THE UNIVERSITY
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Assumptions & Diagnostics
More random effects

Data Analysis for Psychology in R 3

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AY 2021-2022

Part 1: Assumptions

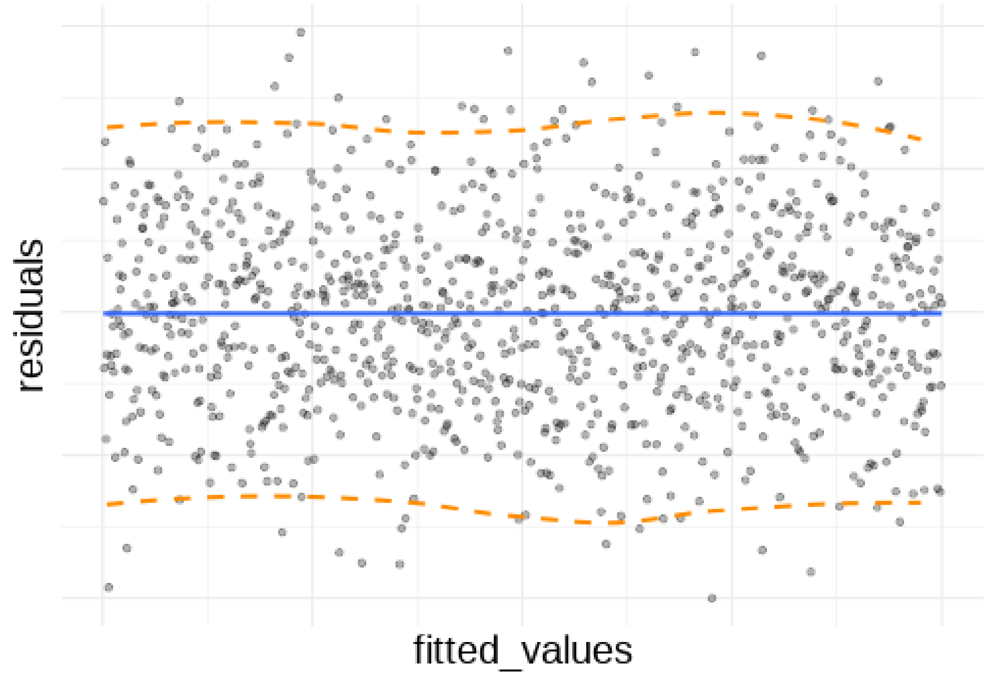
Part 2: Case Diagnostics in MLM

Part 3: Random Effect Structures

Assumptions in LM

The general idea

- $\varepsilon_i \sim N(0, \sigma^2)$ iid
- "zero mean and constant variance"



Assumptions in LM

The general idea

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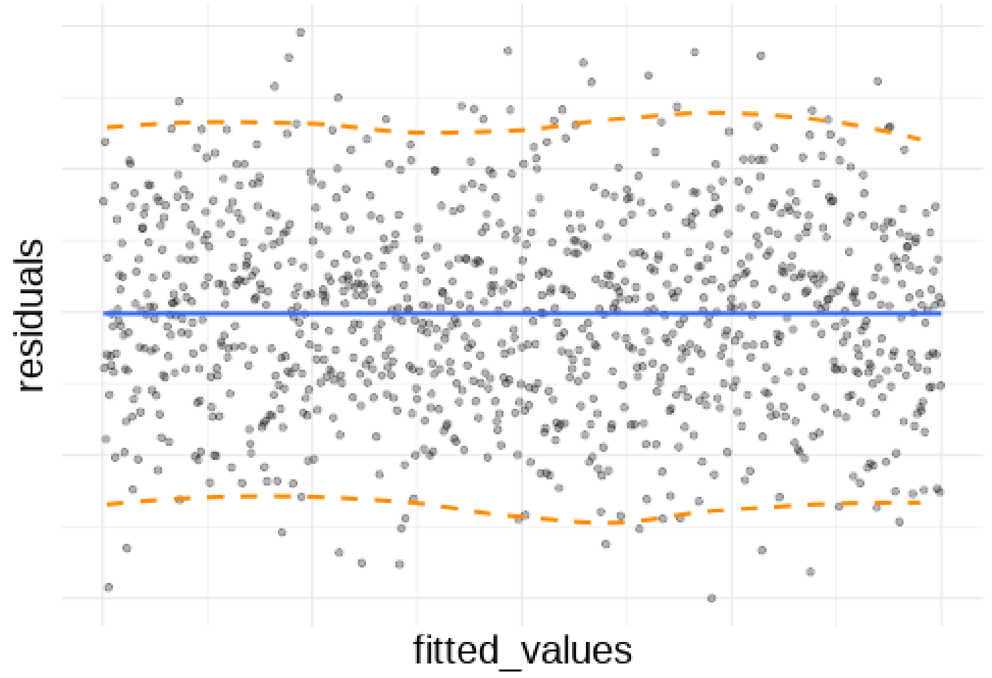
- "zero mean and constant variance"



Recipe book

- Linearity
- Independence
- Normality
- Equal Variances

What's different in MLM?

- Not much is different!

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- General idea is unchanged: error is random

What's different in MLM?

- Not much is different!
- General idea is unchanged: error is random
- We now have residuals at multiple levels!

Random effects as level 2 residuals

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Random effects as level 2 residuals

for observation j in group i

Level 1:
$y_{ij} = \beta_{0i} \cdot 1 + \beta_{1i} \cdot x_{ij} + \varepsilon_{ij}$
Level 2:
$\beta_{0i} = \gamma_{00} + \zeta_{0i}$
$\beta_{1i} = \gamma_{10} + \zeta_{1i}$

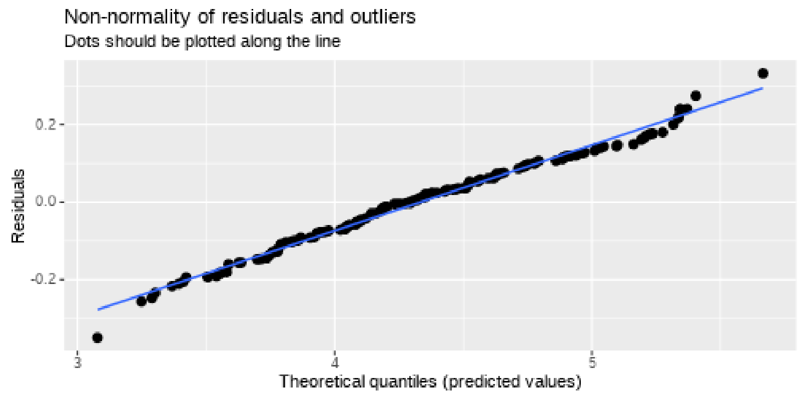
$\varepsilon, \zeta_0,$ and ζ_1 are all assumed to be normally distributed with mean 0.

Random effects as level 2 residuals

ε

`resid(model)`

mean zero, constant variance

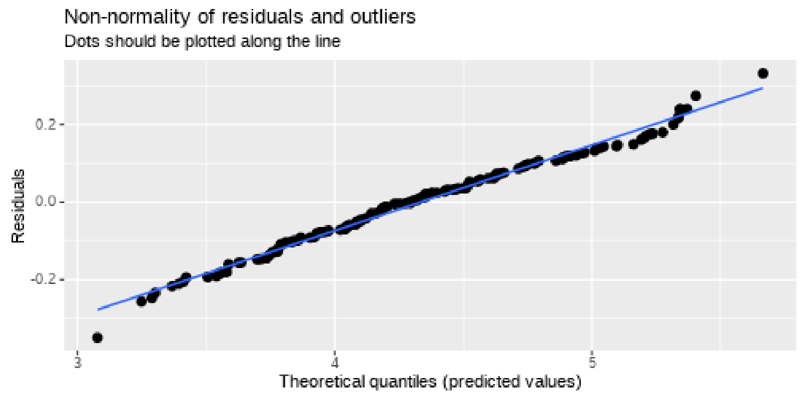


Random effects as level 2 residuals

ε

`resid(model)`

mean zero, constant variance

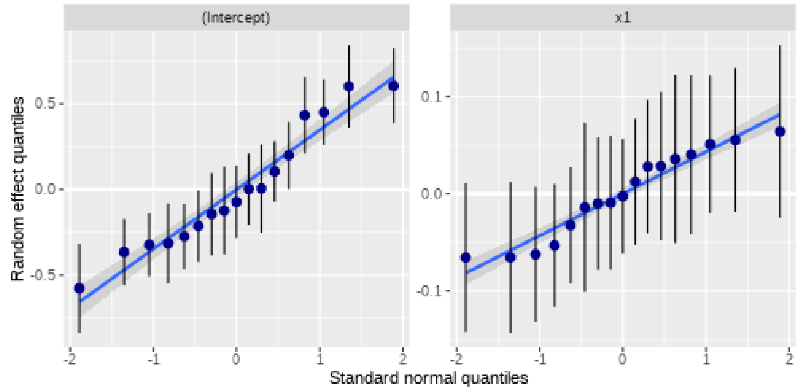


ζ

`ranef(model)`

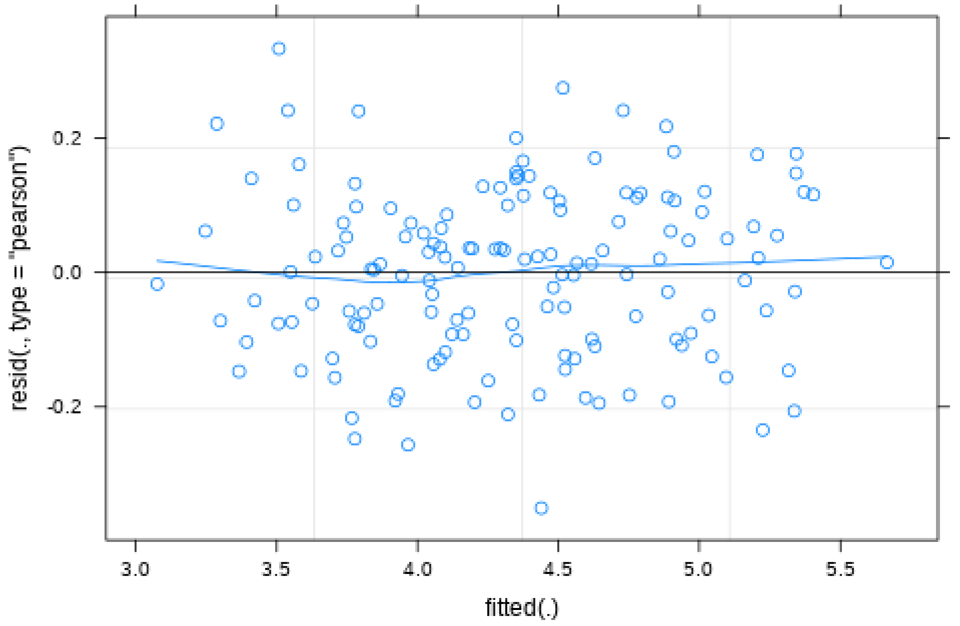
mean zero, constant variance

```
## $cluster
```



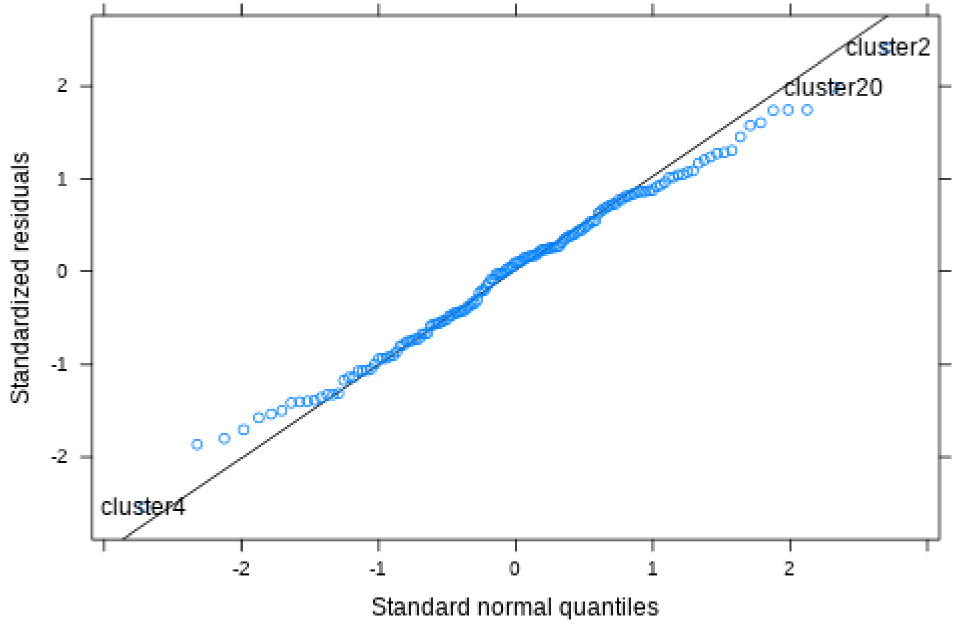
Assumption Plots: Residuals vs Fitted

```r
plot(model, type=c("p","smooth"))
```



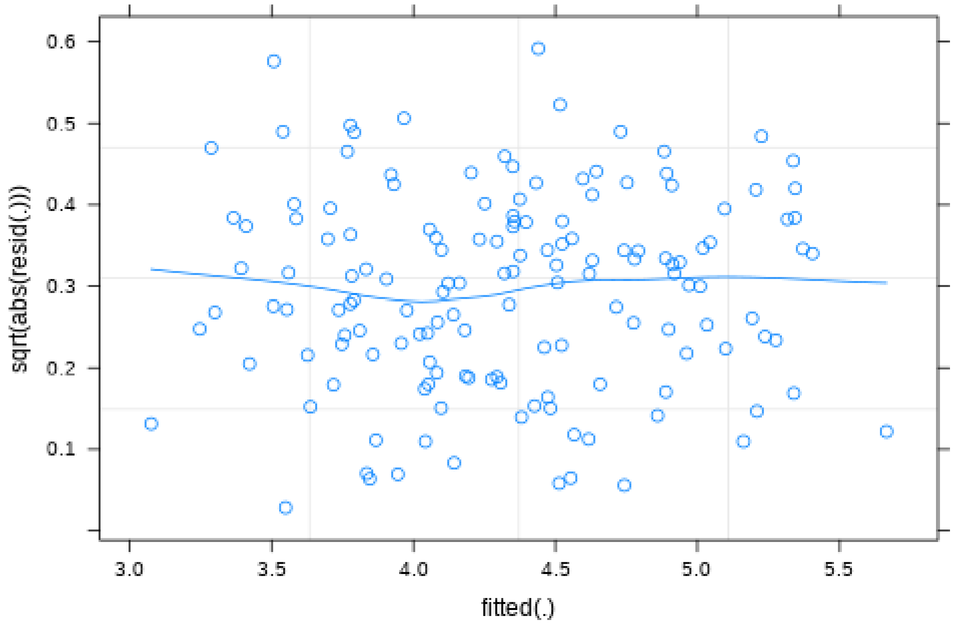
Assumption Plots: qqplots

```
library(lattice)
qqmath(model, id=.05)
```



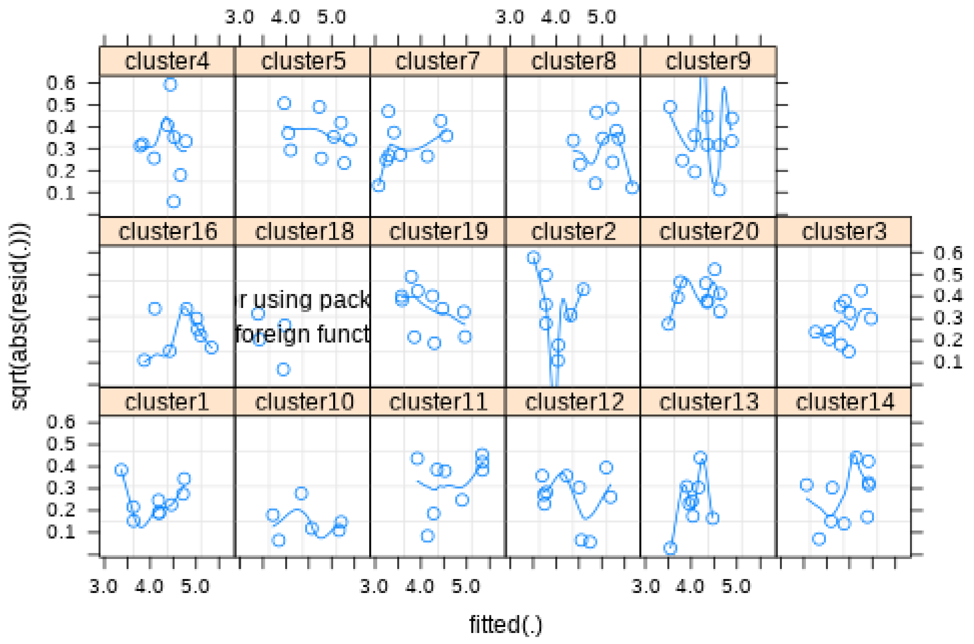
Assumption Plots: Scale-Location

```
plot(model,
     form = sqrt(abs(resid(.))) ~ fitted(.),
     type = c("p","smooth"))
```



Assumption Plots: Scale-Location

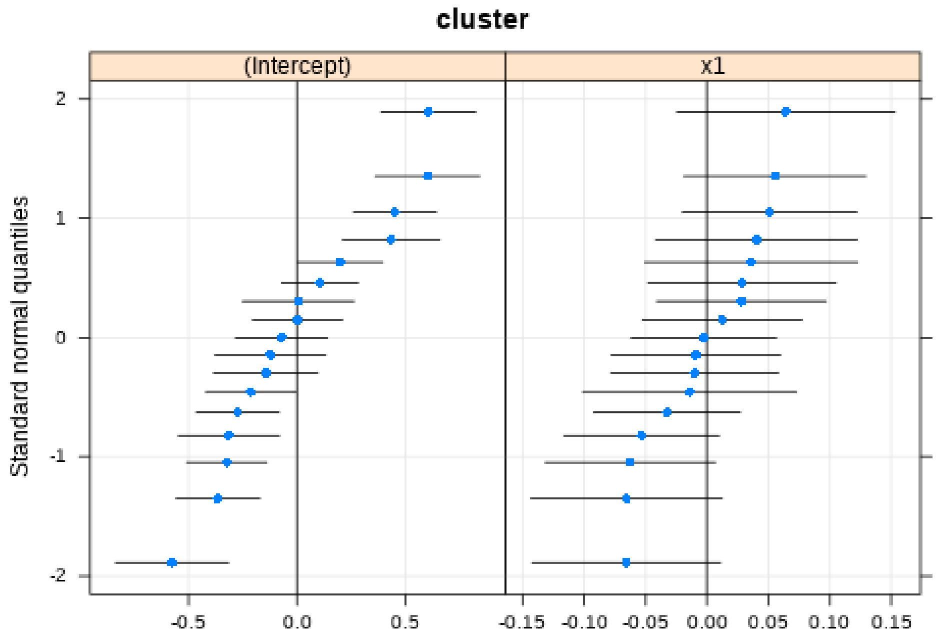
```
plot(model,
     form = sqrt(abs(resid(.))) ~ fitted(.) | cluster,
     type = c("p","smooth"))
```



Assumption Plots: Ranefs

```r
qqmath(ranef(model))
```

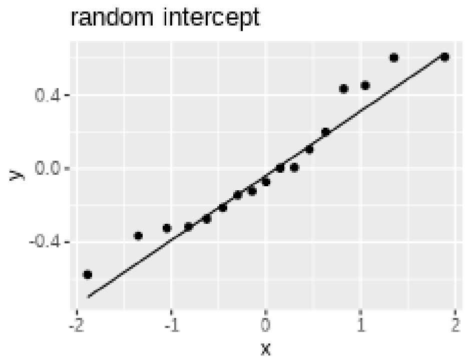
```
## $cluster
```

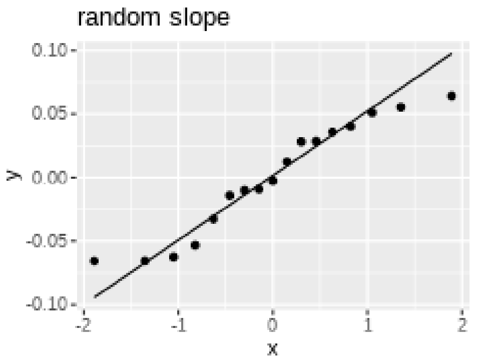


```r
rans <- as.data.frame(ranef(model)$cluster)

ggplot(rans, aes(sample = `(Intercept)`)) +
  stat_qq() + stat_qq_line() +
  labs(title="random intercept")

ggplot(rans, aes(sample = x1)) +
  stat_qq() + stat_qq_line()
  labs(title="random slope")
```

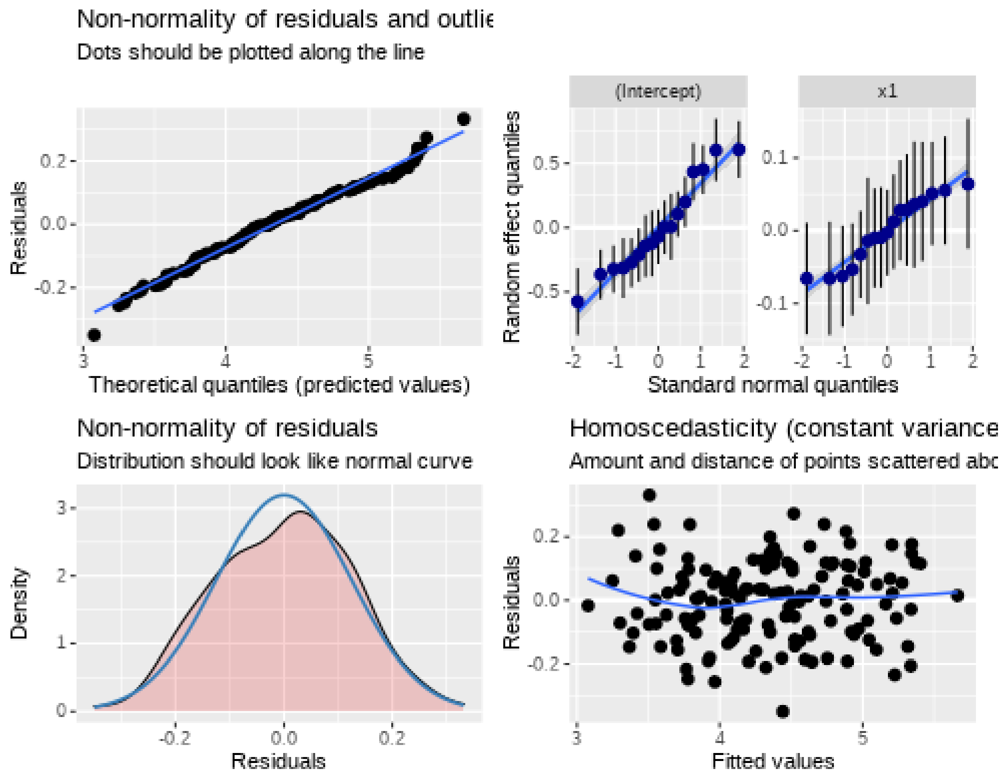




for a quick check

if nothing else...

```r
sjPlot::plot_model(model, type = "diag")
```



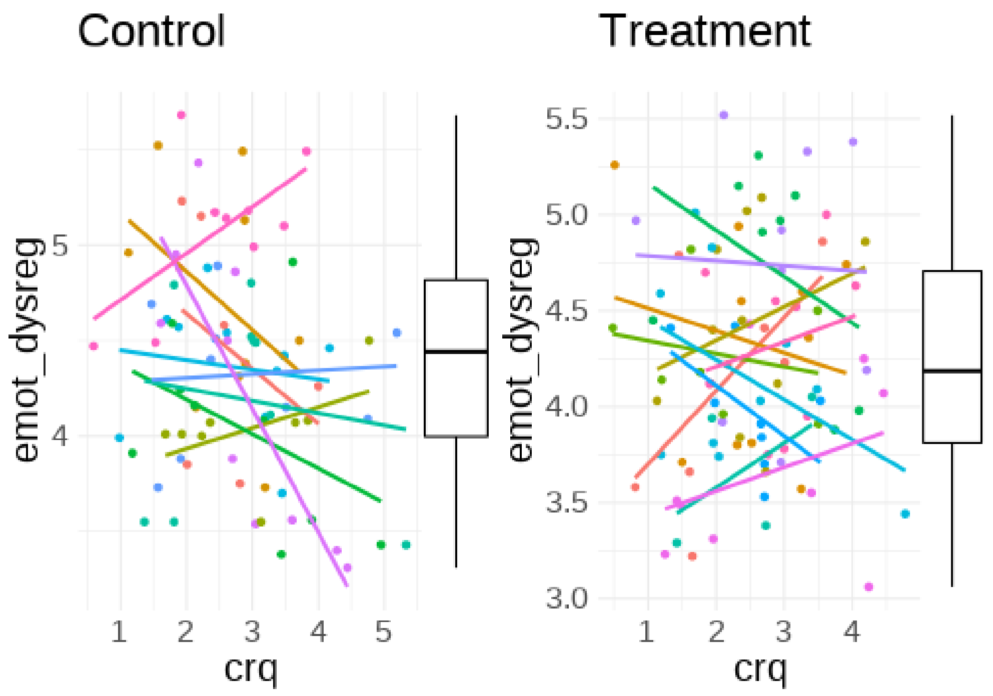
Part 1: Assumptions Troubleshooting

Part 2: Case Diagnostics in MLM

Part 3: Random Effect Structures

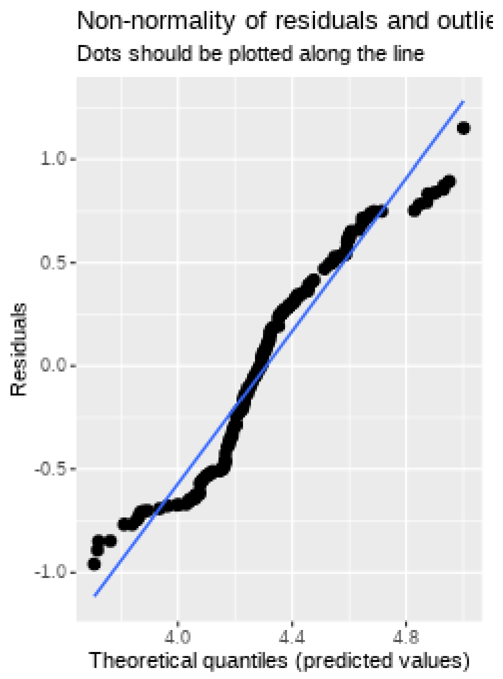
Some Data

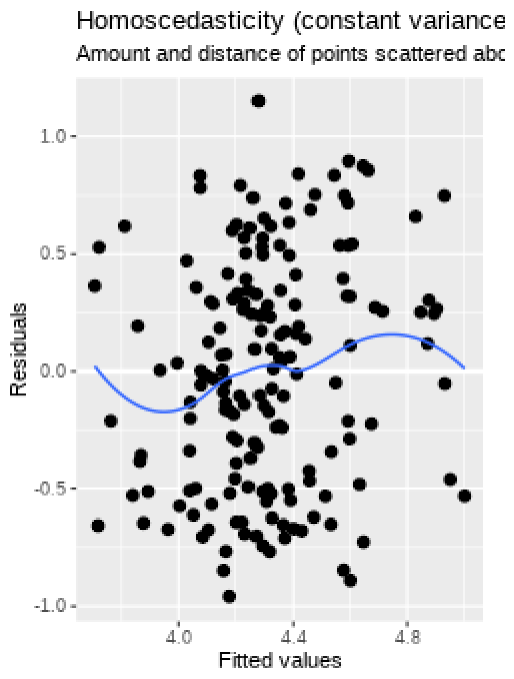
> 200 pupils from 20 schools completed a survey containing the Emotion Dysregulation Scale (EDS) and the Child Routines Questionnaire (CRQ). Eleven of the schools were taking part in an initiative to specifically teach emotion regulation as part of the curriculum.
>
> Adjusting for levels of daily routines, do children from schools partaking in the intervention present with lower levels of emotional dysregulation?



When things look wrong

```
mymodel <- lmer(emot_dysreg ~ crq + int + (1 | schoolid), data = crq)
```

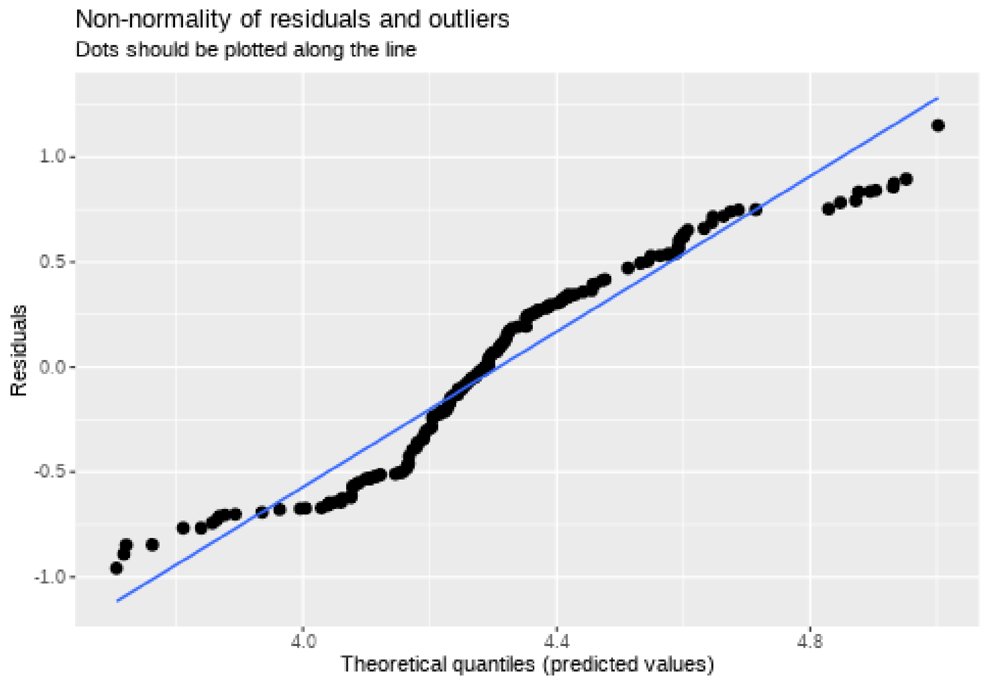




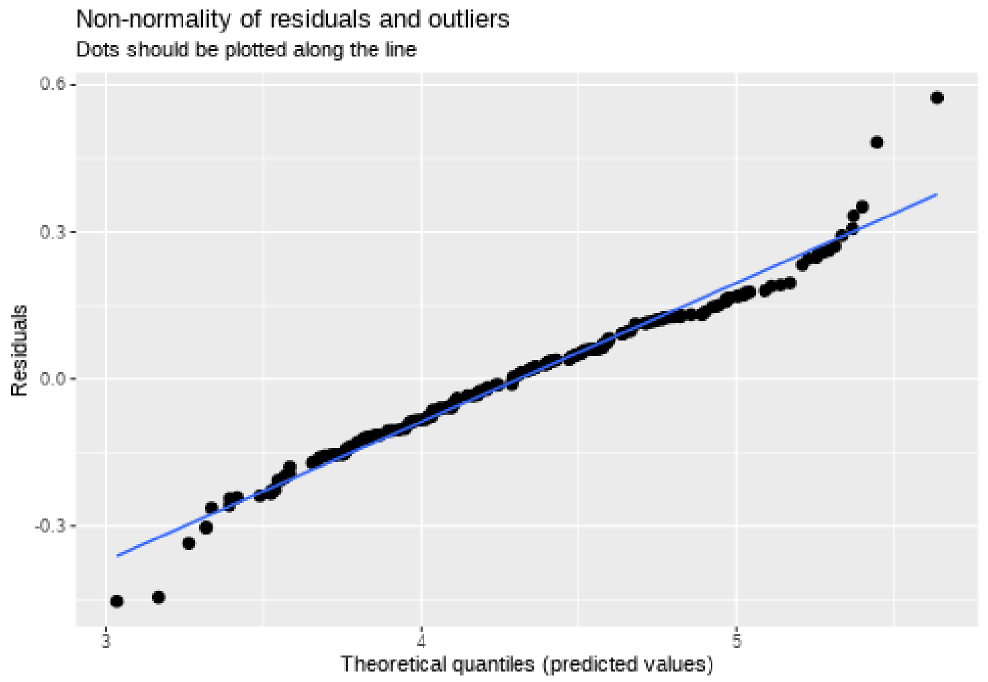
When things look wrong

Model mis-specification?

```
mymodel <- lmer(emot_dysreg ~ crq + int + (1 | schoolid), dat
```



```
mymodel <- lmer(emot_dysreg ~ crq + age + int + (1 | schoolid
```



When things look wrong

Transformations?

- Transforming your outcome variable may help to satisfy model assumptions

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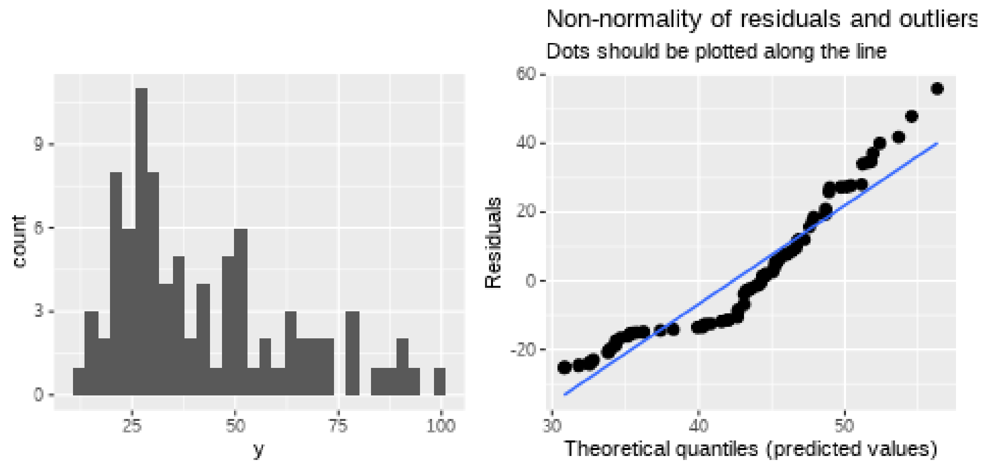
- log(y)
- 1/y
- sqrt(y)
- forecast::BoxCox(y)

When things look wrong

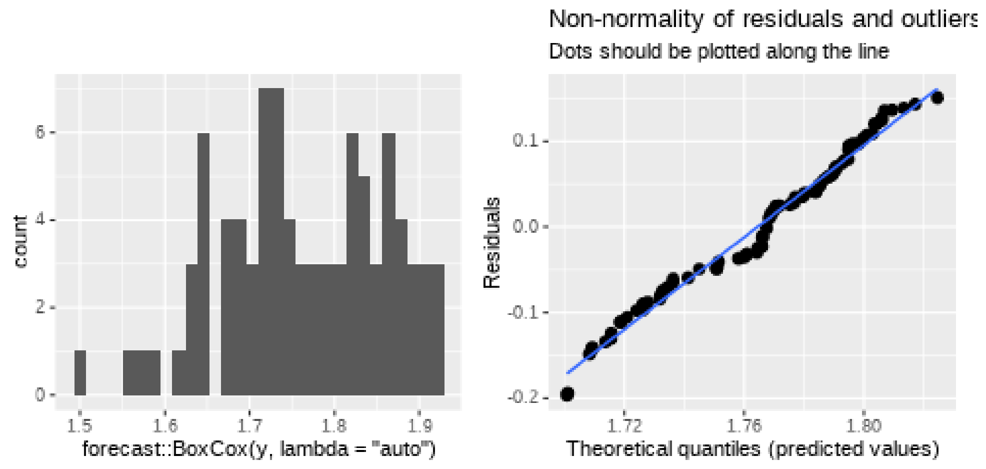
Transformations?

- Transforming your outcome variable may help to satisfy model assumptions

```
lmer(y ~ x1 + g + (1 | cluster), df)
```



```
lmer(forecast::BoxCox(y,lambda="auto") ~ x1 + g + (1 | cluste
```



When things look wrong

Transformations?

- Transforming your outcome variable may help to satisfy model assumptions **but it comes at the expense of interpretability.**

```r
lmer(y ~ x1 + g + (1 | cluster), df)
```

```
## (Intercept)          x1           g
##      36.137       1.615      10.020
```

```r
lmer(forecast::BoxCox(y,lambda="auto") ~ x1 + g + (1 | cluste
```

```
## (Intercept)          x1           g
##    1.733760    0.006857    0.048426
```

When things look wrong

Bootstrap?

basic idea:

1. do many many times:
   a. take a sample (e.g. sample with replacement from your data, or simulated from your model parameters)
   b. fit the model to the sample
2. then:
   a. based on all the models fitted in step 1, obtain a distribution of parameter estimate of interest.
   b. based on the bootstrap distribution from 2a, compute a confidence interval for estimate.
   c. celebrate

Bootstrap: What do we (re)sample?

resample based on the estimated distributions of parameters?

- assumes explanatory variables are fixed, model specification and the distributions (e.g. $\zeta \sim N(0, \sigma_\zeta)$ and $\varepsilon \sim N(0, \sigma_\varepsilon)$) are correct.

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resample residuals

- $y* = \hat{y} + \hat{\varepsilon}_{\text{sampled with replacement}}$
- assumes explanatory variables are fixed, and model specification is correct.

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resample residuals

- $y* = \hat{y} + \hat{\varepsilon}_{\text{sampled with replacement}}$
- assumes explanatory variables are fixed, and model specification is correct.

resample cases

- minimal assumptions - that we have correctly specified the hierarchical structure of data
- But do we resample:
  - observations?
  - clusters?
  - both?

Bootstrap: Parametric

```r
reducedmodel <- lmer(emot_dysreg ~ crq + age + (1 | schoolid), data = crq)
mymodel <- lmer(emot_dysreg ~ crq + age + int + (1 | schoolid), data = crq)
```

- bootstrap LRT

  ```r
  library(pbkrtest)
  PBmodcomp(mymodel, reducedmodel)
  ```

- bootstrap CIs

  ```r
  confint(mymodel, method="boot")
  ```

Bootstrap: Parametric

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- bootstrap LRT

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  library(pbkrtest)
  PBmodcomp(mymodel, reducedmodel)
  ```

- bootstrap CIs

  ```r
  confint(mymodel, method="boot")
  ```

- **lmeresampler** package bootstrap() function

  ```r
  library(lmeresampler)
  mymodelBS <- bootstrap(mymodel, .f = fixef, type = "parametric", B = 2000)
  confint(mymodelBS, type = "norm")
  ```

At time of writing, there is a minor bug with the version of **lmeresampler** that you can download from CRAN, so we recommend installing directly from the package maintainer: `devtools::install_github("aloy/lmeresampler")`

Bootstrap: Cases

```r
mymodel <- lmer(emot_dysreg ~ crq + age + int + (1 | schoolid), data = crq)
```

```r
# devtools::install_github("aloy/lmeresampler")
library(lmeresampler)
# resample only children, not schools
mymodelBScase <- bootstrap(mymodel, .f = fixef,
                           type = "case", B = 2000,
                           resample = c(FALSE, TRUE))
summary(mymodelBScase)
```

```
## Bootstrap type: case
##
## Number of resamples: 2000
##
##            term observed rep.mean        se        bias
## 1   (Intercept)   0.9563   0.9514 0.106136 -0.0049006
## 2           crq  -0.1004  -0.1007 0.013939 -0.0003475
## 3           age   0.2727   0.2731 0.007825  0.0004362
## 4  intTreatment  -0.1520  -0.1525 0.024481 -0.0005422
##
## There were 0 messages, 0 warnings, and 0 errors.
```

```r
confint(mymodelBScase, type = "basic")
```

```
## # A tibble: 4 × 6
##   term         estimate  lower   upper type  level
##   <chr>           <dbl>  <dbl>   <dbl> <chr> <dbl>
## 1 (Intercept)     0.956  0.747  1.17   basic  0.95
## 2 crq            -0.100 -0.129 -0.0731 basic  0.95
## 3 age             0.273  0.257  0.288  basic  0.95
## 4 intTreatment   -0.152 -0.199 -0.104  basic  0.95
```

For a nice how-to guide on the lmeresampler package, see http://aloy.github.io/lmeresampler/articles/lmeresampler-vignette.html.
For a discussion of different bootstrap methods for multilevel models, see Leeden R.., Meijer E., Busing F.M. (2008) Resampling Multilevel Models. In: Leeuw J.., Meijer E. (eds) Handbook of Multilevel Analysis. Springer, New York, NY. DOI: 10.1007/978-0-387-73186-5_11

Bootstrap: Cases

```r
mymodel <- lmer(emot_dysreg ~ crq + age + int + (1 | schoolid), data = crq)
```

```r
# devtools::install_github("aloy/lmeresampler")
library(lmeresampler)
# resample only children, not schools
mymodelBScase <- bootstrap(mymodel, .f = fixef,
                           type = "case", B = 2000,
                           resample = c(FALSE, TRUE))
summary(mymodelBScase)
```

```
## Bootstrap type: case
##
## Number of resamples: 2000
##
##            term observed rep.mean       se       bias
## 1   (Intercept)   0.9563   0.9514 0.106136 -0.0049006
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## 4  intTreatment  -0.1520  -0.1525 0.024481 -0.0005422
##
## There were 0 messages, 0 warnings, and 0 errors.
```
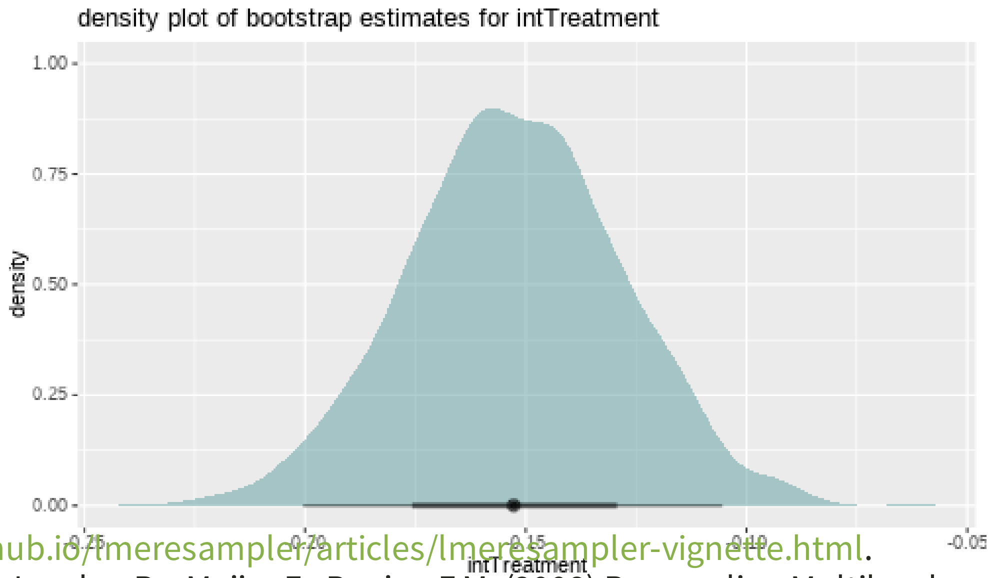

```r
plot(mymodelBScase,"intTreatment")
```



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Summary

- Our assumptions for multi-level models are similar to that of a standard linear model in that we are concerned with the our residuals
    - in the multi-level case, we have residuals are multiple levels.
- When assumptions appear violated, there are various courses of action to consider.
    - primarily, we should think about whether our model makes theoretical sense
- Resampling methods (e.g. Bootstrapping) can be used to obtain confidence intervals and bias-corrected estimates of model parameters.
    - There are various forms of the bootstrap, with varying assumptions.

End of Part 1

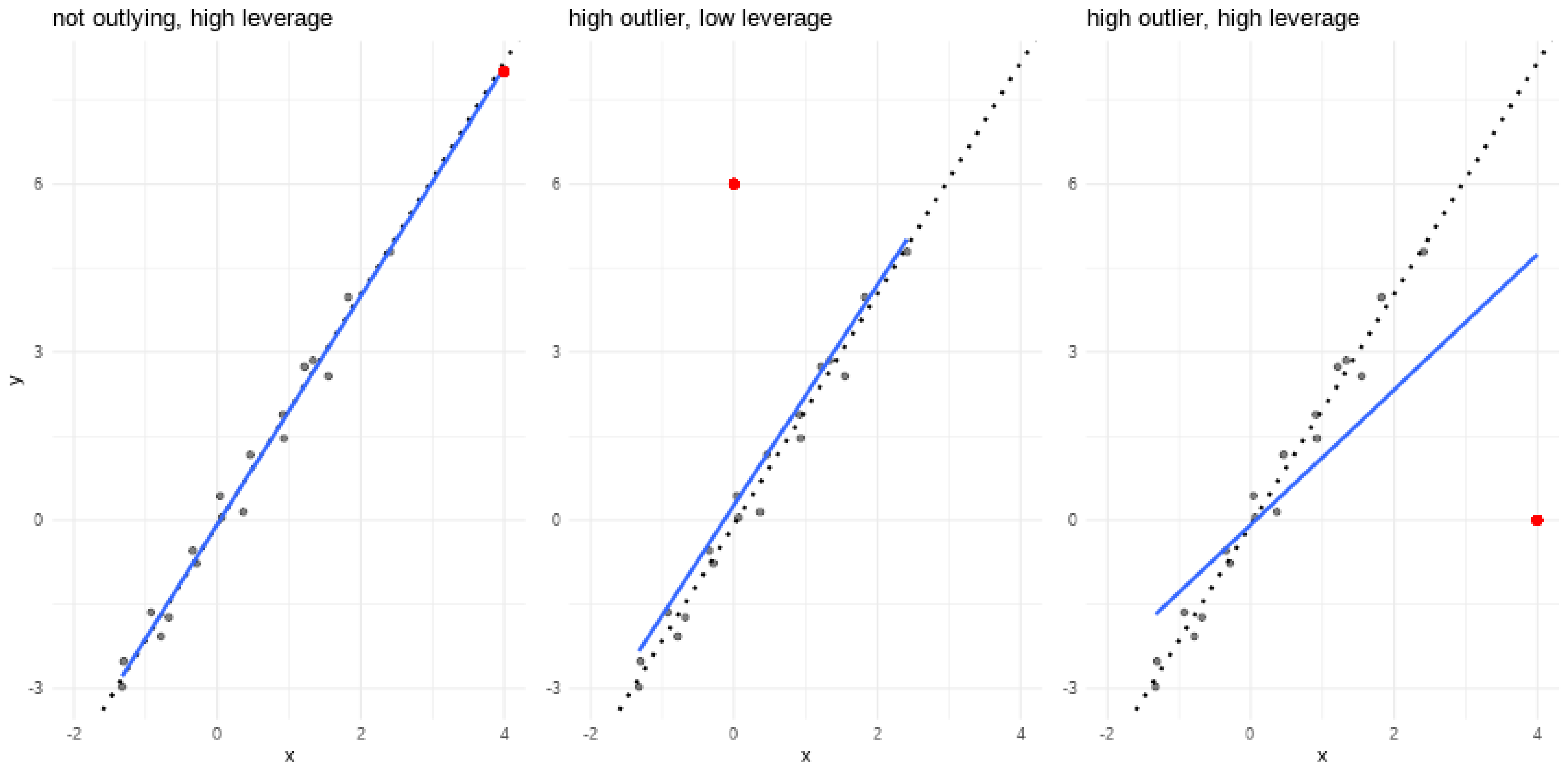
Part 1: Assumptions

Part 2: Case Diagnostics in MLM

Part 3: Random Effect Structures

Influence

Just like standard `lm()`, observations can have unduly high influence on our model through a combination of high leverage and outlyingness.



multiple levels...

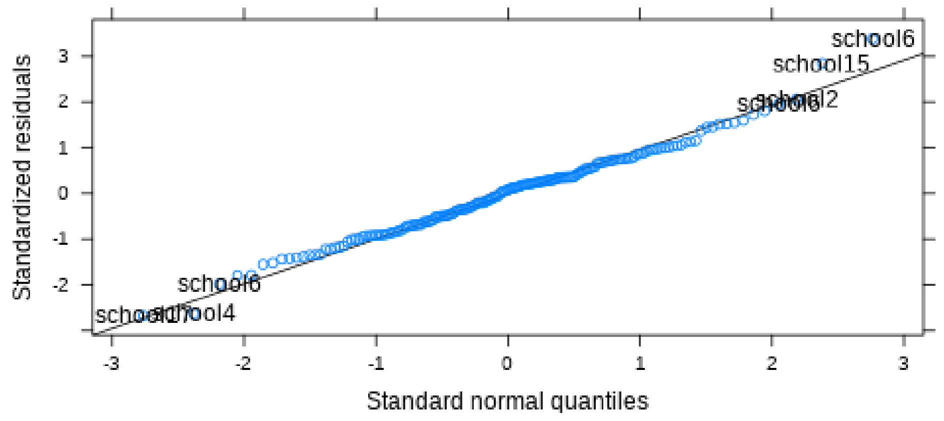
- Both observations (level 1 units) **and** clusters (level 2+ units) can be influential.

multiple levels...

- Both observations (level 1 units) **and** clusters (level 2+ units) can be influential.
- several packages, but current recommendation is **HLMdiag:** http://aloy.github.io/HLMdiag/index.html

Level 1 influential points

```
mymodel <- lmer(emot_dysreg ~ crq + age +
                  int + (1 | schoolid),
                data = crq)
qqmath(mymodel, id=0.05)
```



Level 1 influential points

```r
mymodel <- lmer(emot_dysreg ~ crq + age +
                  int + (1 | schoolid),
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qqmath(mymodel, id=0.05)
```
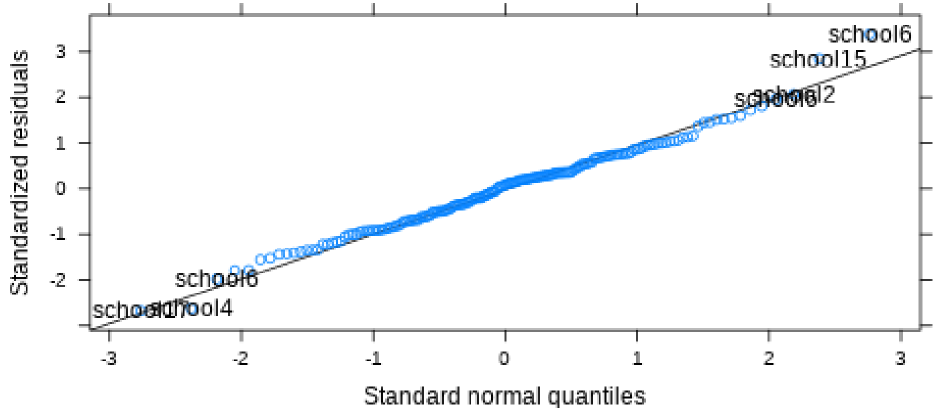



```r
library(HLMdiag)
infl1 <- hlm_influence(mymodel, level = 1)
names(infl1)
```

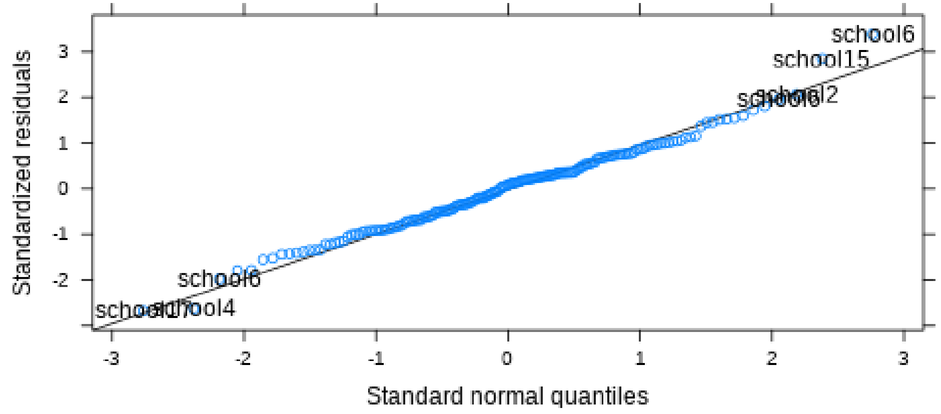
```
##  [1] "id"                "emot_dysreg"       "crq"               "age"
##  [5] "int"               "schoolid"          "cooksd"            "mdffit
##  [9] "covtrace"          "covratio"          "leverage.overall"
```

```r
infl1
```

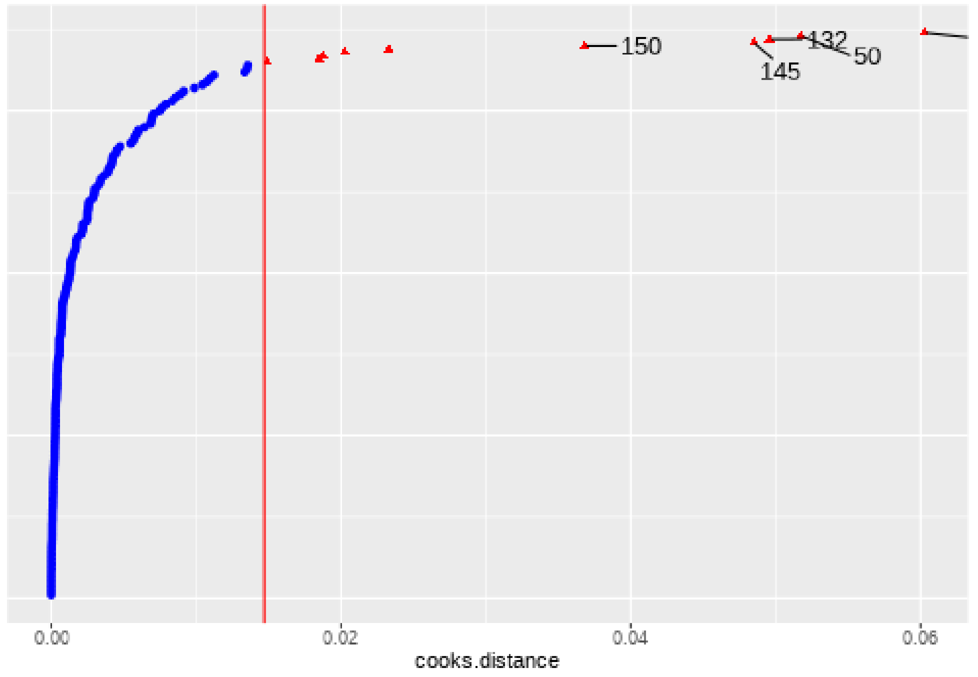
```
## # A tibble: 174 × 11
##       id emot_dysreg   crq   age int       schoolid     cooksd  mdffi
##    <int>       <dbl> <dbl> <dbl> <fct>     <fct>         <dbl>   <db
##  1     1        4.12  1.92    14 Treatment school1  0.0000660   6.59e
##  2     2        3.22  1.65    11 Treatment school1  0.00749     7.34e
##  3     3        4.86  3.56    16 Treatment school1  0.0185      1.80e
##  4     4        4.79  1.45    16 Treatment school1  0.0000195   1.92e
##  5     5        3.58  0.81    12 Treatment school1  0.00692     6.79e
##  6     6        4.41  2.71    15 Treatment school1  0.00000410  4.07e
##  7     7        4.23  3.01    14 Treatment school1  0.00104     1.04e
##  8     8        3.66  1.61    12 Treatment school1  0.000102    1.01e
##  9     9        4.22  2.17    14 Treatment school1  0.00000750  7.50e
## 10    10        4.42  2.28    14 Treatment school2  0.000254    2.53e
## # … with 164 more rows, and 2 more variables: covratio <dbl>,
## #   leverage.overall <dbl>
```

Level 1 influential points

```r
mymodel <- lmer(emot_dysreg ~ crq + age +
                  int + (1 | schoolid),
                data = crq)
qqmath(mymodel, id=0.05)
```

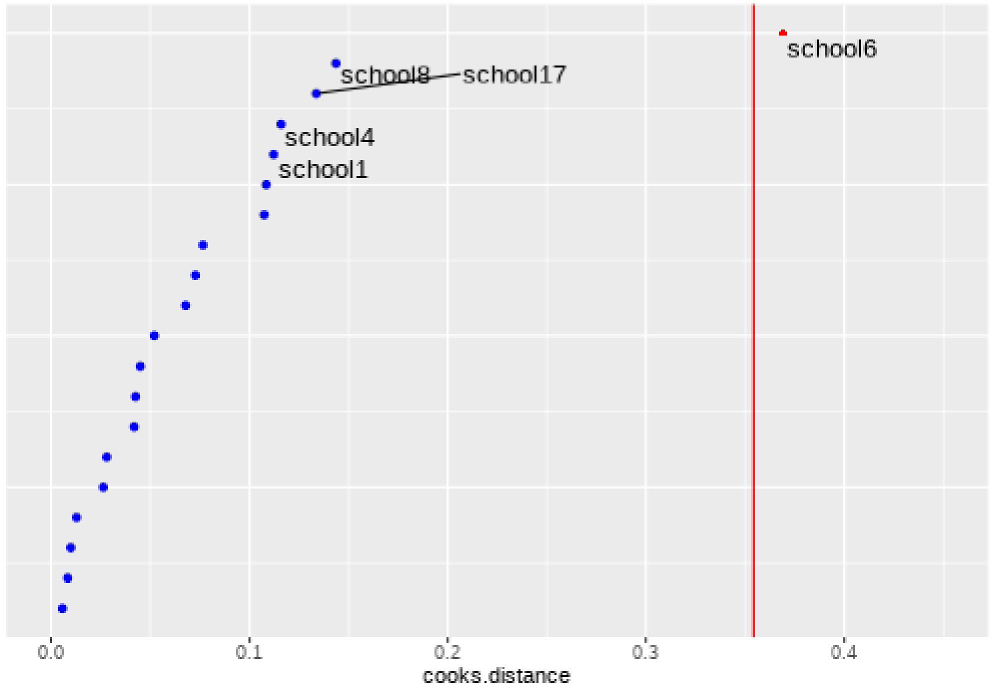


```r
library(HLMdiag)
infl1 <- hlm_influence(mymodel, level = 1)
dotplot_diag(infl1$cooksd, cutoff = "internal")
```



Level 2 influential clusters

```
infl2 <- hlm_influence(mymodel, level = "schoolid")
dotplot_diag(infl2$cooksd, cutoff = "internal", index=infl2$schoolid)
```



What to do?

- In this context (children from schools), I would be inclined not to worry too much about the individual children who have high values on cook's distance, if we plan on case-based bootstrap for our inferential tests (and plan on resampling the level 1 units - the children).

What to do?

- In this context (children from schools), I would be inclined not to worry too much about the individual children who have high values on cook's distance, if we plan on case-based bootstrap for our inferential tests (and plan on resampling the level 1 units - the children).
- It's worth looking into school 6 a bit further.
- `mdffits` is a measure of multivariate "difference in fixed effects"

```
infl2 %>% arrange(desc(mdffits))
```

```
## # A tibble: 20 × 6
##    schoolid  cooksd mdffits covtrace covratio leverage.overall
##    <fct>      <dbl>   <dbl>    <dbl>    <dbl>            <dbl>
##  1 school6  0.369   0.330      0.253     1.27            0.107
##  2 school8  0.144   0.128      0.245     1.26            0.131
##  3 school17 0.134   0.121      0.267     1.29            0.108
##  4 school1  0.112   0.104      0.193     1.20            0.117
##  5 school4  0.116   0.103      0.267     1.29            0.111
##  6 school5  0.108   0.0992     0.239     1.26            0.129
##  7 school11 0.107   0.0990     0.229     1.24            0.110
##  8 school7  0.0767  0.0701     0.283     1.31            0.148
##  9 school18 0.0730  0.0675     0.118     1.12            0.126
## 10 school16 0.0680  0.0620     0.195     1.21            0.122
## 11 school15 0.0522  0.0503     0.185     1.19            0.122
## 12 school20 0.0451  0.0426     0.242     1.26            0.105
## 13 school2  0.0427  0.0411     0.148     1.15            0.171
## 14 school9  0.0420  0.0405     0.186     1.20            0.122
## 15 school12 0.0281  0.0259     0.256     1.28            0.126
```

What to do?

- In this context (children from schools), I would be inclined not to worry too much about the individual children who have high values on cook's distance, if we plan on bootstrapping our inferential tests (and plan on resampling the level 1 units - the children).

- It's worth looking into school 6 a bit further.

- examine fixed effects upon deletion of schools 6

```
delete6 <- case_delete(mymodel, level = "schoolid", type = "fixef", delete = "school6")
cbind(delete6$fixef.original, delete6$fixef.delete)
```

```
##                  [,1]     [,2]
## (Intercept)   0.9563  1.06034
## crq          -0.1004 -0.08985
## age           0.2727  0.26519
## intTreatment -0.1520 -0.18202
```

Sensitivity Analysis?

Would our conclusions change if we excluded these schools?

```
mymodelrm6 <- lmer(emot_dysreg ~ crq + age +
                  int + (1 | schoolid),
                data = crq %>%
                  filter(!schoolid %in% c("school6")))
mymodelrm6BS <- bootstrap(mymodelrm6, .f = fixef,
                           type = "case", B = 2000,
                           resample = c(FALSE, TRUE))
confint(mymodelrm6BS, type = "basic")
```

```
## # A tibble: 4 × 6
##   term         estimate  lower   upper type  level
##   <chr>           <dbl>  <dbl>   <dbl> <chr> <dbl>
## 1 (Intercept)    1.06    0.857  1.26   basic  0.95
## 2 crq           -0.0899 -0.117 -0.0627 basic  0.95
## 3 age            0.265   0.251  0.280  basic  0.95
## 4 intTreatment  -0.182  -0.229 -0.136  basic  0.95
```

Summary

- Influence can be exerted by individual observations and higher lever groups of observations
    - e.g. by children and by schools, or by individual trials and by participants.
- We can get measures of influence at different levels, and consider how estimates and conclusions might change when certain observations (or groups) are excluded
- Bootstrapping is relevant as whether we are resampling at the level of an influential group/observation is going to affect the extent to which our estimates are biased by that observation/group

End of Part 3

Part 1: Assumptions

Part 2: Case Diagnostics in MLM

Part 3: Random Effect Structures

What have we seen so far?

- children within schools
- birds within gardens
- measurements within participants
- nurses within hospitals
- and probably some others...

Nested

- the level j observations in a level i group belong **only** to that level i group.

Nested

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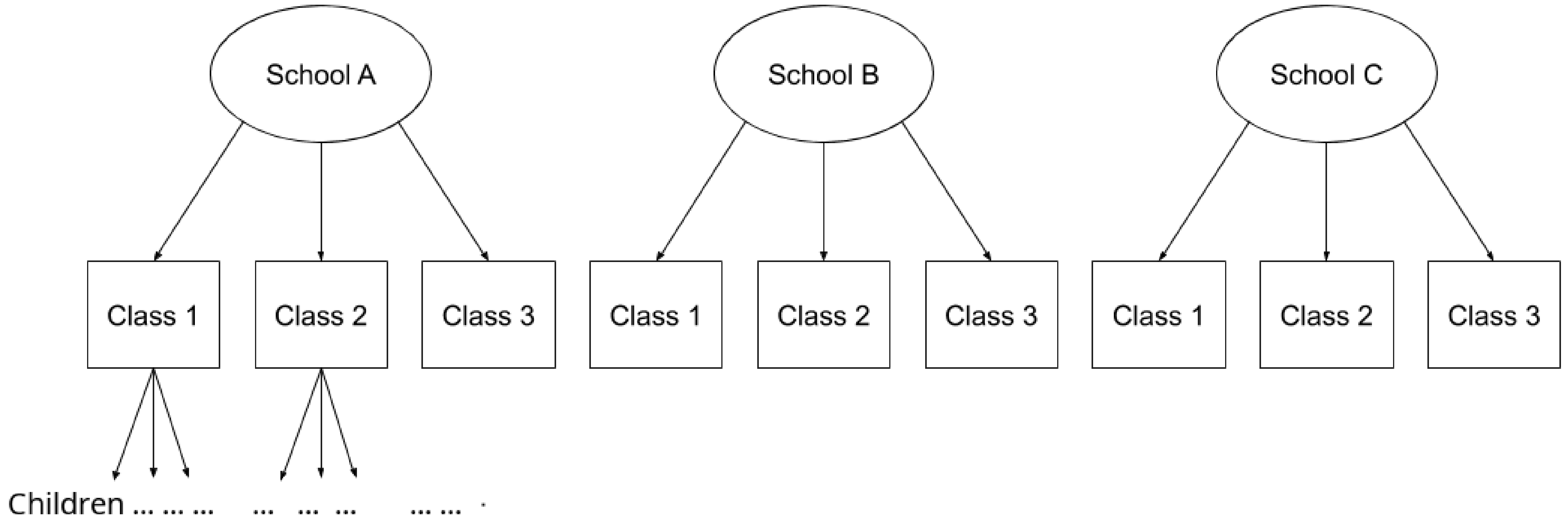
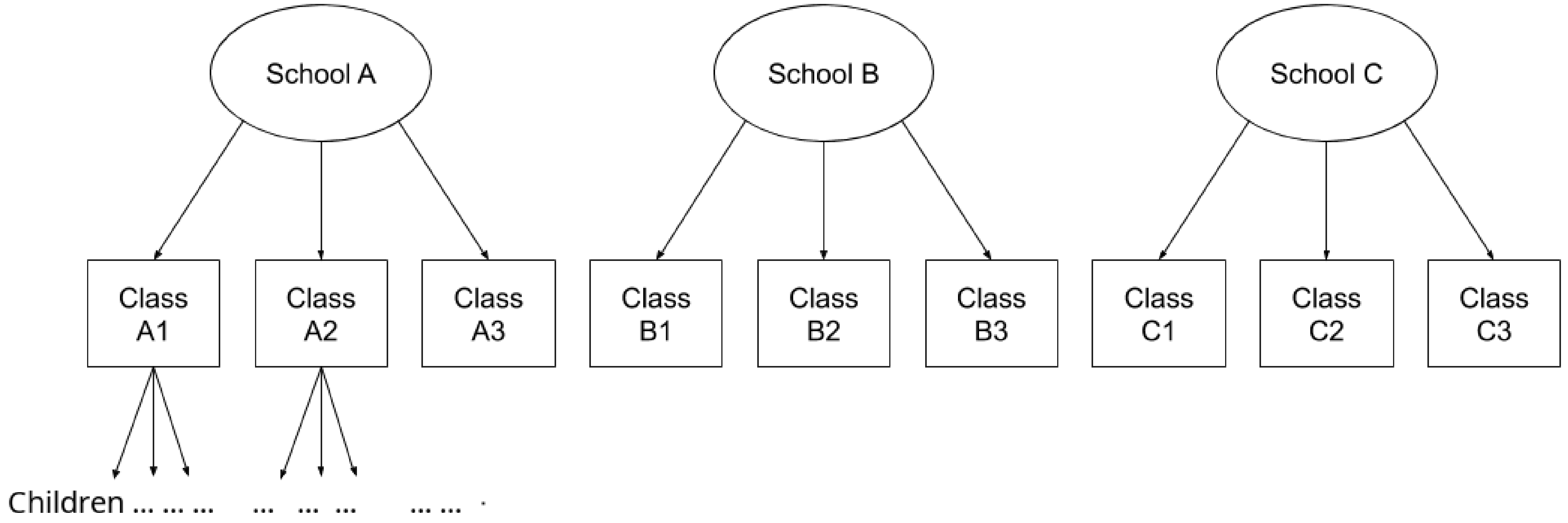
- `(1 | school/class)` or `(1 | school) + (1 | class:school)`



Nested

- the level j observations in a level i group belong **only** to that level i group.
- If labels are unique, `(1 | school) + (1 | class)` is the same as `(1 | school/class)`



Crossed

- "crossed" = not nested!

Crossed

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- `(1 | subject) + (1 | task)`

Fixed or random

Criterion:	**Repetition:** *If the experiment were repeated:*	**Desired inference:** *The conclusions refer to:*
Fixed effects	Same levels would be used	The levels used
Random effects	Different levels would be used	A population from which the levels used are just a (random) sample

- If only small number of clusters, estimating variance components may be unstable.
- Partialling out cluster-differences as fixed effects *may* be preferable.

Maximal Structures

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```
maxmodel <- lmer(emot_dysreg ~ crq + age + int + (1 + crq + age | schoolid), data = crq)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00275817 (tol = 0.002, component 1)
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```

another example: 16 items each occur in 4 different combinations: condition A vs B $\times$ type 1 vs 2.
40 participants see all items in all conditions (64 trials each participant).

```
mmod <- lmer(outcome ~ condition * type + (1 + condition * type | ppt) +
               (1 + condition * type | item), data = kelly)
```

```
## boundary (singular) fit: see ?isSingular
```

Model Convergence

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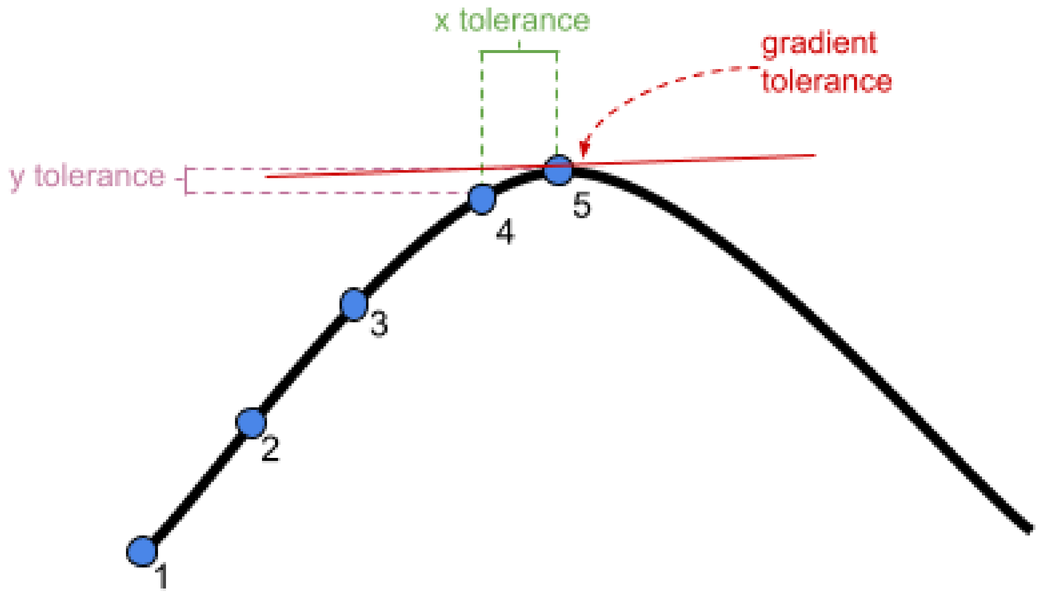

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- Remove random effects with least variance until model converges (see Barr et al., 2013)
- Use a criterion for model selection (e.g. AIC, BIC) to choose a random effect structure that is supported by the data (see Matsuchek et al., 2017)

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- Remove random effects with least variance until model converges (see Barr et al., 2013)
- Use a criterion for model selection (e.g. AIC, BIC) to choose a random effect structure that is supported by the data (see Matsuchek et al., 2017)
- **No right answer**

correlations between random effects

```
##  Groups   Name              Std.Dev. Corr
##  ppt      (Intercept)        91.7
##           conditionB         59.1    -0.21
##           type2              27.6     0.25 -0.42
##           conditionB:type2   22.4    -0.32 -0.86  0.26
##  item     (Intercept)        37.0
##           conditionB         35.8    -0.18
##           type2              20.2     0.14 -0.40
##           conditionB:type2   65.6     0.25  0.27 -0.92
##  Residual                   203.2
```

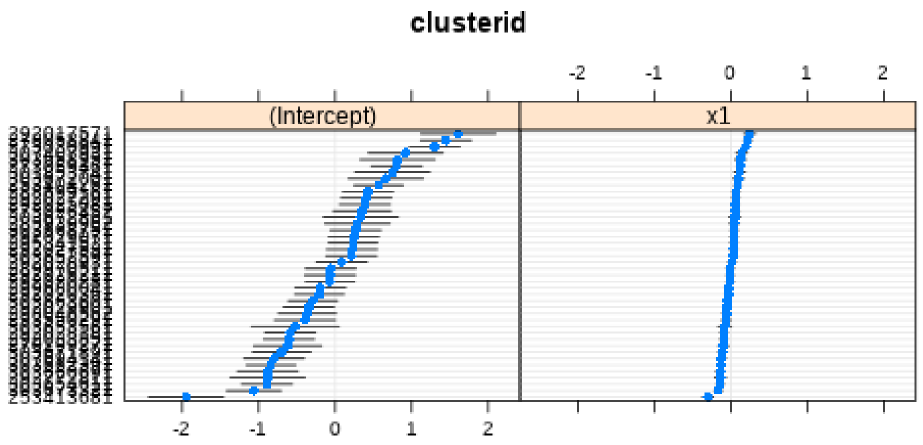
correlations between random effects

perfect correlations

```
m1 <- lmer(y ~ 1 + x1 +
             (1 + x1 | clusterid), data = df)
VarCorr(m1)
```

```
##  Groups    Name        Std.Dev. Corr
##  clusterid (Intercept) 0.759
##            x1          0.117    1.00
##  Residual              0.428
```

```
## $clusterid
```



correlations between random effects

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```r
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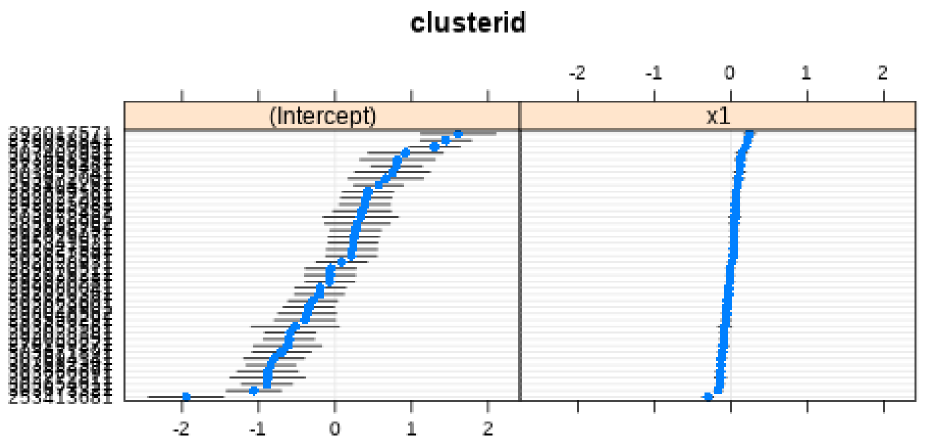
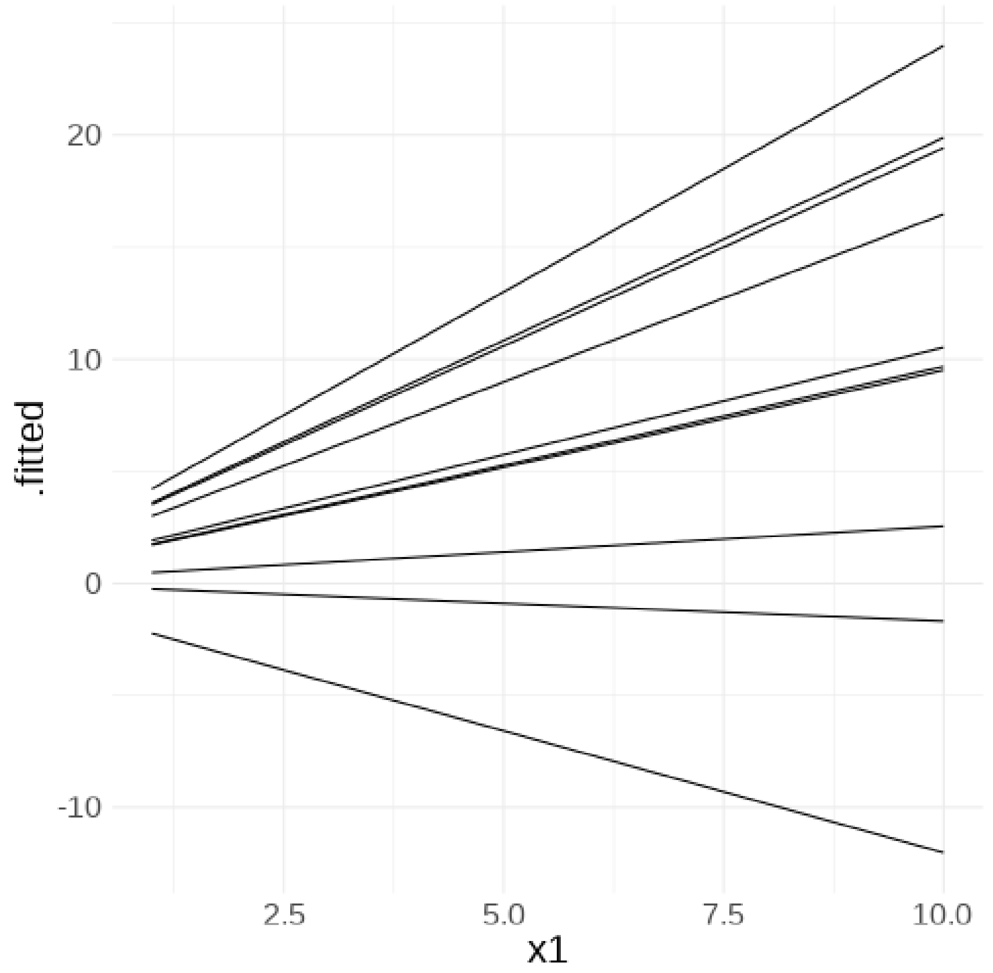
```





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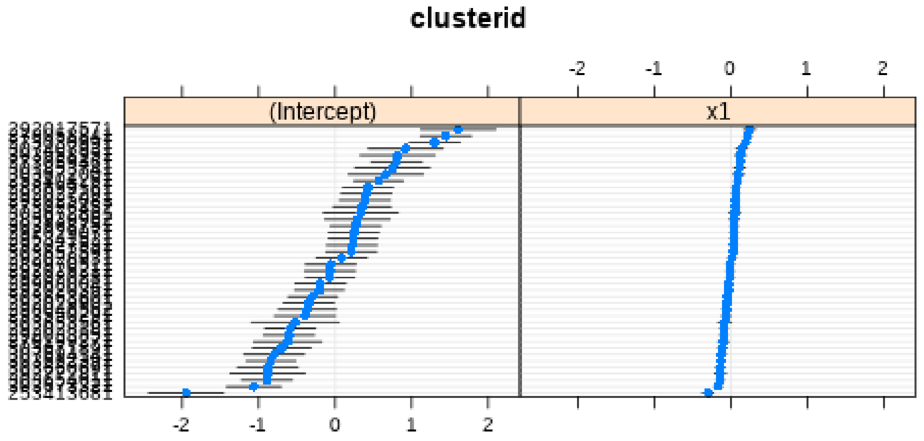
```

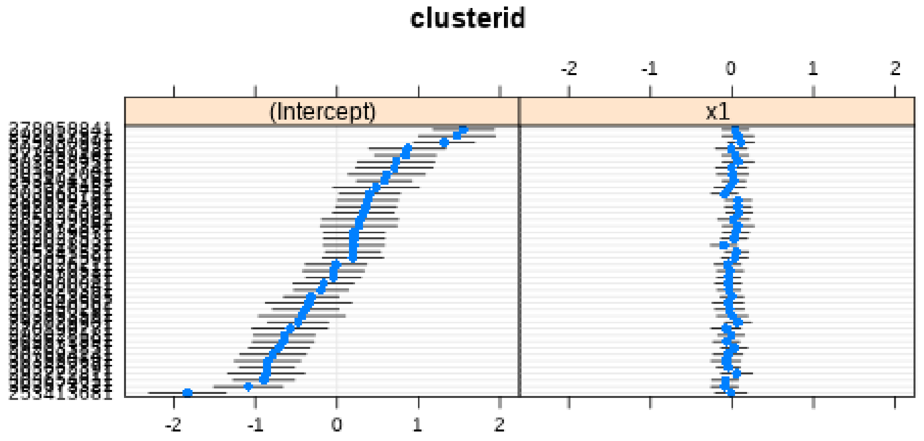


zero correlations

```
zcpmodel <- lmer(y ~ 1 + x1 +
                   (1 + x1 || clusterid), data = df)
VarCorr(zcpmodel)
```

```
##  Groups      Name        Std.Dev.
##  clusterid   (Intercept) 0.751
##  clusterid.1 x1          0.104
##  Residual                0.432
```

```
## $clusterid
```



correlations between random effects

When should we remove them?

correlations between random effects

When should we remove them?

When it makes theoretical sense to do so.

Summary

- random effect structures can get complicated quite quickly
    - we can have multiple levels of nesting
    - we can have crossed random effects
- the maximal random effect structure is the most complex structure we can fit to the data.
    - it often leads to problems with model convergence
- building MLMs is a balancing act between accounting for different sources of variance and attempting to fit a model that is too complex for our data.

End