ADVANCED DATA ANALYSIS FOR PSYCHOLOGICAL SCIENCE

Part 1. Introduction to multilevel modeling

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Outline of Part 1

- **LM recap**: Short recap of linear regression modeling
- **LMER**: Introduction to multilevel modeling (*linear mixed-effects regression*)
- **Data processing**: How to approach a multilevel data structure? How to manipulate and pre-process multilevel data?
- **Descriptives**: Which descriptive stats should be reported from a multilevel dataset? How to compute and interpret them?
- **Model fit**: How to fit a multilevel model in R? How to inspect, report, visualize, and interpret the results of a multilevel model?
- **Model evaluation**: Which are the assumptions of multilevel models? How to evaluate them? How to compare multiple models and select the best model?
- **Related**: Summaries & in-depth topics related to multilevel modeling (e.g., generalized and Bayesian LMER, power analysis)

= not for the exam

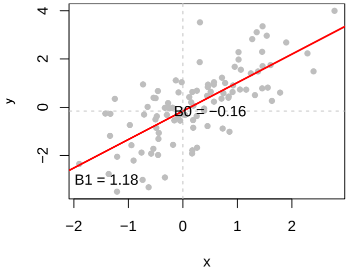
= exercises with R (bring your laptop!)

LM recap: Linear regression models

Linear models (LM) allow to determinate the link between two variables as expressed by a linear function: $y_i = \beta_0 + \beta_1 x_i + \epsilon_i$

Such a function can be graphically represented as a **straight line**, where:

- β_0 is the **intercept** (value assumed by y when x = 0)
- β_1 is the **slope** (predicted change in y when x increases by 1 unit)
- ϵ_i are the **errors** (distance between observation i and the regression line)



x_i and y_i are the values of observation i for the **casual variables** x and y

β_0, β_1, and ϵ_i are called "**parameters**", or "**coefficients**". They are *estimated* from the sampled data and *generalized* to the whole population.

Fitting linear models in R

```r
data("children", package = "npregfast") # loading children dataset from npregfast pkg
```

R uses the `lm()` function to fit linear models with the arguments `formula` (`y ~ x1 + x2 + ...`) and `data` (identifying the dataframe with the model variables).

Null model

Children' `height` is only predicted by the model **intercept** β_0 = expected (i.e., mean) value of `height` in the sample. σ^2 is the **variance of the residuals** ϵ_i (deviations from the intercept).

```r
m0 <- lm(formula = height ~ 1,
         data = children)
coefficients(m0) # model parameters
```

```
(Intercept)
   153.4013
```

```r
summary(m0)$sigma^2 # residual variance
```

```
[1] 243.9085
```

Simple regression model

`height` is now predicted by the **intercept** β_0 (mean value when `age` is 0), the **slope** β_1 (expected change for 1-unit increase in `age`), and the **residual variance** σ^2.

```r
m1 <- lm(formula = height ~ age,
         data = children)
coefficients(m1) # model parameters
```

```
(Intercept)         age
  94.904099    4.388803
```

```r
summary(m1)$sigma^2 # residual variance
```

```
[1] 56.19656
```

Multiple regression & interactions

LM also allow to include **multiple predictors** and the **interactions**[1] among them. This is done by estimating a separate slope (thus, a separate line) for each predictor by *holding constant* the value of the other predictors, which are fixed to zero.

Multiple regression model

β_0 = expected value in girls with `age` = 0

β_1 = `age` effect[2] within the same `sex`

β_2 = `sex` difference when `age` = 0

```
m2 <- lm(formula = height ~ age + sex,
         data = children)
coefficients(m2)
```

```
(Intercept)         age     sexmale
 95.0075706   4.3887983  -0.2001025
```

Interactive model

β_1 = `age` effect in girls

β_2 = `sex` difference in `height` when `age` = 0

β_3 = `sex` difference in `age` effect (**interaction**)

```
m3 <- lm(formula = height ~ age * sex,
         data = children)
round(coefficients(m3),2)
```

```
(Intercept)         age     sexmale age:sexmale
     104.25        3.70      -19.04        1.41
```

[1] The **interaction** between x_1 and x_2 is computed as the **product of** x_1 **and** x_2.

[2] In this context, “effect” is used as a synonym of “relationship” (not a *causal* effect).

Model comparison & model selection

Likelihood ratio test

Compares the *fit* of two *nested* models (i.e., predicting the same y variable, with the more complex model including all predictors included in the simpler model).

```
library(lmtest)
lrtest(m0,m1,m2,m3) # returns Chisq statistic
```

```
  #Df    LogLik Df    Chisq   Pr(>Chisq)
1   2 -10417.84 NA       NA           NA
2   3  -8582.42  1 3670.84 0.000000e+00
3   4  -8582.19  1    0.45 5.046155e-01
4   5  -8468.86  1  226.67 3.176229e-51
```

Information criteria

The Akaike (AIC) and the Bayesian Information Criterion (BIC) compare multiple models in terms of *fit & parsimony* (the lower number of parameters the better)

```
AIC(m0,m1,m2,m3) # AIC: the lower the better
```

```
[1] 20839.68 17170.83 17172.39 16947.72
```

```
# Akaike weights: from 0 (-) to 1 (+)
MuMIn::Weights(AIC(m0,m1,m2,m3))
```

```
 model weights
[1] 0 0 0 1
```

Here, *model fit to the data* is expressed by its **likelihood** = probability of observing the sampled data given the parameters estimated by the model, sometimes referred as the *evidence* of a model, or its *ability to predict/forecast* new data that are similar to the sampled data (see interactive visualization by Kristoffer Magnusson).

Parameter estimation in linear regression models

β_0 , β_1 , and ϵ must be **estimated** based on data sampled from a population:
$\hat{\beta}_0 = b_0$; $\hat{\beta}_1 = b_1$; $\hat{\epsilon} = e$).

There are several methods to estimate unknown parameters, such as:

- **Ordinary least squares (OLS)**: finds the *parameter values* that *minimize the sum of the squared residuals* (default LM estimator)
- **Maximum likelihood estimator (MLE)**: finds the *parameter values* that *maximize the model likelihood*, making the observed data the most probable under that model
- **Bayesian estimator**: finds the *parameter posterior distributions* based on prior knowledge/beliefs (*prior*) and observed data (*likelihood*)

Regardless of the used method, parameters values (or distributions) are always accompanied with a measure of the **uncertainty/precision** associated with their estimate:
Standard errors (SE) = predicted *variability* in the parameter estimate if the data were collected from different random samples from the same population.
SE are used for computing *test statistics* (Est/SE) & *confidence intervals* ($Est \pm 1.96 \times SE$)

In LM, under the assumption of normally distributed residuals, OLS = MLE

What are residuals?

Residuals are the model-based estimates of the population errors.

Linear model:

$y_i = \beta_0 + \beta_1 x_i + \epsilon_i$

Predicted values:

$\hat{y}_i = \beta_0 + \beta_1 x_i$

Observed values:

$y_i = \hat{y}_i + \hat{\epsilon}_i$

Residuals = observed - predicted

$\hat{\epsilon}_i = y_i - \hat{y}_i$

```
head(data.frame(observed = children$height,
                predicted = fitted(m3),
                residuals = residuals(m3)
                squared = residuals(m3)^2 ))
```

```
  observed predicted residuals squared
1   150.77    152.90     -2.13    4.55
2   170.59    156.61     13.98  195.33
3   167.31    160.31      7.00   49.01
4   165.72    165.52      0.20    0.04
5   171.67    160.31     11.36  129.06
6   143.74    151.07     -7.33   53.74
```

```
sum(residuals(m3)^2) # sum of squared (SS) residuals
```

```
## [1] 128188.3
```

```
var(residuals(m3)) # residual variance SIGMA2
```

```
## [1] 51.29585
```

In LM, **model parameters** include:

(1) intercept, (2) slope(s), and (3) **residual variance** σ^2

→ *How many parameters in the previous models? (= **No. predictors** + 2)*

Statistical inference on regression coefficients

In the NHST approach, we can **test the statistical significance** of regression coefficients (*two-tail t-test*). This is automatically done by R in the model summary.

```
summary(m3) # model results
```

```
            Estimate Std. Error t value     Pr(>|t|)
(Intercept)   104.25       0.88  118.22 0.000000e+00
age             3.70       0.06   57.45 0.000000e+00
sexmale       -19.04       1.26  -15.14 1.237494e-49
age:sexmale     1.41       0.09   15.39 3.897810e-51
```

- **Estimate** = estimated parameter
- **Std. Error** = parameter standard error
- **t value** = test statistic computed as $t = Estimate/Std.Error$
- **p-value** = p corresponding to the t-value with *No. Obs. − No. Coeff. − 1* degrees of freedom

Effect size:

Coefficient of determination

$R^2 = 1 - SS_{residuals}/SS_{total}$

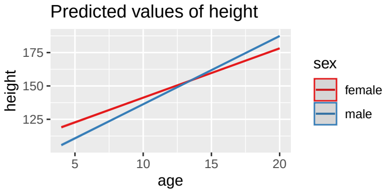
```
summary(m3)$r.squared
```

```
[1] 0.79
```

The model explains 79% of the variance in height.

Plotting effects:

```
sjPlot::plot_model(m3,type="pred",terms=c("age","sex"))
```



Hands on R

1. Download & read the dataset from the *"Pregnancy during pandemics"* study

`depr` = postnatal depression, `age` = mother's age, `NICU` = intensive care, `threat` = fear of COVID

```
library(osfr) # package to interact with the Open Science Framework platform
proj <- "https://osf.io/ha5dp/" # link to the OSF project
osf_download(osf_ls_files(osf_retrieve_node(proj))[2, ],conflicts="overwrite") # download
preg <- na.omit(read.csv("OSFData_Upload_2023_Mar30.csv",stringsAsFactors=TRUE)) # read data
colnames(preg)[c(2,5,12,14)] <- c("age","depr","NICU","threat") # set variable names
```

2. Explore the the variables `depr`, `threat`, `NICU`, and `age` (descr., corr., & plots)
3. Fit a null model `m0` of `depr`
4. Fit a simple regression model `m1` with `depr` being predicted by `threat`
5. Fit a multiple regression model `m2` also controlling for `NICU` and `age`
6. Fit an interactive model `m3` to check whether `age` moderates the relationship between `threat` and `depr`.
7. Compare the models with AIC and likelihood ratio test: which is the best model?
8. Print & interpret the coefficients estimated by the selected model
9. Print & interpret the statistical significance of the estimated coefficients
10. Plot the effects of the selected model
11. Compute the determination coefficient of the selected model

One step back: Linear model assumptions

Core assumptions:

1. Linearity: x_i and y_i are linearly associated $\rightarrow$ the expected (mean) value of ϵ_i is zero

2. Normality: residuals ϵ_i are normally distributed with $\epsilon_i \sim \mathcal{N}(0, \sigma^2)$

3. Homoscedasticity: ϵ_i variance is constant over the levels of x_i (homogeneity of variance)

4. Independence of predictors & errors: predictors x_i are unrelated to residuals ϵ_i

5. Independence of observations: for any two observations i and j with $i \neq j$,
the residual terms ϵ_i and ϵ_j are independent (no common disturbance factors)

Additional assumptions:

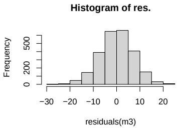
6. Absence of influential observations (multivariate outliers)

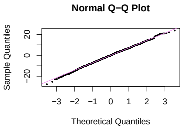
7. Absence of multicollinearity (for multiple regression):
lack of linear relationship between x_1 and x_2

Model diagnostics: Assessing LM assumptions

Normality & linearity ☺

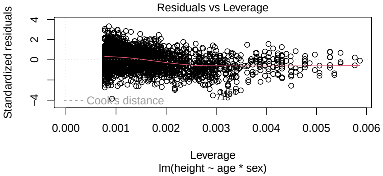
```
hist(residuals(m3))
qqnorm(residuals(m3)); qqline(residuals(m3))
```





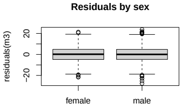
Absence of influential cases ☺

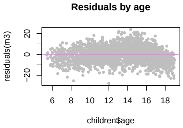
```
plot(m3,which=5)
```



Homoscedasticity & independence x, ϵ ☺

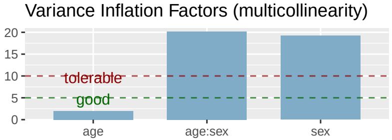
```
plot(residuals(m3) ~ children$sex)
plot(residuals(m3) ~ children$age)
```





Absence of multicollinearity ☹

```
sjPlot::plot_model(m3,"diag")[[1]]
```



Independence of observations ?

Are the unmeasured factors influencing y unrelated from one individual to another?

Cluster variables & nested data

In many cases, the *sampling method* creates **clusters** of *individual observations*

- students → schools
- children → families → neighborhoods → cities → regions → states → planets

Nested data structure (= *multilevel* or *hierarchical* data structure)
= when data points at the **individual level** appear *in only one group* of the **cluster level** variable

→ individual observations are ***nested*** within clusters

How do you imagine such a nested dataset?

Individual observation = statistical unit = individual entity within a sample or population that is the subject of data collection & analysis (not necessarily a person)

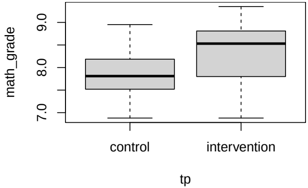
Case study: Innovative math teaching program

We're hired by a school principal to assess whether an *innovative teaching program* can improve *math achievement* in first-year high-school students.

```
# reading data
itp <- read.csv("data/studentData.csv")
# frequency table class by intervention
table(itp[,c("classID","tp")])
```

```
       tp
classID control intervention
      A      30            0
      B      22            0
      C       0           27
      D       0           11
```

```
boxplot(math_grade ~ tp, data=itp)
```



The teaching program `tp` was delivered over the first semester to 2 out of 4 classes and we got the students' end-of-semester `math_grade` (1-10).

Nested dataset: students are *nested within* classes, with each student only belonging to one class.

```
head(itp[,1:4],12)
```

```
   studID classID      tp math_grade
1      s1       A control       7.74
2      s2       A control       8.31
3      s3       A control       7.09
4      s4       A control       7.80
5      s5       A control       7.21
6      s6       A control       8.95
7      s7       A control       7.48
8      s8       A control       7.86
9      s9       A control       7.85
10    s10       A control       7.13
11    s11       A control       7.87
12    s12       A control       6.88
```

Non-independence of observations with nested data

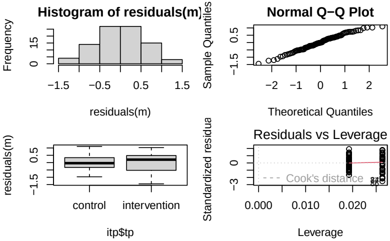
Let's try with a linear regression model:

```
m <- lm(math_grade ~ tp, data=itp)
summary(m)$coefficients[,1:3]
```

```
##                 Estimate Std. Error t value
## (Intercept)         7.85       0.08   97.60
## tpintervention      0.48       0.12    3.87
```

Model diagnostics (see slide #11):

```
hist(residuals(m)); qqnorm(residuals(m))
boxplot(residuals(m)~itp$tp); plot(m,5)
```



- Coefficient meaning?
- Linear model assumptions?

- **Independent observations**?

Are ϵ_i and ϵ_j independent for any $i \neq j$? Are the unmeasured factors influencing y unrelated from one individual to another?

NO: students are nested within classes and such cluster variable is likely to explain differences in the y variable (as well as in the relationship between x and y)

Thus, **we cannot rely on linear models** to analyze these data.

Local dependencies

Local dependencies = correlations that exist among observations within a specific cluster (but the software doesn't know that!)

e.g., grades from the same class will be more correlated than they are between different classes

Why is this a problem?

1) Can result in **biased estimates of the standard errors** → underestimated p-values (+false positive)

2) Potentially important **variables at the cluster level** are neglected

e.g., teachers' characteristics, teaching CV, class social climate

When is this a problem?

Virtually, any time that a cluster variable is potentially related to y

Pragmatically, we cannot account for all potential clusters

e.g., children → families → neighborhoods → cities → regions → states → planets

Based on theory & logic, we should focus on what we consider the most influential clustering factors for both y and x

Mixed-effects models

Multilevel models are part of the largest **linear mixed-effects regression (LMER)** family that include **additional variance terms** for handling local dependencies.

Why 'mixed-effects'?

Because such additional terms come from the distinction between:

- **Fixed effects**: effects that remain ***constant across clusters***, whose levels are *exhaustively considered* (e.g., gender, levels of a Likert scale) and generally controlled by the researcher (e.g., experimental conditions)
- **Random effects**: effects that ***vary from cluster to cluster***, whose levels are *randomly sampled* from a population (e.g., schools)

When individual observations can change cluster over time, it is still a mixed-effects model but not a multilevel model.

Here, "levels" refers to the possible categories/classes of a categorical variable, but from now on we will use this term with a different meaning...

From LM to LMER

LM formula: $y_i = \beta_0 + \beta_1 x_i + \epsilon_i$

Intercept and slope are **constant across all individual observations** i within the population; x, y, and the error term ϵ only variate across individual observations i

LMER formula: $y_{ij} = \beta_{0j} + \beta_{1j} x_{ij} + \epsilon_{ij}$

Intercept and slope have both a **fixed** ($_{0/1}$) and a **random** component ($_j$); y, x, and ϵ variate across **individual observations** i as well as across **clusters** j

$$y_{ij} = \beta_{0j} + \beta_{1j} x_{ij} + \epsilon_{ij} = (\beta_{00} + \lambda_{0j}) + (\beta_{10} + \lambda_{1j}) x + \epsilon_{ij}$$

LMER are an extension of LM where the intercept and the slope are decomposed into the **fixed components** β_{00} and β_{10} referred to the whole sample, and the **random components** λ_{0j} and λ_{1j} randomly varying across clusters.

In LMER, x **variables (predictors) always variate across clusters** j**, but not necessarily across individual observations** i (e.g., school principals' age only variate across schools, whereas students' age variate across students within schools)

Random intercept

Let's start with an **intercept-only model** (i.e., ***unconditional*** or ***null model***), where math grades (y_{ij}) are only predicted by the intercept β_{00} and the residuals ϵ_{ij}

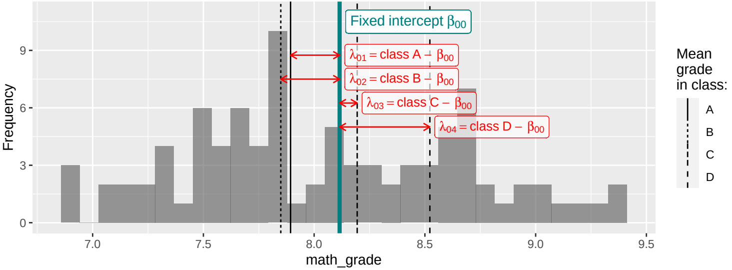
- *Linear model*: $y_i = \beta_0 + \epsilon_i$

  The intercept value β_0 is common to all individuals within the population

- *Linear mixed-effects model*: $y_{ij} = \beta_{0j} + \epsilon_{ij} = (\beta_{00} + \lambda_{0j}) + \epsilon_{ij}$

  - β_{00} is the **fixed intercept** (also called 'average' or 'general intercept') that applies to the whole population

  - λ_{0j} is the **random intercept** = *cluster-specific deviation from the fixed intercept* (i.e., mean class grade - fixed intercept)



Random slope

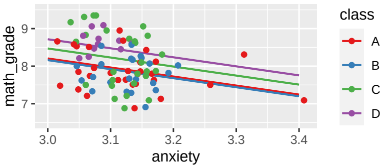
Let's now add a predictor: students' `anxiety` levels x_{ij}.

Random intercept model

$y_{ij} = \beta_{0j} + \beta_1 x_{ij} + \epsilon_{ij}$

$= (\beta_{00} + \lambda_{0j}) + \beta_1 x_{ij} + \epsilon_{ij}$

Math grades y_{ij} are predicted by the overall mean grade β_{00}, their ***average relationship*** with anxiety β_{10}, the random variation among clusters λ_{0j} (*random intercept*), and the random variation among individuals within clusters ϵ_{ij} (*residuals*).



Random slope

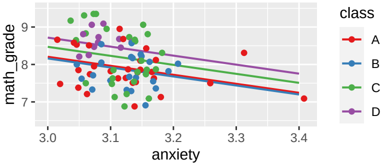
Let's now add a predictor: students' `anxiety` levels x_{ij}.

Random intercept model

$y_{ij} = \beta_{0j} + \beta_1 x_{ij} + \epsilon_{ij}$

$= (\beta_{00} + \lambda_{0j}) + \beta_1 x_{ij} + \epsilon_{ij}$

Math grades y_{ij} are predicted by the overall mean grade β_{00}, their ***average relationship*** with anxiety β_{10}, the random variation among clusters λ_{0j} (*random intercept*), and the random variation among individuals within clusters ϵ_{ij} (*residuals*).

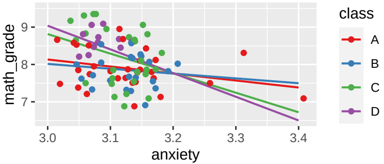


Random intercept & **random slope** model

$y_{ij} = \beta_{0j} + \beta_{1j} x_{ij} + \epsilon_{ij}$

$= (\beta_{00} + \lambda_{0j}) + (\beta_{10} + \lambda_{1j})\ x_{ij} + \epsilon_{ij}$

Since the effect of anxiety might not be the same across all classes, we partition β_1 into the overall ***average relationship*** between anxiety and grades β_{10} (*fixed slope*) and the cluster-specific variation in the relationship λ_{1j} (***random slope***) - basically, an interaction between anxiety and class.



From LMER to multilevel modeling

LMER is often called *'multilevel modeling'* due to the underlying **variance decomposition** of the y_{ij} variable into the *within-cluster* and the *between-cluster* levels.

That is, the LMER formula $y_{ij} = (\beta_{00} + \lambda_{0j}) + (\beta_{10} + \lambda_{1j}) + \epsilon_{ij}$ can be expressed in two separate levels:

$$\begin{aligned} \textit{Level 1 (within)}: y_{ij} &= \beta_{0j} + \beta_{1j} x_{ij} + \epsilon_{ij} \\ \textit{Level 2 (between)}: \beta_{0j} &= \beta_{00} + \lambda_{0j} \\ \beta_{1j} &= \beta_{10} + \lambda_{1j} \end{aligned}$$

In some papers and textbooks, the coefficients β_{00} and β_{01} are indicated with γ_{00} and γ_{01}, while λ_{0j} and λ_{1j} are sometimes indicated with U_{0j} and U_{1j}, respectively.

That's all for now!

Questions?

Homework (optional):

- read the slides presented today
  and write in the Moodle forum if you have any doubts
- refresh your familiarity with R: `R-intro.pdf`
- **exeRcises 1-3** from `exeRcises.pdf`

For each exercise, the solution (or one of the possible solutions) can be found in dedicated chunk of commented code within the `exeRcises.Rmd` file

Credits

The present slides are partially based on:

- Altoè, G. (2023) Corso Modelli lineari generalizzati ad effetti misti - 2023. https://osf.io/b7tkp/
- Beaujean, A. A. (2014) Latent Variable Modeling Using R. A Step-by-Step Guide. New york: Routledge
- Finch, W. H., Bolin, J. E., Kelley, K. (2014). Multilevel Modeling Using R (2nd edition). Boca Raton: CRC Press
- Pastore, M. (2015). Analisi dei dati in psicologie (e applicazioni in R). Il Mulino.

Useful resources on multilevel modeling

- Bates, D. (2022). lme4: Mixed-effects modeling with R. https://stat.ethz.ch/~maechler/MEMo-pages/lMMwR.pdf
- Baayen, R. H., Davidson, D. J., & Bates, D. M. (2008). Mixed-effects modeling with crossed random effects for subjects and items. *Journal of memory and language, 59*(4), 390-412.
- Bliese, P. (2022). Multilevel modeling in R (2.7). https://cran.r-project.org/doc/contrib/Bliese_Multilevel.pdf
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- Jason Fernando (2023) R-Squared: Definition, Calculation Formula, Uses, and Limitations. Available at this link

Achronyms & Greek letters

- AIC = Akaike Information Criterion
- BIC = Bayesian Information Criterion
- LM = linear models
- CI = confidence intervals
- MLE = maximum likelihood estimator
- OLS = ordinary least squares
- NHST = null hypothesis significance testing
- SE = standard error
- SS = sum of squares

- β = *beta*, used to index population-level intercept (β_0) and slope (β_1, β_2, etc.) parameters
- ϵ = *epsilon*, used to index population-level errors to be estimated based on model residuals
- σ = *sigma*, used to index the variance σ^2 of population-level errors (or model residual)
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