

# Integrated Data Analysis

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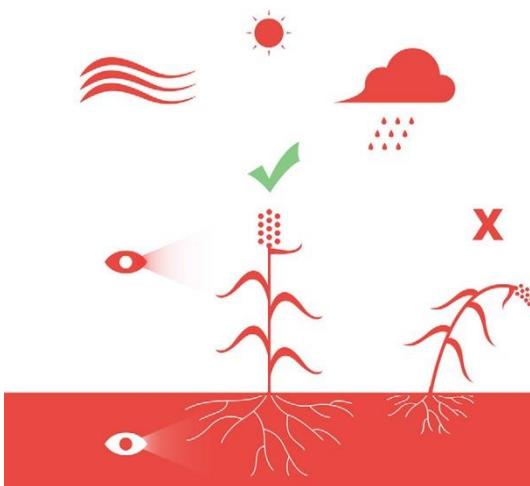
Institute of field and vegetable crops, Novi Sad  
Center of Excellence for Legumes

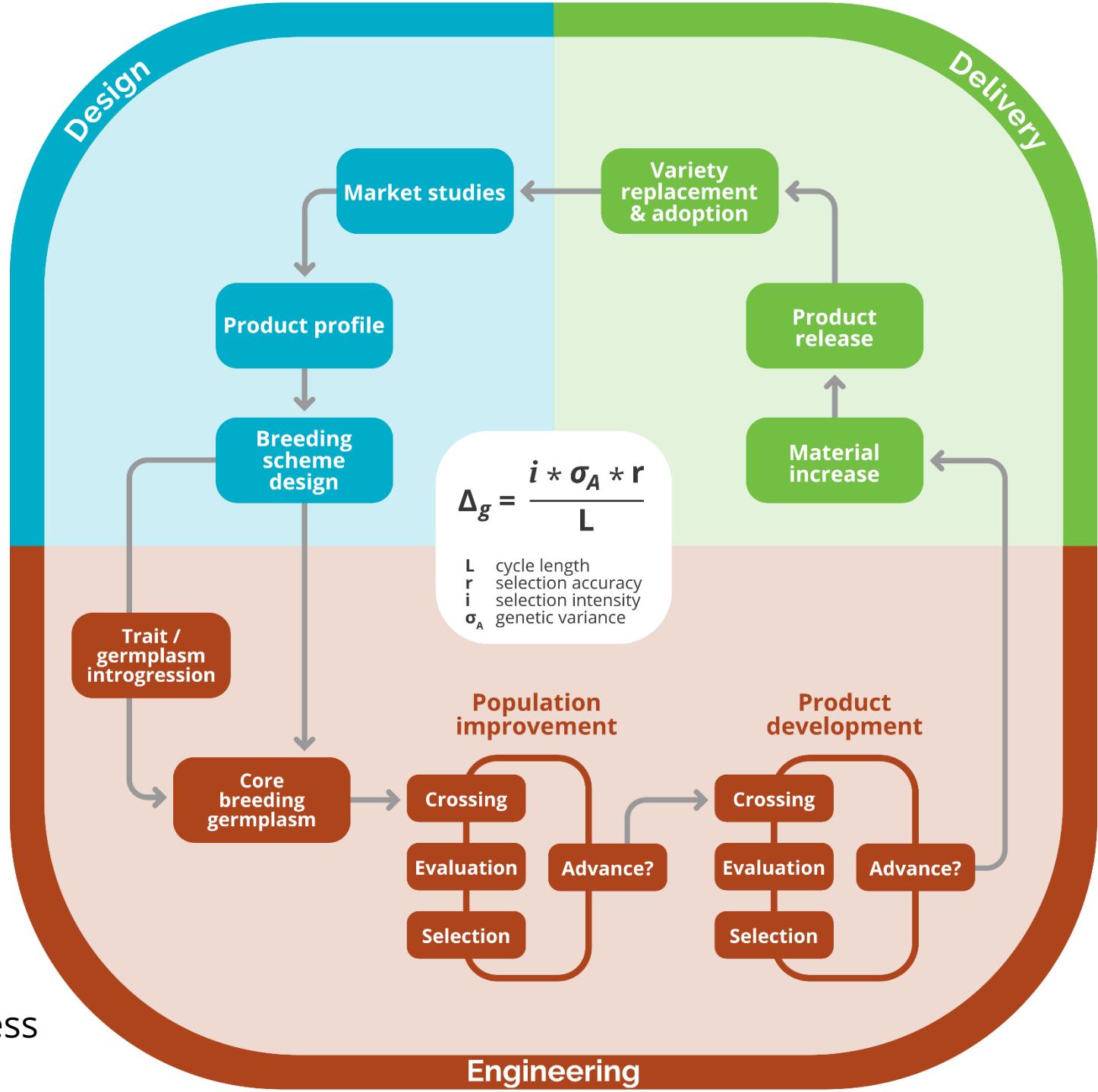


# Key Concepts

- **Pooling Raw Data**
- **Expanded Inquiry**
- **Increased Power**
- **Cumulative Science**

- Integrated Data Analysis is a powerful approach for synthesizing information from multiple sources to advance scientific knowledge and address complex research questions. It offers the potential to move beyond the limitations of individual studies and build a more robust and advanced understanding of phenomena.



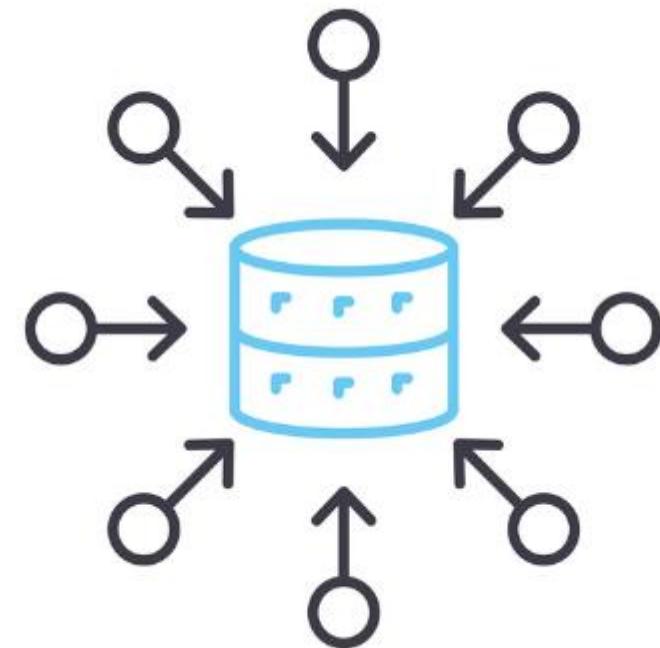


Breeding as a process

Source: EiB

# Single data source

- Single experiment/trial
- Single survey
- Data base query
- Simulation and modeling
- ....



# Data types

## Qualitative Data (Categorical Data):

**Nominal Data:** categories without any inherent order or ranking.

Examples: colors (red, blue, green), types of fruit (apple, banana, orange)

**Ordinal Data:** categories with a meaningful order or ranking.

Examples: survey responses like "strongly agree, agree, neutral, disagree, strongly disagree," or disease score (S, MS, M, MR, R).

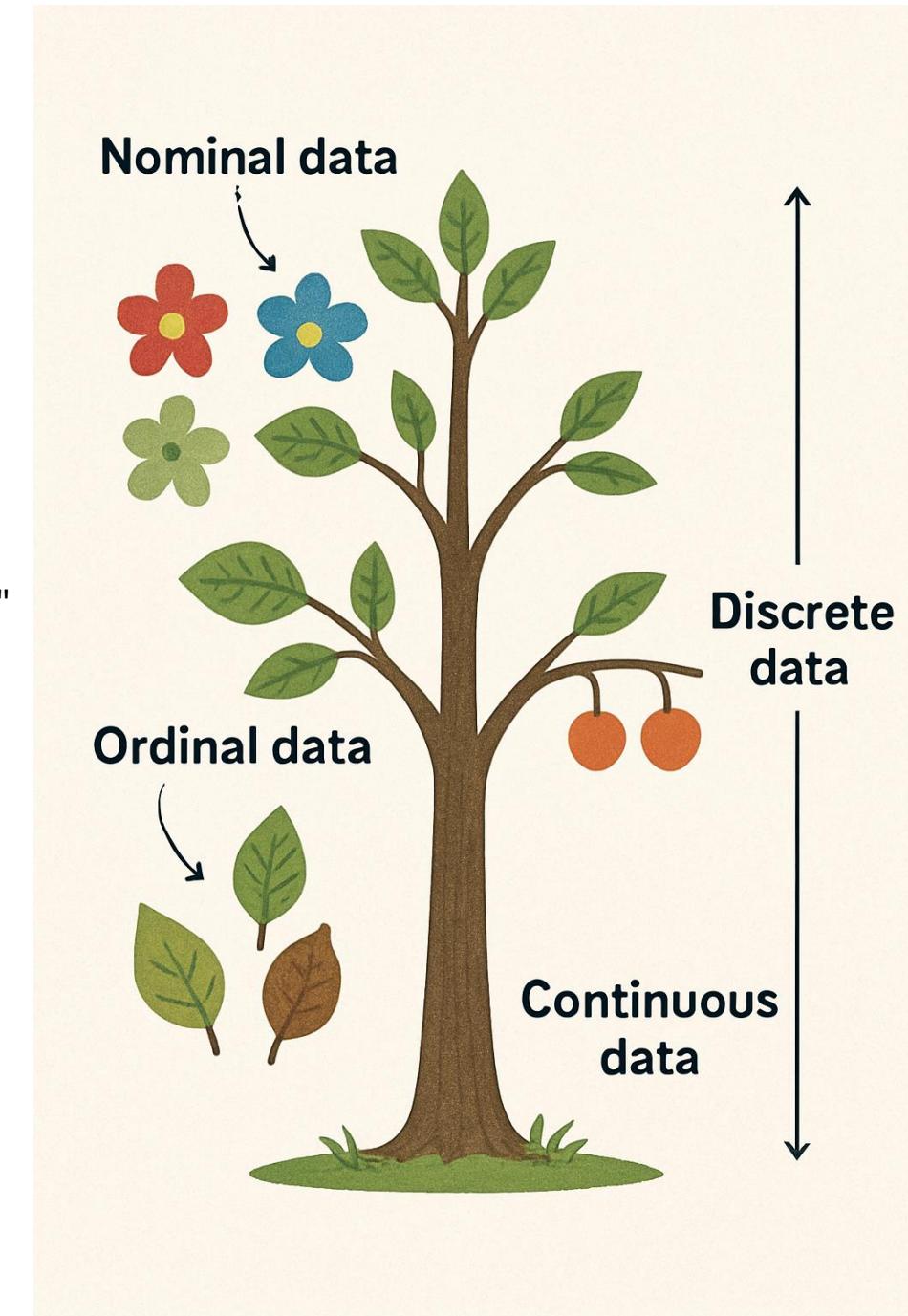
## Quantitative Data (Numerical Data):

**Discrete Data:** countable values that can only take specific, separate values with gaps in between.

Examples: number of students, number of fruits.

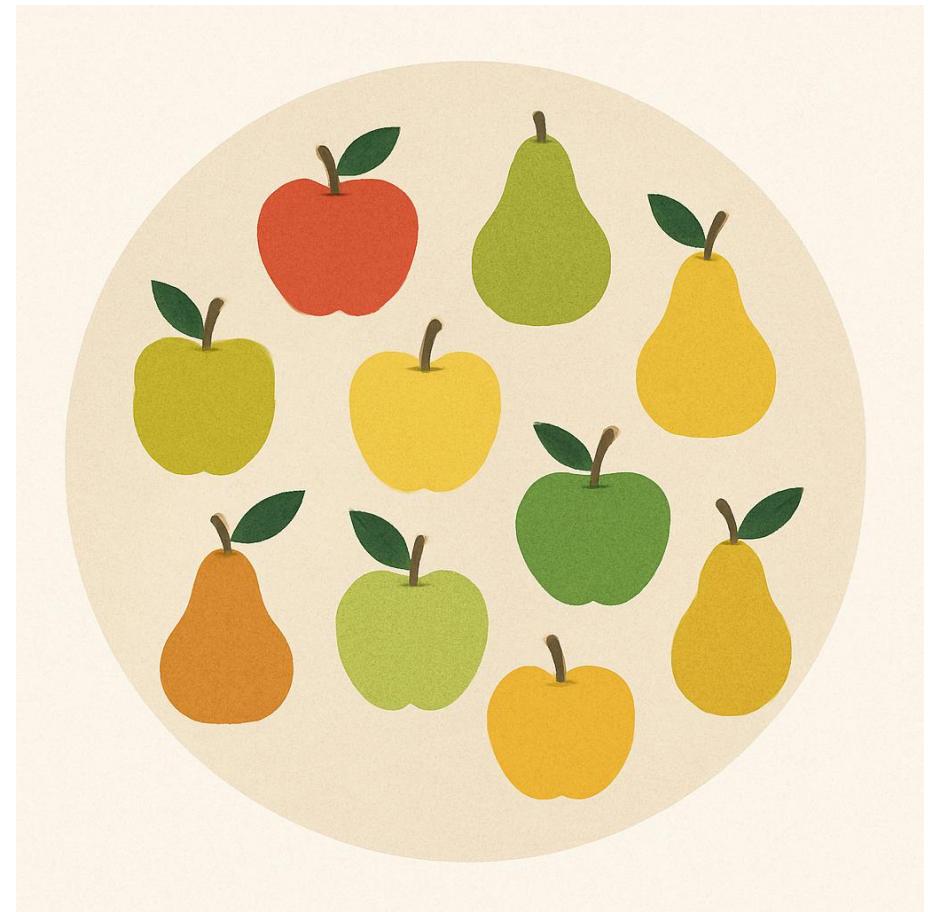
**Continuous Data:** values that can fall anywhere within a given range.

Examples: height, weight, temperature, time.



# Nominal Data

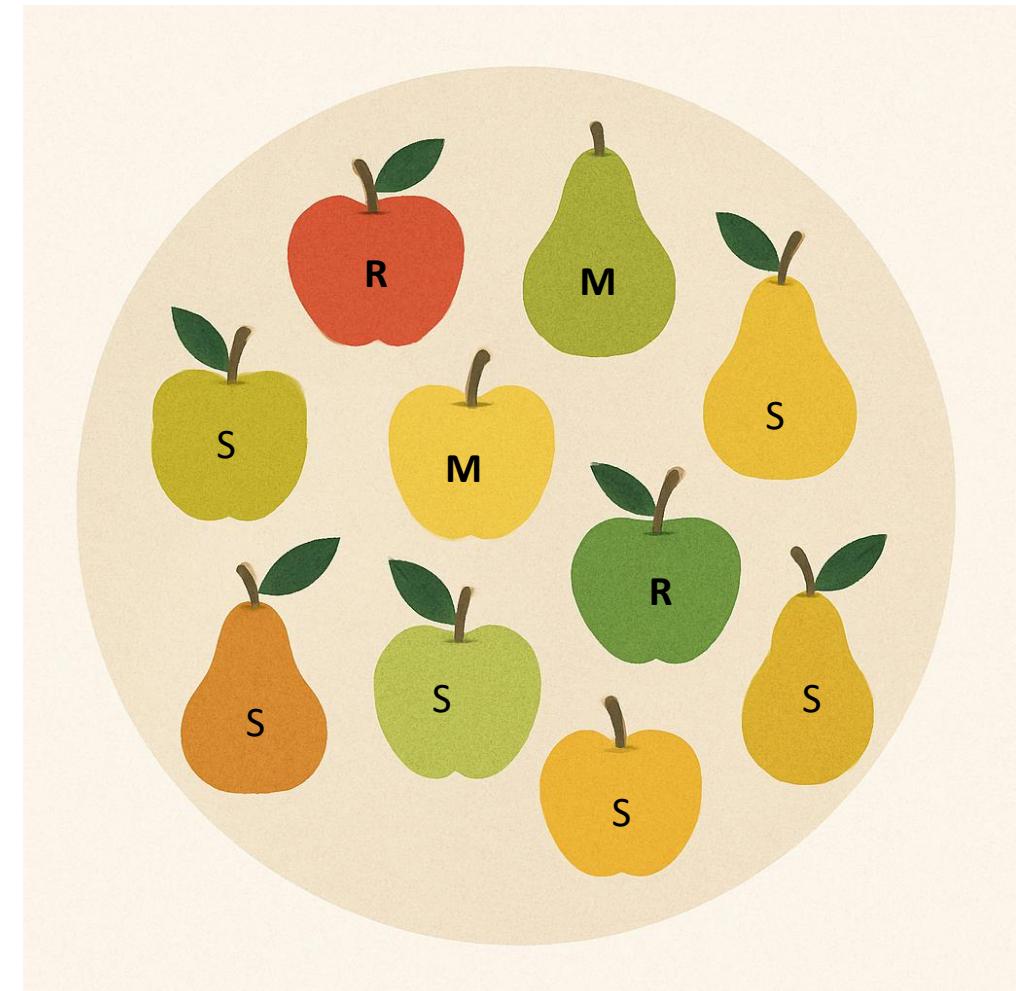
			
<b>Frequencies</b>	The number of times each category appears in the data	6	4
<b>Proportions Percentages</b>	The frequency of a category divided by the total number of observations	60 %	40 %
<b>Mode</b>	The category with the highest frequency	x	



Do not use mean and standard deviation !

# Ordinal Data

		R (1)	M (2)	S (3)
<b>Frequency</b>	raw counts or percentages	2	2	6
<b>Mode</b>	most frequently occurring value			x
<b>Median</b>	middle value when the data is ordered	1, 1, 2, 2, <b>3, 3</b> , 3, 3, 3		
<b>Range</b>	difference between the highest and lowest values		2	
<b>Interquartile Range (IQR)</b>	difference between the 75th and 25th percentiles		$Q75 = 3, Q25 = 2$ $IQR = 1$	



Do not use mean and standard deviation !

# Quantitative Data (Numerical Data)

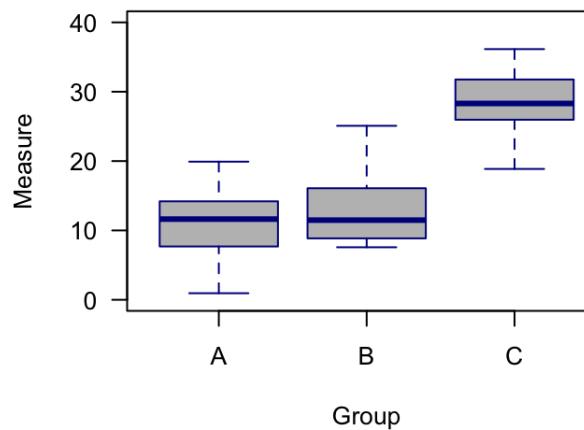
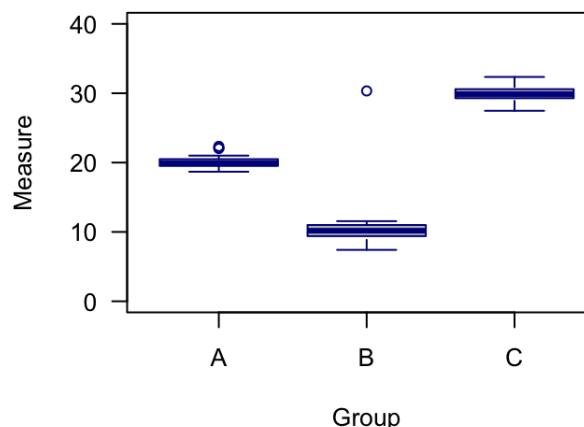
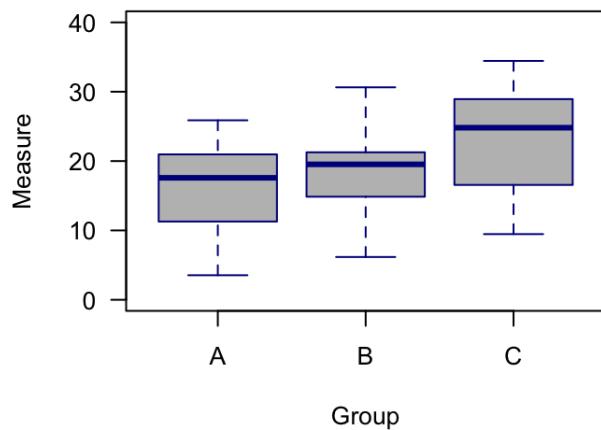
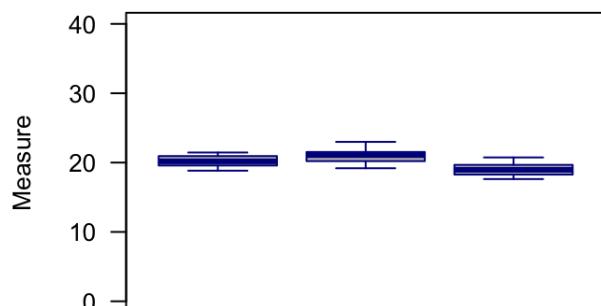
## Discrete Data and Continuous Data



<b>Measures of Center</b>	
<b>Mean</b>	The average of all values in the dataset
<b>Median</b>	The middle value when the data is sorted
<b>Mode</b>	The value that appears most frequently
<b>Measures of Dispersion</b>	
<b>Range</b>	The difference between the maximum and minimum values
<b>Variance</b>	A measure of how spread out the data is from the mean
<b>Standard Deviation</b>	The square root of the variance, providing a more interpretable measure of spread

# ANalysis Of VAriance

two sources of variance



**between-group variance**

comparing the mean of each group with the overall mean

**within-group variance**

variation of each observation from its group mean

**sums of squares (SS)** = is the numerical metric distances of each point to the mean

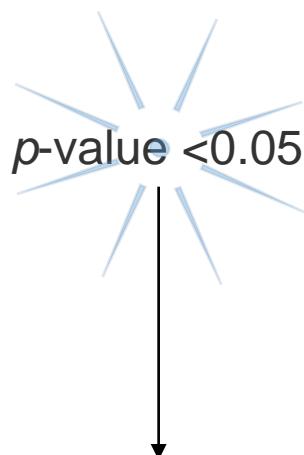
# ANOVA terminology

- **Factor:** different groups (eg. Genotypes, locations, years....)
- **Level:** categories within the factor (# of genotypes, # locations...)
- One way ANOA, Two way ANOVA

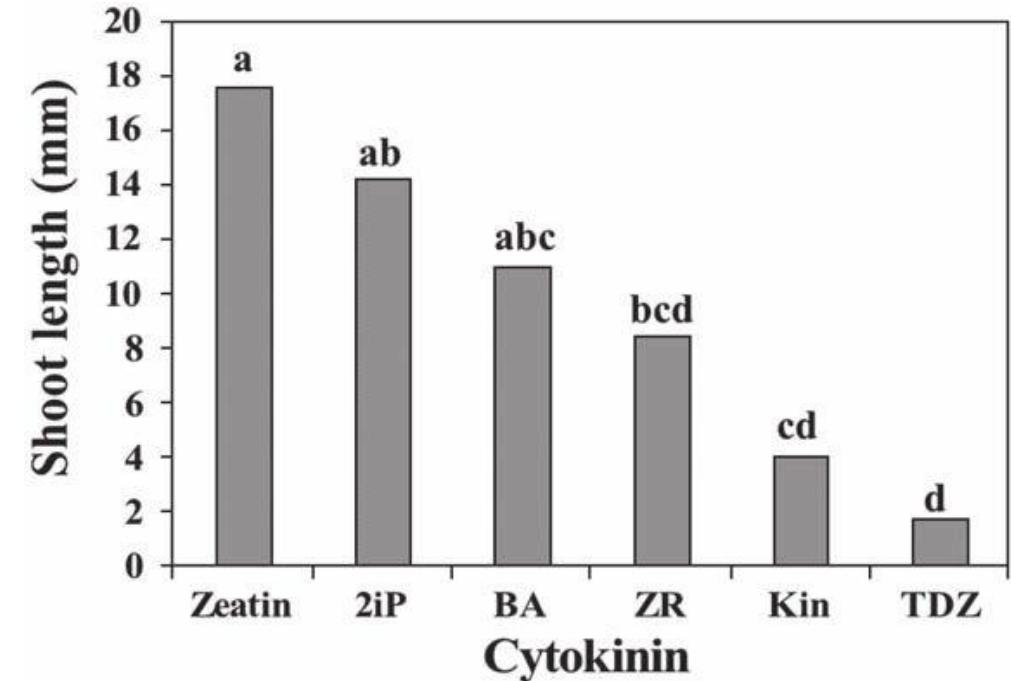
```
aov.model <- aov(size ~ pop)
```

```
summary(aov.model)
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
## pop        2  34.67  17.333   10.4 0.00457 **
## Residuals  9  15.00   1.667
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



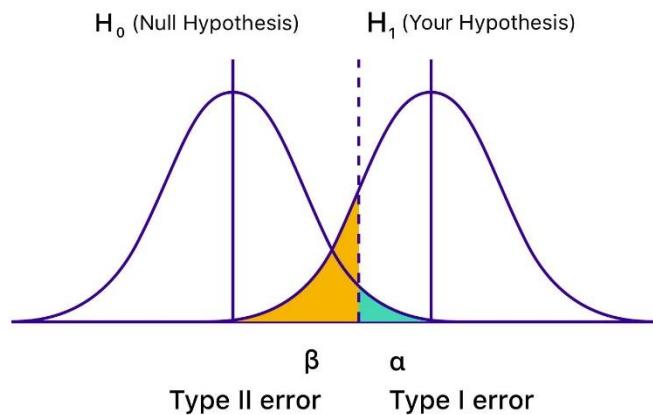
significant difference between the means, it only indicates that at least two means are different, not which specific pairs



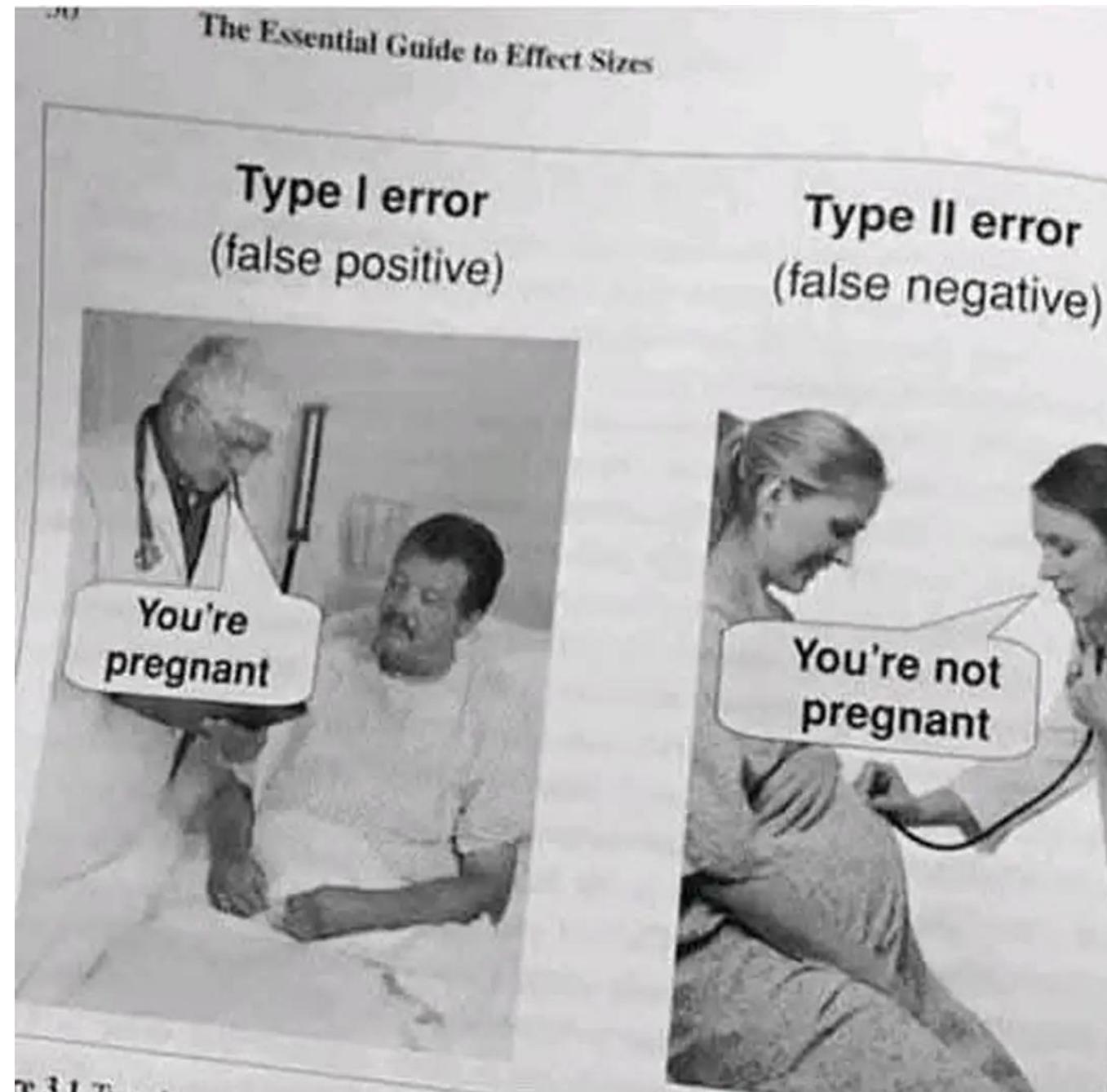
Tukey's Honest Significant Differences (HSD)

post-hoc comparisons or means comparisons

# Error types



Reality		
Test	TRUE	FALES
TRUE		Type II
FALES	Type I	



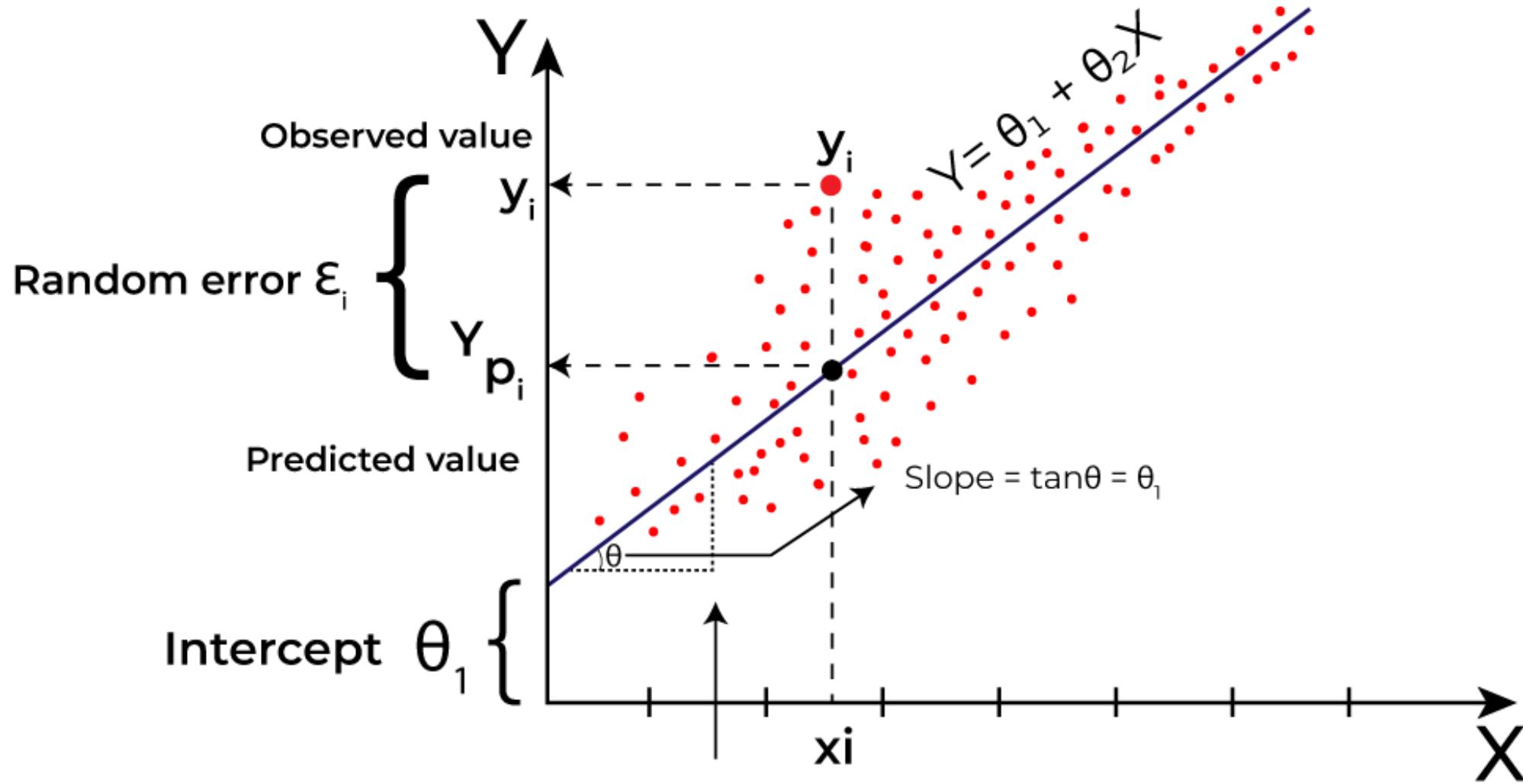
# ANOVA interpretation

## SCENARIO

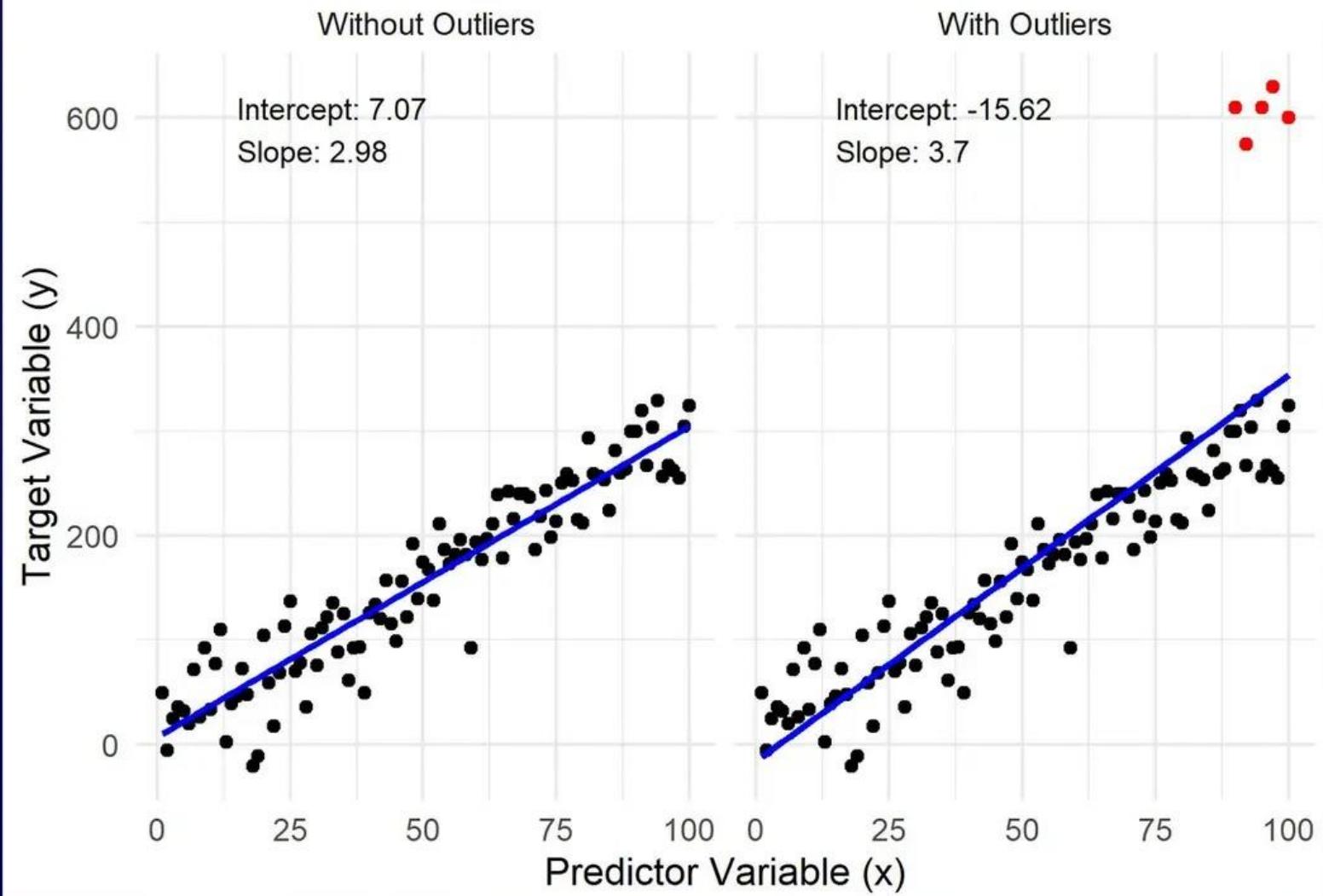
	1	2	3	4
Genotype	<b>0.45</b>	<b>0.30</b>	<b>0.30</b>	<b>0.25</b>
Locations	<b>0.30</b>	<b>0.20</b>	0.10	0.15
Year	0.10	0.05	0.20	0.15
Genotype x Location	0.05	<b>0.35</b>	0.05	0.05
Genotype x Year	0.05	0.05	<b>0.30</b>	0.05
Genotype x Location x Year	0.05	0.05	0.05	<b>0.35</b>



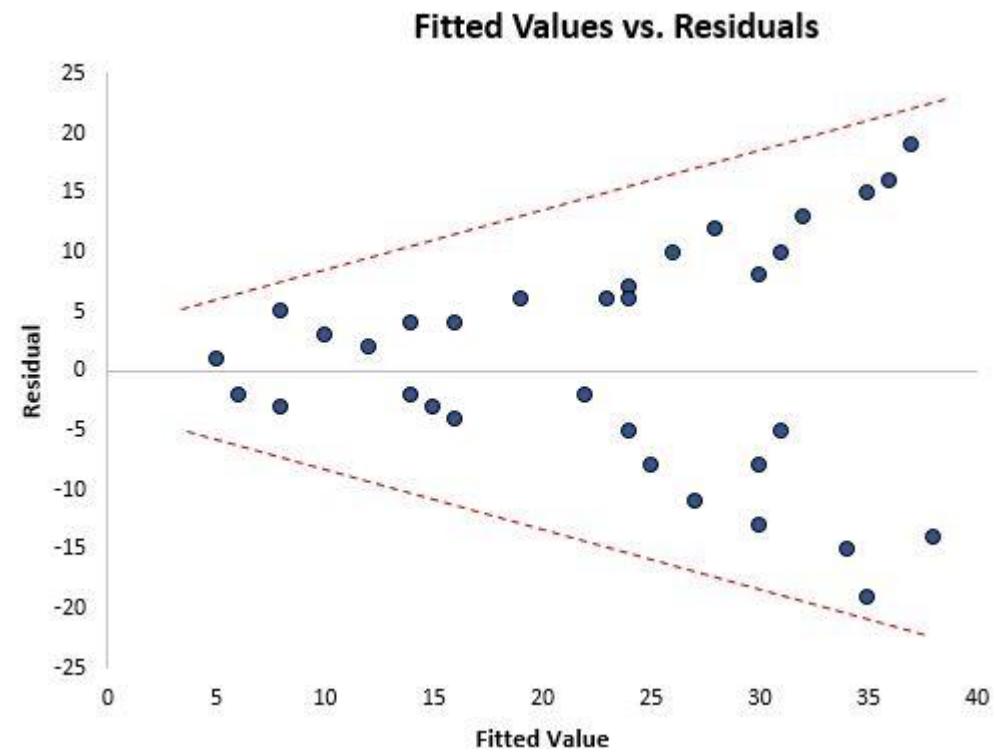
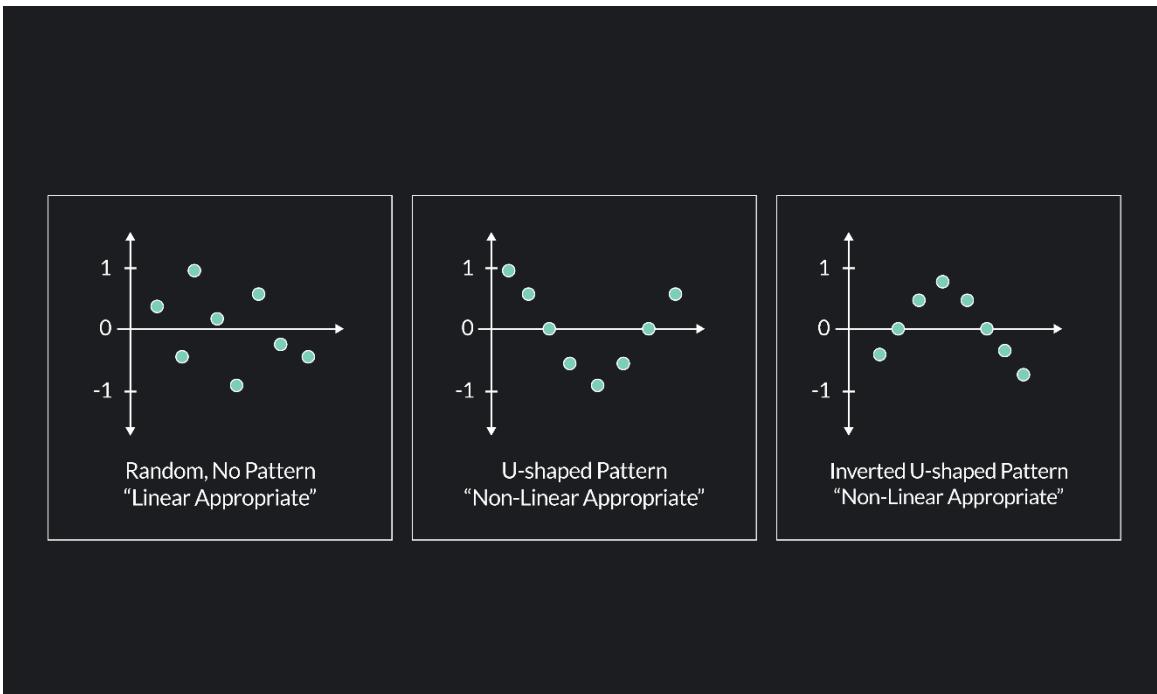
# Linear regression



## Impact of Outliers on Linear Regression



# Residuals (actual vs predicted)



# Fix vs random linear models

Model is a relationship between variables

**Fixed Effects Models:** In fixed effects models, **the effects of the independent variables are assumed to be constant across all groups or levels** in the data.

standard regression coefficients representing factors

**Random Effects Models:** Random effects models, on the other hand, assume that **the variation across entities can be captured in a random component of the model.**

variation introduced by grouping or clustering

# Why Use Mixed Models?

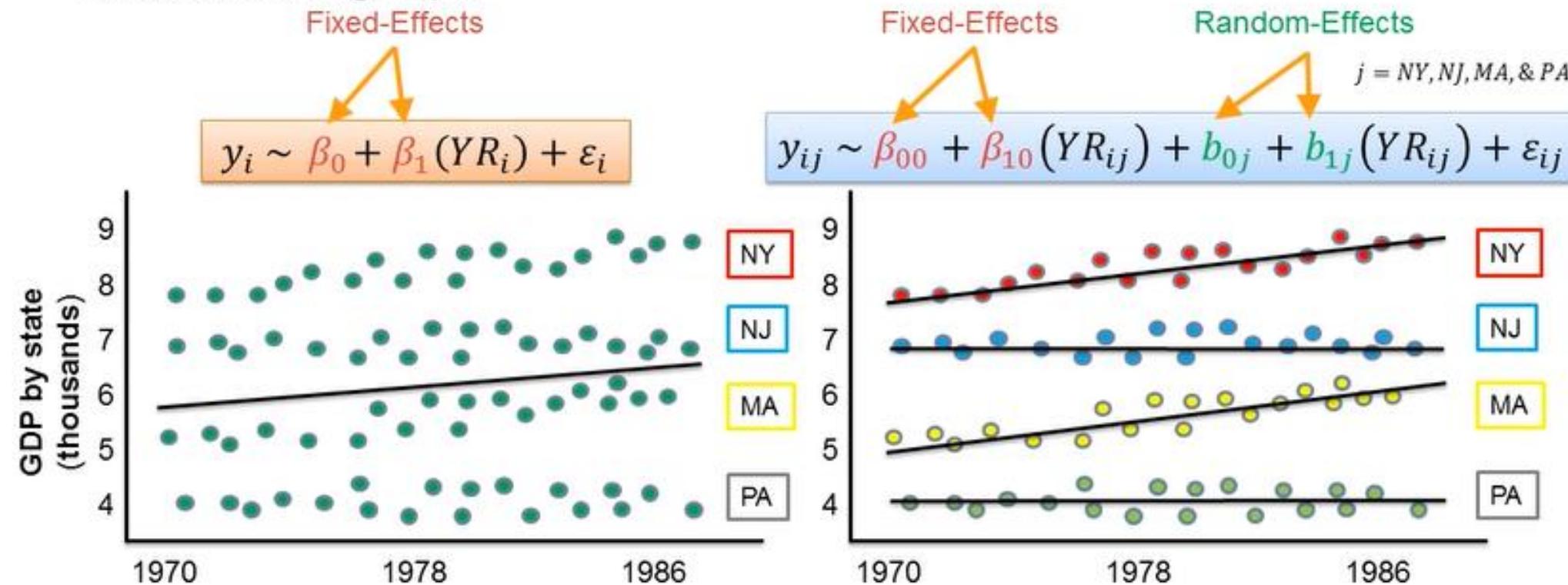
**Account for Non-Independence:** Mixed models explicitly handle the non-independence that arises from hierarchical data, where observations within the same group are correlated.

**Reduce Pseudoreplication:** They avoid the problem of pseudoreplication, which occurs when analyses treat non-independent data points as if they were independent.

**Model Variability:** By modeling variance at different levels, mixed models provide a more accurate understanding of the relationships between variables.

**Linear mixed models (LMMs)** are applied across many scientific fields to analyze clustered, longitudinal, or repeated-measures data where observations within groups are not independent

Extensions of Linear regression models for data that are collected and summarized in groups.



Trial design

Multi-environment testing

Genotype by environment interaction

Handles Non-Independence

Accounts for Within- and Between-Subject Variability

Flexible for Unbalanced Data

# Mathematical Representation of Linear Mixed-Effects Models

## Mathematical Representation of Linear Mixed-Effects Models

The general form of a linear mixed-effects model can be represented as:

$$y_{ij} = \beta_0 + \beta_1 x_{ij} + u_j + \epsilon_{ij}$$

Where:

- $y_{ij}$  is the outcome variable for the  $i$ -th observation in the  $j$ -th group.
- $\beta_0$  and  $\beta_1$  are the fixed-effect coefficients (intercept and slope).
- $x_{ij}$  is the predictor variable for the  $i$ -th observation in the  $j$ -th group.
- $u_j$  is the random effect for the  $j$ -th group.
- $\epsilon_{ij}$  is the residual error for the  $i$ -th observation in the  $j$ -th group.

The random effect  $u_j$  is assumed to follow a normal distribution with mean zero and variance  $\sigma_u^2$ , and the residuals  $\epsilon_{ij}$  are also assumed to be normally distributed with variance  $\sigma^2$ .

**Fixed effects** give the estimate of the average effect of the characteristic in the population

**Random effects** model group-specific deviations of this common average

**Input # of Treatments:** 18

**Input # of Full Reps:** 3

**Input # of Locations:** 1

**Plot Order Layout:** serpentine

**Starting Plot Number(s):** 101  Continuous Plot

**Input Location:** FARGO

**Random Seed:** 123

Randomized Complete Block Design 9X6						
ROWS	G-16	G-17	G-4	G-3	G-8	G-14
	G-5	G-15	G-13	G-6	G-1	G-2
	G-9	G-18	G-10	G-7	G-11	G-12
	G-15	G-7	G-10	G-8	G-3	G-9
	G-14	G-11	G-1	G-4	G-17	G-18
	G-6	G-12	G-2	G-16	G-13	G-5
	G-16	G-12	G-9	G-18	G-8	G-7
	G-11	G-5	G-4	G-13	G-1	G-17
	G-15	G-14	G-3	G-10	G-2	G-6

**Select a Factorial Design Type:** Factorial in a RCBD

**Input # of Entries for Each Factor: (Separated by Comma)** 2,2,3

**Input # of Full Reps:** 3 **Input # of Locations:** 1

**Starting Plot Number:** 101 **Input Location:** FARGO

**Plot Order Layout:** serpentine

**Random Seed:** 123

**Run!** **Simulate!** **Save Experiment!**

Full Factorial Design (RCBD) 9X4				
ROWS	1*0*2	0*0*2	1*1*2	1*0*0
	1*0*1	1*1*0	0*1*0	0*1*1
	0*0*1	1*1*1	0*1*2	0*0*0
	0*0*1	1*0*0	1*1*1	0*1*2
	0*1*0	1*1*0	1*1*2	0*0*0
	0*0*2	1*0*1	0*1*1	1*0*2
	1*0*1	0*1*0	1*1*0	0*1*1
	0*0*2	0*1*2	1*1*2	0*0*0
	1*1*1	1*0*0	0*0*1	1*0*2

COLUMNS

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10
10	28	71	29	9	7	21	76	22	30	37
9	77	40	5	10	78	13	6	14	18	3
8	69	12	10	74	64	62	16	25	12	13
7	8	24	31	49	68	73	60	33	5	38
6	57	59	58	53	75	27	2	34	63	70
5	72	19	15	42	44	29	50	51	20	48
4	3	36	43	65	52	8	39	41	80	7
3	4	69	11	47	56	55	54	61	19	7
2	46	66	67	16	35	7	2	19	10	7
1	17	45	1	16	26	6	4	23	8	7

p-rep design

	V1	V2	V3	V4	V5	V6	V7	V8	V9
Row5	8	29	2	6	11	4	1	5	
Row4	15	22	18	4	2	26	1	9	
Row3	10	14	1	4	23	3	27	20	2
Row2	2	3	19	21	4	13	24	16	1
Row1	1	4	7	28	12	25	1	17	

Augmented RCBD

	LOC1	LOC2	LOC3	LOC4	LOC5	LOC6	Copies	Avg
Gen-3	1	1	1	1	2	2	8	1.3
Gen-4	1	1	1	2	1	2	8	1.3
Gen-6	1	1	2	1	2	1	8	1.3
Gen-7	1	2	2	1	1	1	8	1.3
Gen-9	1	1	1	2	2	1	8	1.3
Gen-11	1	1	1	2	1	2	8	1.3
Gen-12	1	2	1	1	2	1	8	1.3
Gen-13	1	1	2	2	1	1	8	1.3
Gen-16	1	2	1	1	1	2	8	1.3

Multi-Location P-rep Design

# Example of LMM

## Dataset: Sleep Study

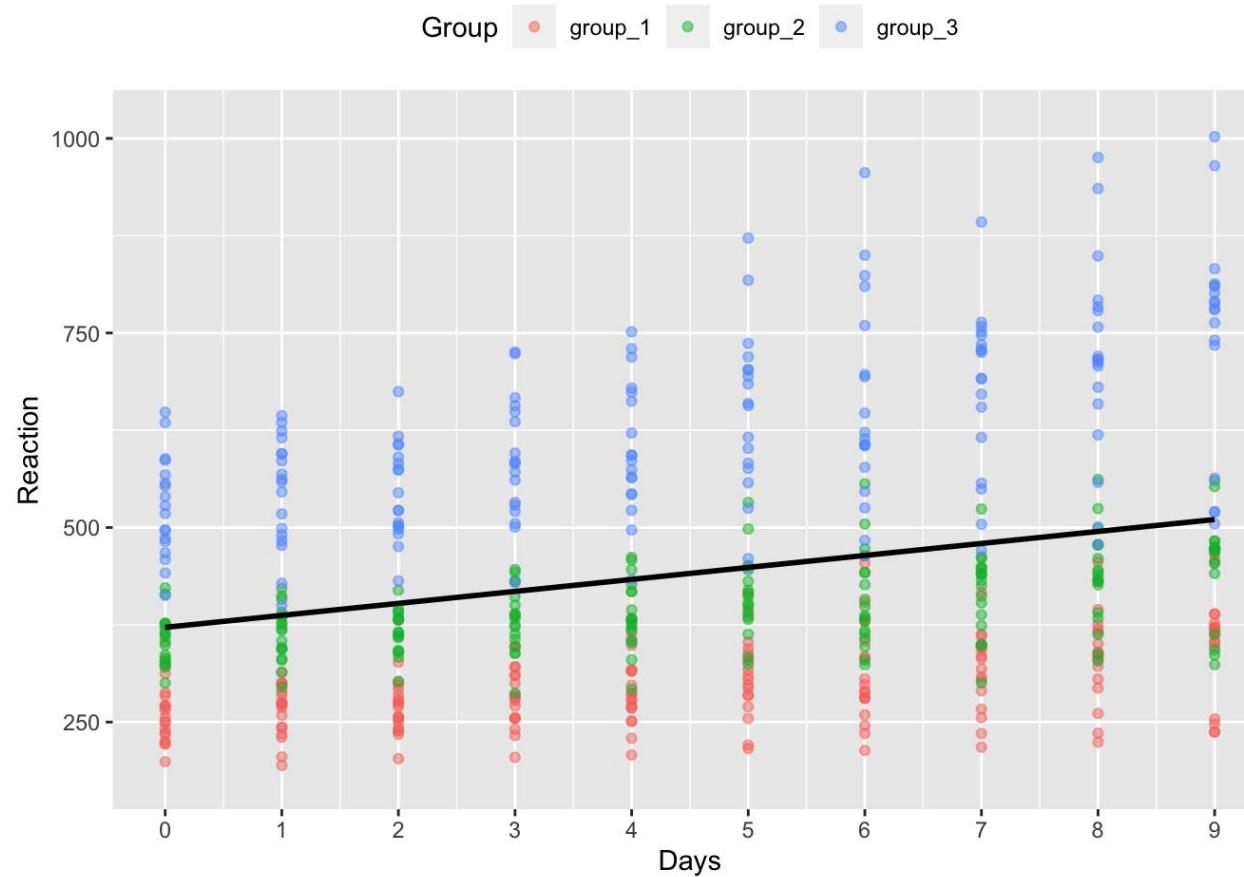
A survey-based study of the sleeping habits of individuals

The sleepstudy data set is from an experiment that examined reaction times of sleep deprived individuals over the course of a few days (individuals only got 3h of sleep each day), with three different groups of people

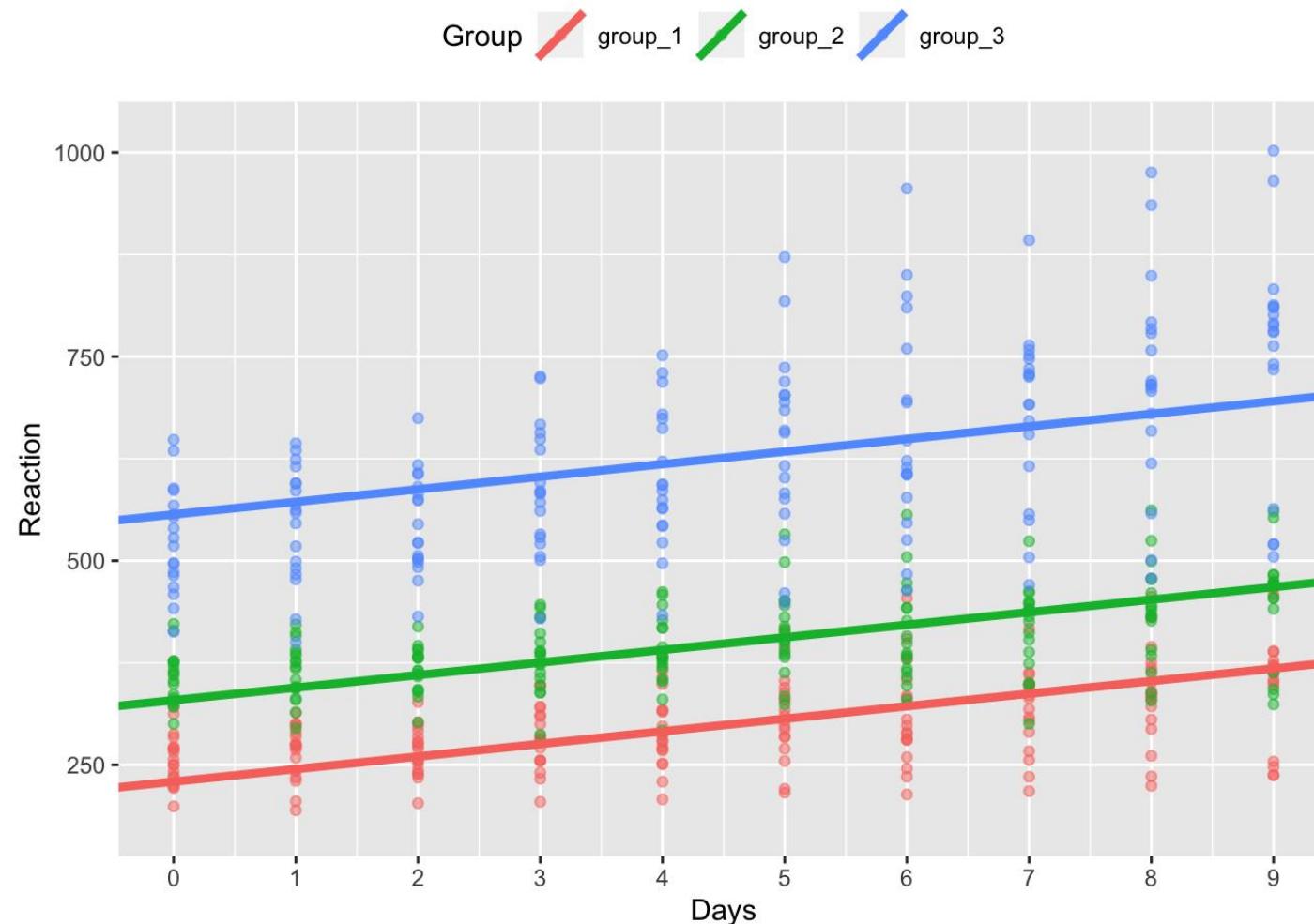
```
head(sleepstudy, 20)
```

	Reaction	Days	Subject
## 1	249.5600	0	308
## 2	258.7047	1	308
## 3	250.8006	2	308
## 4	321.4398	3	308
## 5	356.8519	4	308
## 6	414.6901	5	308
## 7	382.2038	6	308
## 8	290.1486	7	308
## 9	430.5853	8	308
## 10	466.3535	9	308
## 11	222.7339	0	309
## 12	205.2658	1	309
## 13	202.9778	2	309
## 14	204.7070	3	309
## 15	207.7161	4	309
## 16	215.9618	5	309
## 17	213.6303	6	309
## 18	217.7272	7	309
## 19	224.2957	8	309
## 20	237.3142	9	309

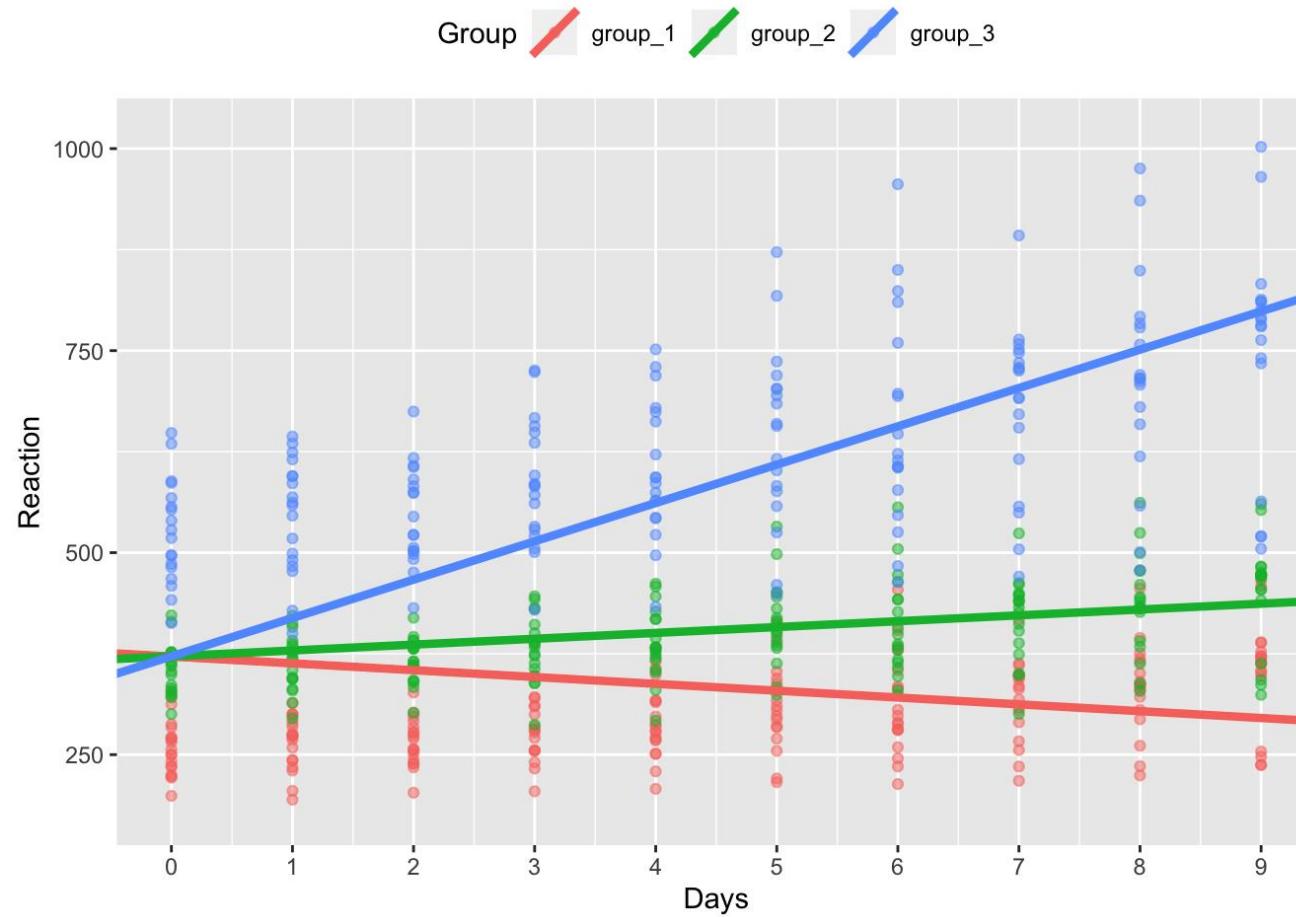
# Fix slope and intercept



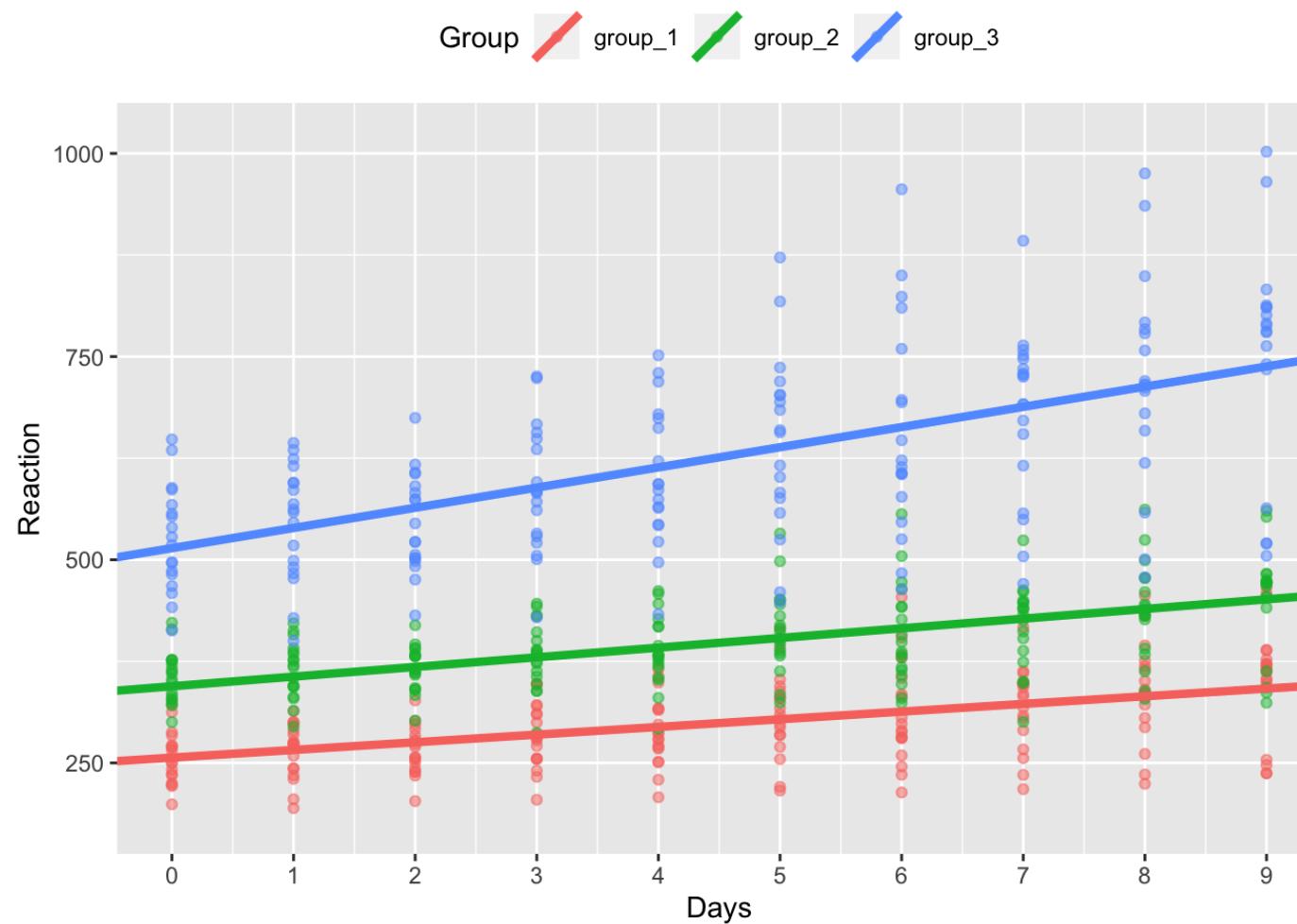
# Random intercept

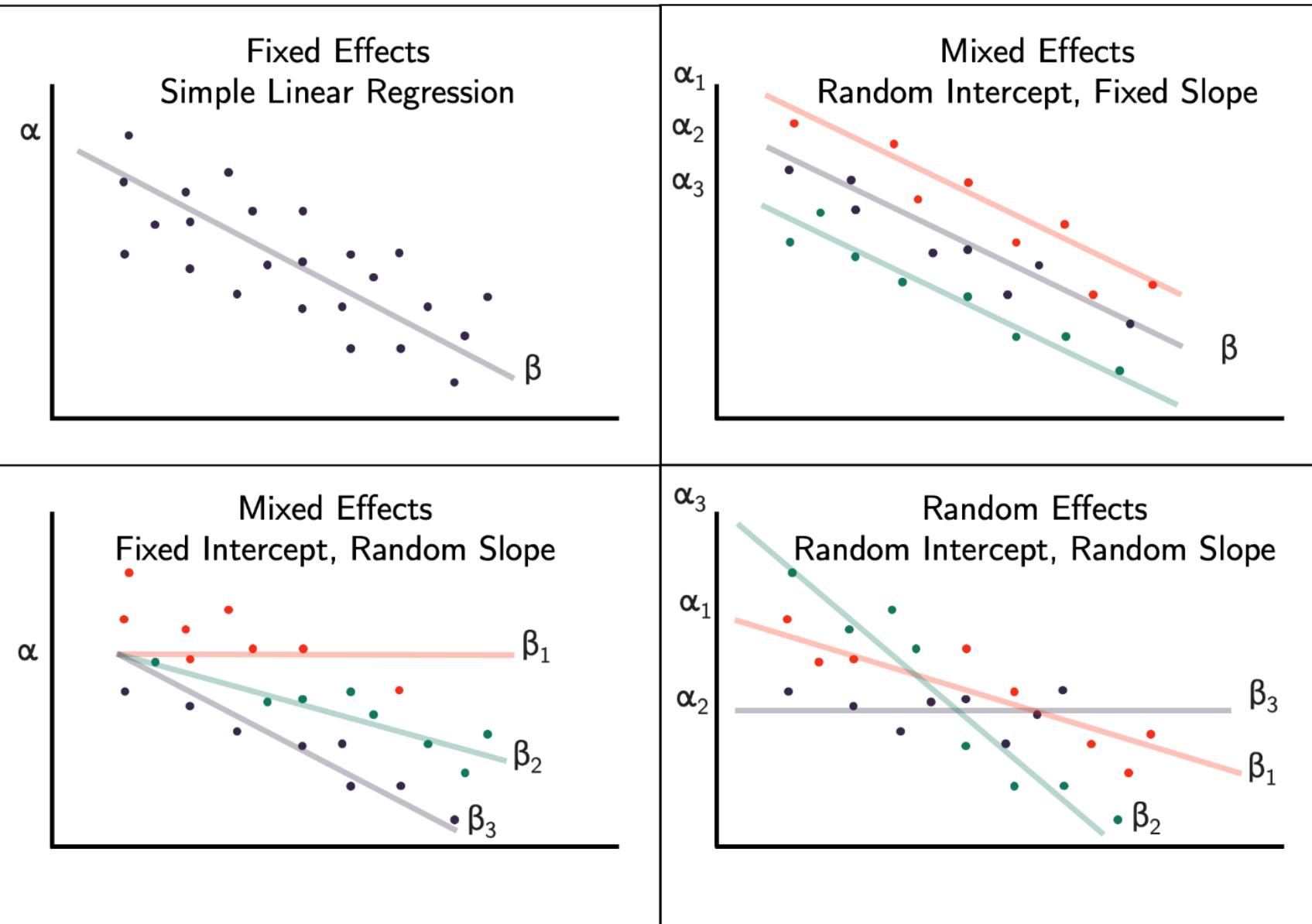


# Random slope



# Random intercept and slope





“simplest, most complete”

# Model selection

## AIC (Akaike Information Criterion)

$$AIC = -2 \ln(\text{Likelihood}) + 2k$$

- **Likelihood** measures how well the model explains the data.
- **k** is the number of parameters in the model.

## BIC (Bayesian Information Criterion)

$$BIC = -2 \ln(\text{Likelihood}) + k \ln(n)$$

- **n** is the number of observations in the dataset.
- The **penalty term** increases with the size of the dataset.

**lower values indicating a better model**

# Data Integration and Analysis

combining or merging of data from multiple sources in an effort to extract better and/or more information

merging data by common data elements

linking data sets through a common factor

example: meta analysis

