Applied Bayesian Modeling - module 7

Leontine Alkema

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1 Read in radon data

Read in the radon data and process (copied from earlier module)

```
# house level data
d <- read.table(url("http://www.stat.columbia.edu/~gelman/arm/examples/radon/srrs2.dat"),
                header=T, sep=",")

# deal with zeros, select what we want, make a fips (county) variable to match on
d <- d %>%
  mutate(activity = ifelse(activity==0, 0.1, activity)) %>%
  mutate(fips = stfips * 1000 + cntyfips) %>%
  dplyr::select(fips, state, county, floor, activity)

# county level data
cty <- read.table(url("http://www.stat.columbia.edu/~gelman/arm/examples/radon/cty.dat"),
                  header = T, sep = ",")
cty <-
  cty %>%
  mutate(fips = 1000 * stfips + ctfips) %>%
  dplyr::select(fips, Uppm) %>%
  rename(ura_county = (Uppm))

dmn <- d %>%
  filter(state=="MN") %>% # Minnesota data only
  dplyr::select(fips, county, floor, activity) %>%
  left_join(cty)
```

1.1 More data processing for multilevel modeling

Some more data processing first, to produce a data set that has county info and to produce the plot with means from the slides. In the data set:

- y_i is log(activity)
- county gives county name (fips gives the unique county ID)
- x_i is floor
- u_i is log_ur = log(ura_county)

(the last two are added for module 8, when including predictors)

```r
dat <-
  dmn%>%
  mutate(y = log(activity), log_ur = log(ura_county))
head(dat)
```

```
##    fips               county floor activity ura_county         y     log_ur
## 1 27001 AITKIN                   1      2.2   0.502054 0.7884574 -0.6890476
## 2 27001 AITKIN                   0      2.2   0.502054 0.7884574 -0.6890476
## 3 27001 AITKIN                   0      2.9   0.502054 1.0647107 -0.6890476
## 4 27001 AITKIN                   0      1.0   0.502054 0.0000000 -0.6890476
## 5 27003 ANOKA                    0      3.1   0.428565 1.1314021 -0.8473129
## 6 27003 ANOKA                    0      2.5   0.428565 0.9162907 -0.8473129
```

Create summary data set with info for each county:

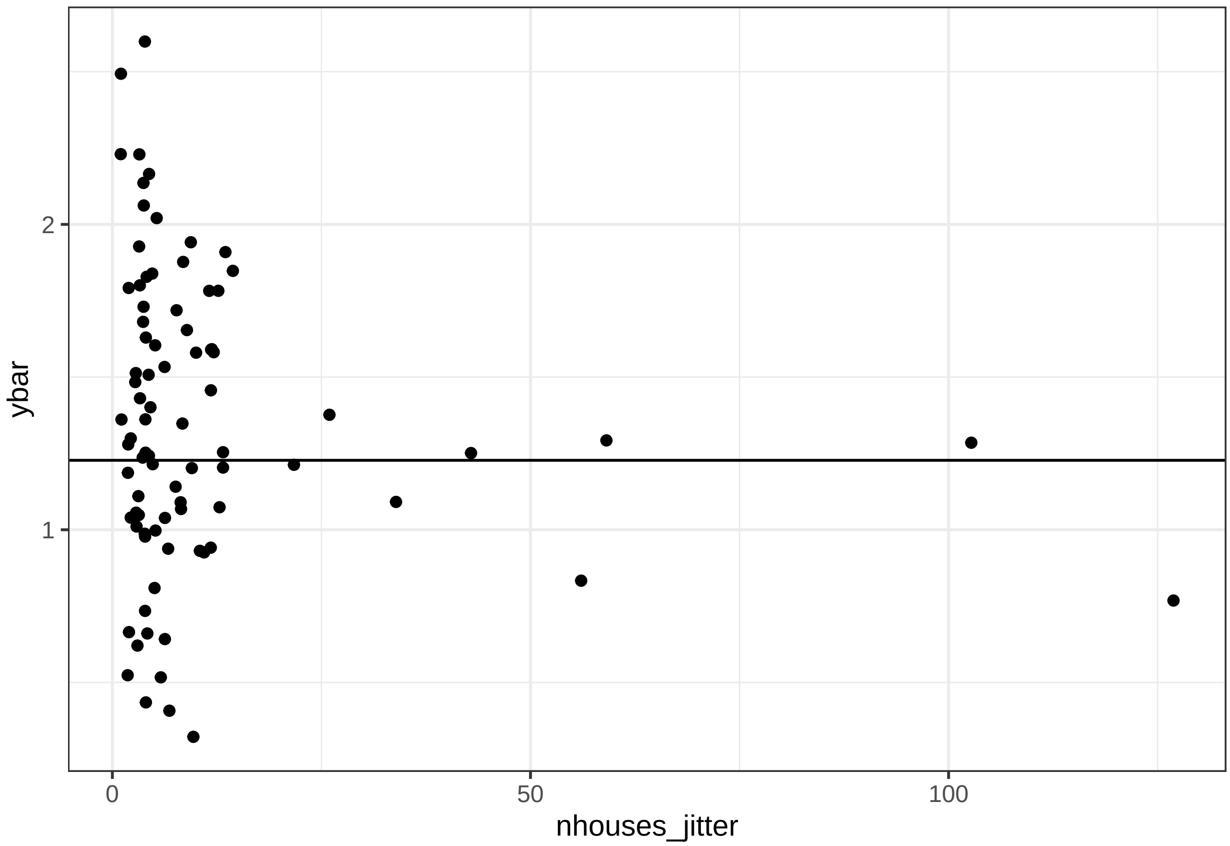
```r
# to plot observations and county means ~ sample sizes,
# easier to see if sample sizes are slighly jittered
set.seed(12345)

datcounty <- dat %>%
  group_by(fips) %>%
  summarize(nhouses = n(), ybar = mean(y), county = county[1], log_ur = log_ur[1]) %>%
  mutate(nhouses_jitter = nhouses*exp(runif (length(nhouses), -.1, .1)))
ngroups <- dim(datcounty)[1]
head(datcounty)
```

```
## # A tibble: 6 x 6
##    fips nhouses  ybar county                  log_ur nhouses_jitter
##   <dbl>   <int> <dbl> <chr>                    <dbl>          <dbl>
## 1 27001       4 0.660 "AITKIN              " -0.689           4.18
## 2 27003      52 0.833 "ANOKA               " -0.847          56.1
## 3 27005       3 1.05  "BECKER              " -0.113           3.16
## 4 27007       7 1.14  "BELTRAMI            " -0.593           7.56
## 5 27009       4 1.25  "BENTON              " -0.143           3.97
## 6 27011       3 1.51  "BIG STONE           "  0.387           2.81
```

```r
ybarbar <- mean(dat$y) # population (here state) mean
```

```r
datcounty %>%
  ggplot(aes(x = nhouses_jitter, y = ybar)) +
  geom_point() +
  geom_hline(mapping = aes(yintercept = ybarbar)) +
  theme_bw()
```



2 Model fitting

```
fit <- brm(y ~ (1|county),
        data = dat,
        file = "output/mod7ex2",
        iter = 1000,
        chains = 4,
        cores = getOption("mc.cores", 4))
```

Summary of model fit:

```
summary(fit)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: y ~ (1 | county)
##    Data: dat (Number of observations: 927)
##   Draws: 4 chains, each with iter = 1000; warmup = 500; thin = 1;
##          total post-warmup draws = 2000
##
## Group-Level Effects:
## ~county (Number of levels: 85)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
```

```
## sd(Intercept)     0.32      0.05     0.23     0.42 1.00      804     1189
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept     1.32      0.05     1.22     1.42 1.00     1242     1326
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     0.81      0.02     0.77     0.85 1.00     3773     1593
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

3 Visualizing the group-level mean parameters

Coefficients can be obtained using coef(fit), you can get the help file here:

```
#?coef.brmsfit
```

Just showing some function calls here first, ie for mu_alpha:

```
fixef(fit)
```

```
##           Estimate  Est.Error     Q2.5   Q97.5
## Intercept 1.317962 0.05025675 1.224561 1.41716
```

eta = alpha - mu_alpha (as compared to notation in slides), labeled here as random effects

```
eta <- as_tibble(ranef(fit)$county[,,"Intercept"], rownames = "county")
head(eta)
```

```
## # A tibble: 6 x 5
##   county                Estimate Est.Error   Q2.5  Q97.5
##   <chr>                    <dbl>     <dbl>  <dbl>  <dbl>
## 1 "AITKIN              "  -0.256      0.251 -0.772  0.238
## 2 "ANOKA               "  -0.430      0.114 -0.658 -0.212
## 3 "BECKER              "  -0.0834     0.260 -0.604  0.423
## 4 "BELTRAMI            "  -0.0919     0.214 -0.503  0.323
## 5 "BENTON              "  -0.0261     0.250 -0.524  0.467
## 6 "BIG STONE           "   0.0684     0.267 -0.421  0.631
```

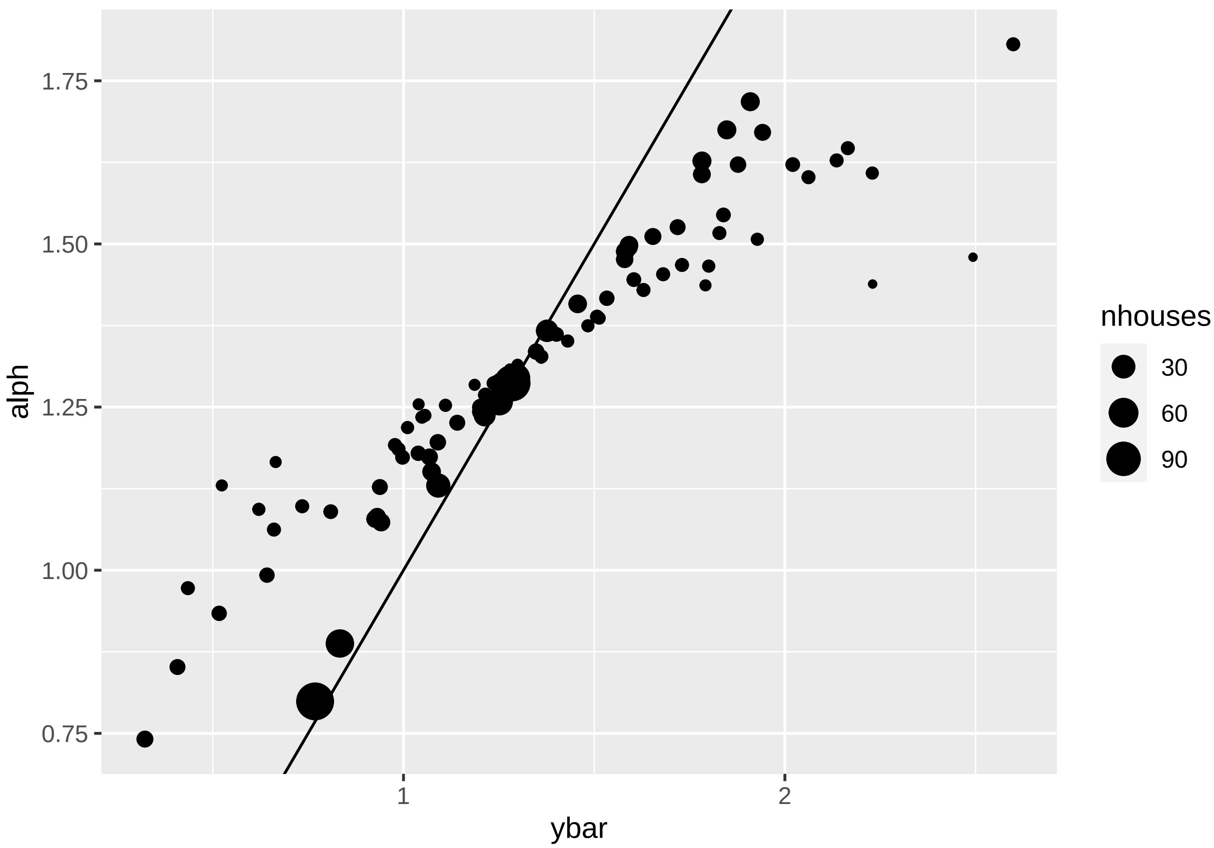
To get the alpha = eta + mu_alpha, we can use the following call

```
alphas <-
  coef(fit, summary = T)$county %>%
  as_tibble(rownames = "county") %>%
  rename(alph = Estimate.Intercept)
alphas
```

```
## # A tibble: 85 x 5
##    county                    alph Est.Error.Intercept Q2.5.Intercept Q97.5.Inter~1
##    <chr>                    <dbl>               <dbl>          <dbl>         <dbl>
##  1 "AITKIN              " 1.06                0.251          0.558          1.53
##  2 "ANOKA               " 0.888               0.104          0.677          1.09
##  3 "BECKER              " 1.23                0.263          0.715          1.75
##  4 "BELTRAMI            " 1.23                0.215          0.816          1.64
##  5 "BENTON              " 1.29                0.252          0.801          1.78
##  6 "BIG STONE           " 1.39                0.268          0.894          1.93
##  7 "BLUE EARTH          " 1.72                0.184          1.37           2.08
##  8 "BROWN               " 1.43                0.249          0.969          1.93
##  9 "CARLTON             " 1.08                0.190          0.723          1.46
## 10 "CARVER              " 1.24                0.188          0.878          1.60
## # ... with 75 more rows, and abbreviated variable name 1: Q97.5.Intercept
```

Make the plot of alpha ~ ybar

```
alphas %>%
  left_join(datcounty) %>%
  ggplot(aes(y = alph, x = ybar, size = nhouses)) +
  geom_point() +
  geom_abline(slope = 1, intercept = 0)
```



Plot of alpha - ybar

```
alphas %>%
  left_join(datcounty) %>%
  ggplot(aes(y = alph - ybar, x = nhouses)) +
  geom_point() +
  geom_hline(yintercept = 0)
```