THE UNIVERSITY
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Centering Predictors Generalisations

Data Analysis for Psychology in R 3

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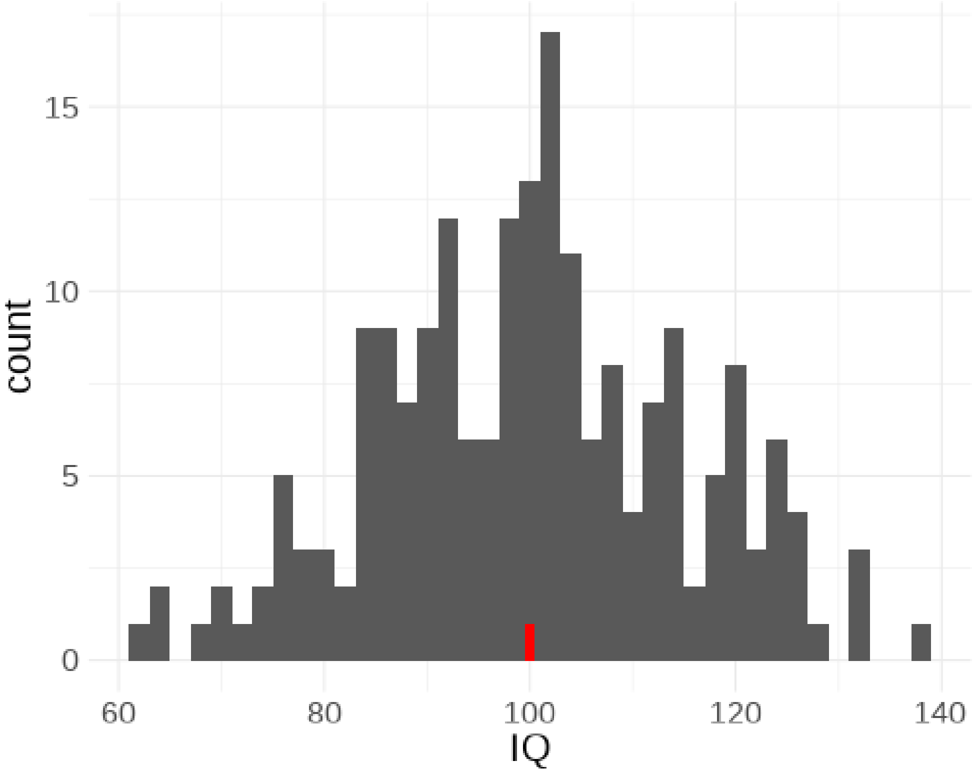
Part 1: Centering Predictors

Part 2: GLMM

Centering

Suppose we have a variable for which the mean is 100.



Centering

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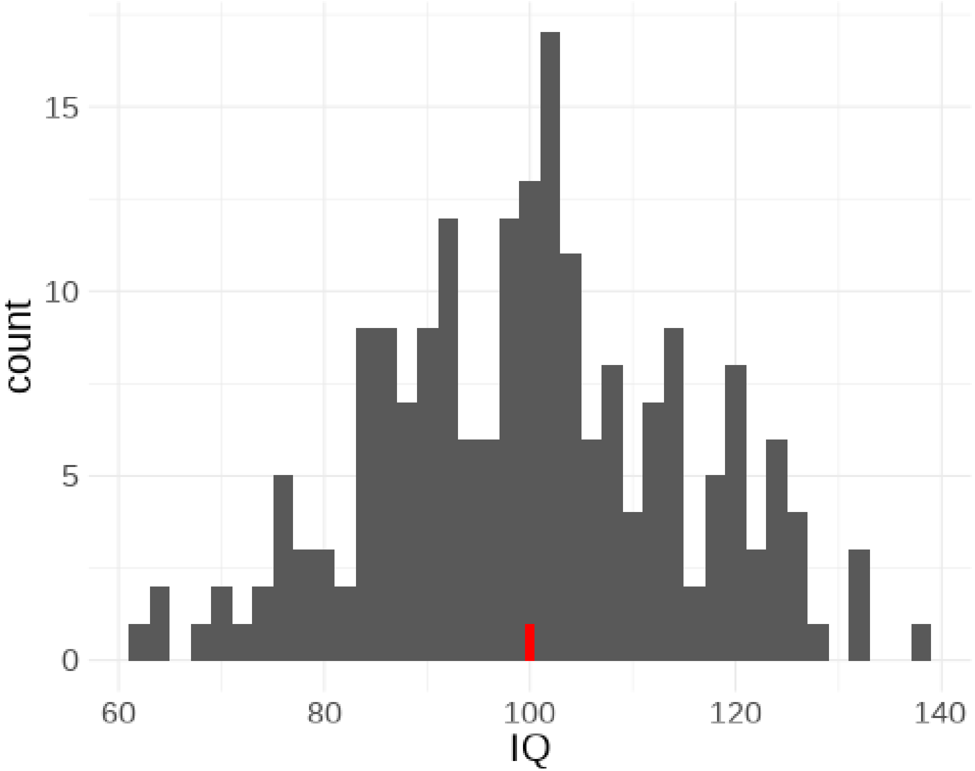
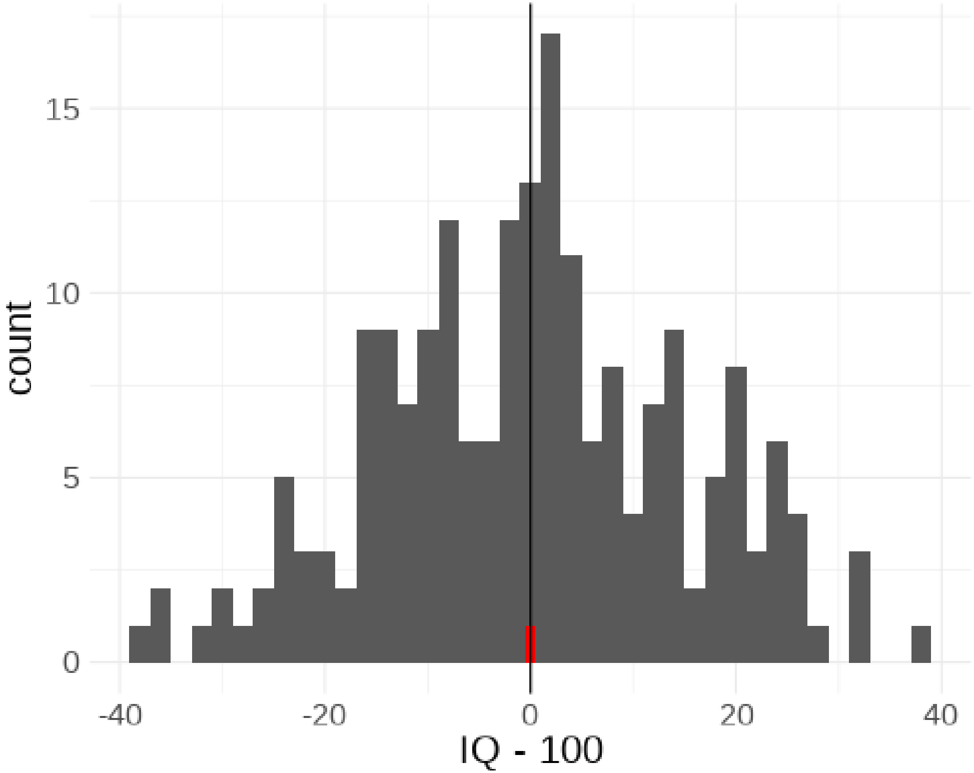


We can re-center this so that the mean becomes zero:



Centering

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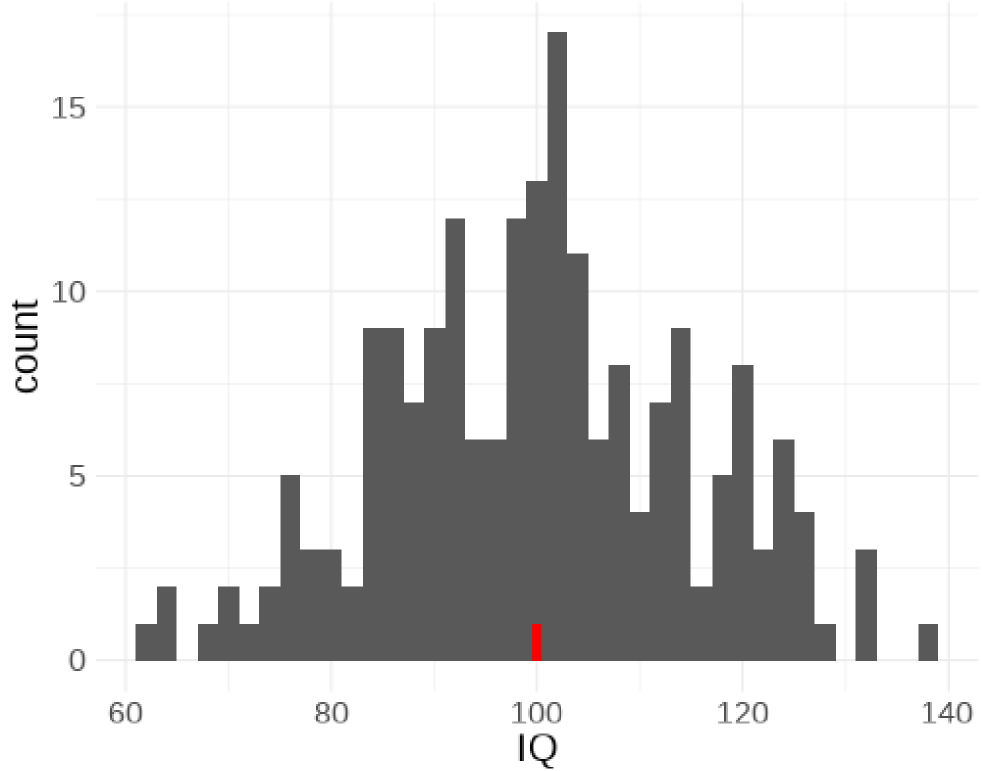
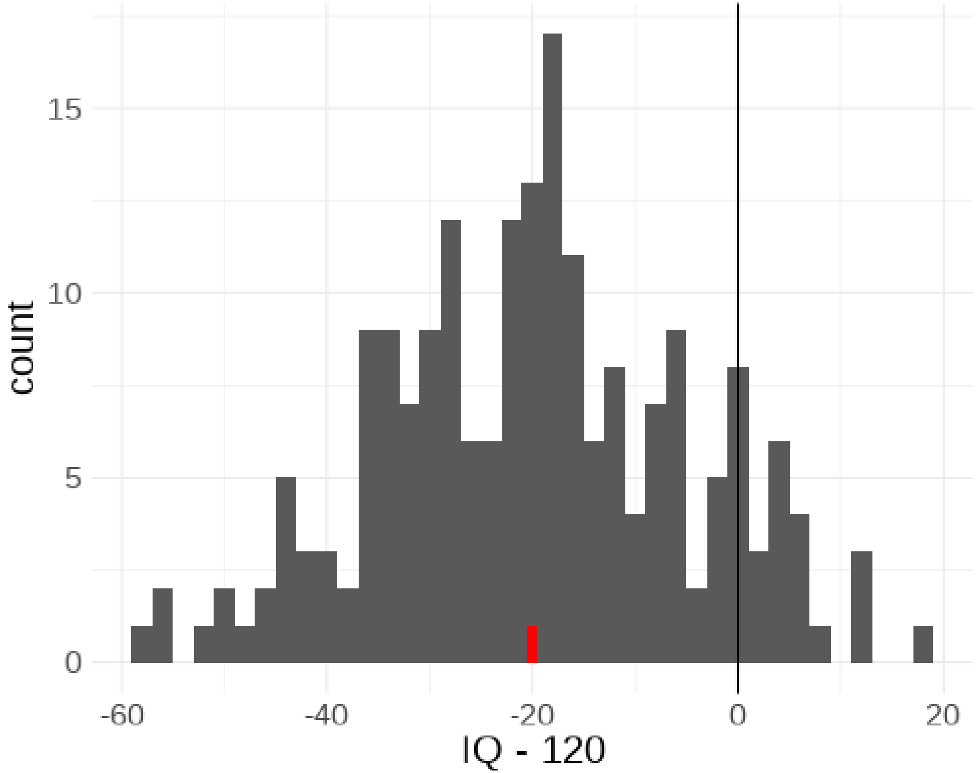
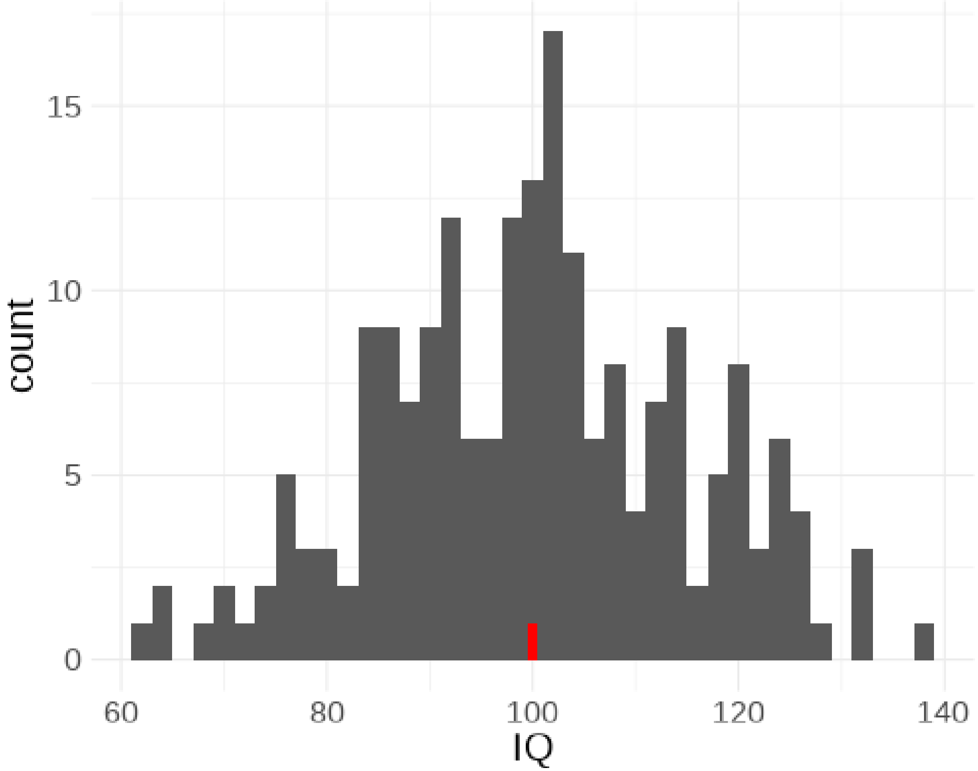


We can re-center this so that *any* value becomes zero:



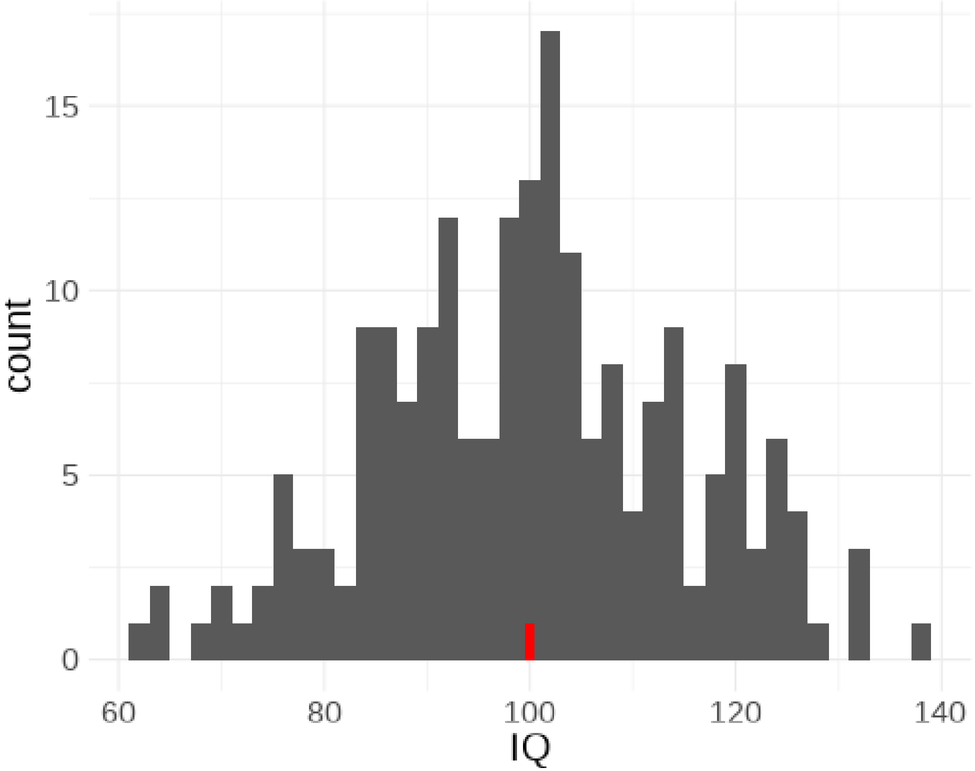
Scaling

Suppose we have a variable for which the mean is 100.
The standard deviation is 15

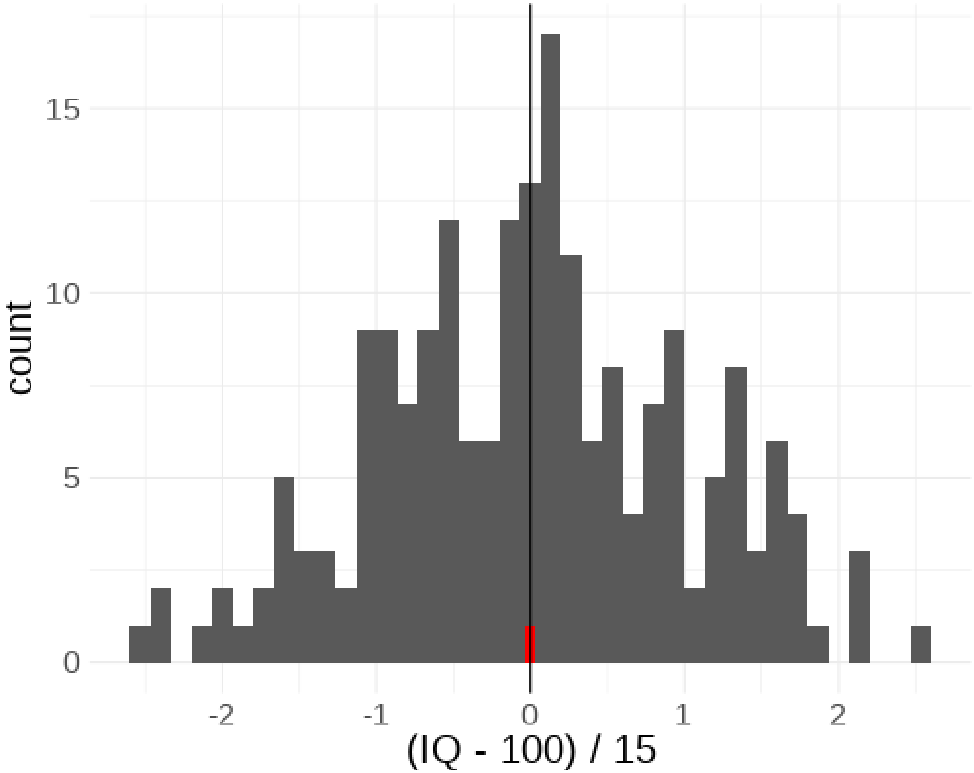


Scaling

Suppose we have a variable for which the mean is 100.
The standard deviation is 15



We can scale this so that a change in 1 is equivalent to a change in 1 standard deviation:



Centering predictors in LM

```
m1 <- lm(y~x,data=df)
m2 <- lm(y~scale(x, center=T,scale=F),data=df)
m3 <- lm(y~scale(x, center=T,scale=T),data=df)
m4 <- lm(y~I(x-5), data=df)
```

Centering predictors in LM

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m1 <- lm(y~x,data=df)
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m3 <- lm(y~scale(x, center=T,scale=T),data=df)
m4 <- lm(y~I(x-5), data=df)
```

```
anova(m1,m2,m3,m4)
```

```
## Analysis of Variance Table
##
## Model 1: y ~ x
## Model 2: y ~ scale(x, center = T, scale = F)
## Model 3: y ~ scale(x, center = T, scale = T)
## Model 4: y ~ I(x - 5)
##   Res.Df RSS Df Sum of Sq F Pr(>F)
## 1    198 177
## 2    198 177  0         0
## 3    198 177  0         0
## 4    198 177  0         0
```

Centering predictors in LM

```r
m1 <- lm(y~x,data=df)
m2 <- lm(y~scale(x, center=T,scale=F),data=df)
m3 <- lm(y~scale(x, center=T,scale=T),data=df)
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anova(m1,m2,m3,m4)
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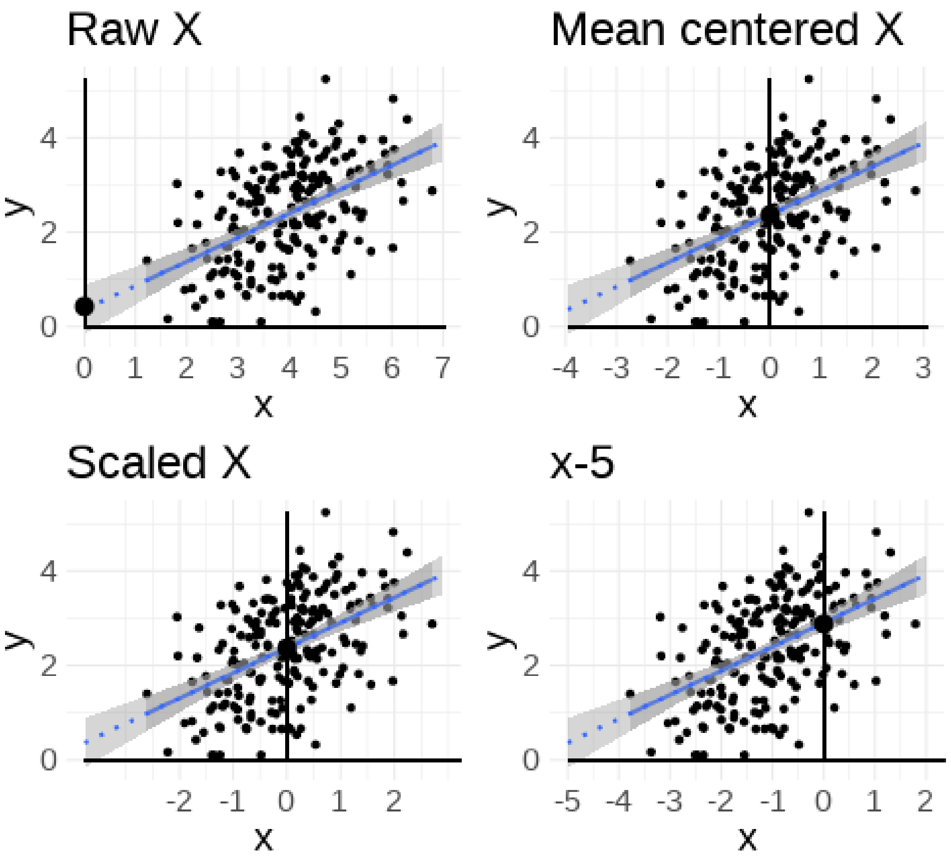
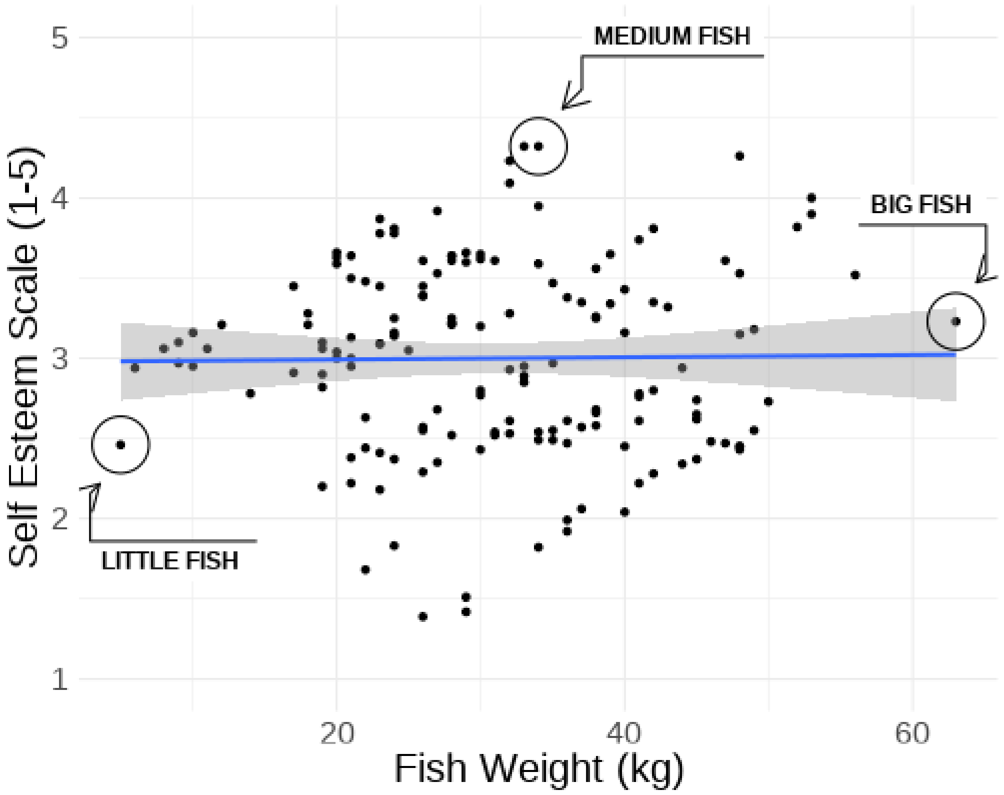
```

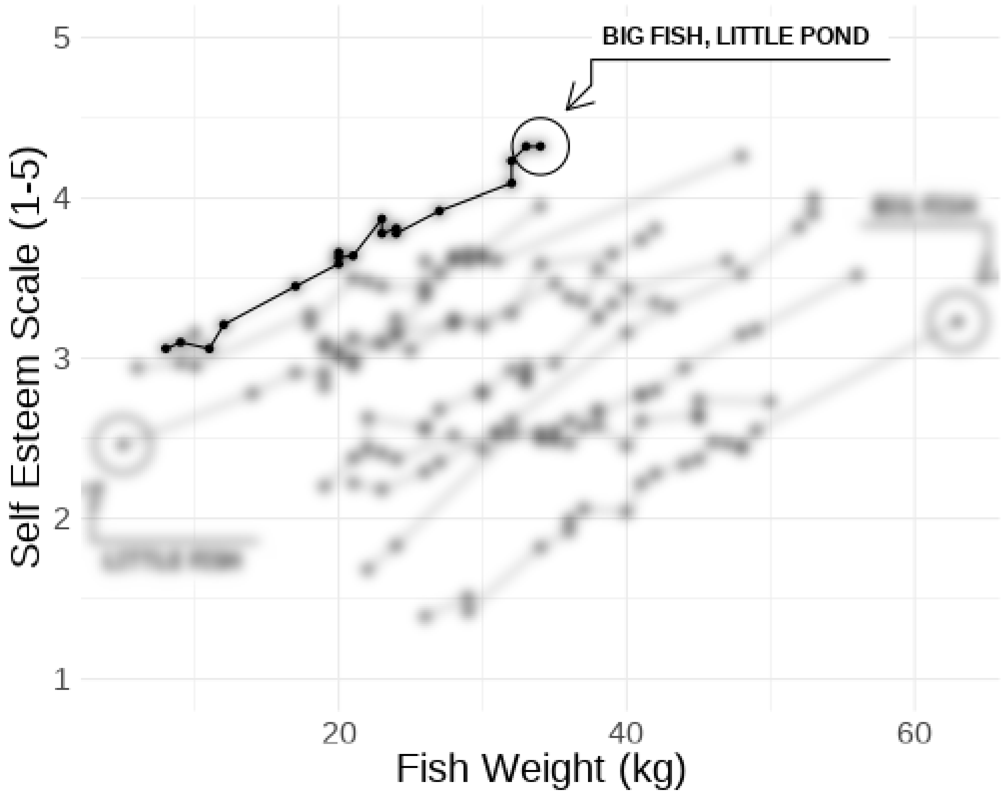


Big Fish Little Fish



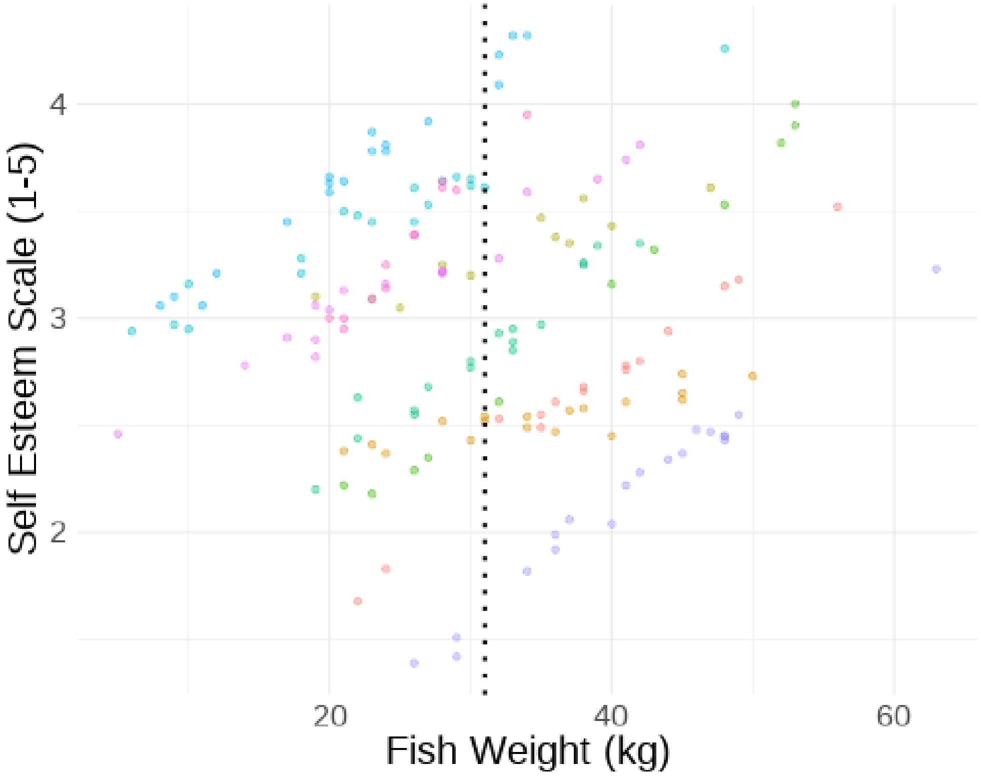
data available at https://uoepsy.github.io/data/bflp.csv

Things are different with multi-level data



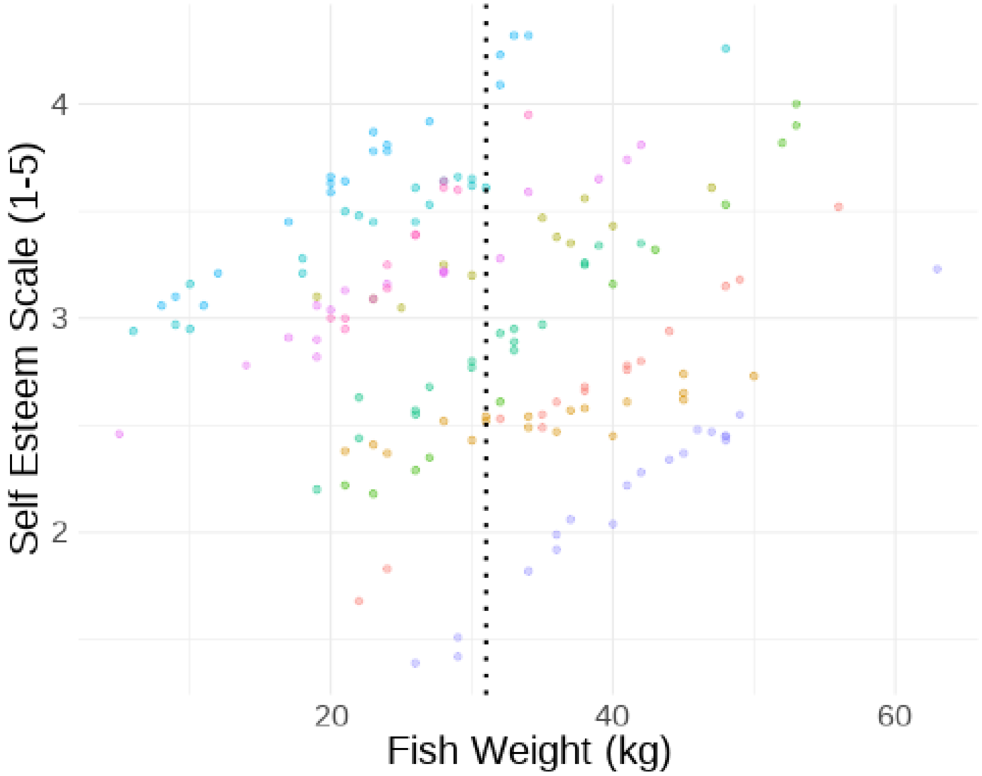
Multiple means

Grand mean

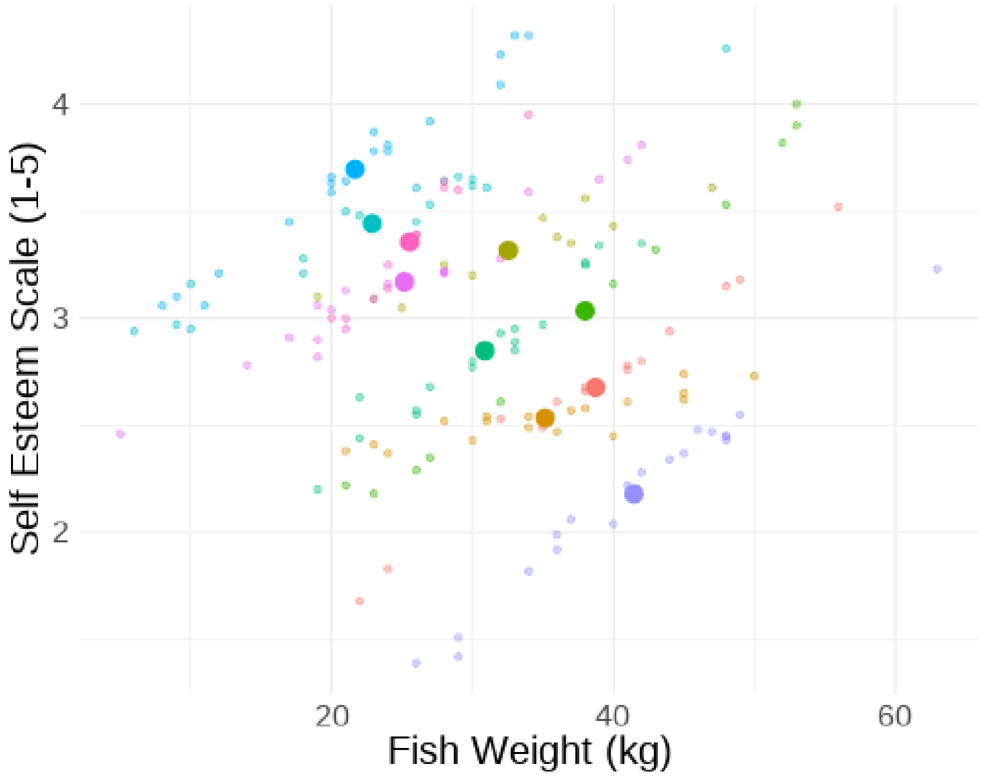


Multiple means

Grand mean

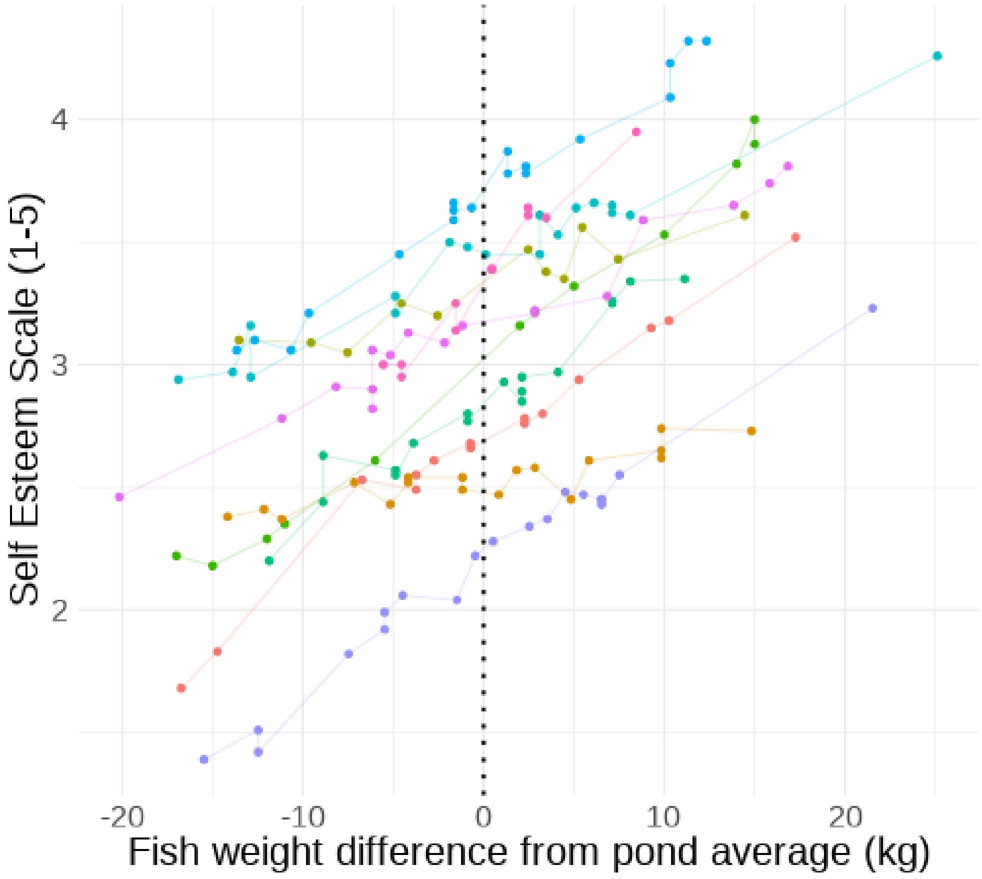


Group means

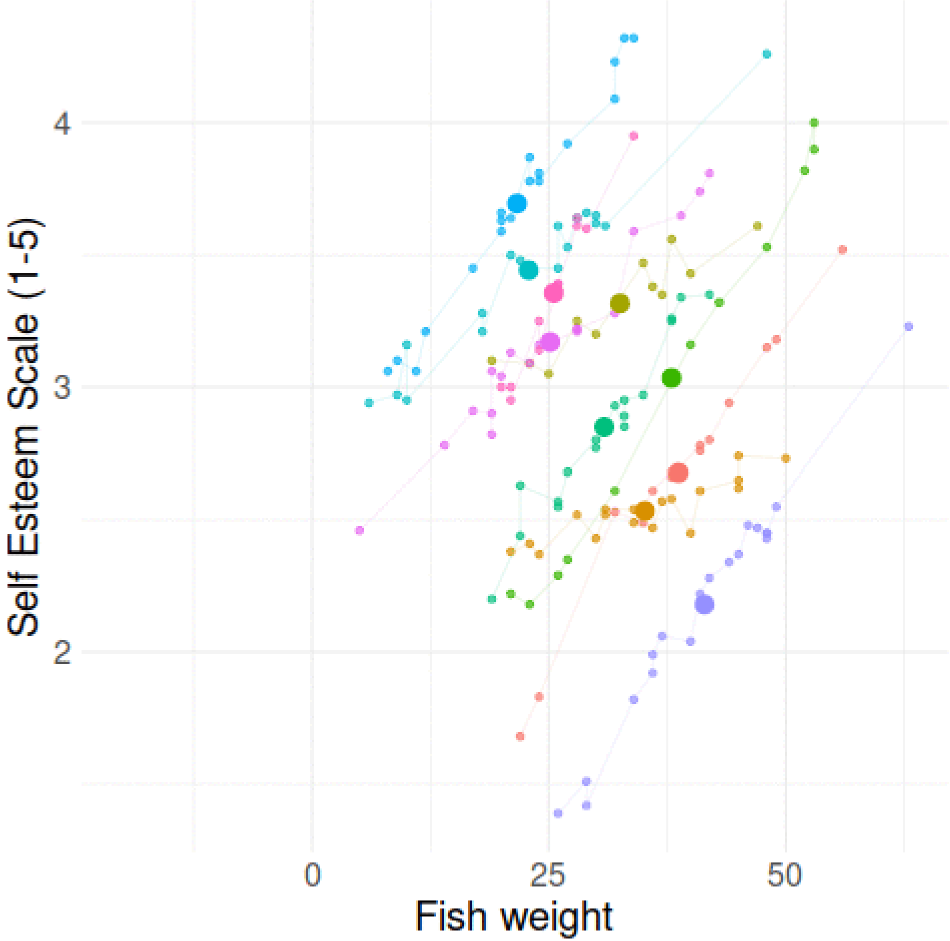


Group mean centering

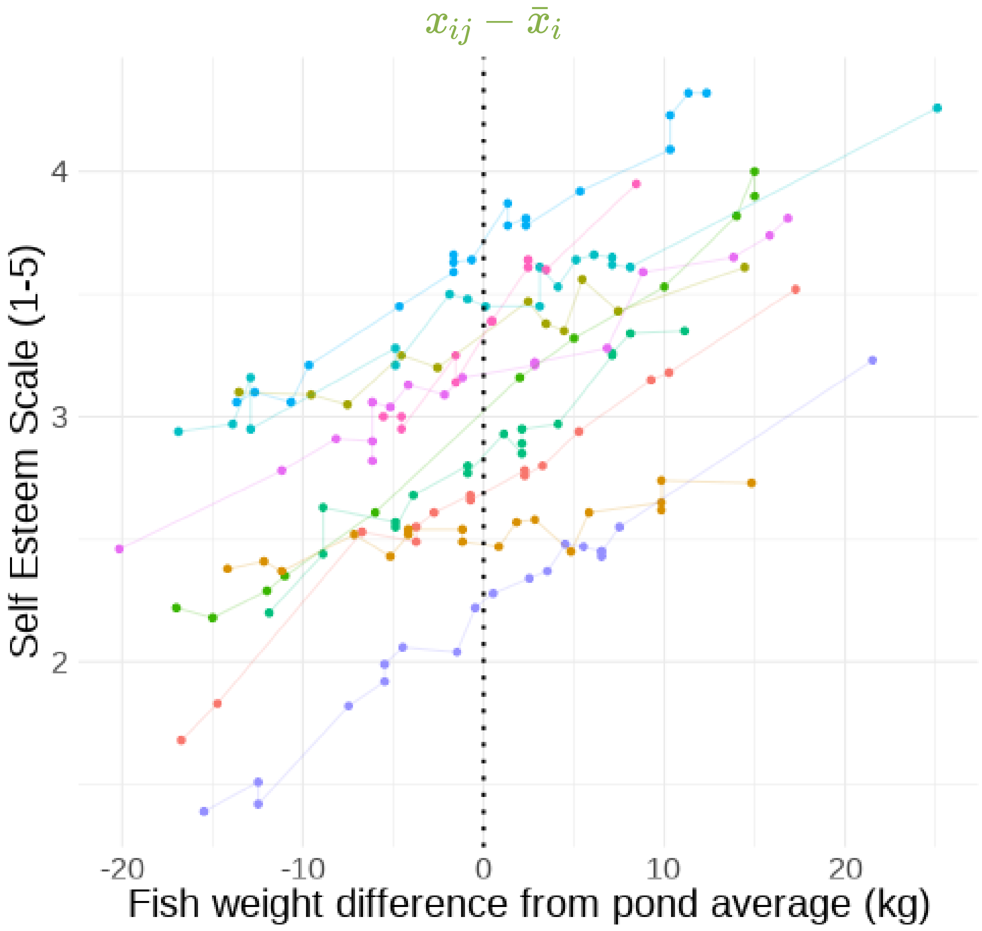
$x_{ij} - \bar{x}_i$

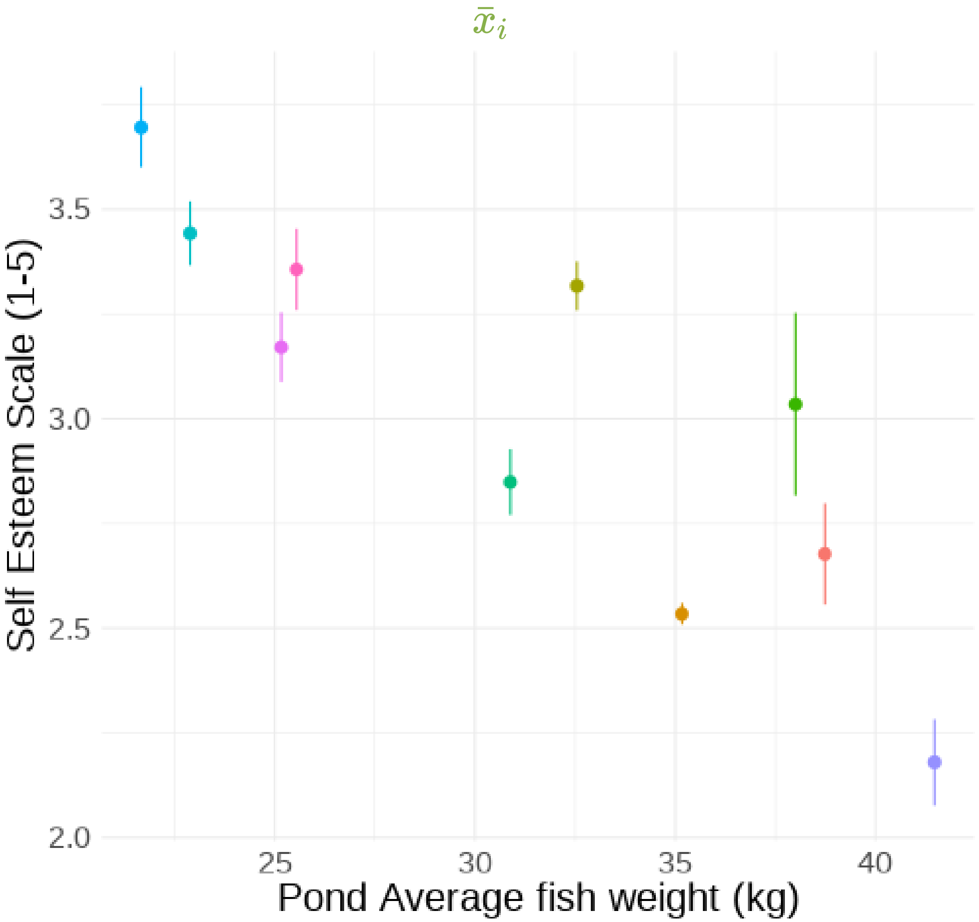


Group-mean centering



Group mean centering





Disaggregating within & between

RE model

$$
\begin{aligned}
y_{ij} &= \beta_{0i} + \beta_1(x_j) + \varepsilon_{ij} \\
\beta_{0i} &= \gamma_{00} + \zeta_{0i} \\
\ldots
\end{aligned}
$$

```
rem <- lmer(self_esteem ~ fish_weight +
              (1 | pond), data=bflp)
```

Disaggregating within & between

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\ldots
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$$

```
rem <- lmer(self_esteem ~ fish_weight +
              (1 | pond), data=bflp)
```

Within-between model

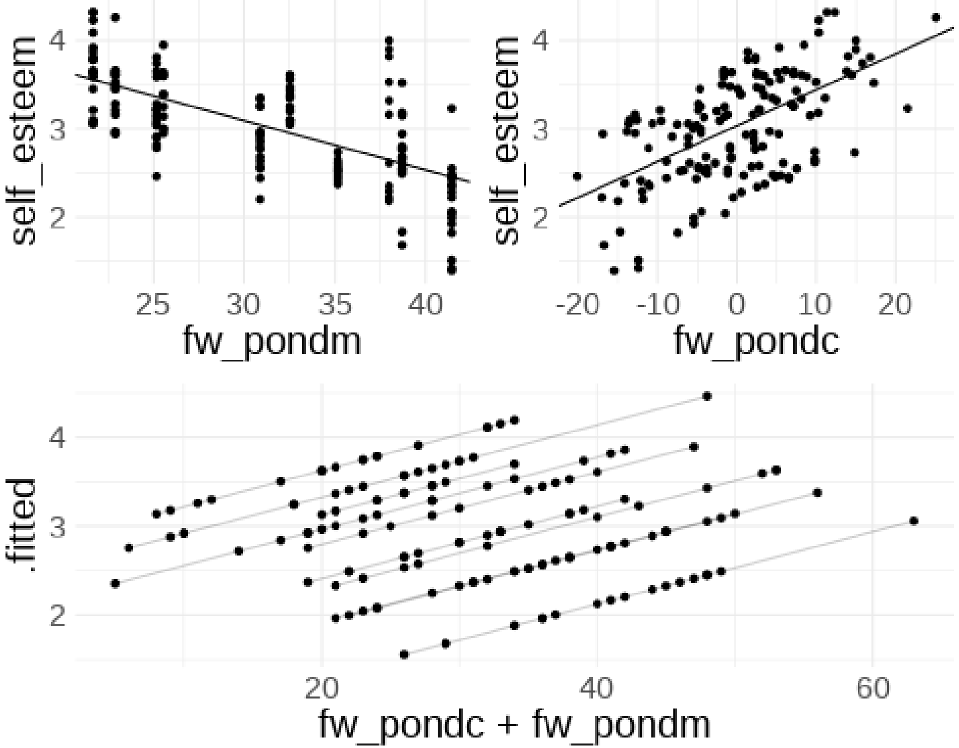
$$
\begin{aligned}
y_{ij} &= \beta_{0i} + \beta_1(\bar{x}_i) + \beta_2(x_{ij} - \bar{x}_i) + \varepsilon_{ij} \\
\beta_{0i} &= \gamma_{00} + \zeta_{0i} \\
\ldots
\end{aligned}
$$

```
bflp <-
  bflp %>% group_by(pond) %>%
    mutate(
      fw_pondm = mean(fish_weight),
      fw_pondc = fish_weight - mean(fish_weight)
    ) %>% ungroup

wbm <- lmer(self_esteem ~ fw_pondm + fw_pondc +
              (1 | pond), data=bflp)
fixef(wbm)
```

```
## (Intercept)    fw_pondm    fw_pondc 
##     4.76802    -0.05586     0.04067
```

Disaggregating within & between



Within-between model

$$
\begin{aligned}
y_{ij} &= \beta_{0i} + \beta_1(\bar{x}_i) + \beta_2(x_{ij} - \bar{x}_i) + \varepsilon_{ij} \\
\beta_{0i} &= \gamma_{00} + \zeta_{0i} \\
&\ldots
\end{aligned}
$$

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bflp <-
  bflp %>% group_by(pond) %>%
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    ) %>% ungroup

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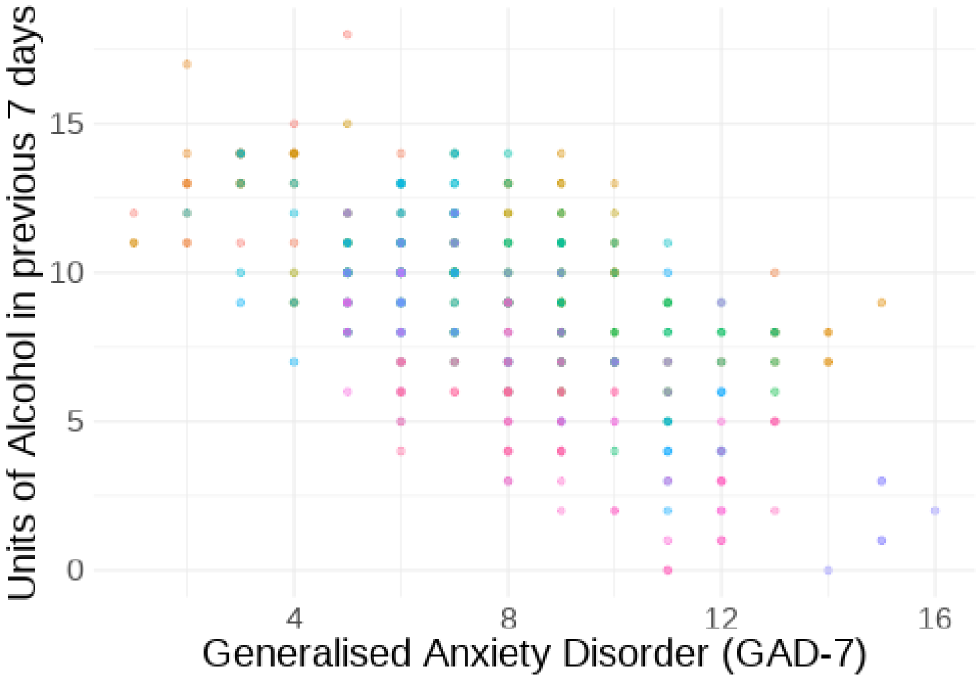
fixef(wbm)
```

```
## (Intercept)    fw_pondm    fw_pondc
##     4.76802    -0.05586     0.04067
```

A more realistic example

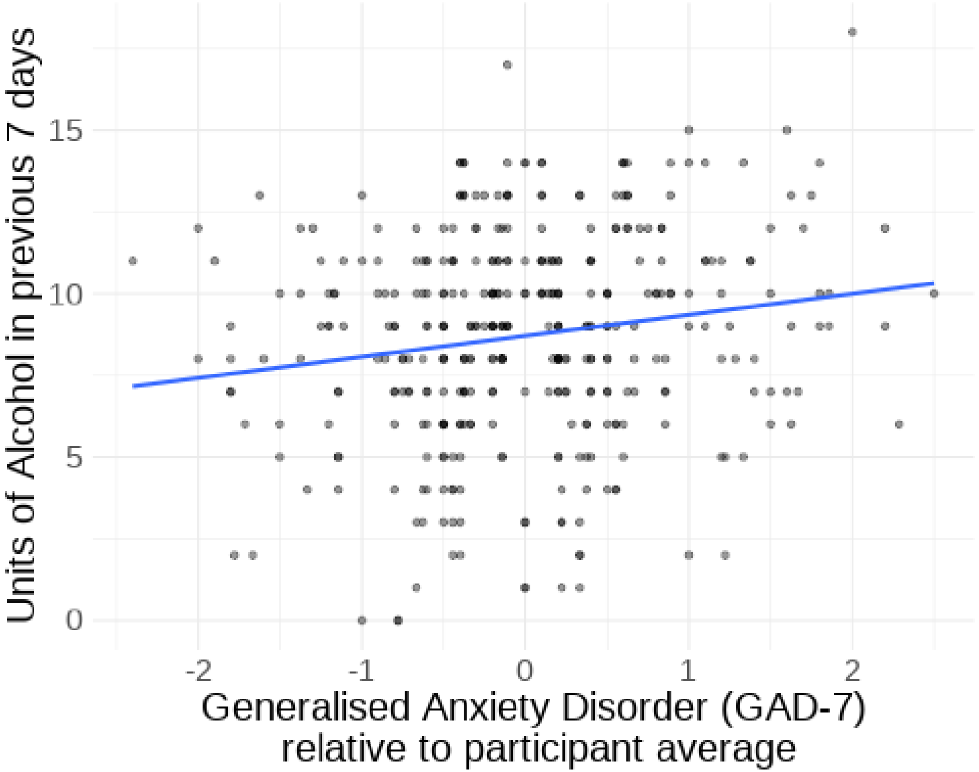
A research study investigates how anxiety is associated with drinking habits. Data was collected from 50 participants. Researchers administered the generalised anxiety disorder (GAD-7) questionnaire to measure levels of anxiety over the past week, and collected information on the units of alcohol participants had consumed within the week. Each participant was observed on 10 different occasions.



data available at https://uoepsy.github.io/data/alcgad.csv

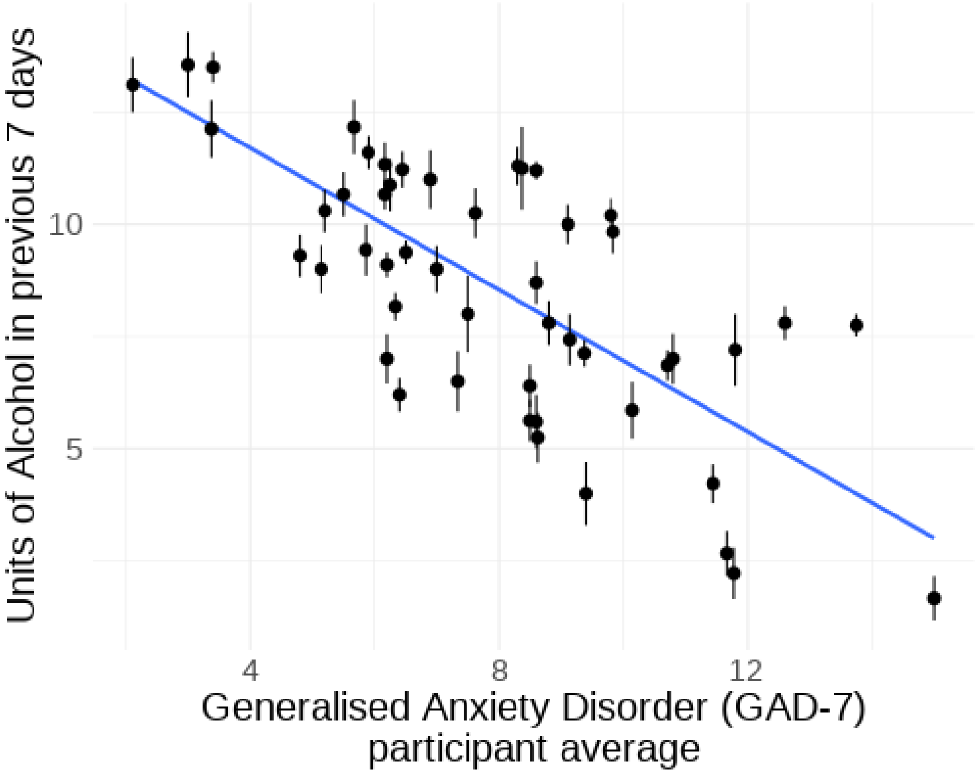
A more realistic example

Is being more nervous (than you usually are) associated with higher consumption of alcohol?



A more realistic example

Is being generally more nervous (relative to others) associated with higher consumption of alcohol?



Modelling within & between effects

```
alcgad <-
  alcgad %>% group_by(ppt) %>%
  mutate(
    gadm=mean(gad),
    gadmc=gad-gadm
  )
alcmod <- lmer(alcunits ~ gadm + gadmc +
                 (1 + gadmc | ppt),
               data=alcgad,
               control=lmerControl(optimizer = "bobyqa"))
```

```
summary(alcmod)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: alcunits ~ gadm + gadmc + (1 + gadmc | ppt)
##    Data: alcgad
## Control: lmerControl(optimizer = "bobyqa")
##
## REML criterion at convergence: 1424
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.8466 -0.6264  0.0642  0.6292  3.0281
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  ppt      (Intercept) 3.7803   1.944
##           gadmc       0.0935   0.306    -0.30
##  Residual             1.7234   1.313
## Number of obs: 375, groups:  ppt, 50
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  14.5802     0.8641   16.87
## gadm         -0.7584     0.1031   -7.35
## gadmc         0.6378     0.0955    6.68
##
## Correlation of Fixed Effects:
##       (Intr) gadm
## gadm  -0.945
## gadmc -0.055  0.012
```

Modelling within & between interactions

```
alcmod <- lmer(alcunits ~ (gadm + gadmc)*interv +
                 (1 | ppt),
               data=alcgad,
               control=lmerControl(optimizer = "bobyqa"))
```

```
summary(alcmod)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: alcunits ~ (gadm + gadmc) * interv + (1 | ppt)
##    Data: alcgad
## Control: lmerControl(optimizer = "bobyqa")
## 
## REML criterion at convergence: 1404
## 
## Scaled residuals: 
##     Min      1Q  Median      3Q     Max 
## -2.8183 -0.6354  0.0142  0.5928  3.0874 
## 
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  ppt      (Intercept) 3.59     1.9     
##  Residual             1.69     1.3     
## Number of obs: 375, groups:  ppt, 50
## 
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    14.858      1.275   11.65
## gadm           -0.876      0.154   -5.70
## gadmc           1.092      0.128    8.56
## interv         -0.549      1.711   -0.32
## gadm:interv     0.205      0.205    1.00
## gadmc:interv   -0.757      0.166   -4.57
## 
## Correlation of Fixed Effects:
##              (Intr) gadm   gadmc  interv gdm:nt
```

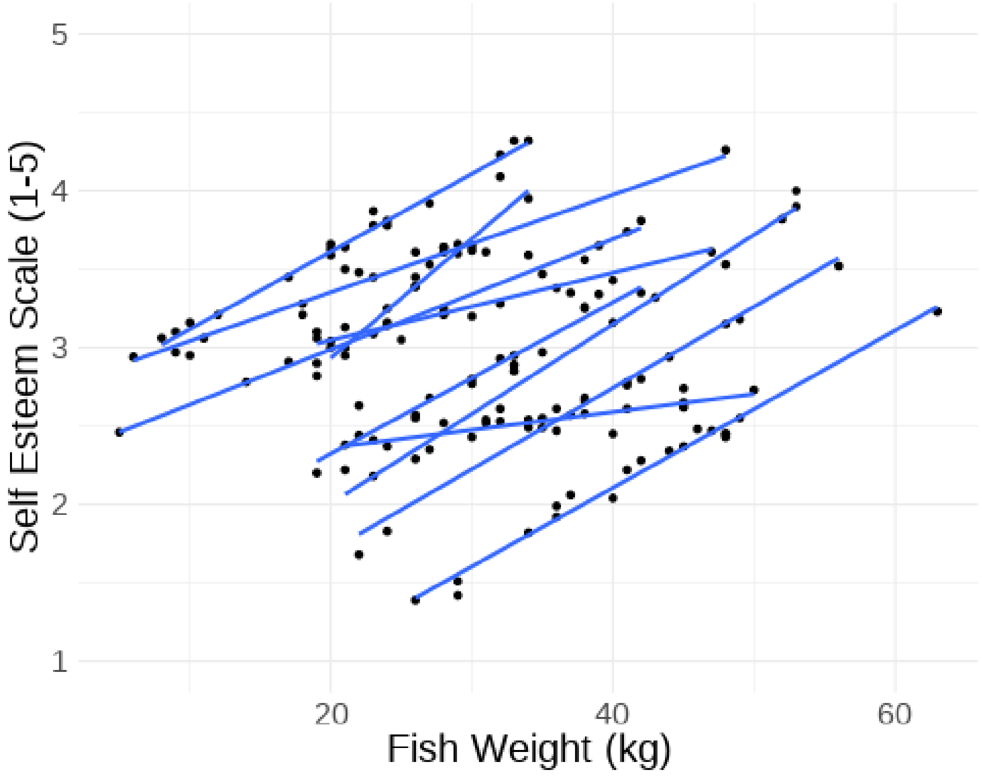
The total effect

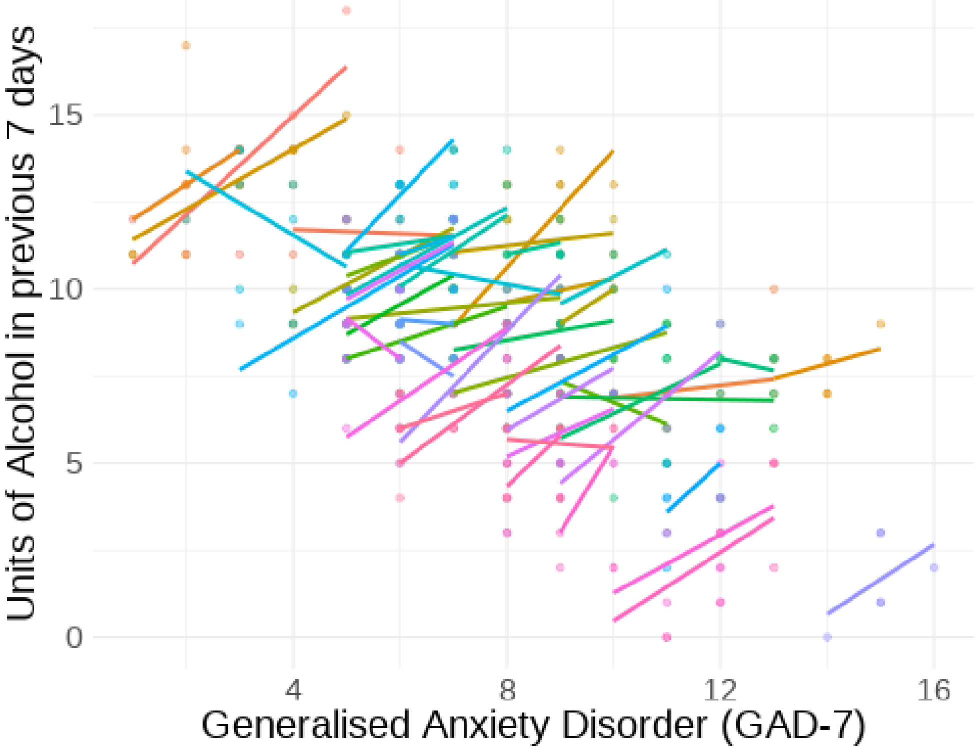
```
alcmod2 <- lmer(alcunits ~ gad + (1 | ppt),
                data=alcgad,
                control=lmerControl(optimizer = "bobyqa"))
```

```
summary(alcmod2)
```

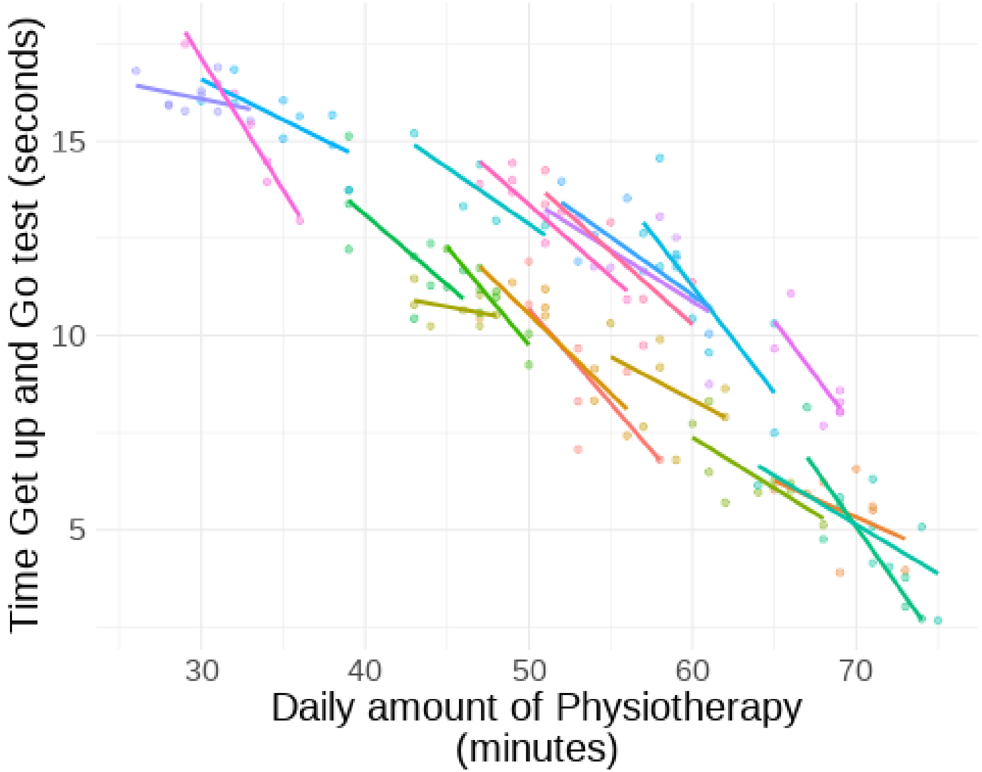
```
## Linear mixed model fit by REML ['lmerMod']
## Formula: alcunits ~ gad + (1 | ppt)
##    Data: alcgad
## Control: lmerControl(optimizer = "bobyqa")
## 
## REML criterion at convergence: 1494
## 
## Scaled residuals: 
##     Min      1Q  Median      3Q     Max 
## -2.9940 -0.6414  0.0258  0.5808  2.9825 
## 
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  ppt      (Intercept) 14.32    3.78    
##  Residual              1.83    1.35    
## Number of obs: 375, groups:  ppt, 50
## 
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   5.1787     0.8198    6.32
## gad           0.4281     0.0779    5.50
## 
## Correlation of Fixed Effects:
##     (Intr)
## gad -0.752
```

Within & Between

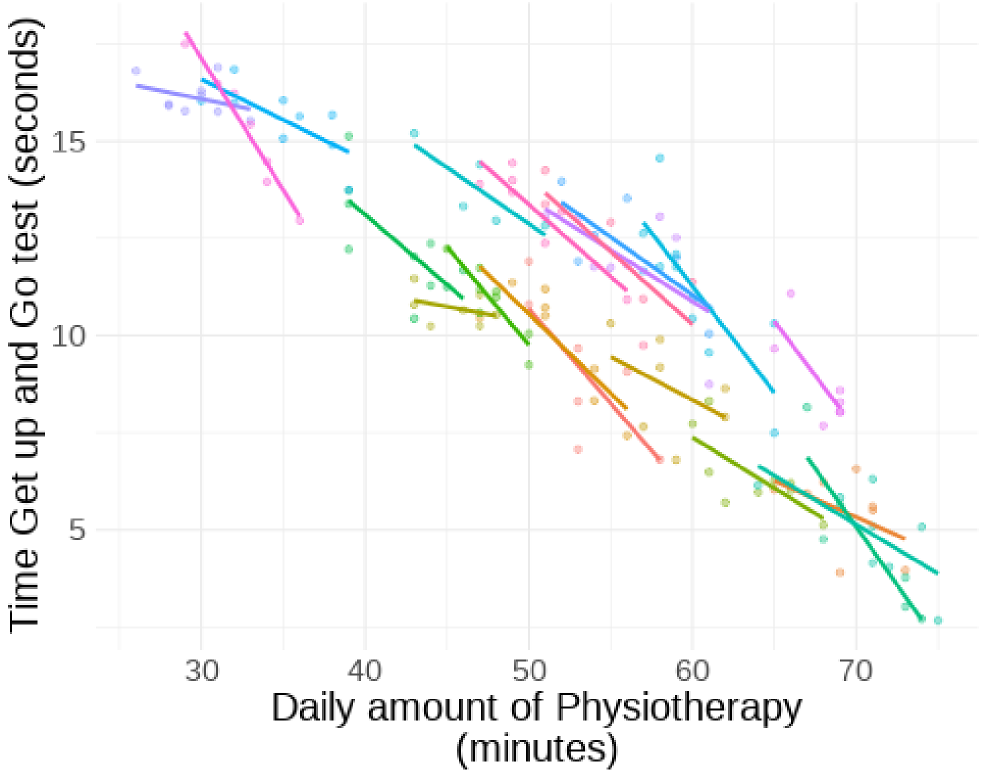


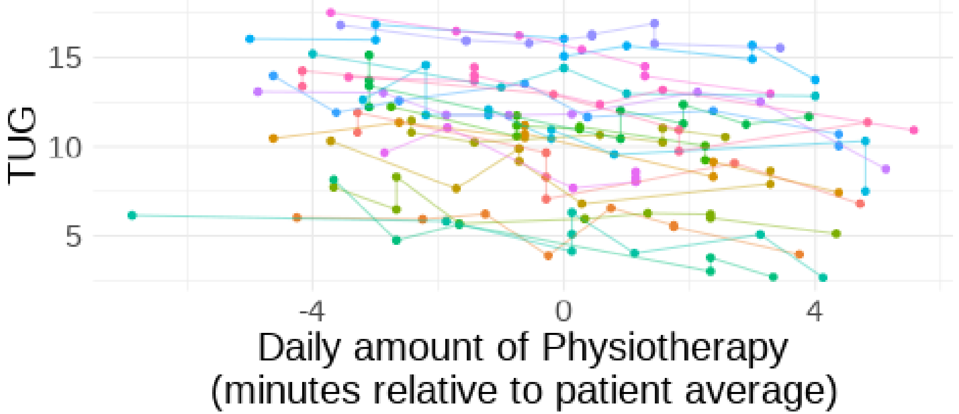


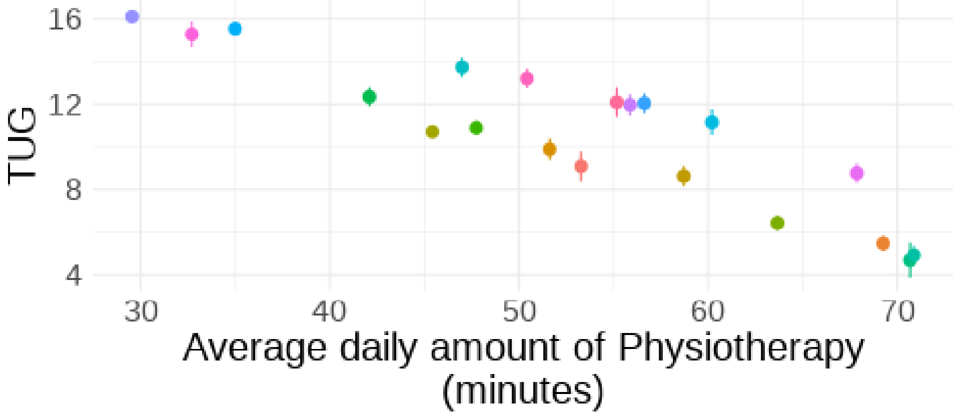
Within & Between



Within & Between







Summary

- Applying the same linear transformation to a predictor (e.g. grand-mean centering, or standardising) makes **no difference** to our model or significance tests
  - but it may change the meaning and/or interpretation of our parameters
- When data are clustered, we can apply group-level transformations, e.g. **group-mean centering.**
- Group-mean centering our predictors allows us to disaggregate **within** from **between** effects.
  - allowing us to ask the theoretical questions that we are actually interested in

End of Part 1

Part 1: Centering Predictors

Part 2: GLMM

lm() and glm()

lm()

$$y = \beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k) + \boldsymbol{\varepsilon}$$

lm() and glm()

lm()

$$y = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\boldsymbol{\beta}} + \boldsymbol{\varepsilon}$$

lm() and glm()

lm()

$$y = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\boldsymbol{\beta}} + \boldsymbol{\varepsilon}$$

$$\text{where } -\infty \leq y \leq \infty$$

lm() and glm()

lm()

$$y = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\boldsymbol{\beta}} + \boldsymbol{\varepsilon}$$

$$\text{where } -\infty \leq y \leq \infty$$

$$?? = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\boldsymbol{\beta}} + \boldsymbol{\varepsilon}$$

lm() and glm()

lm()

$$y = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\boldsymbol{\beta}} + \boldsymbol{\varepsilon}$$

where $-\infty \leq y \leq \infty$

glm()

$$ln\left(\frac{p}{1-p}\right) = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\boldsymbol{\beta}} + \boldsymbol{\varepsilon}$$

where $0 \leq p \leq 1$

lm() and glm()

lm()

$$y = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\beta} + \varepsilon$$

$$\text{where } -\infty \leq y \leq \infty$$

glm()

$$ln\left(\frac{p}{1-p}\right) = \underbrace{\beta_0 + \beta_1(x_1) + \ldots + \beta_k(x_k)}_{\mathbf{X}\beta} + \varepsilon$$

$$\text{where } 0 \leq p \leq 1$$

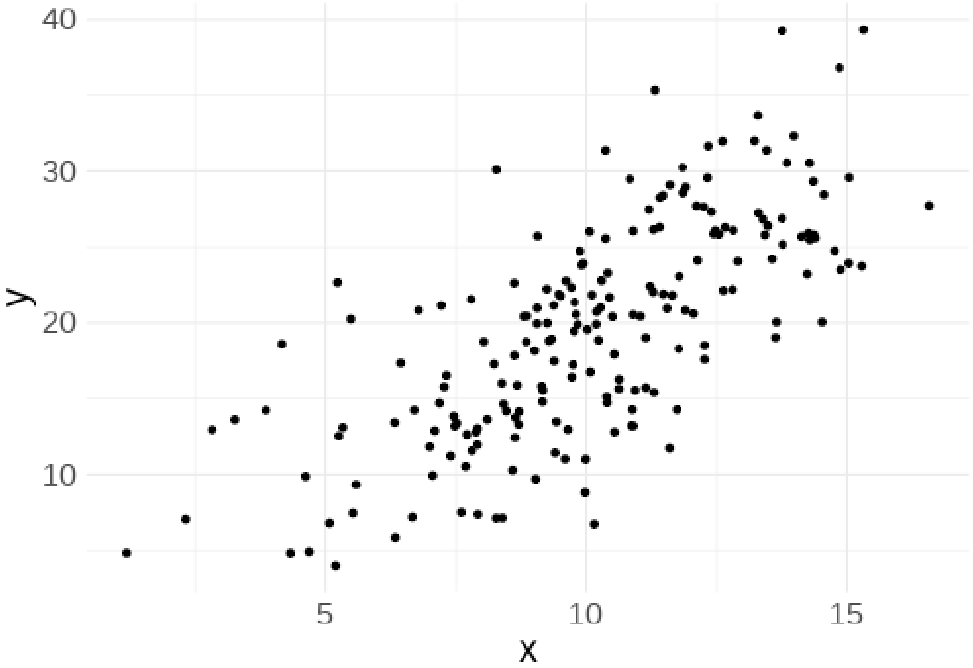
glm() is the **generalised** linear model.

we can specify the link function to model outcomes with different distributions.
this allows us to fit models such as the *logistic* regression model:

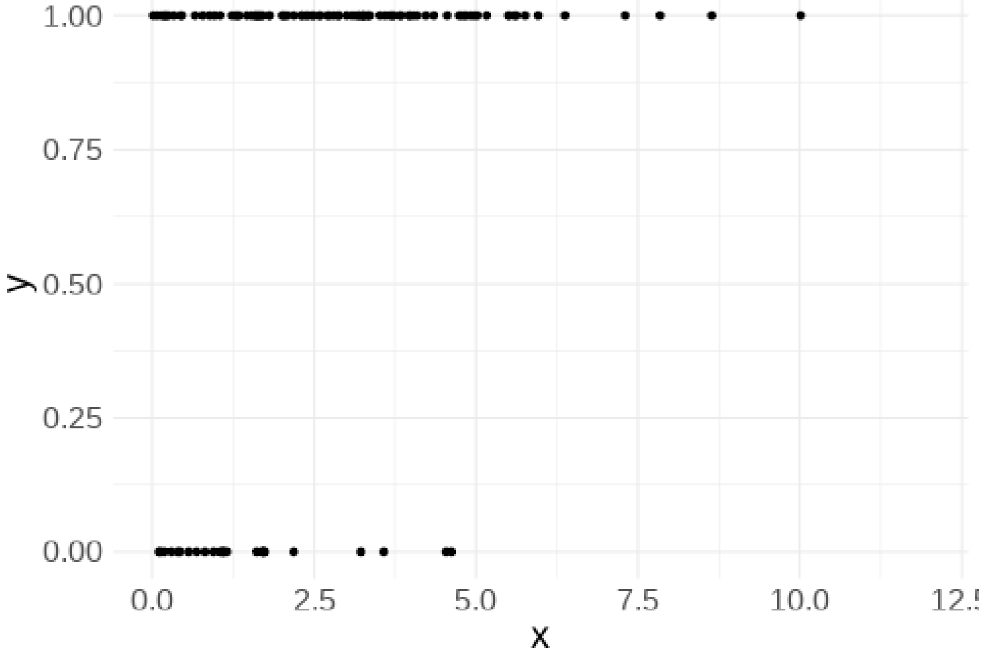
```
glm(y~x, family = binomial(link="logit"))
```

logistic regression visualised

continuous outcome



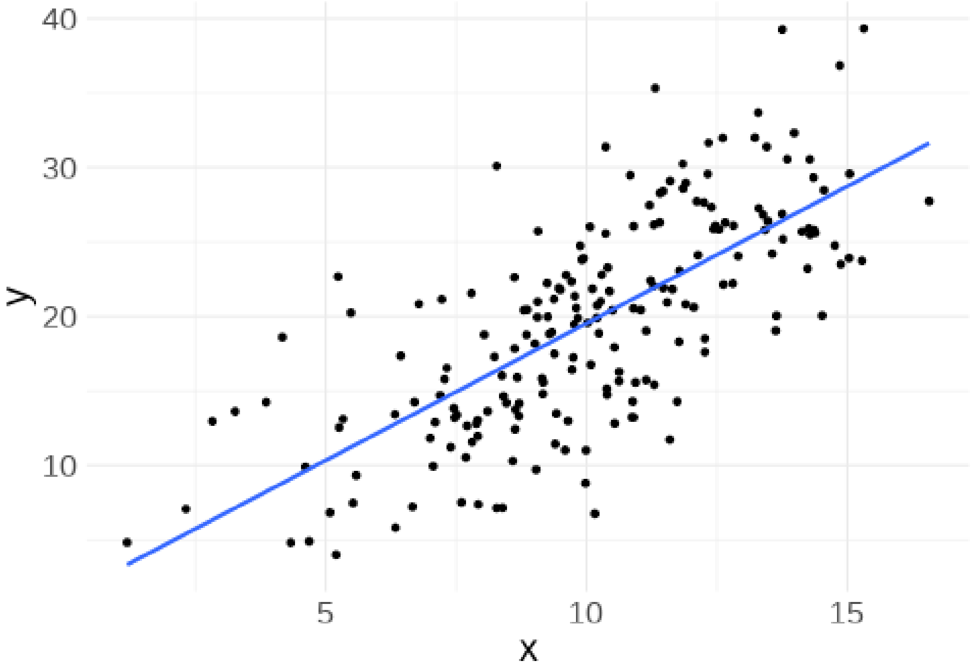
binary outcome



logistic regression visualised

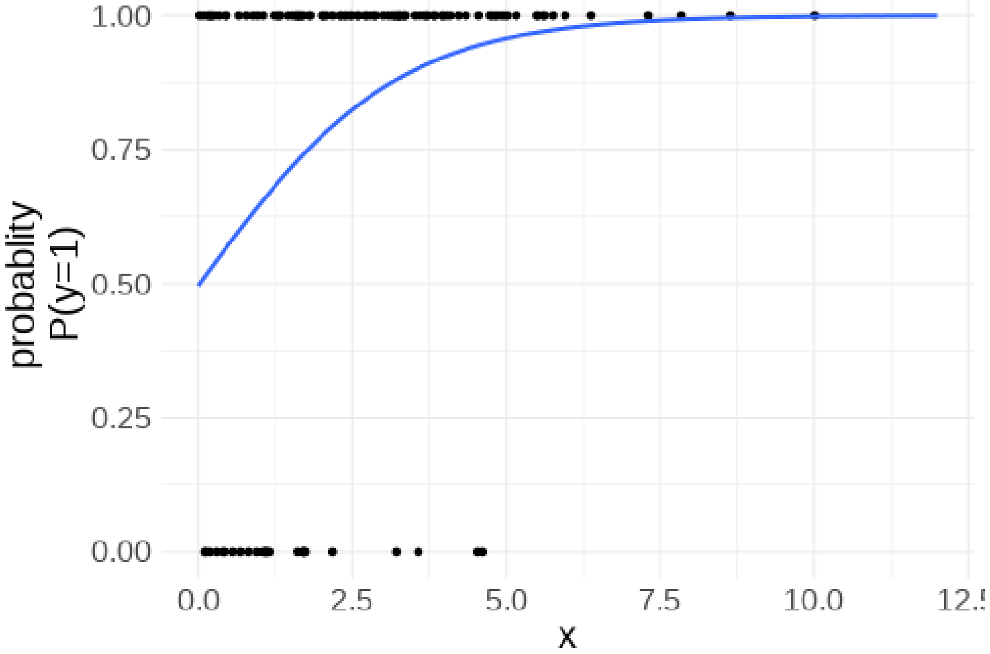
linear regression

we model y directly as linear combination of one or more predictor variables



logistic regression

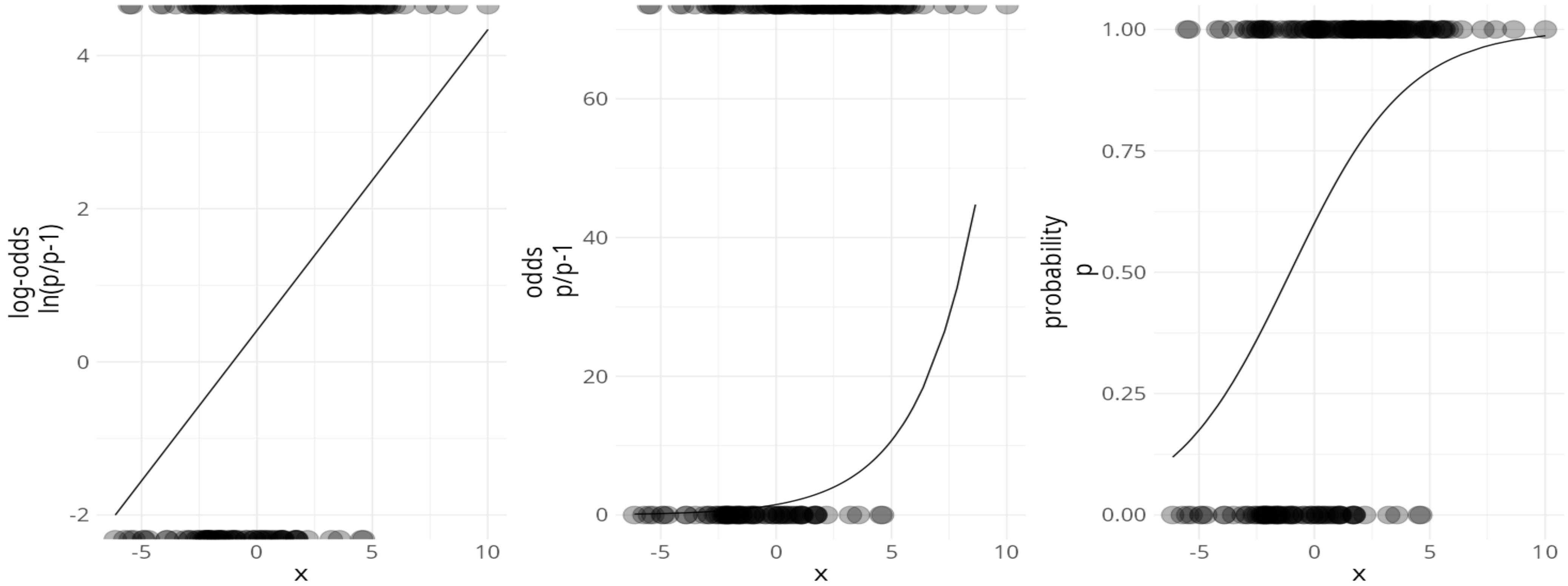
probability is *not* linear..
but we can model it indirectly



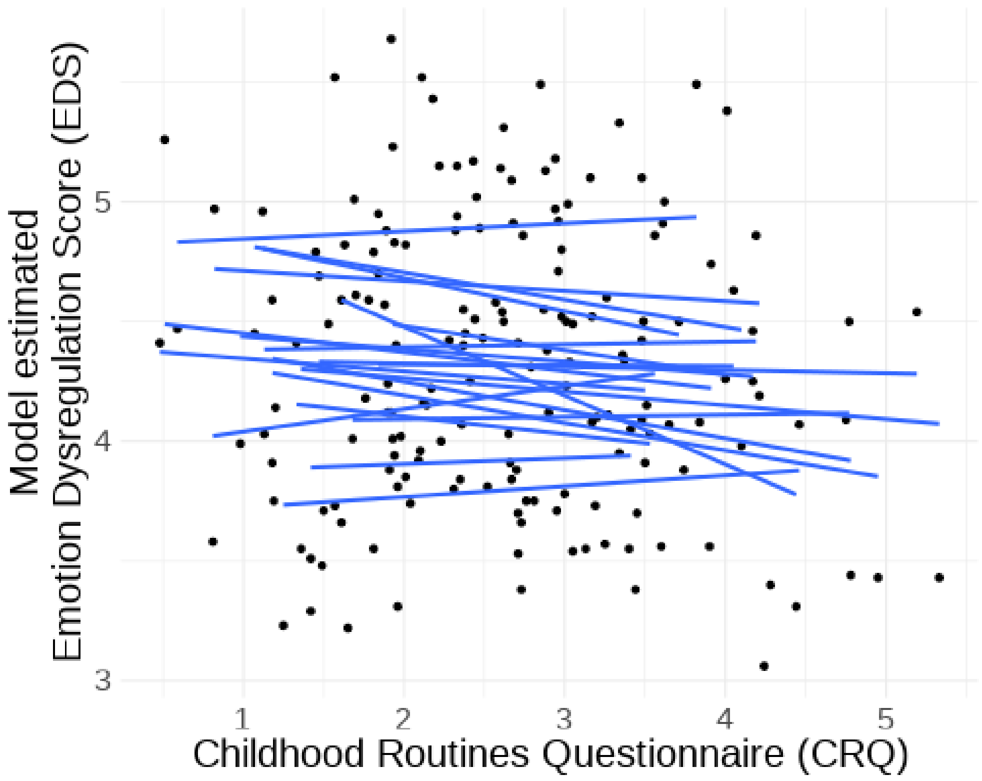
logistic regression visualised

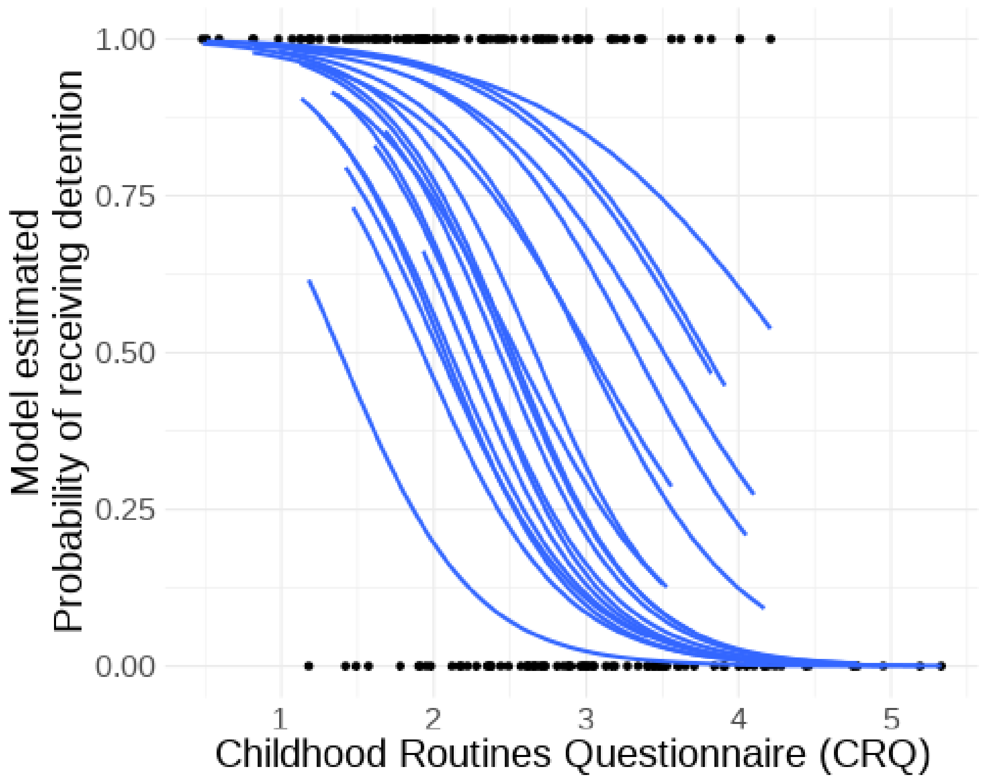
$ln\left(\frac{p}{1-p}\right)$

log-odds are linear

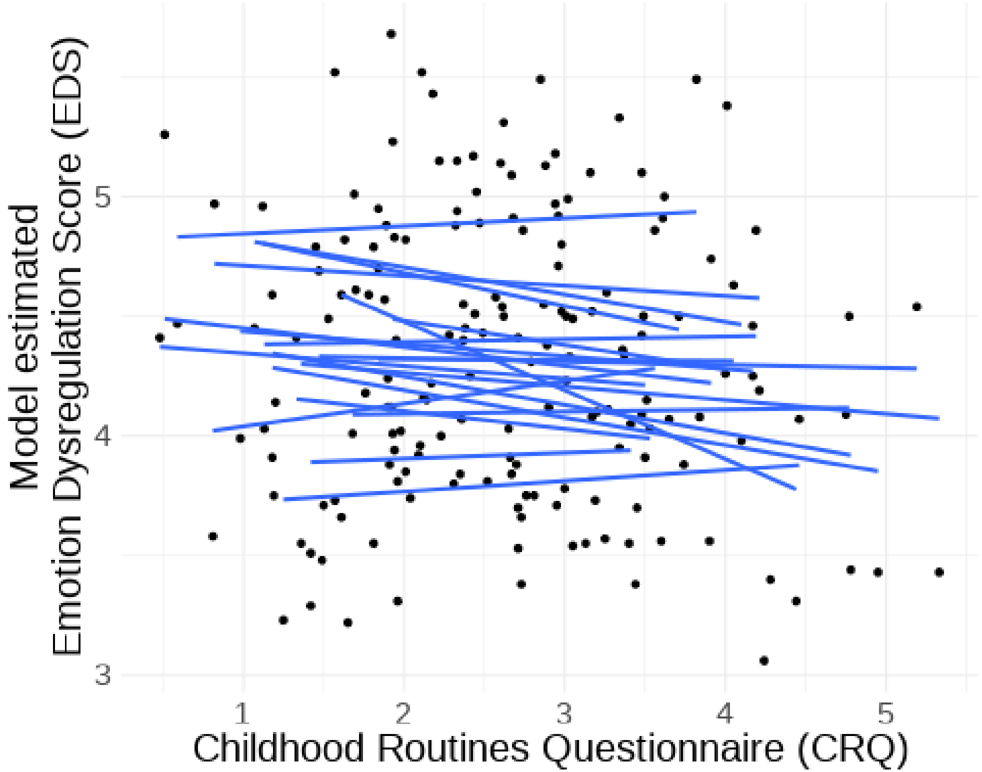


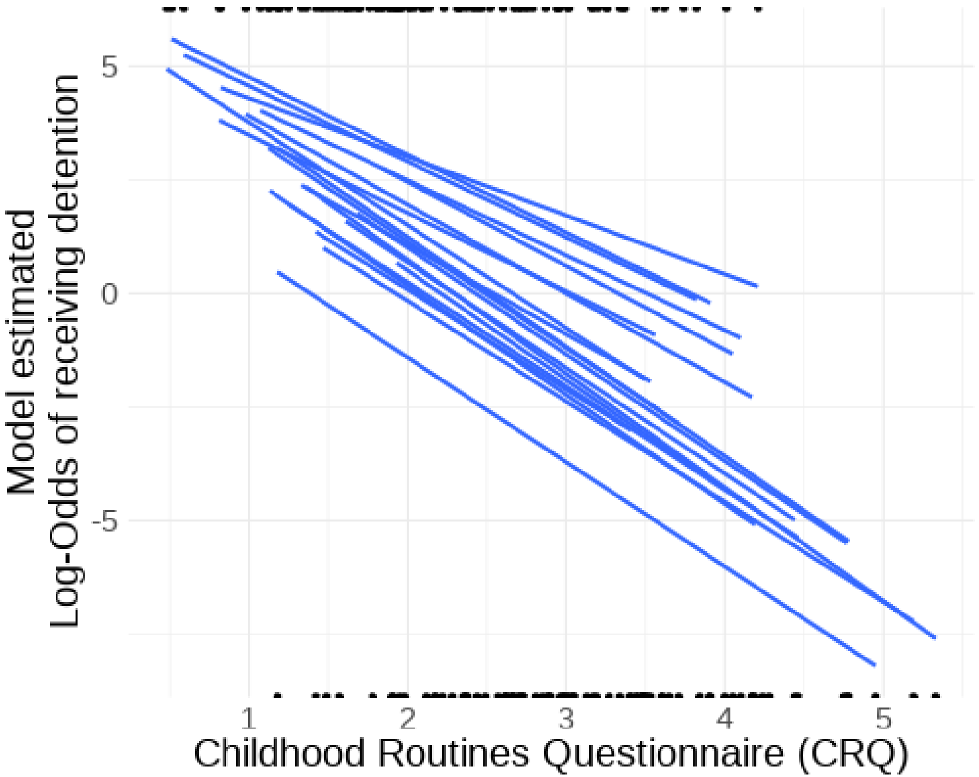
lmer() and glmer()





lmer() and glmer()





fitting a glmer()

> Researchers are interested in whether the level of routine a child has in daily life influences their probability of receiving a detention at school. 200 pupils from 20 schools completed a survey containing the Child Routines Questionnaire (CRQ), and a binary variable indicating whether or not they had received detention in the past school year.

```
crq <- read_csv("https://uoepsy.github.io/data/crqdetentionda
head(crq)
```

```
## # A tibble: 6 × 7
##   emot_dysreg   crq int       schoolid sleep   age detention
##         <dbl> <dbl> <chr>     <chr>    <chr> <dbl>     <dbl>
## 1        4.12  1.92 Treatment school1  <8hr     14         1
## 2        3.22  1.65 Treatment school1  <8hr     11         1
## 3        4.86  3.56 Treatment school1  <8hr     16         1
## 4        4.79  1.45 Treatment school1  8hr+     16         1
## 5        3.58  0.81 Treatment school1  <8hr     12         1
## 6        4.41  2.71 Treatment school1  <8hr     15         0
```

```
detentionmod <- glmer(detention ~ crq + (1 + crq | schoolid),
      data = crq, family="binomial")
summary(detentionmod)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: detention ~ crq + (1 + crq | schoolid)
##    Data: crq
##
##      AIC      BIC   logLik deviance df.resid
##    180.0    195.8    -85.0    170.0      169
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.419 -0.450  0.119  0.504  1.826
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  schoolid (Intercept) 2.577    1.605
##           crq         0.414    0.643    -0.52
## Number of obs: 174, groups:  schoolid, 20
##
## Fixed effects:
##             Estimate Std. Error z value  Pr(>|z|)
## (Intercept)    5.472      1.184    4.62 0.0000038 ***
## crq           -2.126      0.465   -4.57 0.0000049 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

fitting a glmer()

> Researchers are interested in whether the level of routine a child has in daily life influences their probability of receiving a detention at school. 200 pupils from 20 schools completed a survey containing the Child Routines Questionnaire (CRQ), and a binary variable indicating whether or not they had received detention in the past school year.

```
crq <- read_csv("https://uoepsy.github.io/data/crqdetentionda
head(crq)
```

```
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```

```
detentionmod <- glmer(detention ~ crq + (1 + crq | schoolid),
      data = crq, family="binomial")
exp(fixef(detentionmod))
```

```
## (Intercept)         crq
##    237.8341      0.1193
```

interpretating coefficients

- `lm(y ~ x + ...)`
  - β_x denotes the change in the average y when x is increased by one unit and all other covariates are fixed.
- `lmer(y ~ x + ... + (1 + x + ... | cluster))`
  - β_x denotes the change in the average y when x is increased by one unit, averaged across clusters
- `glmer(ybin ~ x + ... + (1 + x + ... | cluster), family=binomial)`
  - e^{β_x} denotes the change in the average y when x is increased by one unit, **holding cluster constant.**

this is optional content

why are glmer() coefficients cluster-specific?

consider a **linear** multilevel model: `lmer(respiratory_rate ~ treatment + (1|hospital))`

Imagine two patients from different hospitals. One is has a treatment, one does not.

- patient j from hospital i is "control"
- patient j' from hospital i' is "treatment"

The difference in estimated outcome between patient j and patient j' is the "the effect of having treatment" plus the distance in random deviations between hospitals i and i'

model for patient j from hospital i
$\hat{y}_{ij} = (\gamma_{00} + \zeta_{0i}) + \beta_1(Treatment_{ij} = 0)$

model for patient j' from hospital i'
$\hat{y}_{i'j'} = (\gamma_{00} + \zeta_{0i'}) + \beta_1(Treatment_{i'j'} = 1)$

difference:
$\hat{y}_{i'j'} - \hat{y}_{ij} = \beta_1 + (\zeta_{0i'} - \zeta_{0i}) = \beta_1$

Because $\zeta \sim N(0, \sigma_\zeta)$, the differences between all different $\zeta_{0i'} - \zeta_{0i}$ average out to be 0.

this is optional content

why are glmer() coefficients cluster-specific?

consider a **logistic** multilevel model: `glmer(needs_op ~ treatment + (1|hospital), family="binomial")`

Imagine two patients from different hospitals. One is has a treatment, one does not.

- patient j from hospital i is "control"
- patient j' from hospital i' is "treatment"

The difference in **probability of outcome** between patient j and patient j' is the "the effect of having treatment" plus the distance in random deviations between hospitals i and i'

model for patient j from hospital i

$$log\left(\frac{p_{ij}}{1-p_{ij}}\right) = (\gamma_{00} + \zeta_{0i}) + \beta_1(Treatment_{ij} = 0)$$

model for patient j' from hospital i'

$$log\left(\frac{p_{i'j'}}{1-p_{i'j'}}\right) = (\gamma_{00} + \zeta_{0i'}) + \beta_1(Treatment_{i'j'} = 1)$$

difference (log odds):

$$log\left(\frac{p_{i'j'}}{1-p_{i'j'}}\right) - log\left(\frac{p_{ij}}{1-p_{ij}}\right) = \beta_1 + (\zeta_{0i'} - \zeta_{0i})$$

this is optional content

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$$log\left(\frac{p_{ij}}{1-p_{ij}}\right) = (\gamma_{00} + \zeta_{0i}) + \beta_1(Treatment_{ij} = 0)$$

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$$log\left(\frac{p_{i'j'}}{1-p_{i'j'}}\right) = (\gamma_{00} + \zeta_{0i'}) + \beta_1(Treatment_{i'j'} = 1)$$

difference (odds ratio):

$$\frac{p_{i'j'}/(1-p_{i'j'})}{p_{ij}/(1-p_{ij})} = \exp(\beta_1 + (\zeta_{0i'} - \zeta_{0i}))$$

this is optional content

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$$log\left(\frac{p_{i'j'}}{1-p_{i'j'}}\right) = (\gamma_{00} + \zeta_{0i'}) + \beta_1(Treatment_{i'j'} = 1)$$

difference (odds ratio):

$$\frac{p_{i'j'}/(1-p_{i'j'})}{p_{ij}/(1-p_{ij})} = \exp(\beta_1 + (\zeta_{0i'} - \zeta_{0i})) \neq \exp(\beta_1)$$

this is optional content

why are glmer() coefficients cluster-specific?

consider a **logistic** multilevel model: `glmer(needs_op ~ treatment + (1|hospital), family="binomial")`

Hence, the interpretation of e^{β_1} is not the odds ratio for the effect of treatment "averaged over hospitals", but rather for patients *from the same hospital*.

Summary

- Differences between linear and logistic multi-level models are analogous to the differences between single-level linear and logistic regression models.
- Fixed effects in logistic multilevel models are "conditional upon" holding the cluster constant.

End