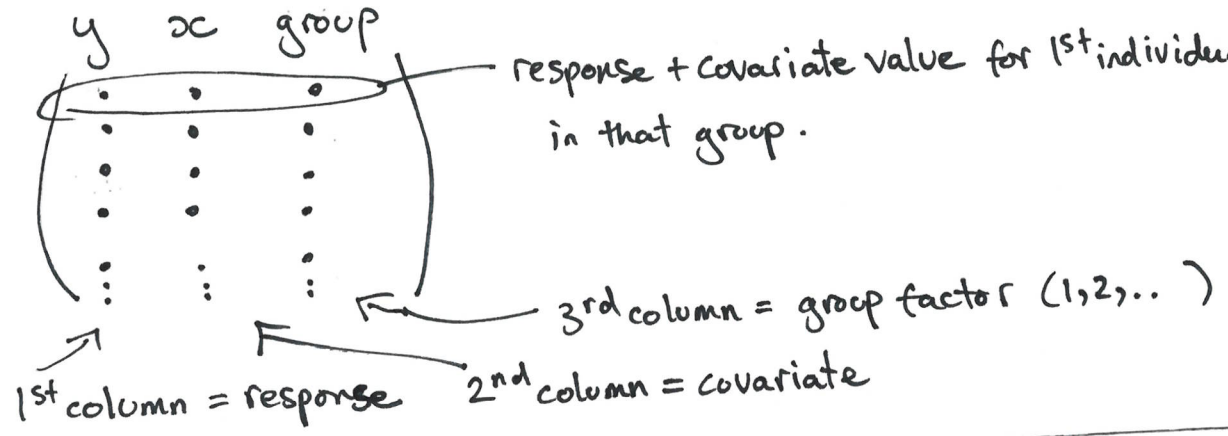
2-level random effects models

Suppose we have a data frame called 'mydata':



Empty model

$N(0,\sigma_u^2)$

$$y_{ij} = \gamma_0 + u_j + \varepsilon_{ij}$$

$N(0,\sigma^2)$

fixed intercept

R code

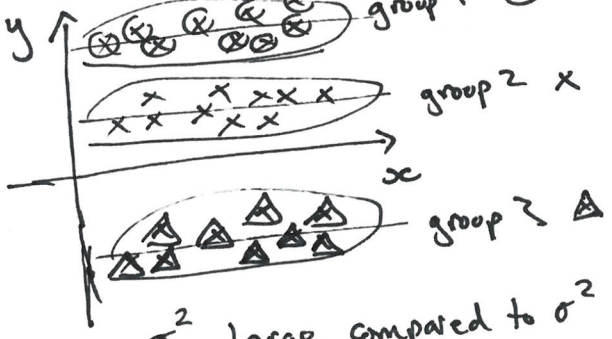
```
ml <- lmer(y~1+(1|group),
           data=mydata)
summary(ml)
```

Useful: use to calculate ICC:

$$\rho = \frac{\sigma_u^2}{\sigma_u^2 + \sigma^2}$$

'rho'

e.g1



σ_u^2 large compared to σ^2.

→ ρ close to 1.

group structure important

e.g2

σ_u^2 small compared to σ^2

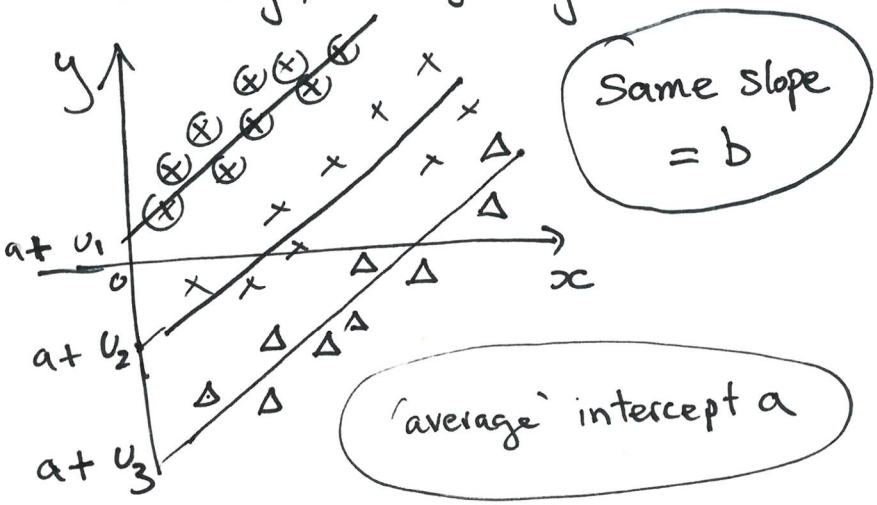
ρ closer to 0.

group structure likely not important.

Random intercept model

$$y_{ij} = a + bx_{ij} + \underbrace{v_j}_{\sim N(0,\sigma_v^2)} + \underbrace{\varepsilon_{ij}}_{\sim N(0,\sigma^2)}$$

$$= (a+v_j) + bx_{ij} + \varepsilon_{ij}$$



Same slope = b

'average' intercept a

Rcode

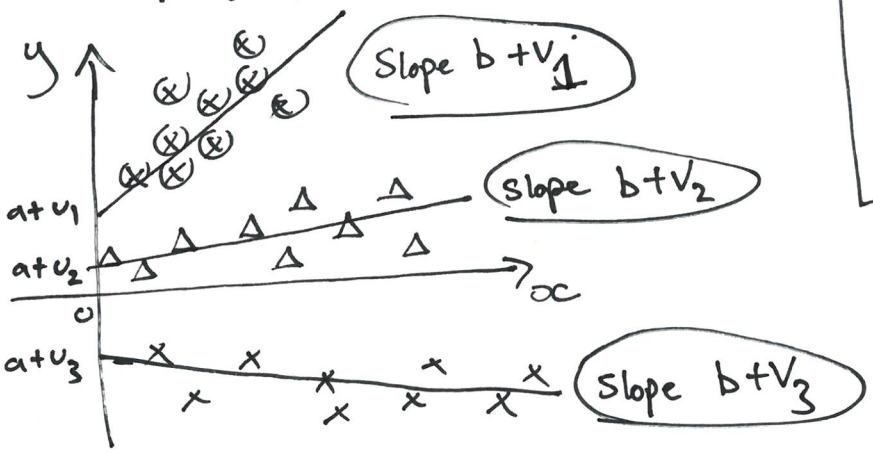
```
ml <- lmer(y ~ 1+x + (1|group),
           data = mydata)

Summary(ml)

# add predictions to mydata
mydata$pred <- predict(ml)
# plot using ggplot(...)
```

Random intercepts + slopes

$$y_{ij} = a + bx_{ij} + v_j + r_j x_{ij} + \varepsilon_{ij}$$

$$= (a+v_j) + (b+r_j)x_{ij} + \varepsilon_{ij}$$

$v_j \sim N(0,\sigma_v^2)$, $r_j \sim N(0,\sigma_r^2)$, $\varepsilon_{ij} \sim N(0,\sigma^2)$



R code

```
ml <- lmer(y ~ 1+x + (1+x|group),
           data = mydata)

Summary(ml)
# predictions
  mydata <- predict(ml)
# plot using ggplot(..)
```

Diagnostics

Similar to regression models. check'.

- Residuals vs fitted values
- Normality of residuals AND random effects.

R code

```
plot(ml)
resid(ml)
ranef(ml)
qqnorm(..)
```