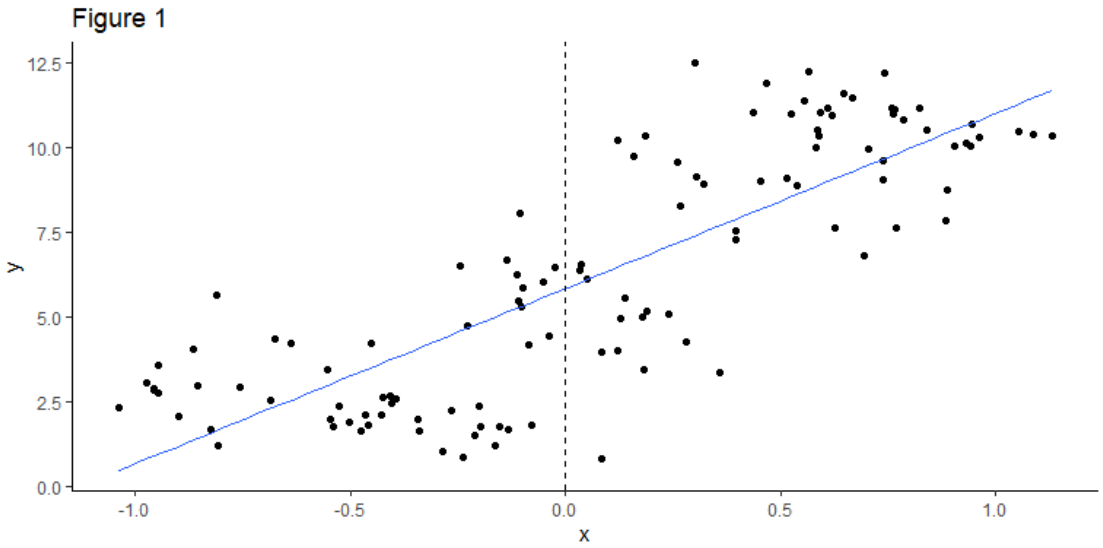
```
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL

#the 95% credible intervals
beta_CI = c(summary(model_fit_1)$summary[1:1, "2.5%"],summary(model_fit_1)$su
mmary[1:1, "97.5%"])
beta_CI

## [1] 4.498770 5.827031
```

The 95% credible intervals of beta which is the slope is between 4.527 and 5.857. It means 0 is not included in the 95% credible intervals. Hence, there is a linear relatiionship between the input and the outcome variable. More details can see next graphic (Figuure1).

```
#draw the graphics for each group
ggplot(df, aes(x, y)) +
  ggtitle("Figure 1")+
  geom_point(shape = 19) +
  geom_smooth(method = "lm", se = FALSE, size = 0.2) +
  scale_color_brewer(palette = "Set1") +
  geom_vline(xintercept = 0, linetype = 2) +
  theme_classic()
```



4.Fit a linear regression with partial pooling. Specifically, allow a random intercept per group. Again, write a brief interpretation about this linear regression. How has your conclusion changed compared to the outcome in Task 3? (10 points)

```
stan_data_2 = list(n_sample = n_sample,
                   n_group = n_group,
                   y_vec = y,
                   x_vec = x,
                   group_idx = group_idx)
```

```
params_monitor = c("beta", "alpha_mean", "eta_alpha", "alpha_sigma", "sigma_r
esid", "log_lik")

test_fit_2 = stan( file = "Intercepts_LinReg.stan",
                   data = stan_data_2,
                   pars = params_monitor,
                   chains = 1,
                   iter = 10,
                   algorithm="NUTS")

##
## SAMPLING FOR MODEL 'Intercepts_LinReg' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would tak
e 0 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: WARNING: No variance estimation is
## Chain 1:          performed for num_warmup < 20
## Chain 1:
## Chain 1: Iteration: 1 / 10 [ 10%]  (Warmup)
## Chain 1: Iteration: 2 / 10 [ 20%]  (Warmup)
## Chain 1: Iteration: 3 / 10 [ 30%]  (Warmup)
## Chain 1: Iteration: 4 / 10 [ 40%]  (Warmup)
## Chain 1: Iteration: 5 / 10 [ 50%]  (Warmup)
## Chain 1: Iteration: 6 / 10 [ 60%]  (Sampling)
## Chain 1: Iteration: 7 / 10 [ 70%]  (Sampling)
## Chain 1: Iteration: 8 / 10 [ 80%]  (Sampling)
## Chain 1: Iteration: 9 / 10 [ 90%]  (Sampling)
## Chain 1: Iteration: 10 / 10 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 0 seconds (Warm-up)
## Chain 1:                0.001 seconds (Sampling)
## Chain 1:                0.001 seconds (Total)
## Chain 1:

## Now we will run our full model:
# How many samples do we want of each parameter, from each chain?
n_mc_samples = 1000
# How much burn-in?
n_burn = 500
# How much thinning? (take the ith value of the chain)
n_thin = 3
# Total iterations needed:
n_iter_total = (n_mc_samples * n_thin) + n_burn
model_fit_2 =
stan(fit = test_fit_2, # So it knows we're already compiled
```

```
     file = "Intercepts_LinReg.stan",
     data = stan_data_2,
     pars = params_monitor,
     chains = 3,
     warmup = n_burn,
     thin = n_thin,
     iter = n_iter_total,
     algorithm="NUTS")
model_out_2 = rstan::extract(model_fit_2)
str(model_out_2)
```

```
## List of 7
##  $ beta       : num [1:3000(1d)] -3.29 -3.05 -2.84 -3.48 -3.44 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
##  $ alpha_mean : num [1:3000(1d)] 10.39 5.76 5.56 6.15 9.47 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
##  $ eta_alpha  : num [1:3000, 1:5] -10.71 -5.9 -5.52 -6.45 -9.63 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ iterations: NULL
##   .. ..$           : NULL
##  $ alpha_sigma: num [1:3000(1d)] 7.08 5.59 5.37 4.63 5.5 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
##  $ sigma_resid: num [1:3000(1d)] 0.83 0.843 0.921 0.798 0.847 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
##  $ log_lik    : num [1:3000, 1:117] -0.812 -0.803 -0.861 -0.73 -0.758 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ iterations: NULL
##   .. ..$           : NULL
##  $ lp__       : num [1:3000(1d)] -48.9 -46.4 -48.6 -45.7 -48.6 ...
##   ..- attr(*, "dimnames")=List of 1
##   .. ..$ iterations: NULL
```

```
#summary(model_fit_2)$summary
#first we visualize tabularly, the 95% CI for estimated parameters and compar
e these the the true values
model_sum = summary(model_fit_2)$summary
model_sum[c(1:9),c(4,6,8)]
```

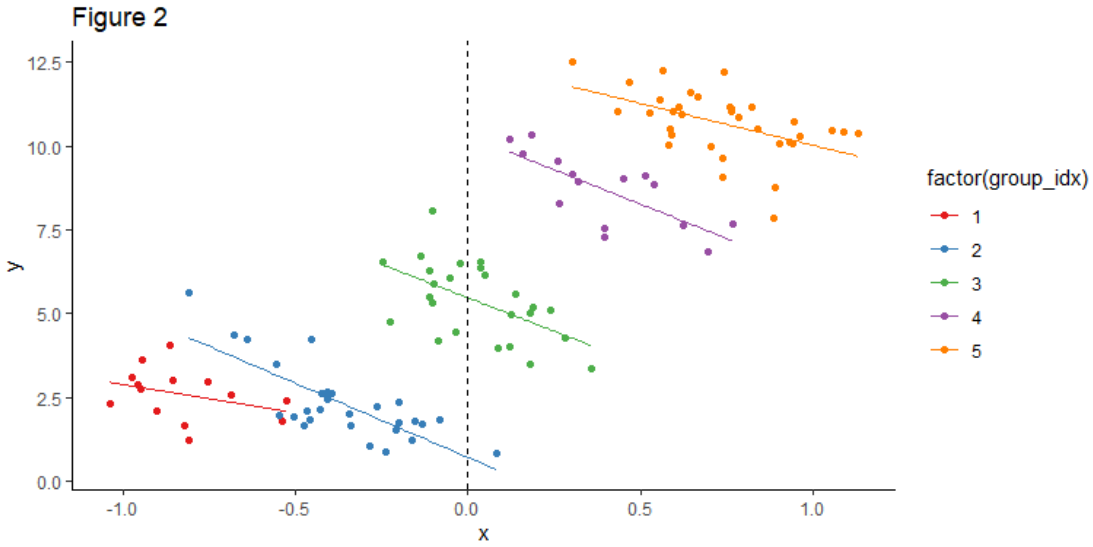
```
##                      2.5%        50%      97.5%
## beta          -4.2255768 -3.3612860 -2.4824869
## alpha_mean    -0.8538509  5.9136786 12.4329932
## eta_alpha[1] -12.5813342 -6.1110159  0.6856631
## eta_alpha[2] -11.3661183 -4.8081377  1.8366116
## eta_alpha[3]  -7.0311699 -0.4578394  6.3970286
## eta_alpha[4]  -2.3131249  4.0601165 10.8479128
## eta_alpha[5]   0.8007318  7.1830648 13.9409152
```

```
## alpha_sigma    3.2751447  5.7082367 13.1918307
## sigma_resid    0.7391743  0.8394490  0.9660167

# we can see that few parameters were adequately recoverd. This included alph
a_mean and all of the eta_alphas (9 of 12 params)
```

The 95% credible intervals of beta which is the slope is between -4.171 and -2.473. For each group, it has differnent interception. In task 3, we can find that the slope for all the data is a positive number, however, when we analysis each single group, the slope is a negative number. From Figure 2, we can find it intuitively.

```
#draw the graphics for each group
ggplot(df, aes(x, y, color = factor(group_idx))) +
  ggtitle("Figure 2")+
  geom_point(shape = 19) +
  geom_smooth(method = "lm", se = FALSE, size = 0.2) +
  scale_color_brewer(palette = "Set1") +
  geom_vline(xintercept = 0, linetype = 2) +
  theme_classic()
```



5.Compare your two models using the LOO-IC. Which model provides a more parsimonious explanation of the data? Interpret what this means. (5 points)

```
# Calculate the LOO and WAIC for a single model:
# Full model
log_lik_1 = extract_log_lik(model_fit_1)
loo_1 = loo(log_lik_1)
loo_1$estimates

##              Estimate         SE
## elpd_loo -254.306013  6.5730454
```

```
## p_loo       2.490803  0.3251701
## looic     508.612026 13.1460909

# reduced, intercept RE model
log_lik_2 = extract_log_lik(model_fit_2)
loo_2 = loo(log_lik_2)
loo_2$estimates

##             Estimate         SE
## elpd_loo -148.902259  7.4904658
## p_loo       6.613833  0.9253659
## looic     297.804519 14.9809316

# model comparison of loo
loo::compare(loo_1, loo_2)

## elpd_diff        se
##     105.4       9.8
```

Based on the p_loo values for both models, the estimate 2.46 is lower than the intercept RE model. Additionally, the elpd_loo is lower but not significant because SE ranges overlap for both model estimate of elpd_loo. Therefore, we can conclude that the reduced model is more parsimonious because p_loo is still greater than the number of parameters.

6.This assignment has shown an example of Simpson's Paradox. Look up this term and write a brief interpretation of how it applies to this assignment. What have you learned? (5 points)

Such as we described in the previous questions, we find that if we analysis all the data, the slope in the Figure 1 is postive, however, when we analysis by the group, the slope for each group is negative see Figure 2.