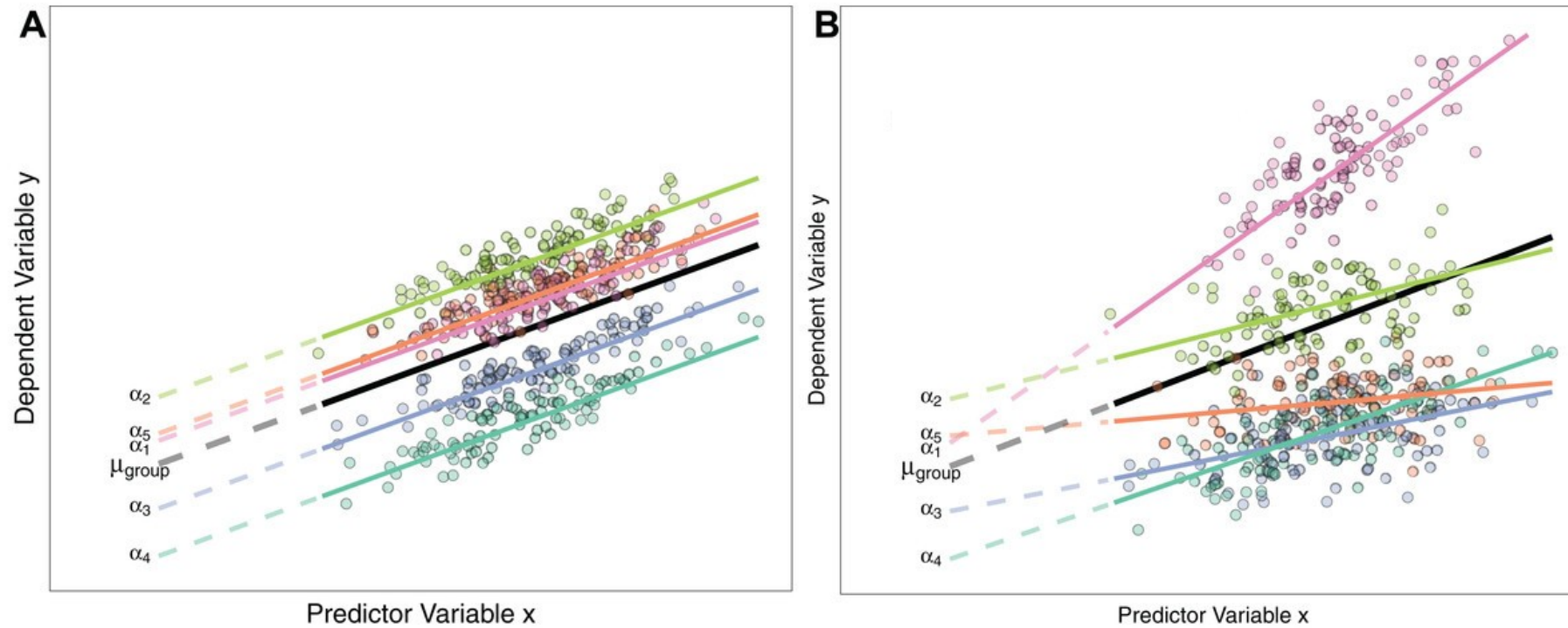


# Introduction to:

## Linear Mixed Effects models



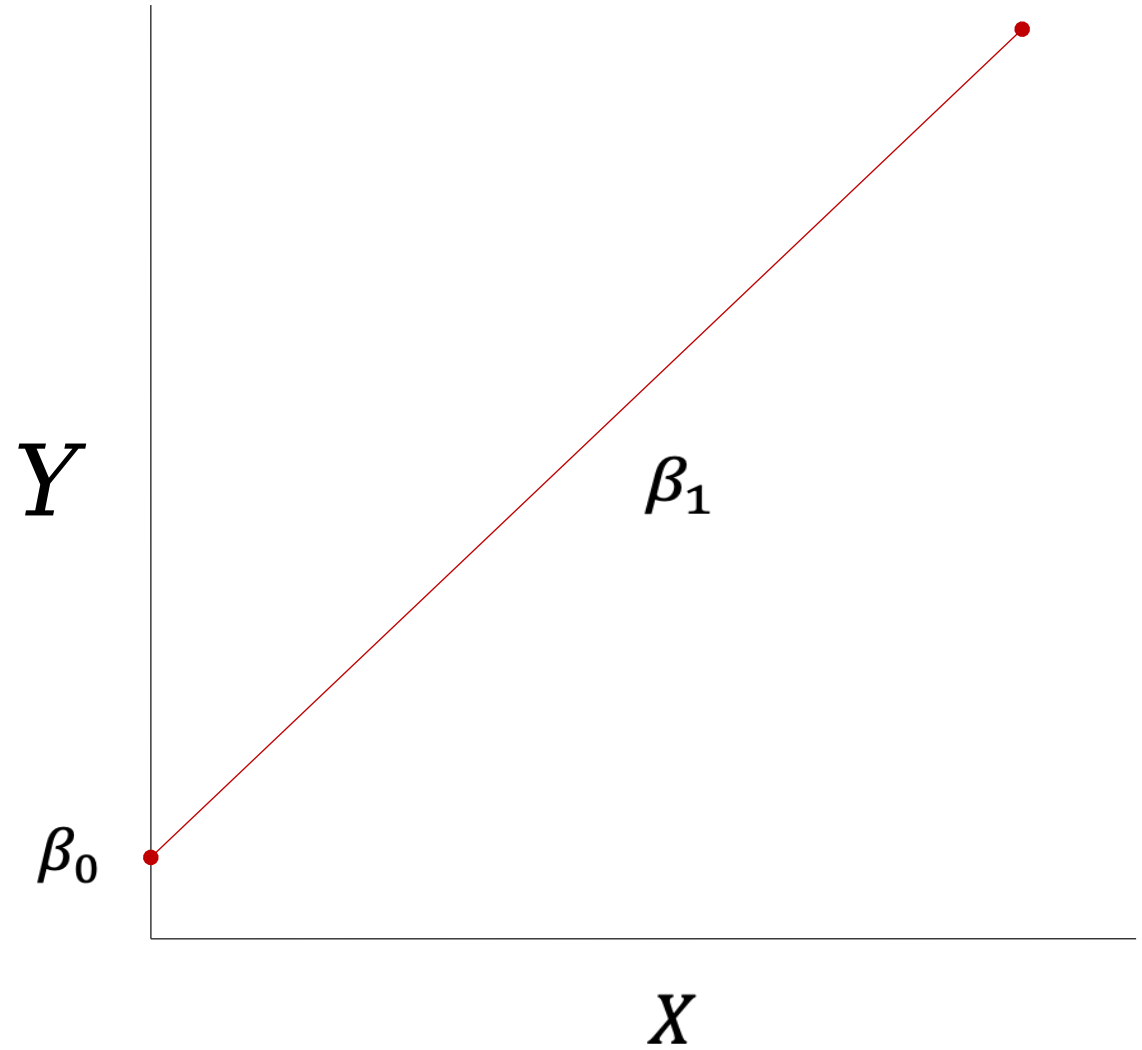
**Linear mixed models**

**Multilevel models**

**Hierarchical linear models**

## Linear mixed models

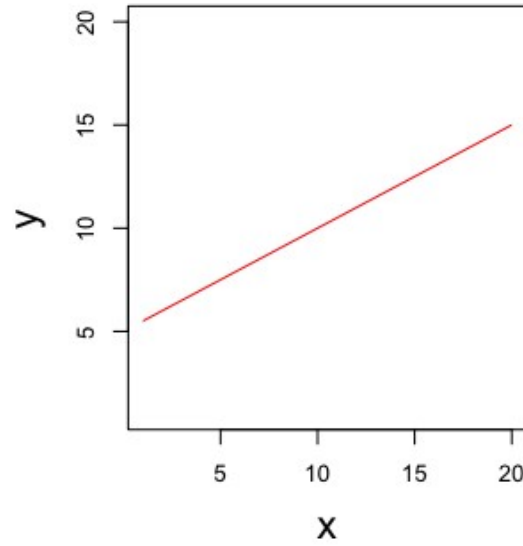
$$Y = \beta_0 + \beta_1 X$$



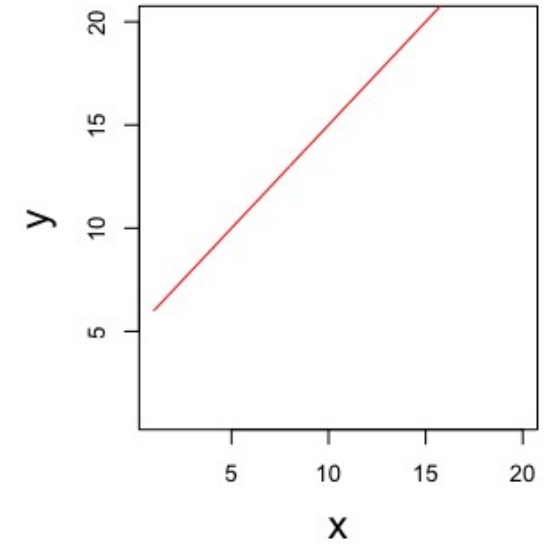
# Linear mixed models

$$Y = \beta_0 + \beta_1 X$$

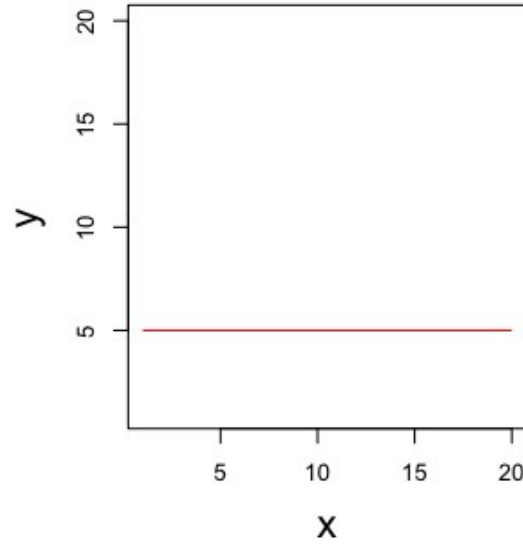
$b_0 = 5, b_1 = 0.5$



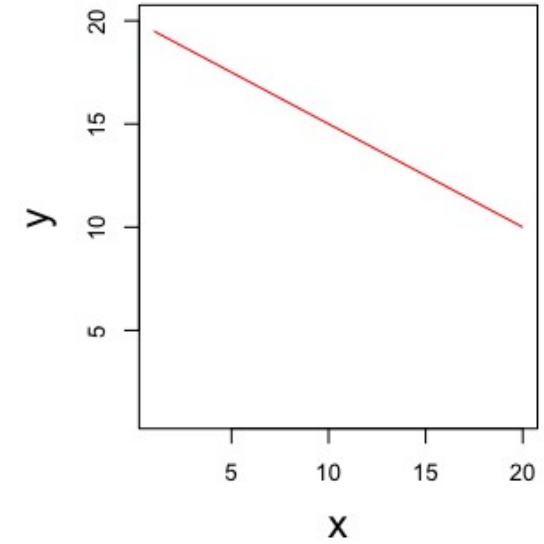
$b_0 = 5, b_1 = 1$



$b_0 = 5, b_1 = 0$



$b_0 = 20, b_1 = -0.5$



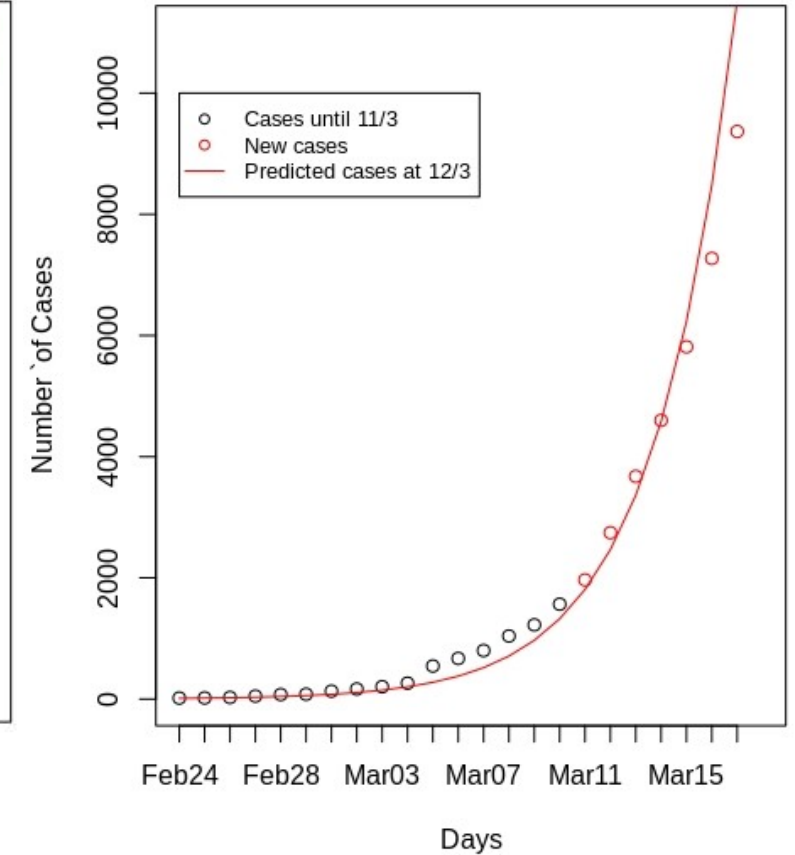
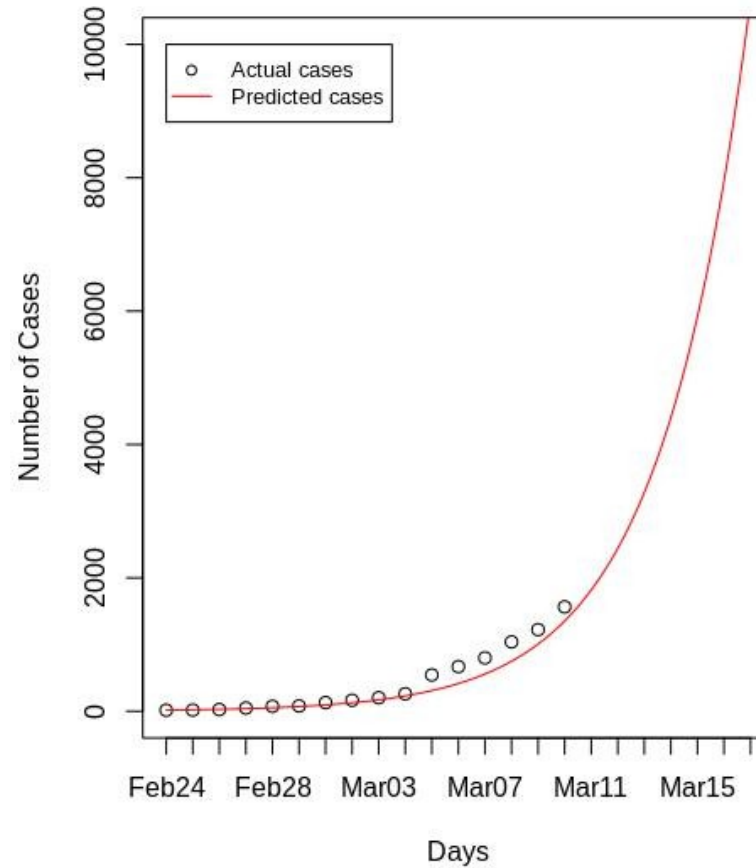
# Linear mixed models

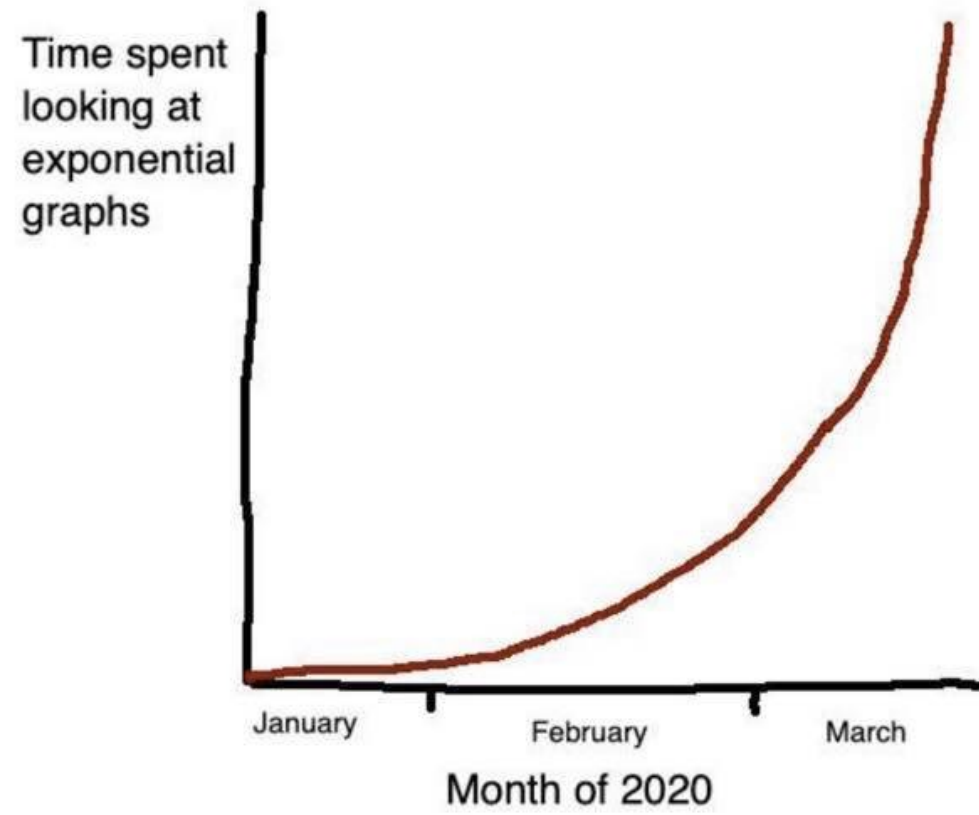
It is a linear model because the parameters combine additively; it is the model that needs to be linear, not necessarily the relationship(s)

$$Y = ae^{\beta x}$$

$$\ln Y = \ln \alpha + \beta x$$

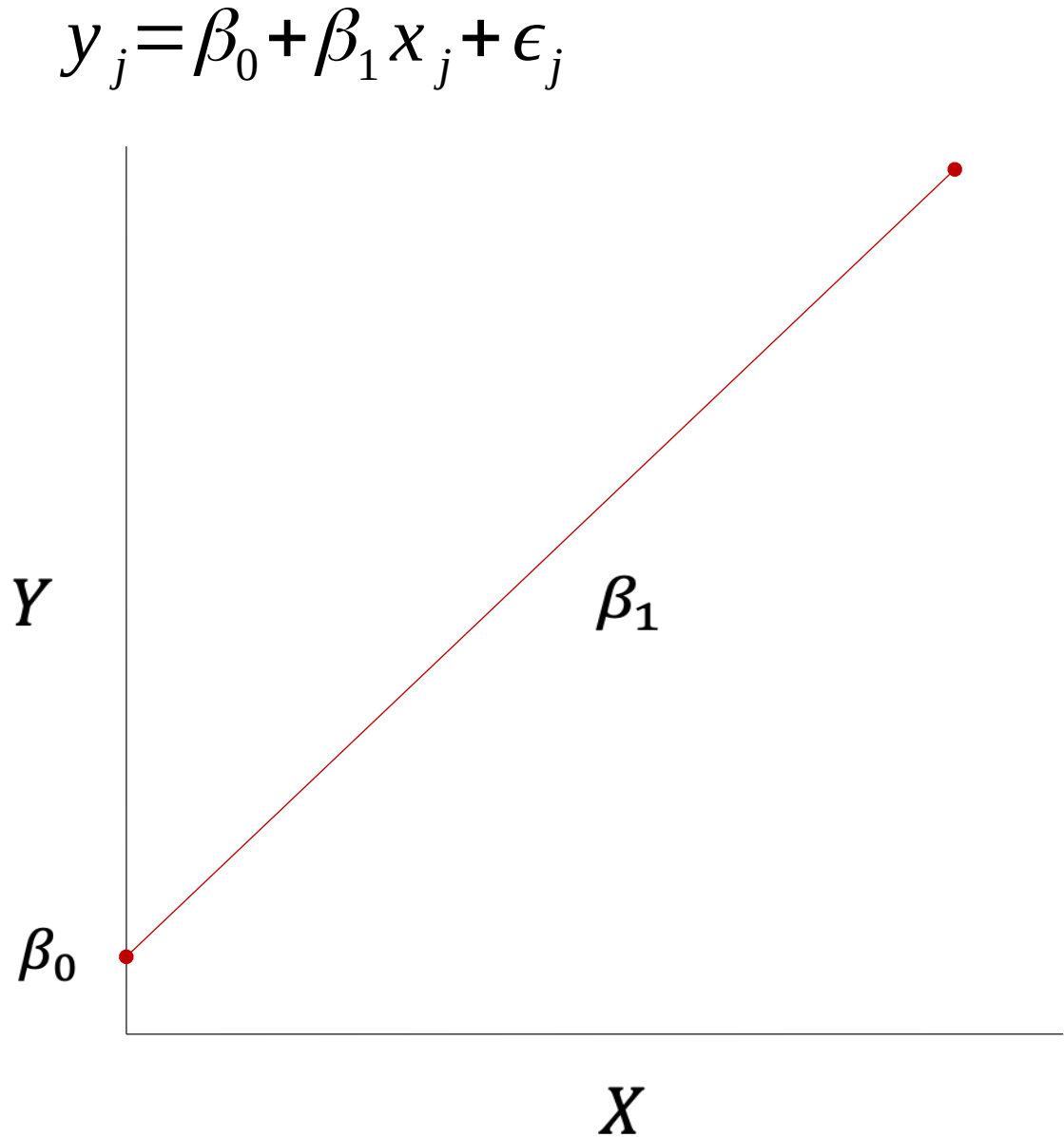
Covid-19 cases in Germany





## Linear mixed models

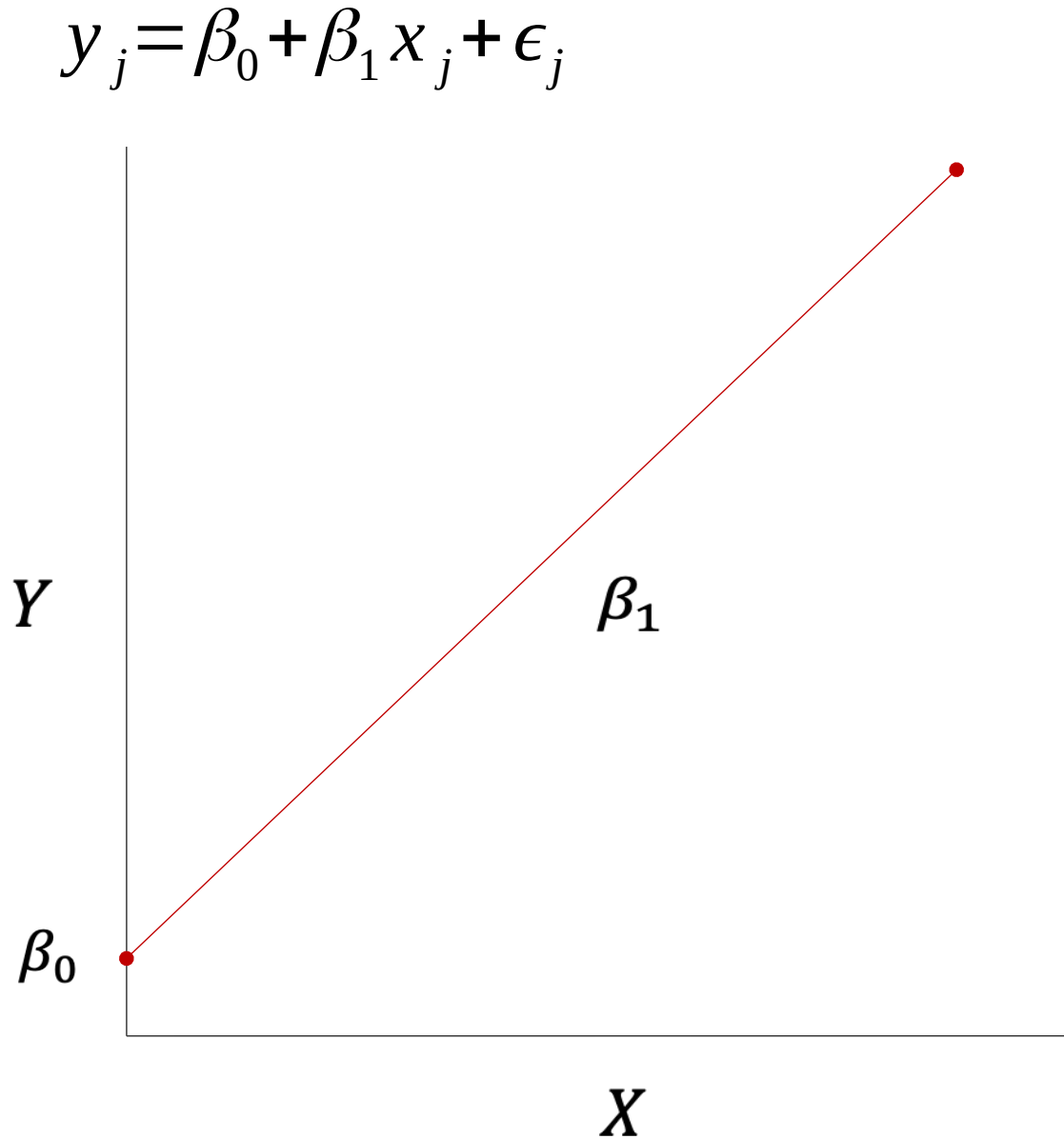
**Fixed effects:** we assume that the model holds true across the entire sample and that for every case of data (participant) in the sample we can predict a score using the same values of the slope and intercept, plus some random error that represents all factors that might influence the dependent variable other than  $x$ .



## Linear mixed models

In linear models, the parameters  $\beta_0$  and  $\beta_1$  are estimated through OLS.

It minimizes the sum of the squared differences between the observed values of  $y$  and the model-predicted values of  $y$  across the entire sample.



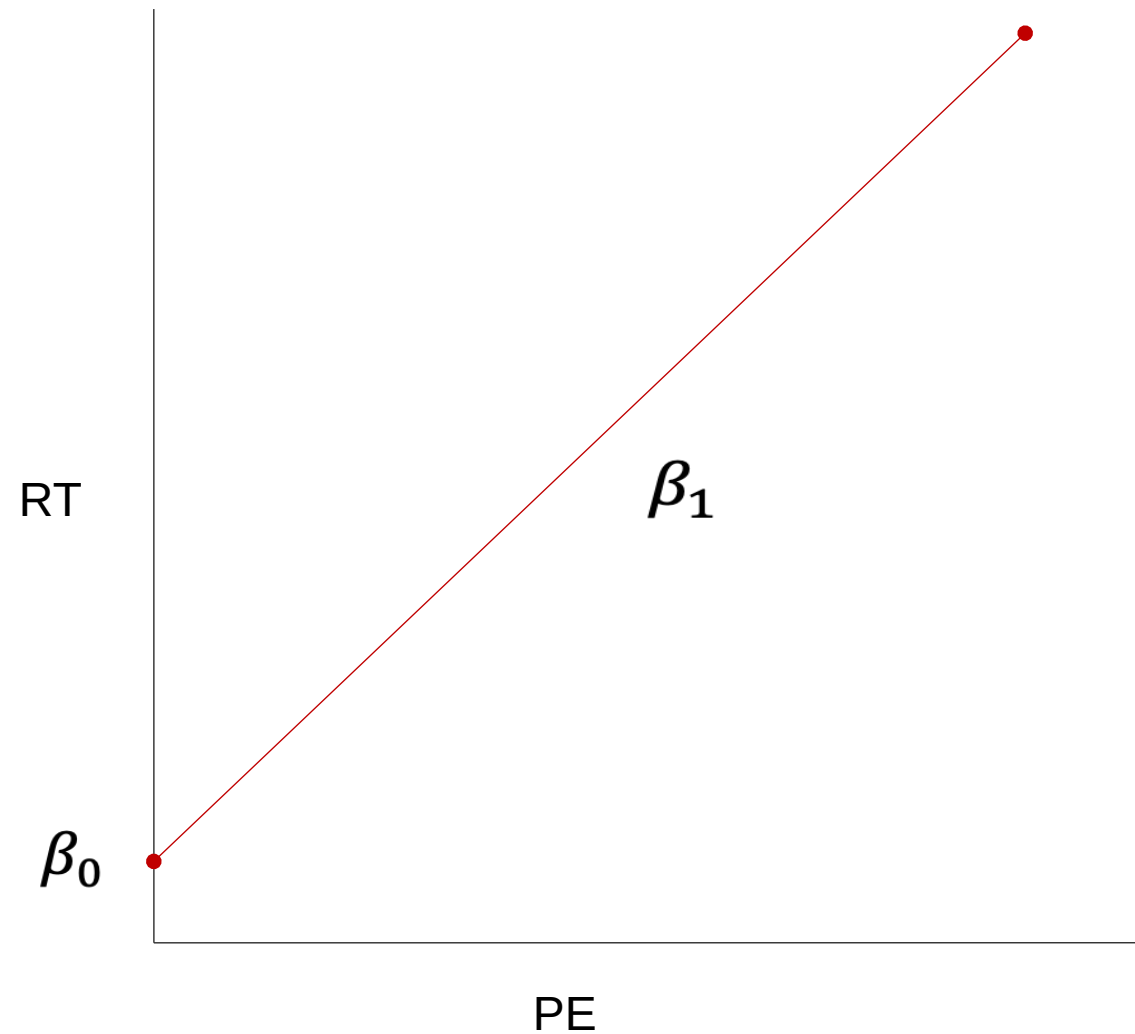


## Linear mixed models

What if we have variables that vary within-participants?

subj_id	item_id	PE	RT
1	1	-2.24718275	3.499112
1	2	0.59722872	3.553017
1	3	2.72881185	3.692639
1	4	-1.72184306	3.295054
1	5	1.07061702	3.166503
1	6	1.01296702	3.070292
1	7	0.84770910	3.440259
1	8	-0.19847366	3.246503
1	9	-0.02643587	3.112401
1	10	0.72538218	3.548040
1	11	0.51826827	3.457657
1	12	-0.72260728	3.783603
1	13	-0.73772957	3.007351
1	14	-0.14433796	3.220507
1	15	1.15225230	3.423374
1	16	0.79673807	3.004323
1	17	-1.93117571	3.193946
1	18	-1.61749030	3.083845

$$y_j = \beta_0 + \beta_1 x_j + \epsilon_j$$



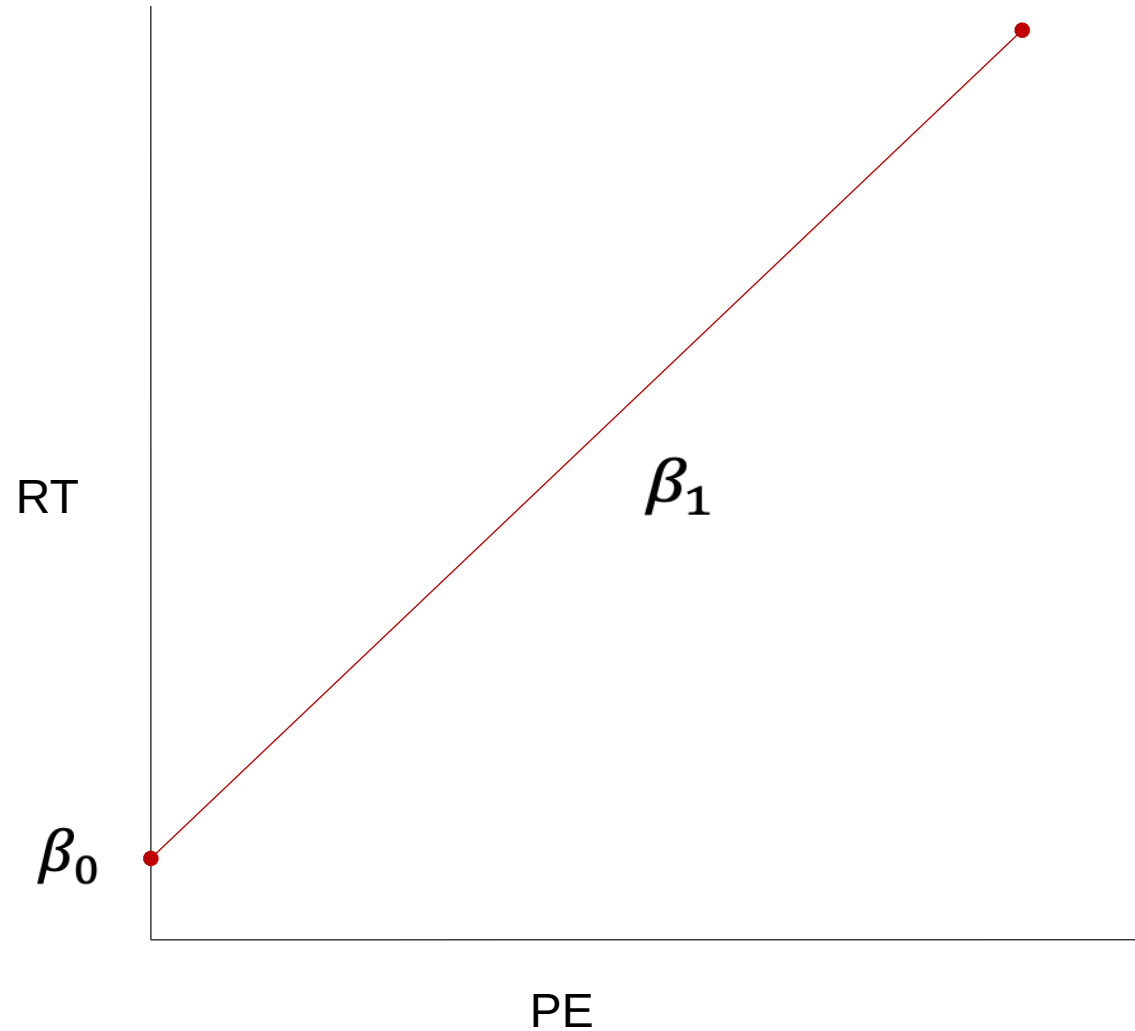
## Linear mixed models

Solution 1: We could fit a OLS regression to the entire Dataset, without aggregating.

What is the problem with that?

Exactly: it violates the assumptions of independence, because participants provide more than one data point. Therefore, their data are correlated (there are clusters in the data).

$$y_j = \beta_0 + \beta_1 x_j + \epsilon_j$$

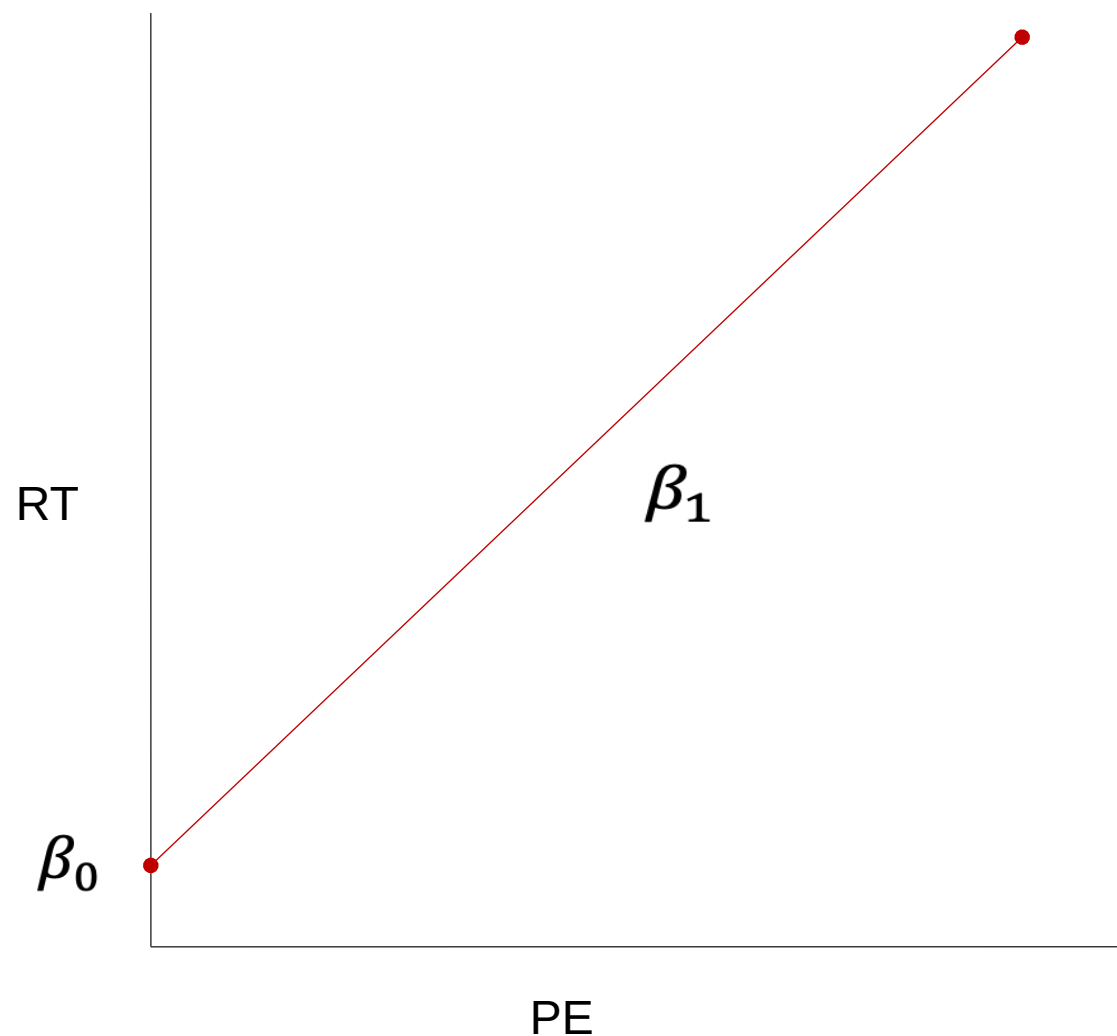


## Linear mixed models

Solution 2: We could aggregate data at the participant level and run OLS regression.

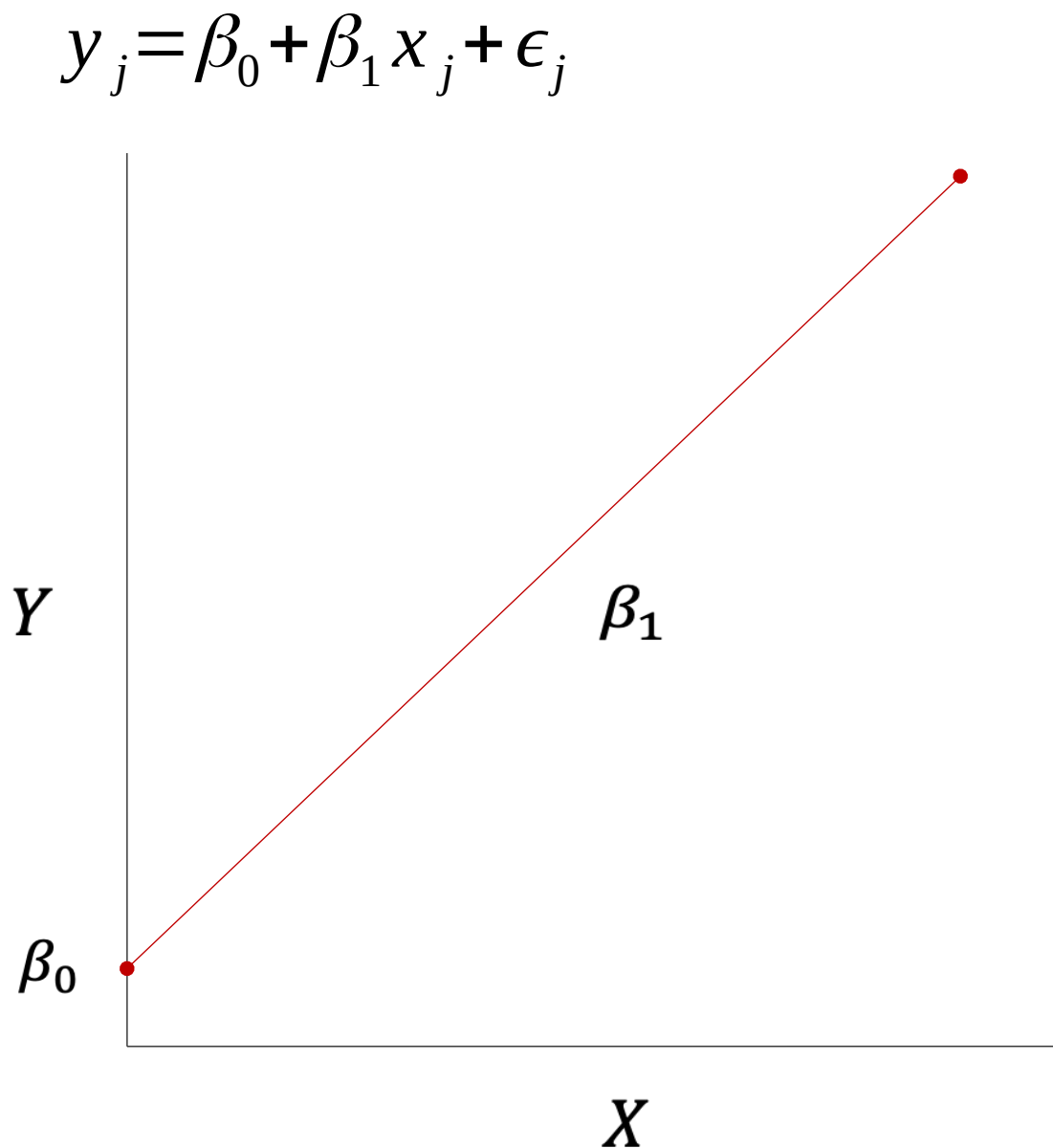
```
Lmmworkshop.Rmd  
```${r aggregate}```
```

$$y_j = \beta_0 + \beta_1 x_j + \epsilon_j$$



## Linear mixed models


```
linearmodel<-lm(outcome~predictor,data=df)
```



# Linear mixed models

```
summary(linearmodel)
```

Call:  
lm(formula = RT ~ PE, data = df\_agg)

$$y_j = \beta_0 + \beta_1 x_j + \epsilon_j$$


Residuals:

Min	1Q	Median	3Q	Max
-4.192	-1.133	-0.148	1.186	3.372

Coefficients:

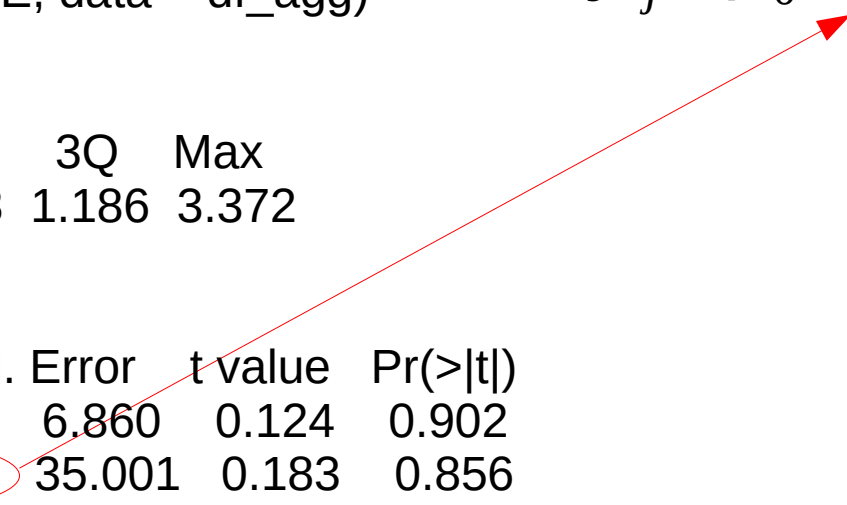
	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	0.852	6.860	0.124	0.902
PE	6.388	35.001	0.183	0.856

Residual standard error: 1.778 on 28 degrees of freedom  
Multiple R-squared: 0.001188, Adjusted R-squared: -0.03448  
F-statistic: 0.03331 on 1 and 28 DF, p-value: 0.8565

# Linear mixed models

```
summary(linearmodel)
```

Call:  
lm(formula = RT ~ PE, data = df\_agg)

$$y_j = \beta_0 + \beta_1 x_j + \epsilon_j$$


Residuals:

Min	1Q	Median	3Q	Max
-4.192	-1.133	-0.148	1.186	3.372

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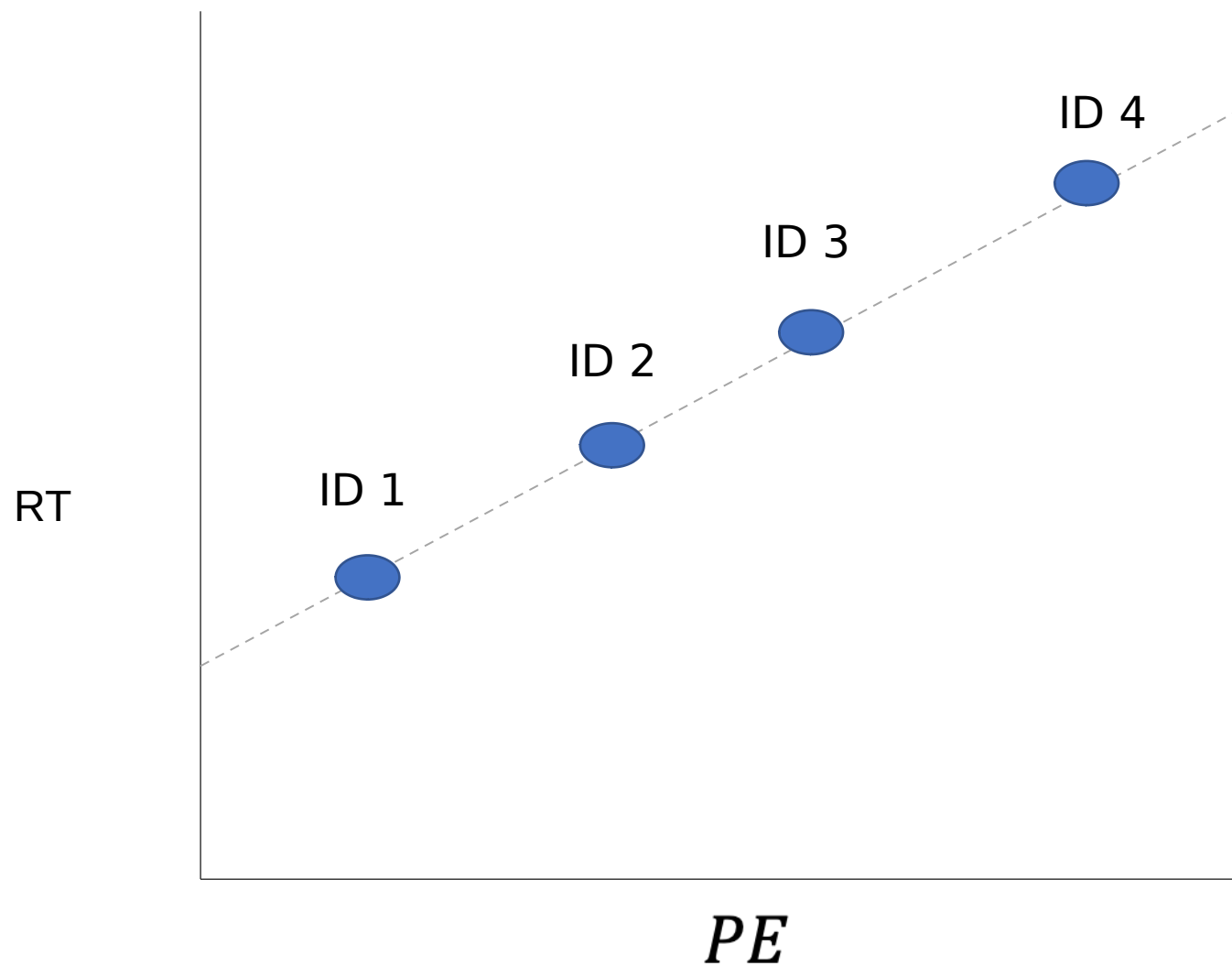
F-statistic: 0.03331 on 1 and 28 DF, p-value: 0.8565

# Linear mixed models

```
Summary.aov(linearmodel)
```

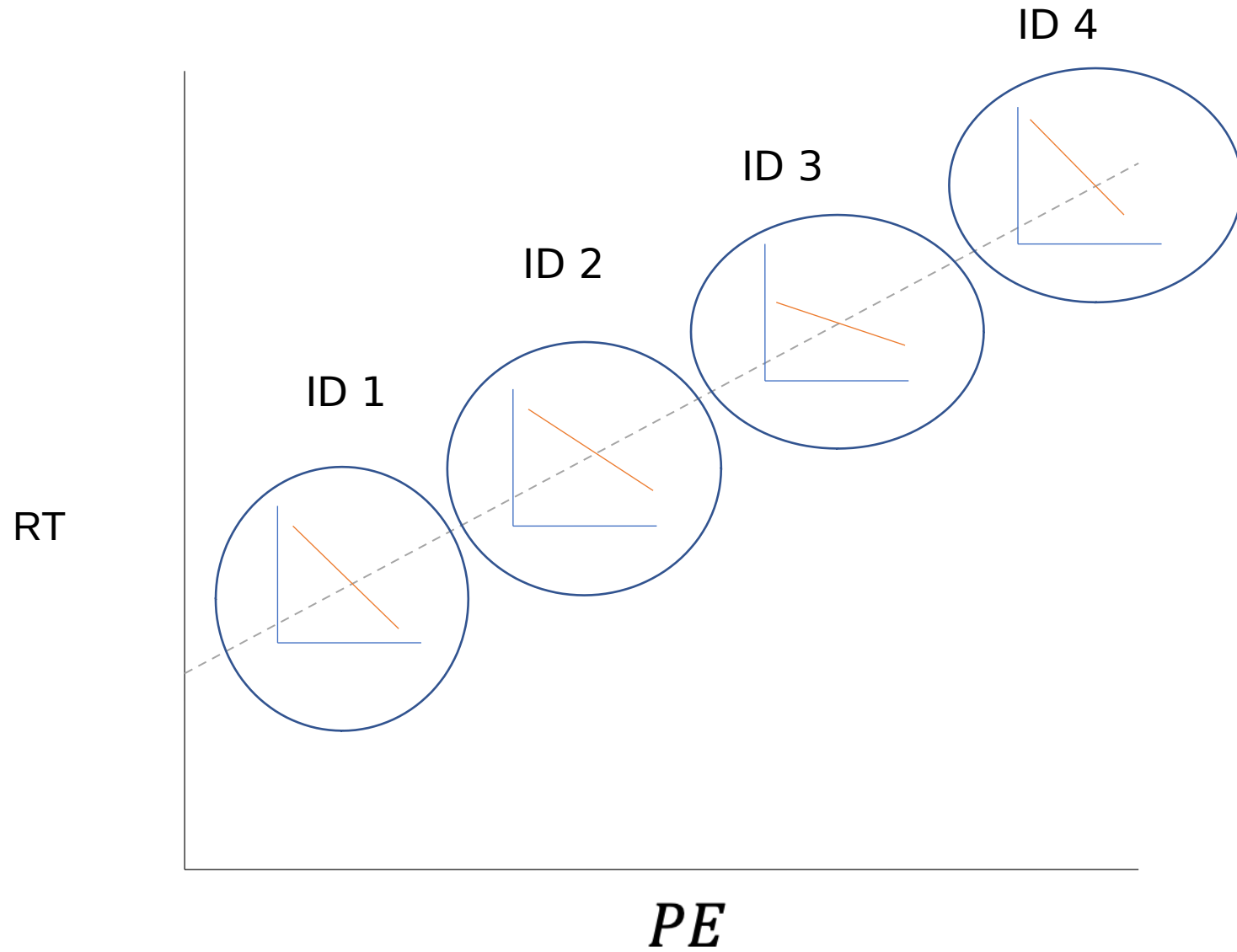
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
PE	1	0.11	0.1053	0.033	0.856
Residuals	28	88.51	3.1612		

What is the problem with that?



Between-participant  
level:  
Participants with  
higher *PE* on average  
have slower *RT*

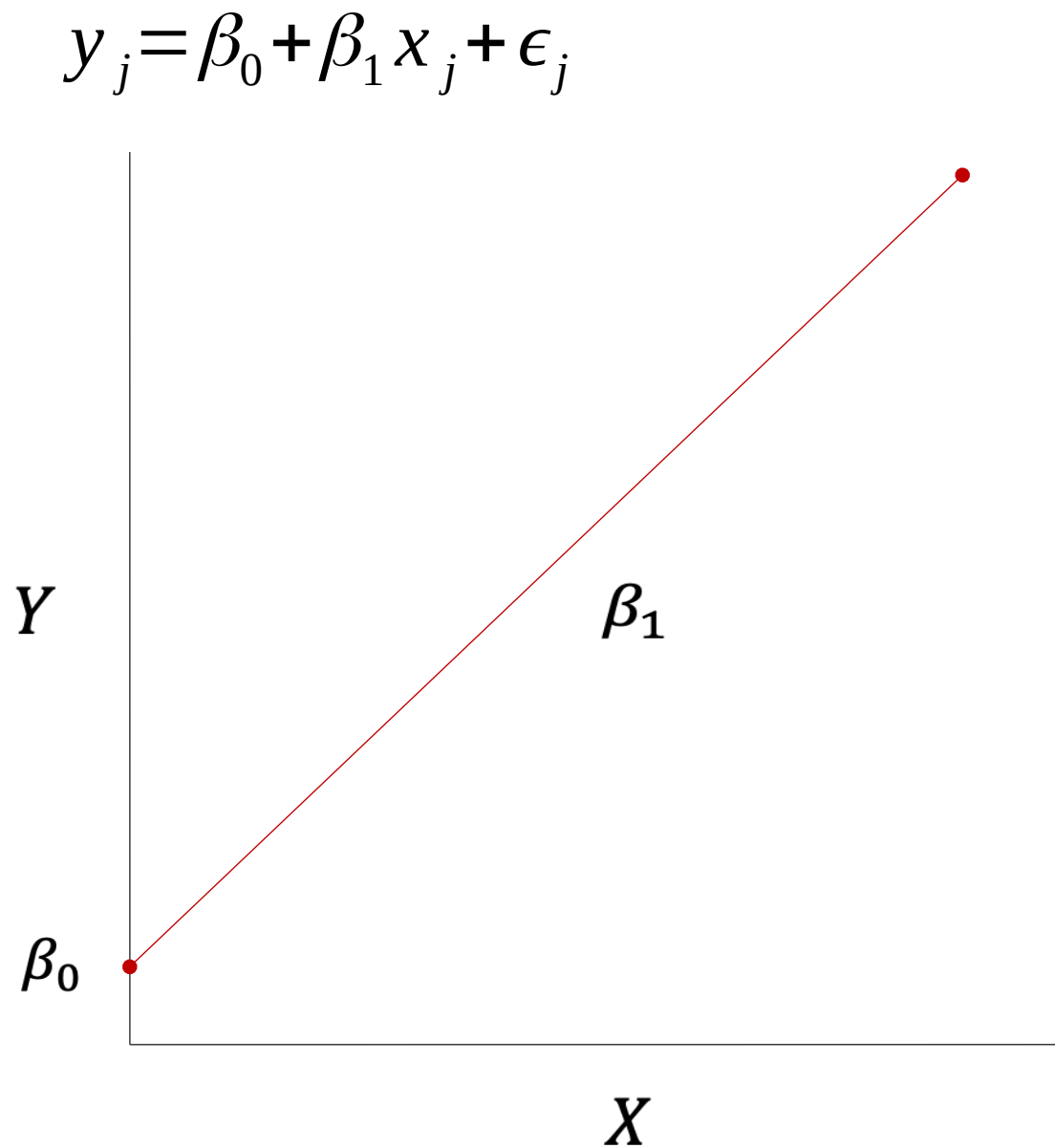




Within-participant  
level:  
When participants  
experienced higher  
PE their RT are faster

## Linear mixed models

So what do we do?

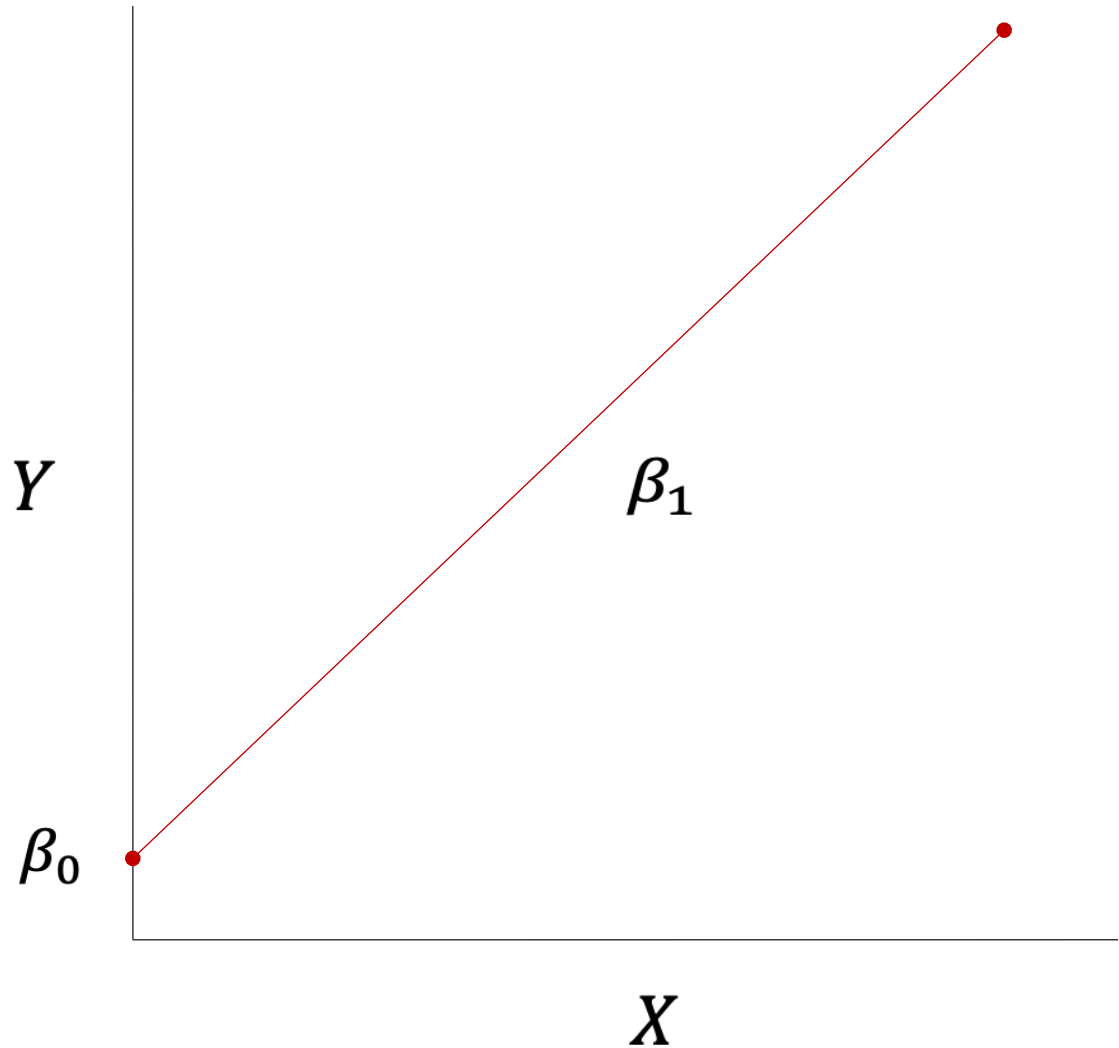


## Linear mixed models

**Random effects:** we say that a parameter is random then we assume not that it is a fixed value, but that its value can vary.

That parameter is also random because we treat it as being randomly selected from the larger population.

$$y_j = \beta_0 + \beta_1 x_j + \epsilon_j$$

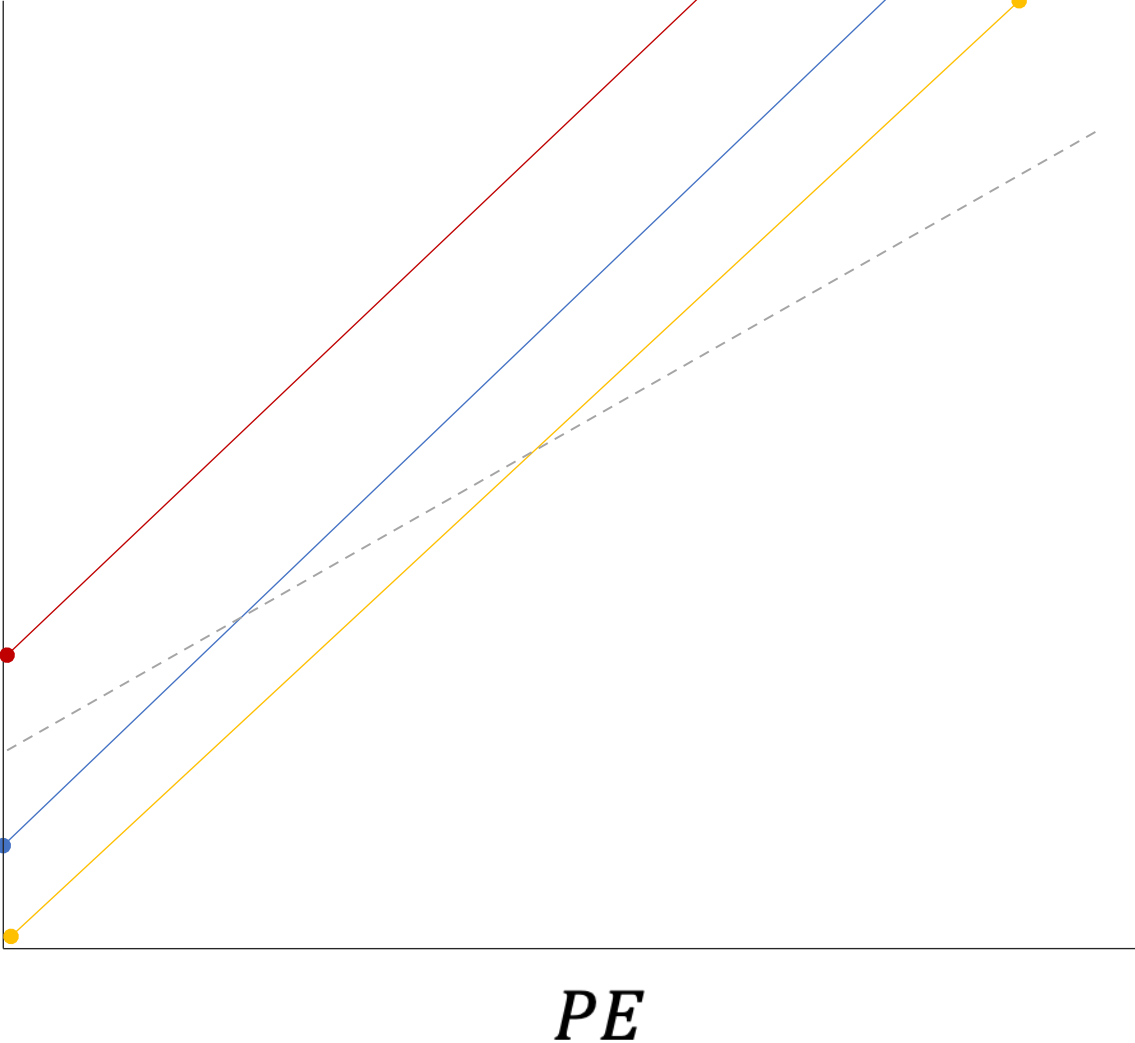


**Random Intercepts**

- Category 1
- Category 2
- Category 3

(i.e., differences in “overall” RT)

RT

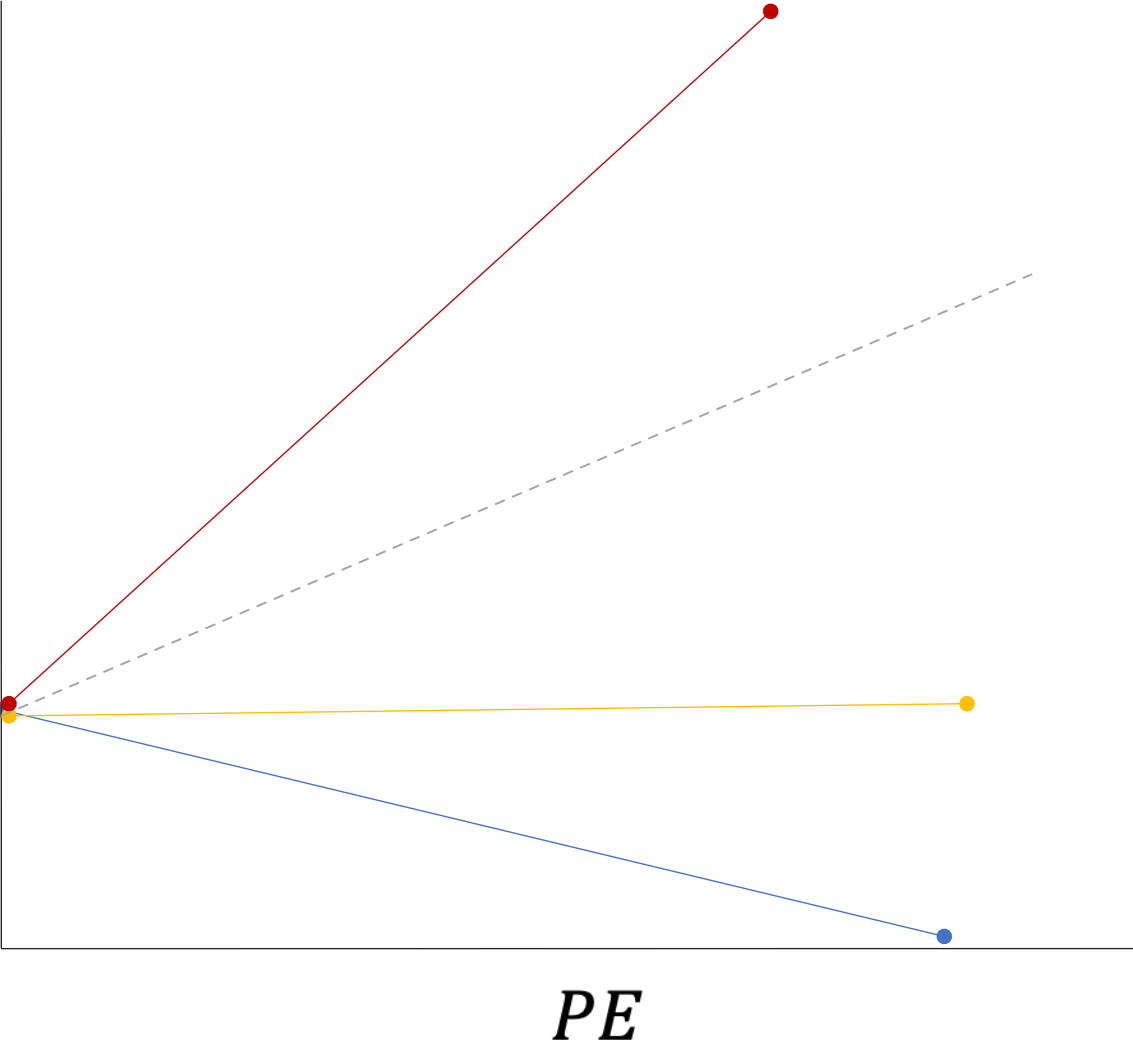


**Random Slopes, fixed intercepts**

- Category 1
- Category 2
- Category 3

RT

i.e., differences in the effect across categories)

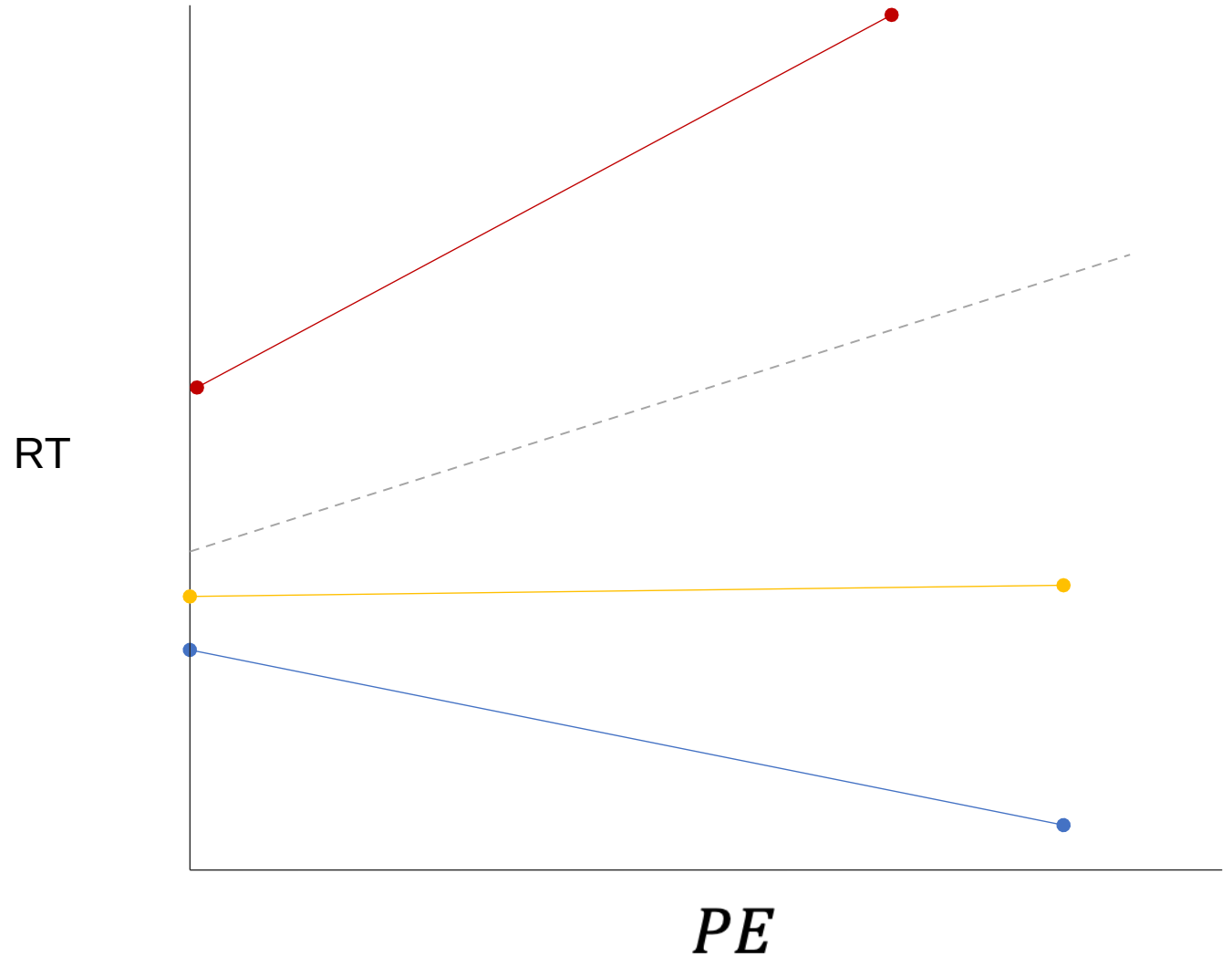


## Random Intercepts and Slopes

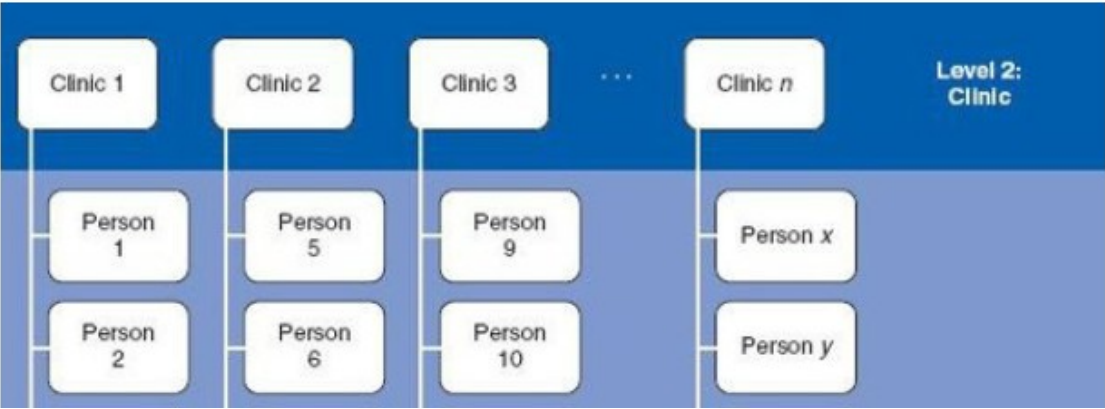
- Category 1
- Category 2
- Category 3

(i.e., differences in the size of the effect across conditions)

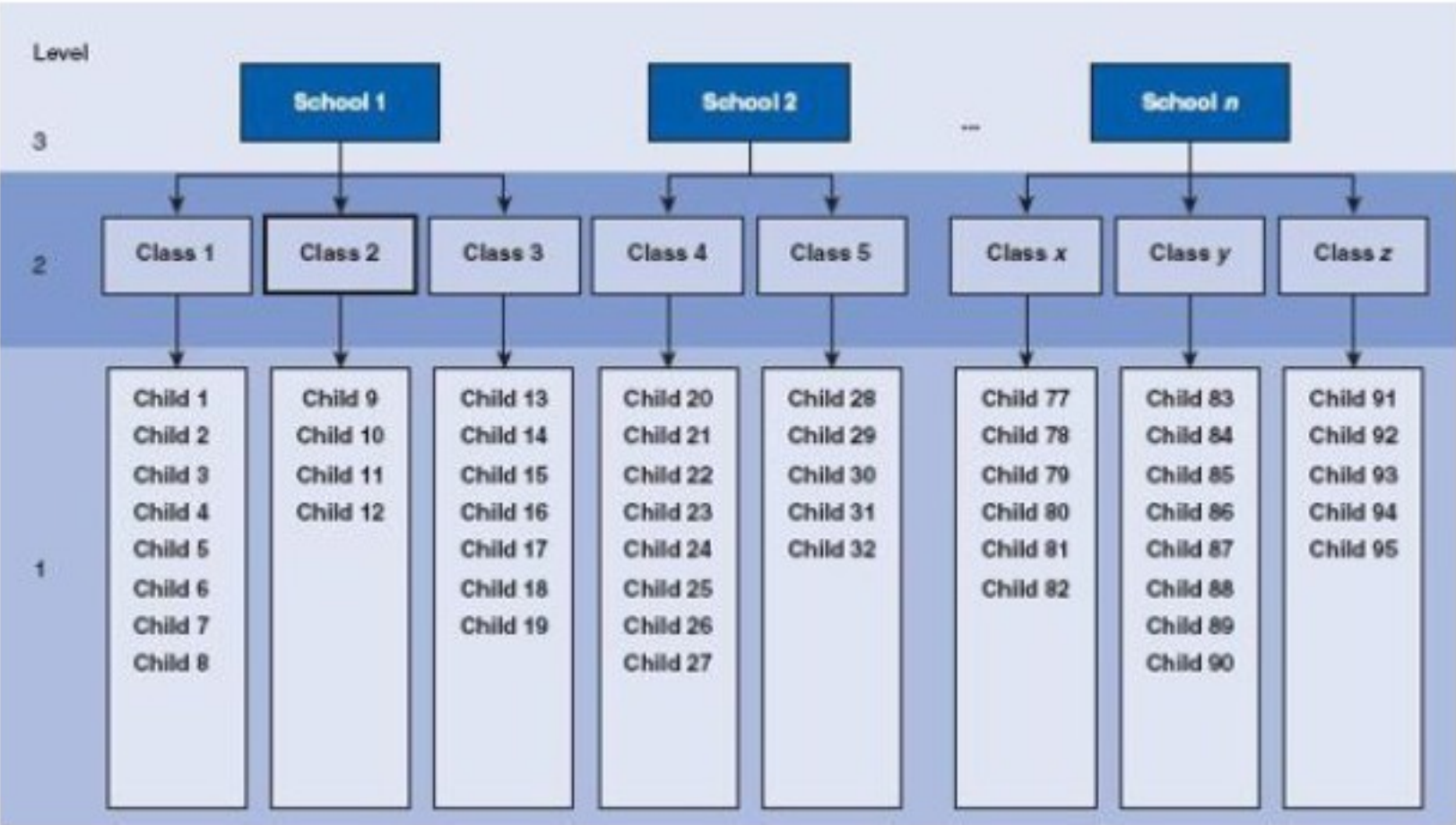
Including random intercepts and slopes allows to control for random variations among items (sampling units)



**Linear mixed models**  
**Multilevel models**  
**Hierarchical linear mod**



Nested data



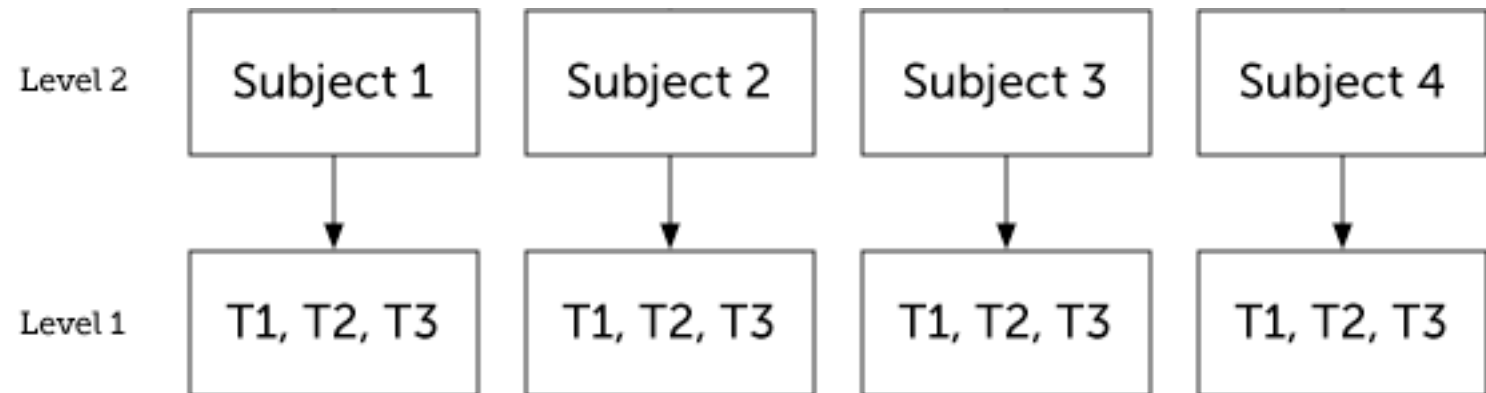
# Linear mixed models

## Multilevel models

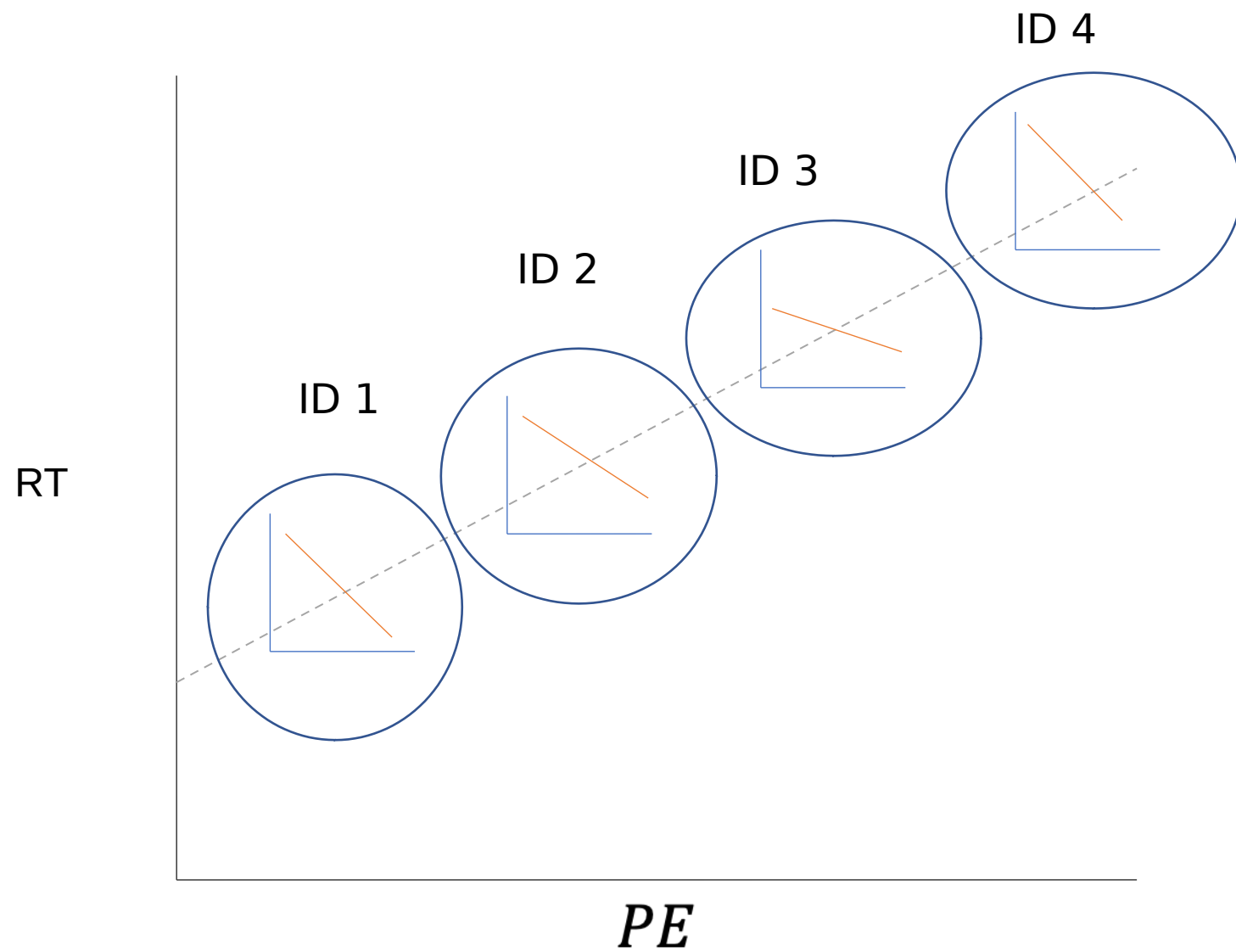
## Hierarchical linear models

Nested data

Taking into account  
within- and between-  
person variability



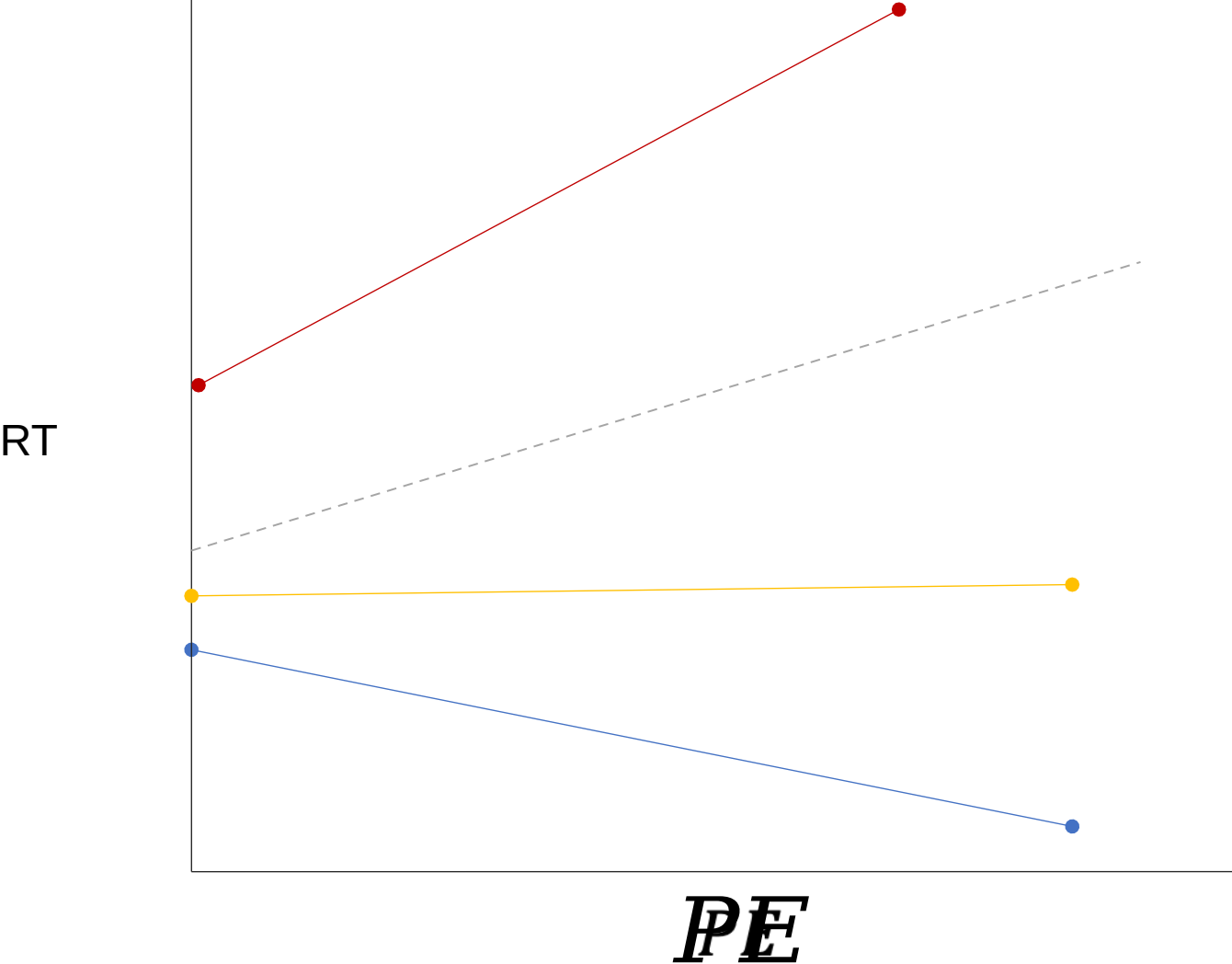




“The reason for favoring the within-subject level is that omitted and confounding variables are less likely to be a problem when analyses focus on how and why people change over time than on how people differ from one another”.  
(Bolger & Laurenceau, *Intensive longitudinal methods: An introduction to diary and experience sampling research*, 2013).

# Random Intercepts and Slopes

- Participant 1
- Participant 2
- Participant 3
- Fixed effect (Intercept and slope for the average person)



Level 1 - dependent variable  $Y$  for observation  $i$  for a particular subject  $j$ .

$$Y_{ij} = \beta_{0j} + \beta_{1j} X_{ij} + \epsilon_{ij}$$

The dependent variable  $Y$  for subject  $j$  for the specific observation  $i$  is given by an subject-specific intercept  $\beta_{0j}$ , a subject specific slope  $\beta_{1j}$ , and a within-subject error term  $\epsilon_{ij}$ .

$$Y_{ij} = \beta_{0j} + \beta_{1j} X_{ij} + \epsilon_{ij}$$

$$\beta_{0j} = \gamma_{00} + u_{0j}$$

Level 2 (between-subjects)

$u_{0j}$  is a random effect because it varies from cluster to cluster

Subject 1

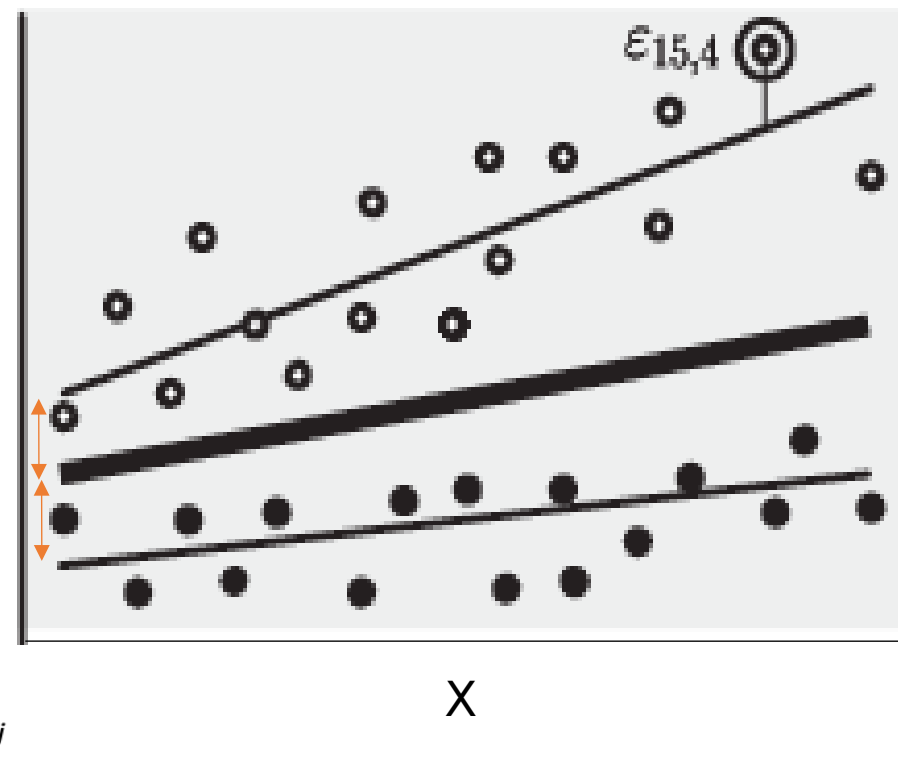
$$Y_{i1} = (\gamma_{00} + u_{01})$$

Typical person

$$Y_{ij} = \gamma_{00}$$

Subject 2

$$Y_{i2} = (\gamma_{00} + u_{02})$$



$$Y_{ij} = \beta_{0j} + \beta_{1j} X_{ij} + \epsilon_{ij}$$

$$\beta_{0j} = \gamma_{00} + u_{0j}$$

$$\beta_{1j} = \gamma_{10} + u_{1j}$$

Level 2 (between-subjects)

Subject 1

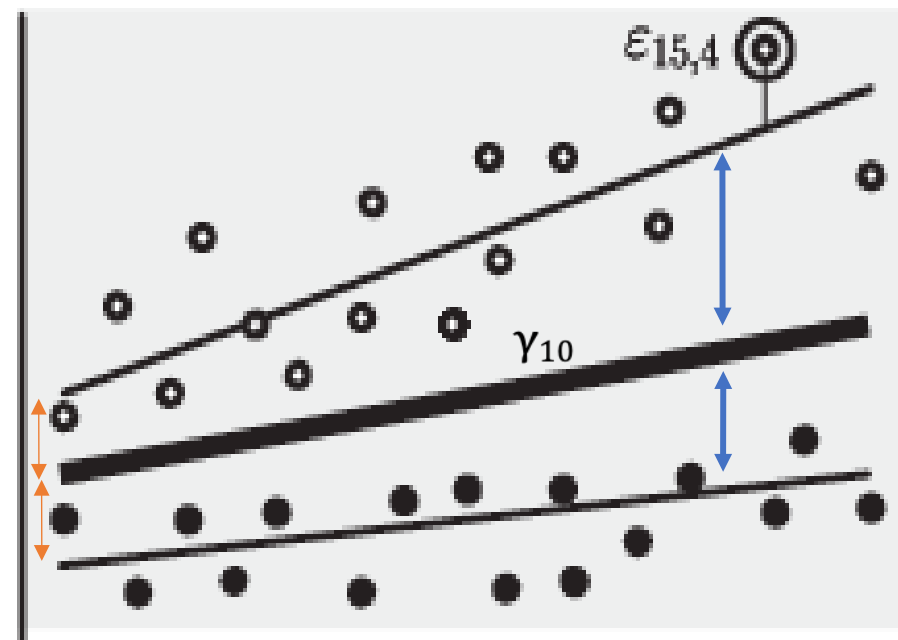
$$Y_{i1} = (\gamma_{00} + u_{01}) + (\gamma_{10} + u_{11}) X_{i1} + \epsilon_{i1}$$

Typical person

$$Y_{ij} = \gamma_{00} + \gamma_{10} X_{ij}$$

Subject 2

$$Y_{i2} = (\gamma_{00} + u_{02}) + (\gamma_{10} + u_{12}) X_{i2} + \epsilon_{i2}$$



X

$u_{0j}$

$u_{1j}$

$Y_{ij} = \beta_{0j} + \beta_{1j} X_{ij} + \epsilon_{ij}$ 
 is a within-subject residual term representing the difference, at a given time point between the predicted Y for a given subject and the actual value.

$$\beta_{0j} = \gamma_{00} + u_{0j}$$

$$\beta_{1j} = \gamma_{10} + u_{1j}$$

Level 2 (between-subjects)

Subject 1

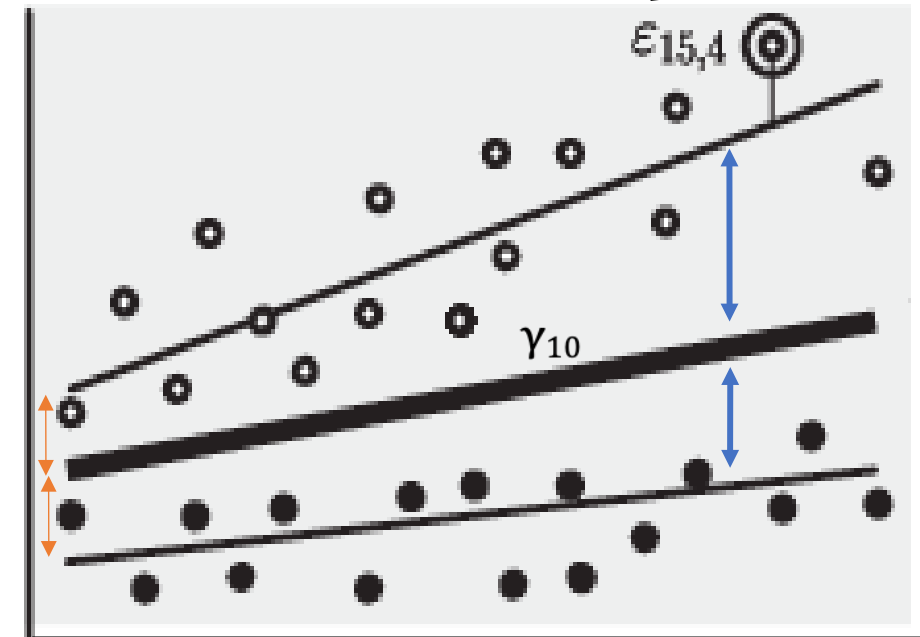
$$Y_{i1} = (\gamma_{00} + u_{01}) + (\gamma_{10} + u_{11}) X_{i1} + \epsilon_{i1}$$

Typical person

$$Y_{ij} = \gamma_{00} + \gamma_{10} X_{ij}$$

Subject 2

$$Y_{i2} = (\gamma_{00} + u_{02}) + (\gamma_{10} + u_{12}) X_{i2} + \epsilon_{i2}$$



X

$u_{0j}$

$u_{1j}$

How are parameters estimated?

Parameters for mixed models are not estimated through OLS, which is not the optimal approach for complex model. Instead, they are estimated through Maximum Likelihood Estimation (MLE) and Restricted Maximum Likelihood (REML).

MLE search for the population model parameters that maximize the likelihood of obtaining our data. In other words, the parameters obtained should maximize the likelihood of our particular sample.

It search through candidate parameters in several iterations using nonlinear optimization algorithms.

RMLE is like MLE, but also takes into account the number of parameters being estimated in the model in order to determine the appropriate degrees of freedom for the estimation of the random components. In contrast, MLE does not account for these. Therefore, it is generally preferred for estimating multilevel models. It is the default for lmer.

Let's do this!

```
lmm<-lmer(DV~IV+(randomeffect|randomintercept),data=df)
```



Random, “stochastic” part of the model, with the random effects. On the right of the | symbol there is the clustering variable. On the left side there are the random slopes.



First, let's fit an unconditional model, a model with only the intercept, to examine the variability between- and within- participant

$$\rho_I = \frac{\tau^2}{\tau^2 + \sigma^2}$$

where

$\tau^2$  = Population variance between clusters

$\sigma^2$  = Population variance within clusters

Relative higher values of  $\rho$  indicate that great amount of variation in the outcome measure (DV) is associated with the cluster membership – observation within participants are correlated.

Variance between-participant is higher than within-participant.

This is called intraclass correlation.

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']  
Formula: RT ~ 1 + (1 | subj\_id)

Random effects:

Groups	Name	Variance	Std.Dev.
subj_id	(Intercept)	3.0549	1.7478
	Residual	0.2816	0.5307

Number of obs: 9000, groups: subj\_id, 30

Lmmworkshop.Rmd

```
```{r lmm rand int}```
```

$$\hat{\rho} = \frac{3.05}{3.05 + 0.28} = 0.91$$

To test whether the addition of the random intercept improves the fit of the model, we can compare a model with random intercept and a model without them

```
Lmmworkshop.Rmd  
```{r Imm rand test sig}  
```
```

This is called “likelihood ratio test”, where the fit of the full and reduced models are compared.

The glmer effect should be called first. `anova(mixmod_unc, mod_unc)`

Data: df

Models:

mod\_unc: RT ~ 1

mixmod\_unc: RT ~ 1 + (1 | subj\_id)

|            | npars | AIC   | BIC   | logLik   | deviance | Chisq | Df | Pr(>Chisq)    |
|------------|-------|-------|-------|----------|----------|-------|----|---------------|
| mod_unc    | 2     | 36110 | 36124 | -18053.1 | 36106    |       |    |               |
| mixmod_unc | 3     | 14385 | 14406 | -7189.3  | 14379    | 21728 | 1  | < 2.2e-16 *** |

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

If models are not fitted with ML, they are refitted with ML, because it makes them comparable.

The chi square difference test is computed on deviance statistics, which is  $-2 \cdot LL$ , and follows a chi-square distribution.

Not everyone agrees that testing significance of random effects is a good idea, as the LRT in some cases are conservative  
Checkout this:

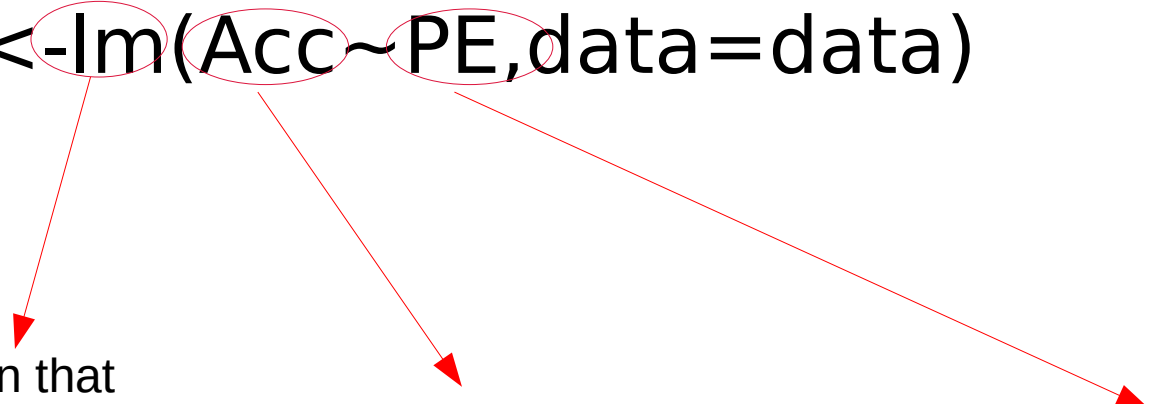
<https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html#testing-significance-of-random-effects>

Consider not testing the significance of random effects. If the random effect is part of the experimental design, this procedure may be considered 'sacrificial pseudoreplication' (Hurlbert 1984). Using stepwise approaches to eliminate non-significant terms in order to squeeze more significance out of the remaining terms is dangerous in any case.

consider using the RLRsim package, which has a fast implementation of simulation-based tests of null hypotheses about zero variances, for simple tests. (However, it only applies to lmer models, and is a bit tricky to use for more complex models.)

```
Lmmworkshop.Rmd  
```${r exactLRT}```  
```
```

LM<-lm(Acc~PE,data=data)




Function that stands for “linear model” and is used in R to calculate regression and its special cases (Anova, multiple regressions, etc.)


Outcome, or dependent variable

On the right side of the ~ symbol there are the predictors (fixed effects)

```
Library("lme4")  
MLM<-lmer(Acc~PE+(PE|PartNumb), data=data)
```



Function for the linear mixed model. It requires that some random effects are added.



Fixed effects part. Same as the lm one.

Within brackets there is the “stochastic” part of the model, with the random effects.  
On the right of the | symbol there is the clustering variable: in our case is the participant number variable. We are adding random intercepts for participants, meaning that we are considering their variance in the average recognition accuracy. On the left side of the | symbol there are the random slopes. In this case, we are considering: random slopes for PE; this means that we are accounting for participants differences in the effects of this variable on accuracy

summary(MLM)

Random effects:

Groups	Name	Variance	Std.Dev.	Corr	
PartNumb	(Intercept)	0.3662782	0.60521		Between participant's variance (and std. dev) in the intercept (overall accuracy)
PE		0.0008159	0.02856	-1.00	Between participant's variance (and std. Dev) in the slope ( effect of PE on accuracy).
Residual		1.2540770	1.11986		
Number of obs: 627, groups: PartNumb, 38					

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )	
(Intercept)	-0.232759	0.133371	41.963984	-1.745	0.0883	
PE 1	0.011369	0.006011	40.291277	1.891	0.0658	Fixed effects. Intercept and coefficient for the entire sample, after accounting for between participants variance.

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

To sum up, benefits of using LMM:

- Control for random variability between items
- Focus on within-participants processes
- Separate within-participant from between-participant variability
- Account for dependency in the data
- Allow to deal with missing data



Please check the practical example  
in the Lab Tutorials for more on LMM