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Multilevel models

Professor Andy Field

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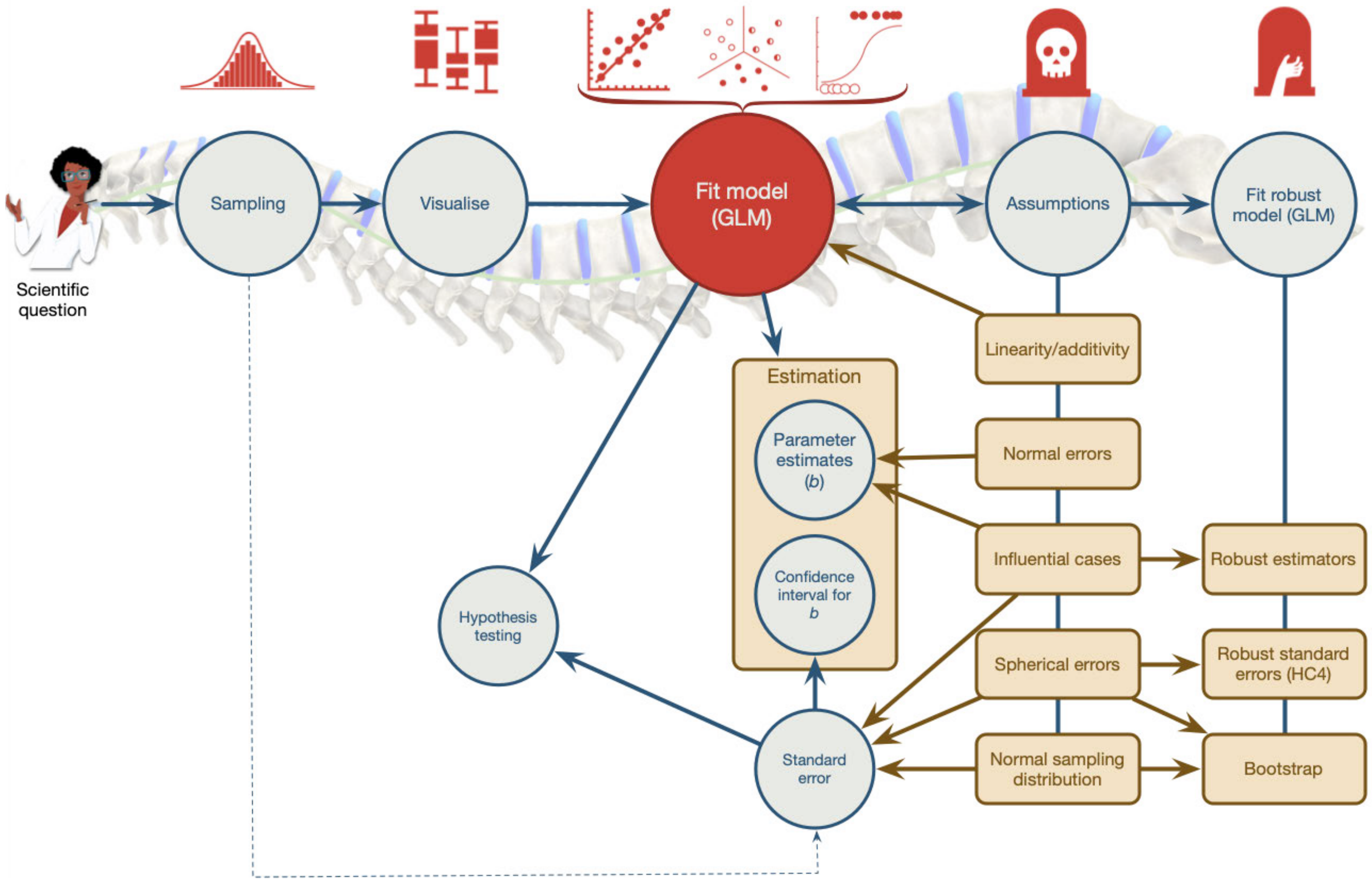
www.youtube.com/user/ProfAndyField/

www.discoveringstatistics.com

www.milton-the-cat.rocks

www.discovr.rocks



Scientific question
Sampling
Visualise
Fit model (GLM)
Assumptions
Fit robust model (GLM)
Estimation
Parameter estimates (b)
Confidence interval for b
Linearity/additivity
Normal errors
Influential cases
Spherical errors
Normal sampling distribution
Robust estimators
Robust standard errors (HC4)
Bootstrap
Hypothesis testing
Standard error

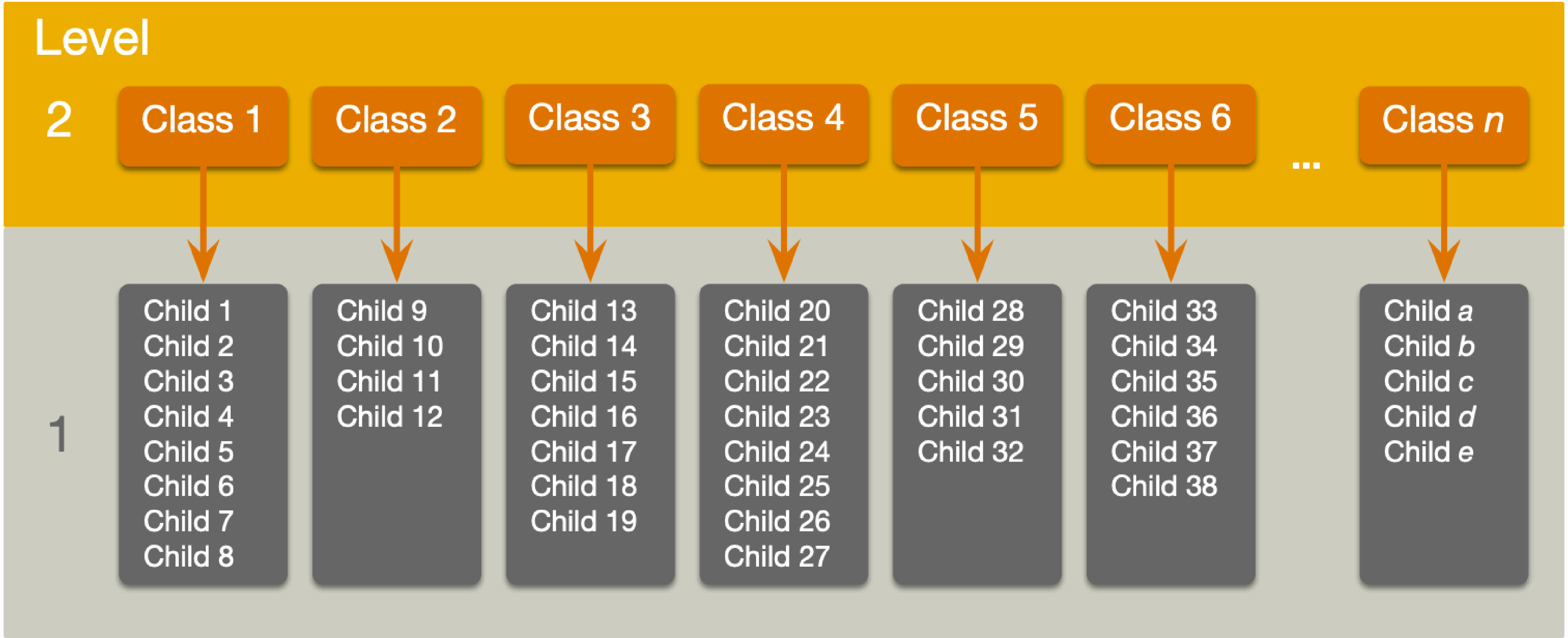
Learning outcomes

- Understand what hierarchical data are
  - Why we can't use the 'normal' GLM
- Understand fixed and random coefficients
- Understand how to build models
- Be able to conduct and interpret models of hierarchical data

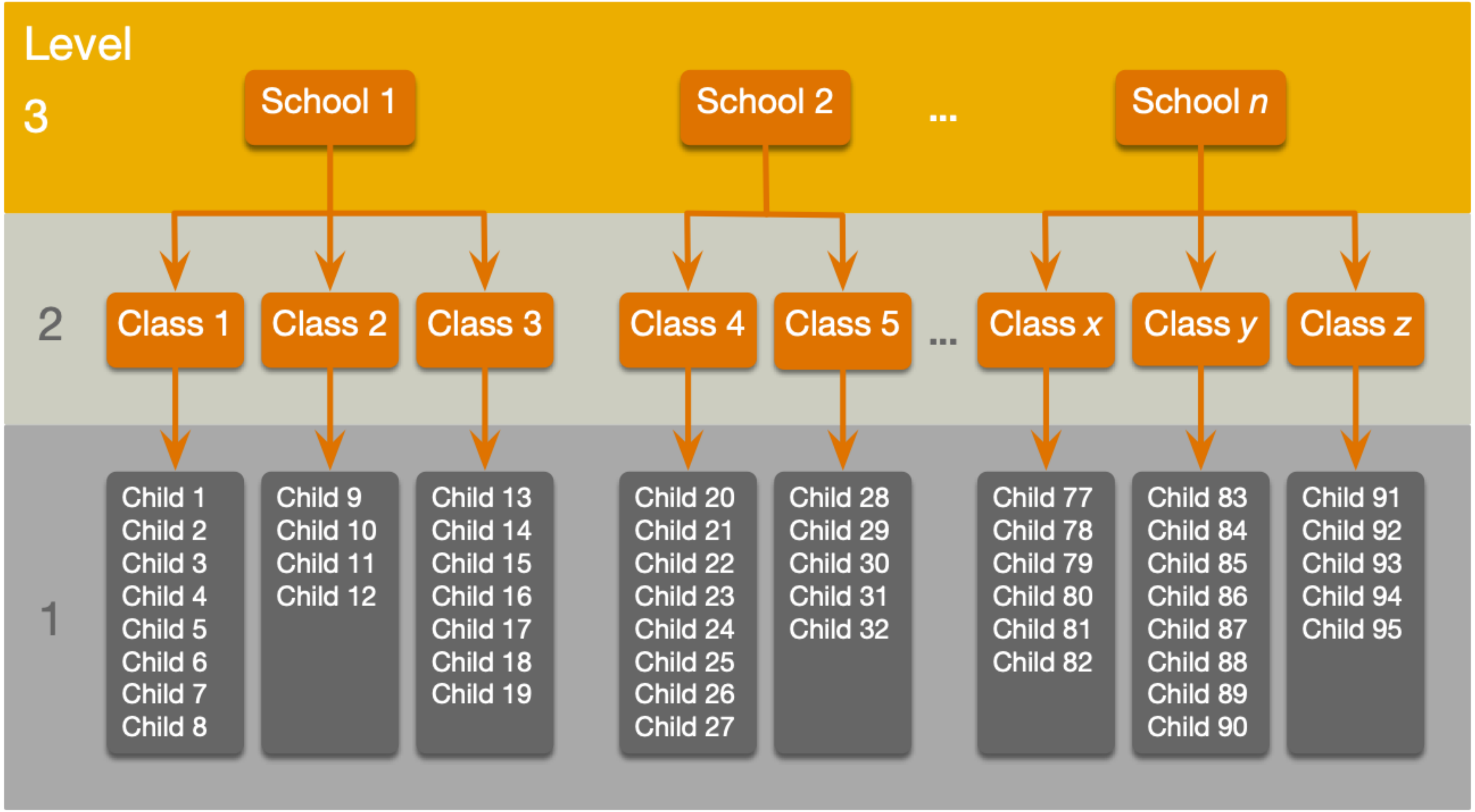
Hierarchical data

- Data structures are often hierarchical
    - Children nested within classrooms
    - Observations nested within people
    - Employees nested within organisations
    - Patients nested within hospitals
    - Patients nested within teams nested within hospitals
    - Service users nested within clinicians nested within hospitals nested within NHS trusts!
    - Zombies nested within rehabilitation clinics 😉

A two-level hierarchy



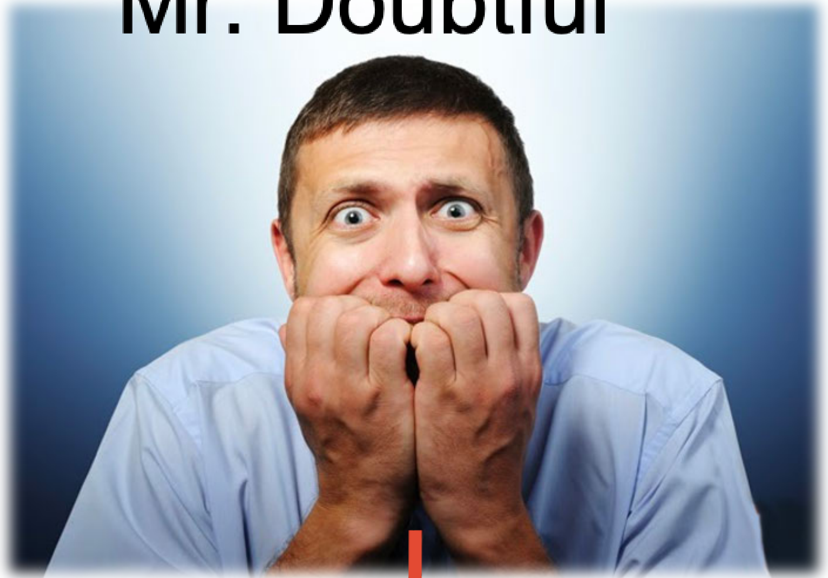
A three-level hierarchy



Why hierarchies matter

- Data from the same context will be more similar than data from different contexts
  - Children in the same class will perform more similarly than children from different classes
  - People treated in the same clinics should be more similar in response than those treated at different clinics
- Lack of independence
  - Violates the assumption of spherical errors (specifically, independence)
  - Biases SEs, CIs and *p* -values

Mr. Doubtful



Ms. Confident

Benefits of multilevel models

- Modelling variability in effects across contexts
    - Model the variability in intercepts
    - Model the variability in slopes
- Model violations of the assumption of spherical errors
    - Model differences in the variability of errors
    - Model relationships between errors
        - (Linear model for repeated observations – two weeks time!)
- Missing data
    - MLMs cope well with missing data (in general)

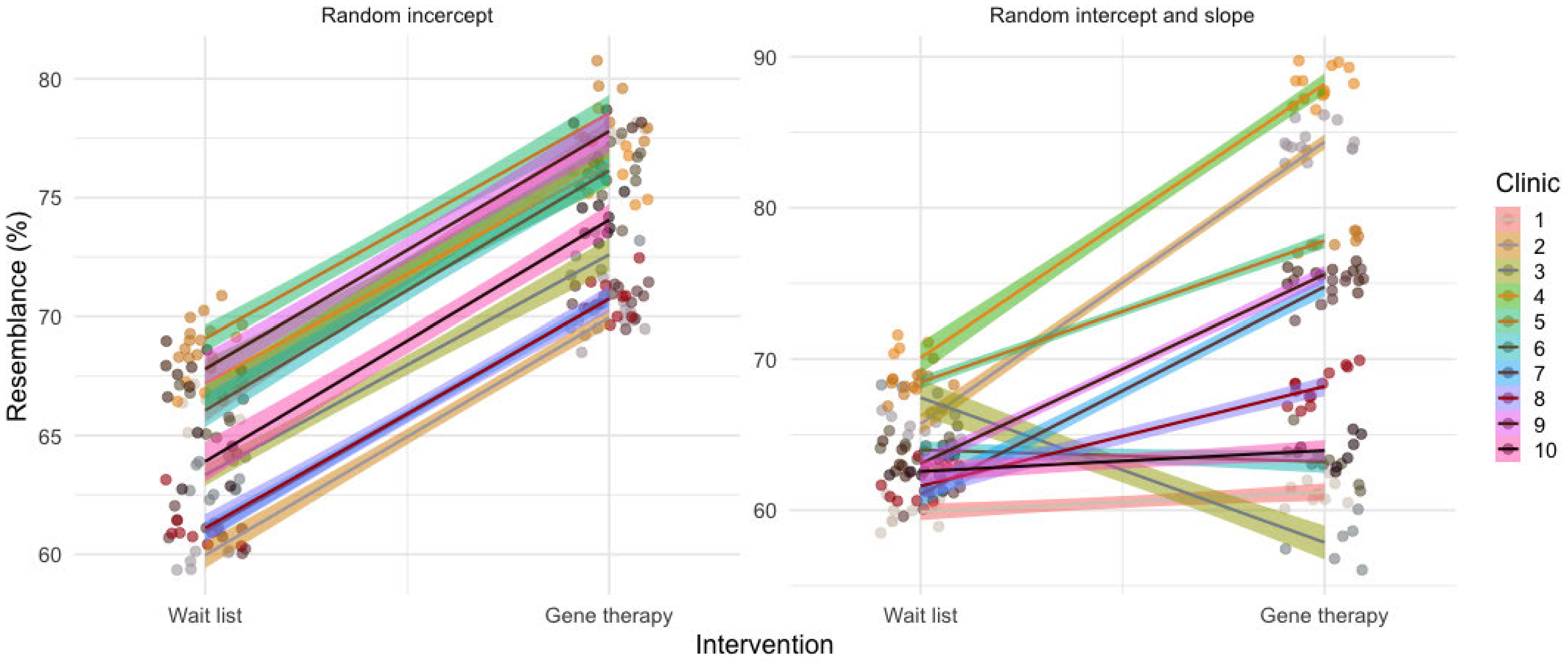
A rehabilitative example

- id_clin: Which of 10 clinics the zombie attended to have the intervention (1 to 10)
- id: Zombie id
- intervention: Was the participant assigned to waiting list (0) or gene therapy (1)?
- gep_level: Genetic Enhancement Program level.
  - Were they originally assigned to the low (0) or high (1) level genetic enhancement program at JIG:SAW?
- tse_months: Time Since Enhancement (months).
  - How long ago did they undergo the original genetic enhancement program (which zombified them)
- resemblance: Resemblance of their face to their pre-zombie state (0% to 100%)

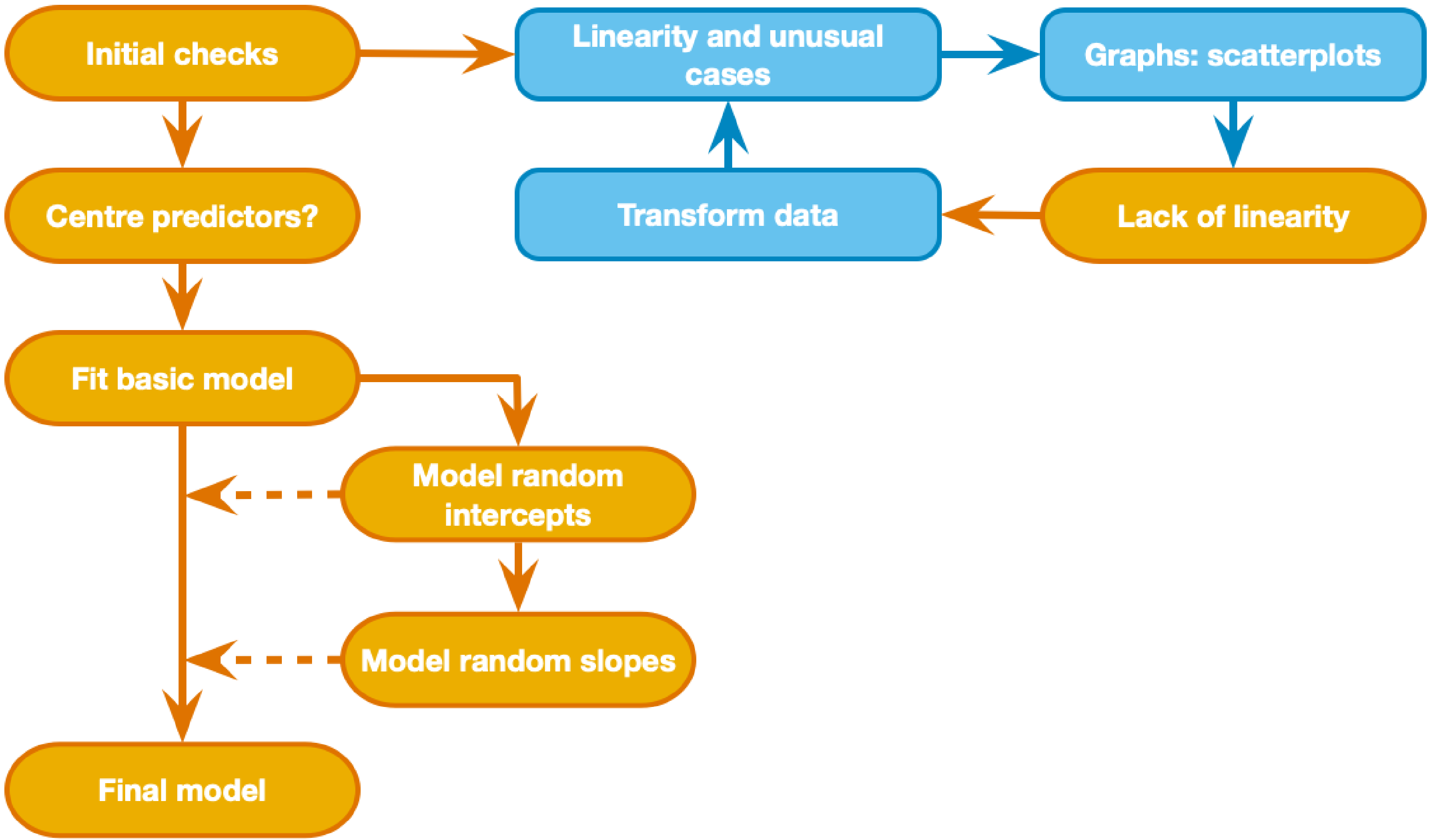
Fixed and random coefficients

- Intercepts and slopes can be fixed or random
  - In OLS regression they are fixed
  - Fixed coefficients
  - Intercepts/slopes are assumed to be the same across different contexts (in this case clinics)
- Random coefficients
  - Intercepts/slopes are allowed to vary across different contexts (in this case clinics)

Intercepts and slopes



The process


Initial checks
Linearity and unusual cases
Graphs: scatterplots
Centre predictors?
Transform data
Lack of linearity
Fit basic model
Model random intercepts
Model random slopes
Final model


Level
2
Clinic 1
Clinic 2
...
Clinic 9
Clinic 10
1
Zombie 1
Zombie 2
Zombie 3
Zombie 4
Zombie 5
Zombie 6
Zombie 7
Zombie 8
Zombie 9
Zombie 10
Zombie 11
Zombie 12
Zombie 13
Zombie 14
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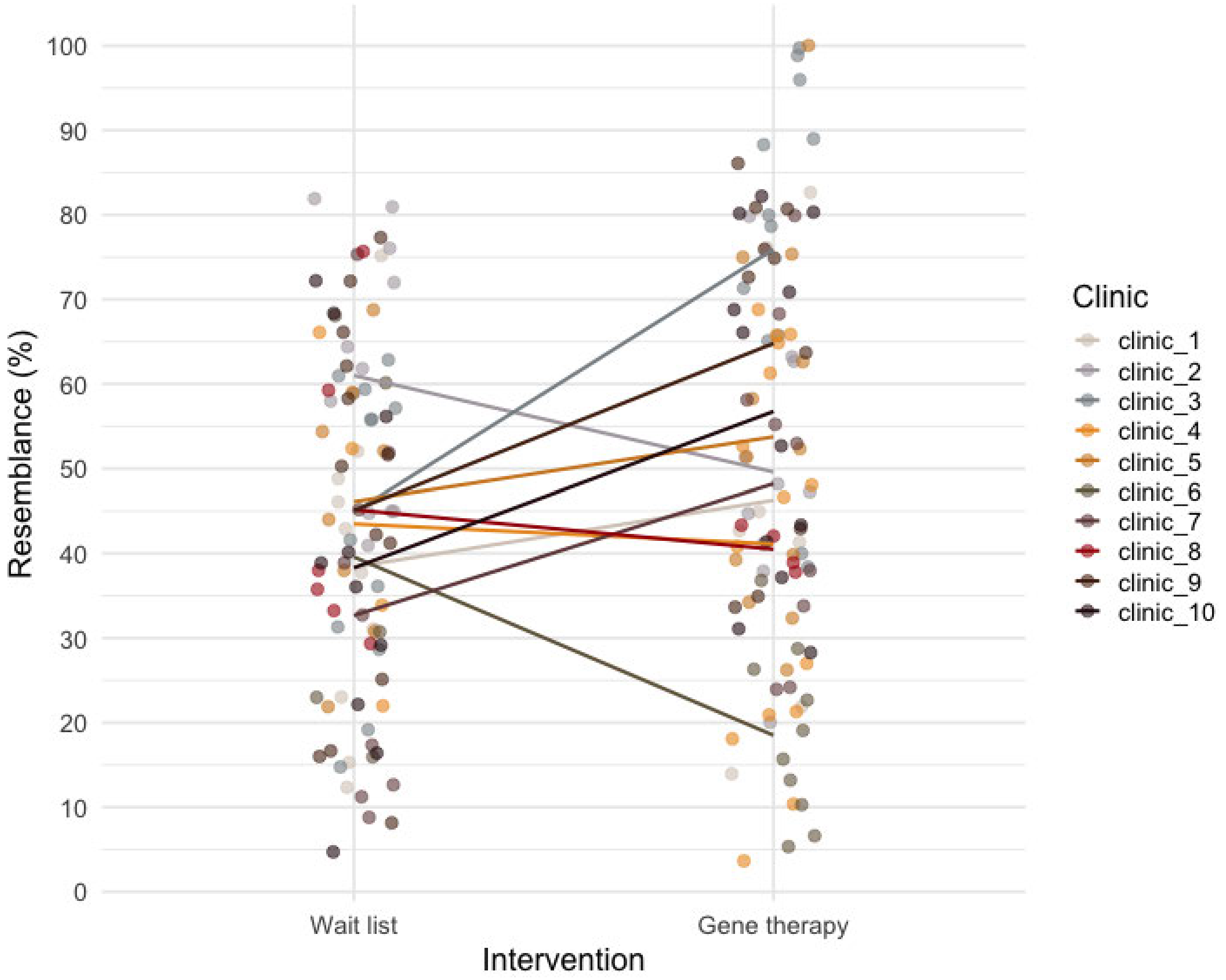
Zombie 190


Resemblance (%)
100
90
80
70
60
50
40
30
20
10
0
Wait list
Gene therapy
Intervention
Clinic
clinic_1
clinic_2
clinic_3
clinic_4
clinic_5
clinic_6
clinic_7
clinic_8
clinic_9
clinic_10

The models (using familiar symbols)

- Fixed intercepts and slopes

$$\text{resem}\hat{\text{b}}\text{lance}_i = \hat{b}_0 + \hat{b}_1\text{Intervention}_i + e_i$$

- Random intercepts but fixed slopes

$$\text{resem}\hat{\text{b}}\text{lance}_{ij} = \hat{b}_{0j} + \hat{b}_1\text{Intervention}_{ij} + e_{ij}$$
$$\hat{b}_{0j} = \hat{b}_0 + \hat{u}_{0j}$$

- Random intercepts and slopes

$$\text{resem}\hat{\text{b}}\text{lance}_{ij} = \hat{b}_{0j} + \hat{b}_{1j}\text{Intervention}_{ij} + e_{ij}$$
$$\hat{b}_{0j} = \hat{b}_0 + \hat{u}_{0j}$$
$$\hat{b}_{1j} = \hat{b}_1 + \hat{u}_{1j}$$

The models (using common notation)

- Fixed intercepts and slopes

$$\widehat{\text{resemblance}}_i = \hat{\gamma}_0 + \hat{\gamma}_1\text{Intervention}_i + e_i$$

- Random intercepts but fixed slopes

$$\widehat{\text{resemblance}}_{ij} = \hat{\gamma}_{0j} + \hat{\gamma}_1\text{Intervention}_{ij} + e_{ij}$$
$$\hat{\gamma}_{0j} = \hat{\gamma}_0 + \hat{u}_{0j}$$

- Random intercepts and slopes

$$\widehat{\text{resemblance}}_{ij} = \hat{\gamma}_{0j} + \hat{\gamma}_{1j}\text{Intervention}_{ij} + e_{ij}$$
$$\hat{\gamma}_{0j} = \hat{\gamma}_0 + \hat{u}_{0j}$$
$$\hat{\gamma}_{1j} = \hat{\gamma}_1 + \hat{u}_{1j}$$

Adding predictors

- Add whether original enhancement was low or high intensity (gep_level)

$$
\begin{aligned}
\widehat{\text{resemblance}}_{ij} &= \hat{\gamma}_{0j} + \hat{\gamma}_{1j}\text{Intervention}_{ij} + \hat{\gamma}_{2}\text{gep\_level}_{ij} + e_{ij} \\
\hat{\gamma}_{0j} &= \hat{\gamma}_{0} + \hat{u}_{0j} \\
\hat{\gamma}_{1j} &= \hat{\gamma}_{1} + \hat{u}_{1j}
\end{aligned}
$$

- Add time since genetic enhancement (tse_months)

$$
\begin{aligned}
\widehat{\text{resemblance}}_{ij} &= \hat{\gamma}_{0j} + \hat{\gamma}_{1j}\text{Intervention}_{ij} + \hat{\gamma}_{2}\text{gep\_level}_{ij} + \hat{\gamma}_{3}\text{tse\_months}_{ij} + e_{ij} \\
\hat{\gamma}_{0j} &= \hat{\gamma}_{0} + \hat{u}_{0j} \\
\hat{\gamma}_{1j} &= \hat{\gamma}_{1} + \hat{u}_{1j}
\end{aligned}
$$

Assessing the fit and comparing models

- Assessing fit
    - AIC
    - BIC
- Models should be built up gradually
    - Start with fixed coefficients
    - Change 1 aspect of the model and compare to the previous with the change in the -2 log likelihood

Model 1:

$$\hat{\text{resemblance}}_i = \hat{\gamma}_0 + e_i$$

```
rehab_base <- nlme::gls(resemblance ~ 1,
                        data = rehab_tib,
                        method = "ML"
                        )
```

Model 2

$$\hat{\text{resemblance}}_{ij} = \hat{\gamma}_0 + \hat{u}_{0j} + e_{ij}$$

```
rehab_ri <- nlme::lme(resemblance ~ 1,
                      random = ~1|id_clin,
                      data = rehab_tib,
                      method = "ML"
                      )
```

Model 3

$$\widehat{\text{resemblance}}_{ij} = \hat{\gamma}_0 + \hat{\gamma}_1 \text{Intervention}_{ij} + \hat{u}_{0j} + e_{ij}$$

```r
rehab_int <- nlme::lme(resemblance ~ intervention,
                       random = ~1|id_clin,
                       data = rehab_tib,
                       method = "ML"
                       )
```

Model 4

$$\widehat{\text{resemblance}}_{ij} = \hat{\gamma}_0 + \hat{\gamma}_1 \text{Intervention}_{ij} + \hat{u}_{0j} + \hat{u}_{1j} + e_{ij}$$

```r
rehab_rs <- nlme::lme(resemblance ~ intervention,
                      random = ~intervention|id_clin,
                      data = rehab_tib,
                      method = "ML"
                      )
```

Model 5

$$\widehat{\text{resemblance}}_{ij} = \hat{\gamma}_0 + \hat{\gamma}_1\text{Intervention}_{ij} + \hat{\gamma}_2\text{gep\_level}_{ij} + e_{ij} + \hat{u}_{0j} + \hat{u}_{1j}$$

```
rehab_gep <- nlme::lme(resemblance ~ intervention + gep_level,
                       random = ~intervention|id_clin,
                       data = rehab_tib,
                       method = "ML"
                       )
```

Model 6

$$\widehat{\text{resemblance}}_{ij} = \hat{\gamma}_0 + \hat{\gamma}_1\text{Intervention}_{ij} + \hat{\gamma}_2\text{gep\_level}_{ij} + \hat{\gamma}_3\text{tse\_months}_{ij} + e_{ij} + \hat{u}_{0j} + \hat{u}_{1j}$$

```
rehab_tse <- nlme::lme(resemblance ~ intervention + gep_level + tse_months,
                       random = ~intervention|id_clin,
                       data = rehab_tib,
                       method = "ML"
                       )
```

Comparing models using R

```
anova(rehab_base, rehab_ri, rehab_int, rehab_rs, rehab_gep, rehab_tse)
```

Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
1	2	1724.75	1731.25	-860.38		NA	NA
2	3	1715.50	1725.24	-854.75	1 vs 2	11.25	0.00
3	4	1710.38	1723.36	-851.19	2 vs 3	7.12	0.01
4	6	1702.11	1721.59	-845.05	3 vs 4	12.27	0.00
5	7	1703.08	1725.81	-844.54	4 vs 5	1.03	0.31
6	8	1103.52	1129.49	-543.76	5 vs 6	601.56	0.00

Model parameters (Fixed effects)

```
broom.mixed::tidy(rehab_tse, effects = "fixed")
```

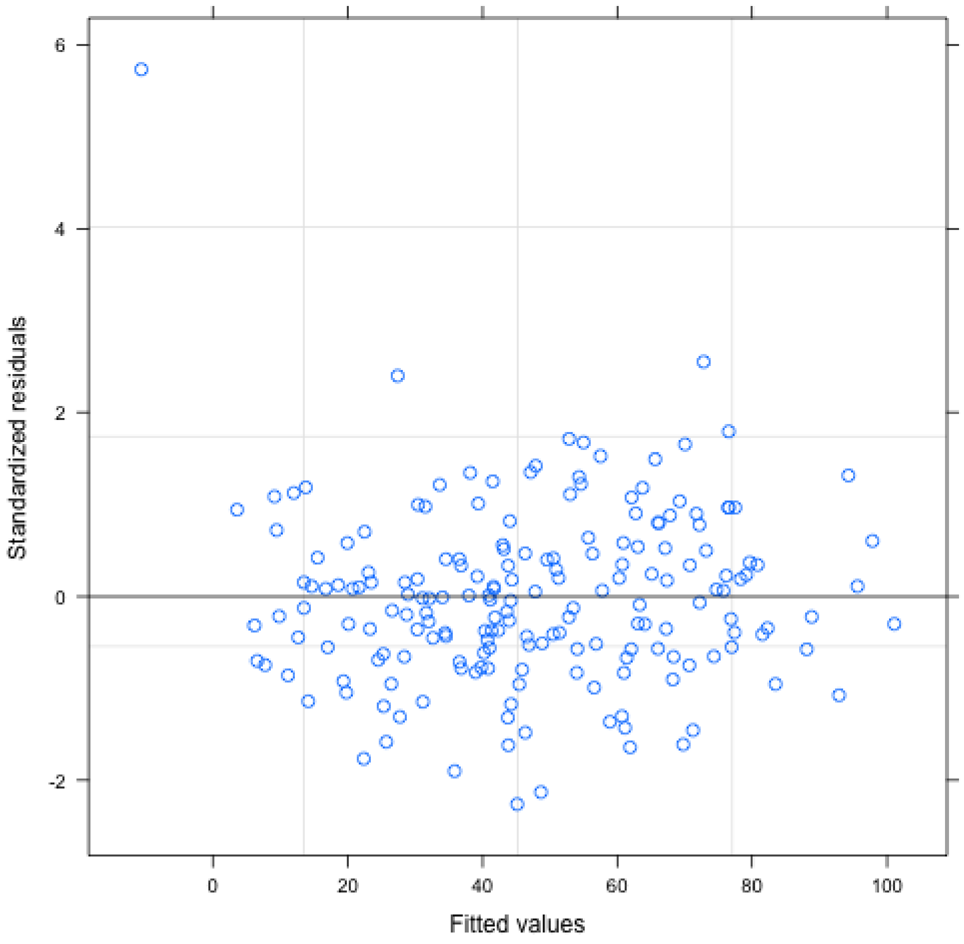
term	estimate	std.error	df	statistic	p.value
(Intercept)	80.933	1.599	177	50.611	0.000
interventionGene therapy	6.794	2.706	177	2.511	0.013
gep_levelHigh intensity	-4.297	0.548	177	-7.844	0.000
tse_months	-1.977	0.028	177	-69.634	0.000

Model parameters (random effects)

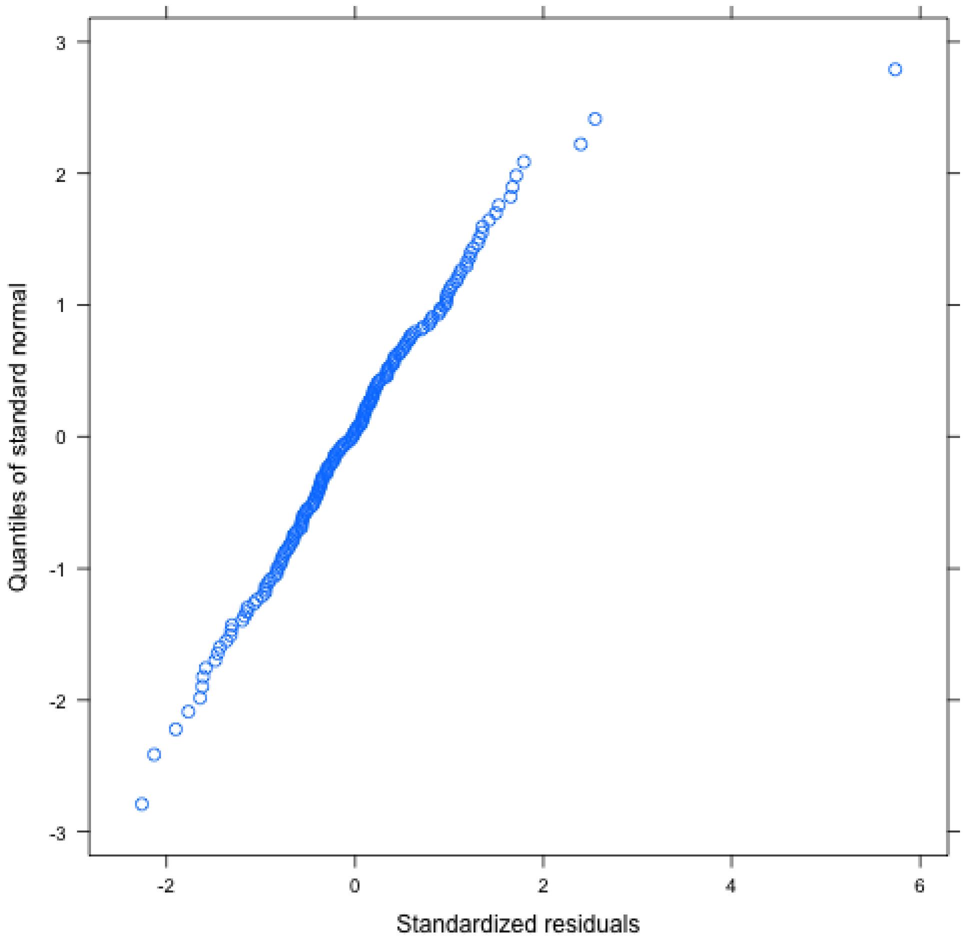
```
broom.mixed::tidy(rehab_tse, effects = "ran_pars")
```

effect	group	term	estimate
ran_pars	id_clin	sd_(Intercept)	4.47
ran_pars	id_clin	cor_interventionGene therapy.(Intercept)	0.66
ran_pars	id_clin	sd_interventionGene therapy	8.28
ran_pars	Residual	sd_Observation	3.60

```
plot(rehab_tse)
```




```
qqnorm(rehab_tse)
```



Robust model parameters

```
rehab_tse_rob <- robustlmm::rlmer(
  resemblance ~ intervention + gep_level + tse_months + (intervention|id_clin),
  data = rehab_tib)
broom.mixed::tidy(rehab_tse_rob, effects = "fixed")
```

effect	term	estimate	std.error	statistic
fixed	(Intercept)	81.70	1.60	51.11
fixed	interventionGene therapy	7.01	3.25	2.16
fixed	gep_levelHigh intensity	-4.58	0.49	-9.29
fixed	tse_months	-1.99	0.03	-77.87

Robust random effects

```
broom.mixed::tidy(rehab_tse_rob, effects = "ran_pars")
```

effect	group	term	estimate
ran_pars	id_clin	sd__(Intercept)	4.47
ran_pars	id_clin	cor__(Intercept).interventionGene therapy	0.55
ran_pars	id_clin	sd__interventionGene therapy	9.83
ran_pars	Residual	sd__Observation	3.18

To sum up …

- Data can be hierarchical and this hierarchical structure can be important.
    - The OLS linear model simply ignores the hierarchy.
- Hierarchical models are just a fancy linear model in which you estimate the variability in the slopes and intercepts within contexts
    - i.e. slopes and intercepts can be random variables (allowed to vary) rather than fixed (assumed to be equal in different situations).
- Start with a model that ignores the hierarchy and then add in random intercepts and slopes to see if they improve the fit of the model.