

# BIOSTATISTICS COURSE #6

SAMPLE SIZE,  
META-ANALYSES  
& LONGITUDINAL  
DATA ANALYSIS

NOVEMBER 2025



## SUMMARY OF THE COURSE #6

**01** INTRODUCTION

**02** SAMPLE SIZE CALCULATION

**03** META-ANALYSIS

**04** CLINICAL TRIALS DATA

**05** LONGITUDINAL DATA ANALYSIS

**06** SURVIVAL ANALYSIS

**07** QUESTIONS

# INTRODUCTION

01

# INTRODUCTION



Here at St Wadlings we like to treat ALL our patients as INDIVIDUALS...this for example is individual No 76/O9bt-c12.

# SAMPLE SIZE CALCULATION

02

# SAMPLE SIZE CALCULATION

## ARTICLE REVIEW

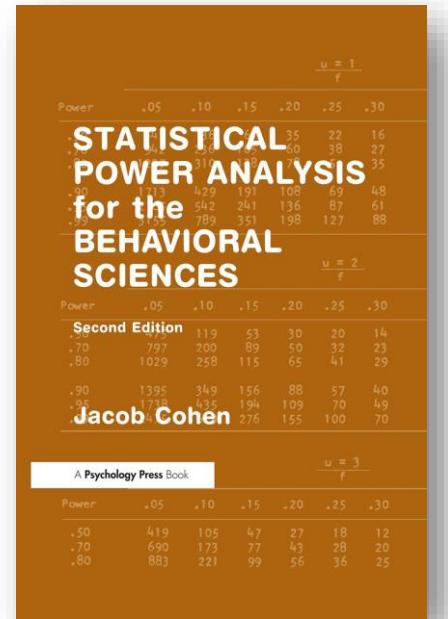
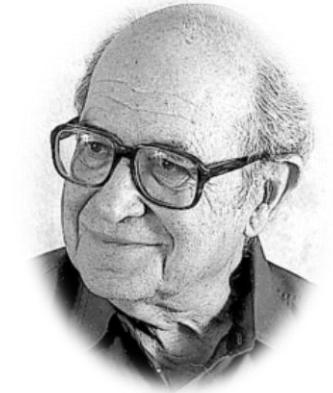


10 minutes

# SAMPLE SIZE CALCULATION

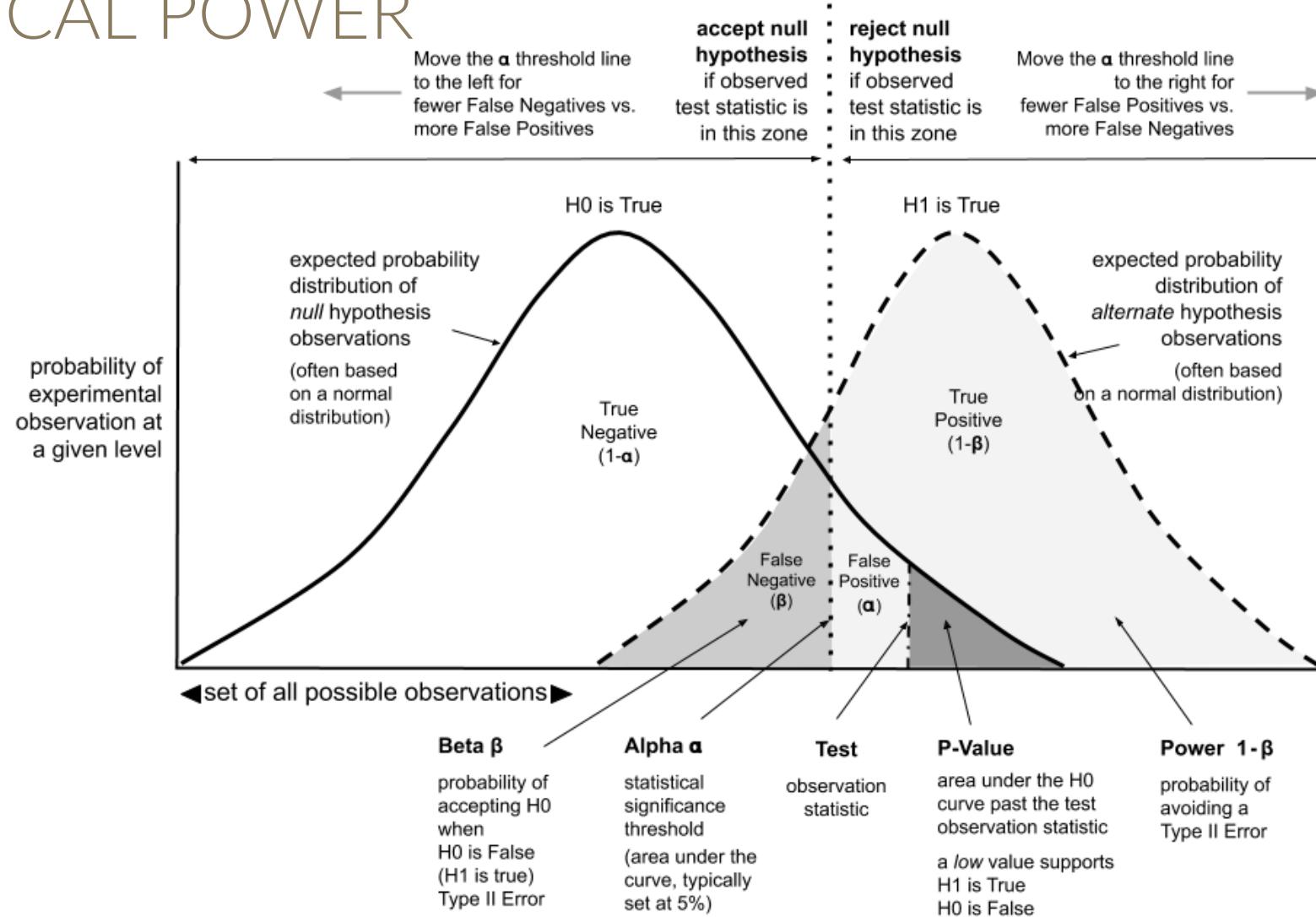
## HISTORY

- Jacob COHEN (1923 – 1998), American Statistician
- Famous for his works on statistical power and sample size calculation
- Invented effect size measures : Cohen's Kappa, Cohen's d and Cohen's h
- Published in 1988 the book “*Statistical Power Analysis for Behavioral Sciences*”
- Pioneered the principles of meta-analyzes



# SAMPLE SIZE CALCULATION

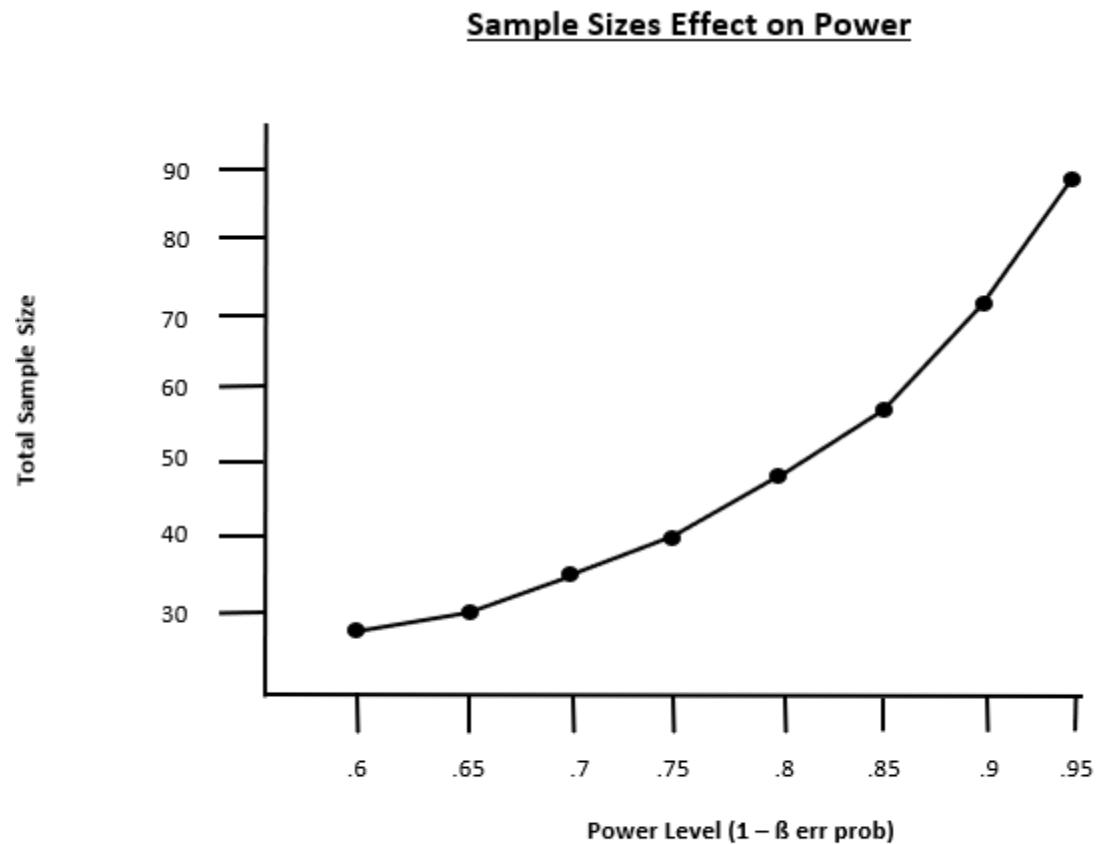
## STATISTICAL POWER



# SAMPLE SIZE CALCULATION

## STATISTICAL POWER

- Statistical power =  $1 - \beta$  (beta risk)
- Represents the ability of a test to detect a significant effect size
- Strongly linked with:
  - Sample size
  - Effect size
  - Significance level



*Note:* As the sample size increases in the model, so does power.

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

Package `pwr` contains many functions for power / sample size calculation :

- `pwr.2p.test` : test of two proportions (same N in groups)
- `pwr.2p2n.test` : test of two proportions (unequal N in groups)
- `pwr.p.test` : Proportion (one sample)
- `pwr.r.test` : Correlation
- `pwr.chisq.test` : Chi-Square test
- `pwr.f2.test` : General Linear Model
- `pwr.anova.test` : balanced one-way ANOVA
- `pwr.norm.test` : Test of a mean to a reference (known variance)
- `pwr.t.test` : T-tests (one sample, two samples, paired)
- `pwr.t2n.test` : T-tests (two samples with unequal N)

Same way to use: all parameter values provided **except one** (result of the function)

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

*pwr.2p.test* function (*pwr* package)

Parameters :  $h$  = effect size :  $2 \times \arcsin(\sqrt{p_1}) - 2 \times \arcsin(\sqrt{p_2})$   
 $n$  = common sample size  
*sig.level* = significance level (default : 5%)  
*power* = power (in %)

*pwr.2p2n.test* function (*pwr* package)

Parameters :  $h$  = effect size :  $2 \times \arcsin(\sqrt{p_1}) - 2 \times \arcsin(\sqrt{p_2})$   
 $n_1$  = sample size group 1  
 $n_2$  = sample size group 2  
*sig.level* = significance level (default : 5%)  
*power* = power (in %)

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

*pwr.p.test* function (*pwr* package)

Parameters :     *h* = effect size :  $2 \times \arcsin(\sqrt{p_1}) - 2 \times \arcsin(\sqrt{p_2})$   
                  *n* = sample size  
                  *sig.level* = significance level (default : 5%)  
                  *power* = power (in %)

*pwr.r.test* function (*pwr* package)

Parameters :     *n* = Total sample size  
                  *r* = correlation  
                  *sig.level* = significance level (default : 5%)  
                  *power* = power (in %)

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

*pwr.chisq.test* function (*pwr* package)

Parameters :

$$w = \text{effect size} : \sqrt{\sum_{i=1}^m \frac{(p_{0i}-p_{1i})^2}{p_{0i}}}$$

with  $m$  : number of cells

$p_{0i}$  : cell probability in ith cell under H0

$p_{1i}$  : cell probability in ith cell under H1

$N$  = Total sample size

$df$  = degrees of freedom (number of categories -1)

$sig.level$  = significance level (default : 5%)

$power$  = power (in %)

Package **effectsize** useful for extracting effect size from an **test** (function **cohens\_w**)

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

*pwr.anova.test* function (*pwr* package)

Parameters :  $k$  = number of groups

$f$  = effect size :  $\sqrt{\frac{\sum_{i=1}^k p_i \times (\mu_i - \mu)^2}{\sigma^2}}$

with  $p_i = \frac{n_i}{N}$  and  $\sigma^2$  : error variance within groups

$n$  = common sample size in each group

*sig.level* = significance level (default : 5%)

*power* = power (in %)

Package *effectsize* useful for extracting f effect size from an ANOVA (function *cohens\_f*)

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

*pwr.t.test* function (*pwr* package)

Parameters :  $d = \text{effect size} : \frac{|\mu_1 - \mu_2|}{\sigma}$   
with  $\mu_1$  : mean of group 1  
 $\mu_2$  : mean of group 2  
 $\sigma$  : common error standard deviation

$n$  = Total sample size

$\text{type}$  = type of data (two.sample, one.sample, paired)

$\text{sig.level}$  = significance level (default : 5%)

$\text{power}$  = power (in %)

*pwr.norm.test* function (*pwr* package)

Parameters : *same as above* but  $d = \text{effect size} : \frac{|\mu - \text{reference}|}{\sigma}$

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

*pwr.t2n.test* function (*pwr* package)

Parameters :  $d = \text{effect size} : \frac{|\mu_1 - \mu_2|}{\sigma}$   
with  $\mu_1$  : mean of group 1  
 $\mu_2$  : mean of group 2  
 $\sigma$  : common error standard deviation

*n1* = Sample size of group 1

*n2* = Sample size of group 2

*type* = type of data (two.sample, one.sample, paired)

*sig.level* = significance level (default : 5%)

*power* = power (in %)

# SAMPLE SIZE CALCULATION

## APPLICATION WITH

Package **pwr** contains other functions for effect size calculation :

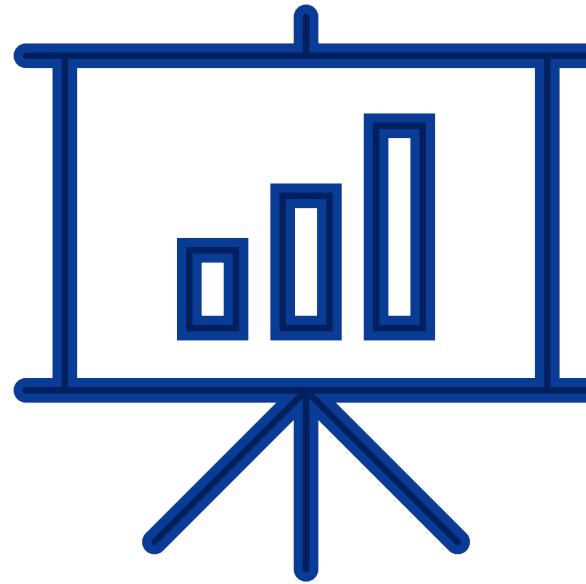
- **cohen.ES**: give the conventional effect size (small, medium, large)
- **ES.h**: calculates effect size for proportion ( $h = \text{effect size} : 2 \times \arcsin(\sqrt{p_1}) - 2 \times \arcsin(\sqrt{p_2})$ )
- **ES.w1** : calculates effect size in the chi-squared test for goodness of fit
- **ES.w2** : calculates effect size in the chi-squared test for association
- **plot** : plot evolution of power vs sample size

**Table I** Values of Effect Sizes and Their Interpretation

Kind of Effect Size	Small	Medium	Large
$r$	.10	.30	.50
$d$	0.20	0.50	0.80
$\eta^2_p$	.01	.06	.14
$f^2$	.02	.15	.35

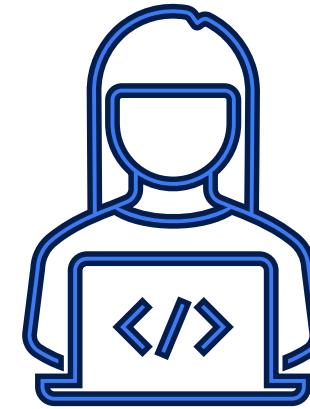
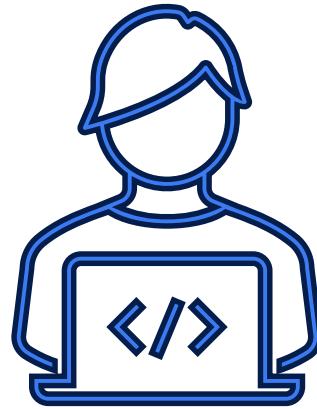
Source: Cohen, J. (1992). A power primer. *Psychological Bulletin*, 112, 155–159. doi:10.1037/0033-2909.112.1.155

# SAMPLE SIZE CALCULATION



Live demo

# SAMPLE SIZE CALCULATION



Time to play !  
(15 minutes)

META-ANALYSIS

03

# META-ANALYSIS

## ARTICLE REVIEW



10 minutes

# META-ANALYSIS

## OVERVIEW

- Definition : method of synthesis of quantitative data from multiple independent studies addressing a common research question.
- The term “*Meta-Analysis*” emerged with Gene GLASS (born in 1940), American statistician specialized in educational psychology and social sciences.
- He published in 1978 his book “*Meta-analysis refers to the analysis of analyses*”
- Goal : combine results of many studies with statistical models in the aim to get more statistical power and get an overall result.



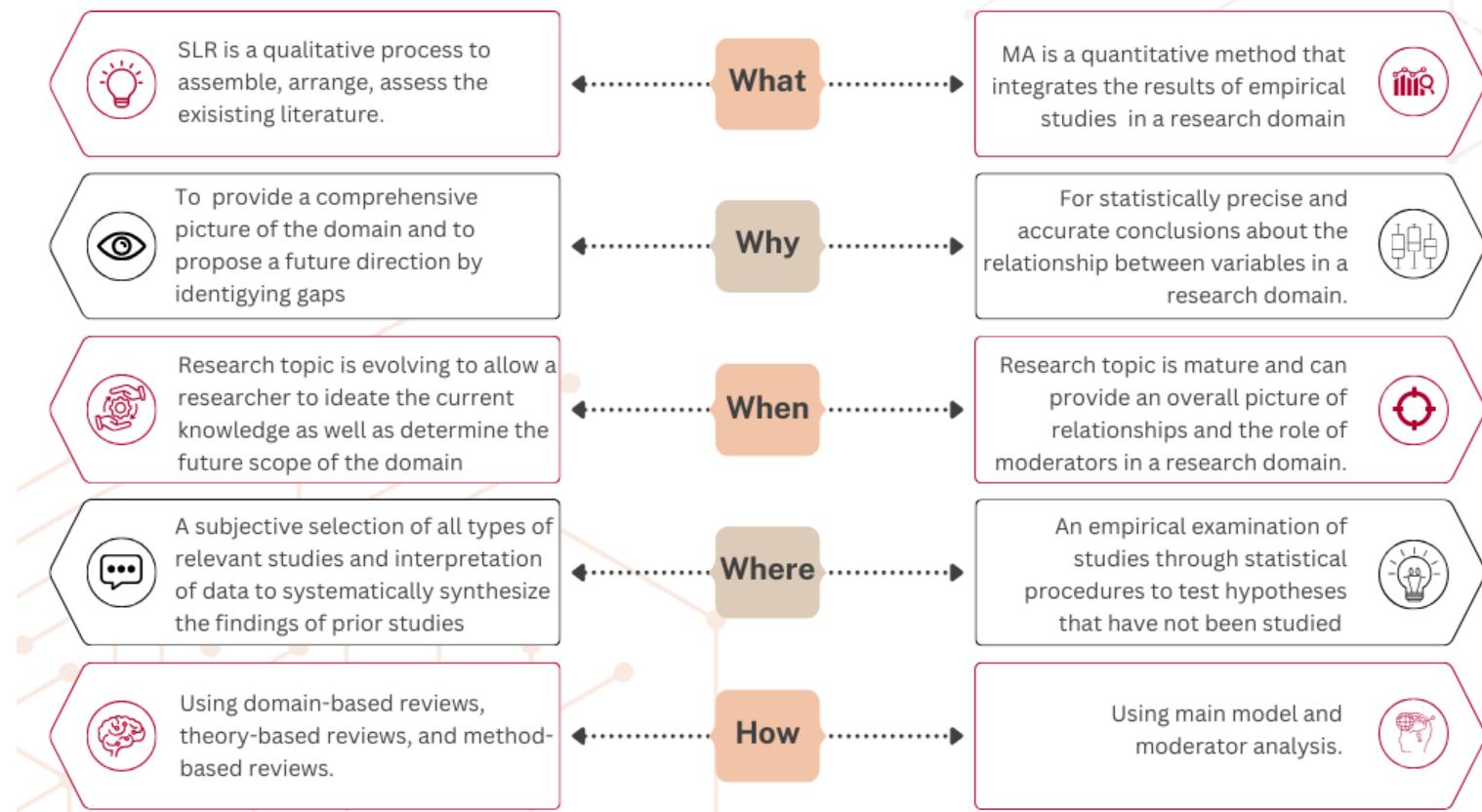
# META-ANALYSIS

## SYSTEMATIC LITTERATURE REVIEW VS META-ANALYSIS

### Systematic Literature Review

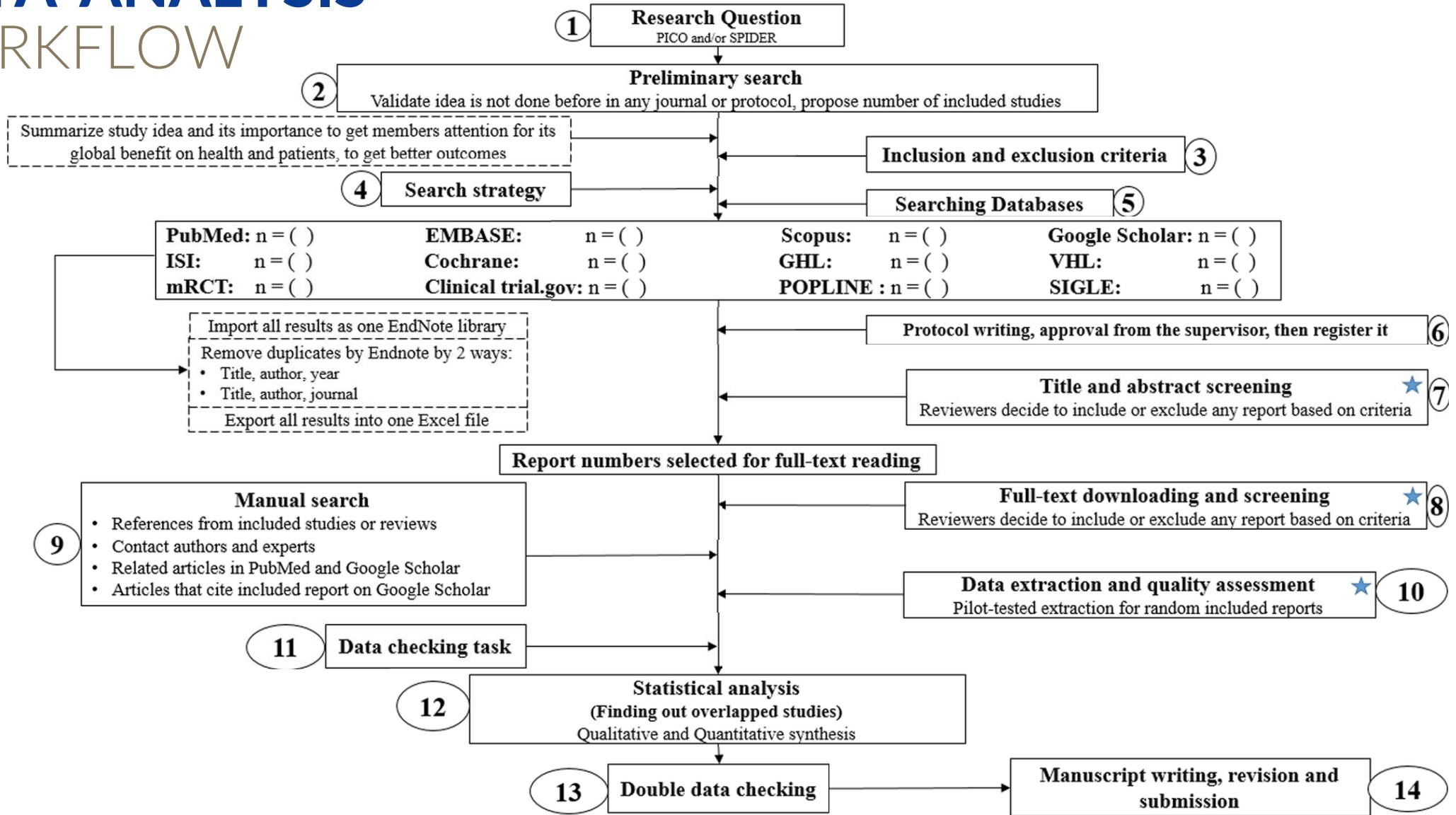
Vs.

### Meta-analysis



# META-ANALYSIS

## WORKFLOW



# META-ANALYSIS

## BIAS

1. Information bias : key study variables are inaccurately measured or classified
2. Interviewer bias : way an interviewer ask questions or react to responses
3. Publication bias : decision to publish research findings is based on their nature or the direction of their results
4. Research bias : researcher's beliefs or expectations influence the research design or data collection process

# META-ANALYSIS

## BIAS

5. Response bias : respondents tend to provide inaccurate or false answers to self-report questions
6. Selection bias : sampling bias, attrition bias, survivorship bias...
7. Other bias : cognitive bias, confirmation bias, framing effect, halo effect, placebo effect...

# META-ANALYSIS

## EFFECT SIZES

1. Arithmetic mean: most commonly used central tendency measure often presented with standard-error of mean (SE)

$$\bar{x} = \frac{\sum_{i=1}^n x_i}{n} \quad \text{and} \quad SE_{\bar{x}} = \frac{s}{\sqrt{n}} \text{ with } s : \text{standard deviation of mean}$$

2. Proportion: outcome measure when we want to examine the prevalence of a disease for example

$$p = \frac{k}{n} \quad \text{and} \quad SE_p = \sqrt{\frac{p(1-p)}{n}}$$

# META-ANALYSIS

## EFFECT SIZES

3. Correlations: effect size which expresses the amount of co-variation between two variables

$$r_{xy} = \frac{\sigma^2_{xy}}{\sigma_x \times \sigma_y} \quad \text{and} \quad SE_{r_{xy}} = \frac{1 - r_{xy}^2}{\sqrt{n-2}}$$

4. Between-Group Mean Difference: raw, un-standardized difference in means between two independent groups.

$$MD = \bar{x}_1 - \bar{x}_2 \quad \text{and} \quad SE_{MD} = s_{pooled} \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

$$s_{pooled} = \sqrt{\frac{(n_1 - 1) \times s_1^2 + (n_2 - 1) \times s_2^2}{(n_1 - 1) + (n_2 - 1)}}$$

# META-ANALYSIS

## EFFECT SIZES

5. Between-Group Standardized Mean Difference: difference in means between two independent groups, standardized by the pooled standard deviation (often called Cohen's d)

$$SMD_{between} = \frac{\bar{x}_1 - \bar{x}_2}{s_{pooled}} \quad \text{and} \quad SE_{SMD} = \sqrt{\frac{n_1 + n_2}{n_1 \times n_2} + \frac{SMD_{between}^2}{2 \times (n_1 + n_2)}}$$

6. Risk-ratio (RR): ratio of two risks. Risks are essentially proportions and can be calculated when we are dealing with binary, or dichotomous, outcome data.

	Event	No Event	
Treatment	a	b	$n_{treat}$
Control	c	d	$n_{control}$
	$n_E$	$n_{\neg E}$	

$$p_{E_{treat}} = \frac{a}{a+b} = \frac{a}{n_{treat}} \quad \text{and} \quad p_{E_{control}} = \frac{c}{c+d} = \frac{c}{n_{control}}$$
$$RR = \frac{p_{E_{treat}}}{p_{E_{control}}}, \text{ often expressed with log}$$

# META-ANALYSIS

## EFFECT SIZES

RR are presented with  $SE_{logRR} = \sqrt{\frac{1}{a} + \frac{1}{c} - \frac{1}{a+b} - \frac{1}{c+d}}$

7. Odd-ratios (OR): similar to Risk-ratio but focus on ratio instead of probability

	Event	No Event	
Treatment	a	b	$n_{treat}$
Control	c	d	$n_{control}$
	$n_E$	$n_{\neg E}$	

$$OR_{treat} = \frac{a}{b} \quad \text{and} \quad OR_{control} = \frac{c}{d}$$

$OR = \frac{OR_{treat}}{OR_{control}}$ , often expressed with log

OR are presented with  $SE_{logOR} = \sqrt{\frac{1}{a} + \frac{1}{b} + \frac{1}{c} + \frac{1}{d}}$

# META-ANALYSIS

## FOREST-PLOT

Studies ID

### Author

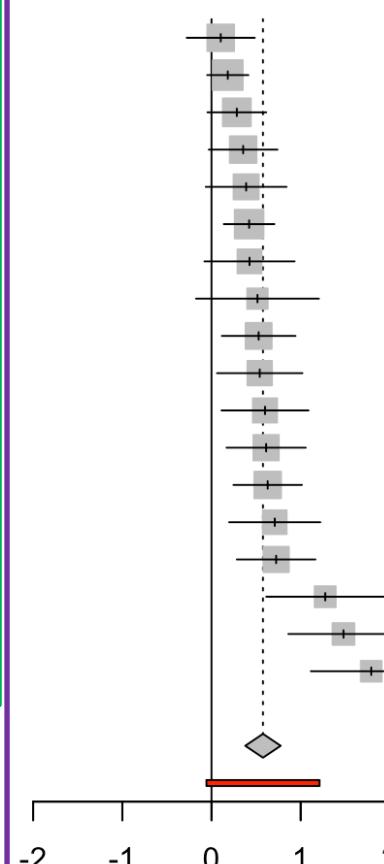
Kuhlmann et al.  
de Vibe et al.  
Hintz et al.  
Cavanagh et al.  
Lever Taylor et al.  
Frazier et al.  
Rasanen et al.  
Ratanasiripong  
Hazlett-Stevens & Oren  
Phang et al.  
Warnecke et al.  
Song & Lindquist  
Frogeli et al.  
Call et al.  
Gallego et al.  
Kang et al.  
Shapiro et al.  
DanitzOrsillo

### Effect size

#### g SE

0.1036	0.1947
0.1825	0.1178
0.2840	0.1680
0.3549	0.1964
0.3884	0.2308
0.4219	0.1448
0.4262	0.2579
0.5154	0.3513
0.5287	0.2105
0.5407	0.2443
0.6000	0.2490
0.6126	0.2267
0.6300	0.1960
0.7091	0.2608
0.7249	0.2247
1.2751	0.3372
1.4797	0.3153
1.7912	0.3456

### Standardised Mean Difference



### Plot

#### SMD 95%-CI Weight

0.58 [ 0.38; 0.78] 100.0%  
[-0.06; 1.21]

Pooled results

Heterogeneity

Heterogeneity:  $I^2 = 63\%, p < 0.01$

Meta-analysis results

# META-ANALYSIS

## HETEROGENEITY

- The more we include studies in a meta-analysis, the more we increase the **variability of measures** (bias...) and then increase **heterogeneity** : clinical diversity, methodological diversity, statistical heterogeneity.
- How to evaluate **heterogeneity** in a meta-analysis :

$I^2$  statistic :  $I^2 = \left( \frac{Q - df}{Q} \right) \times 100\%$  with Q : Chi<sup>2</sup> statistic and df = degrees of freedom

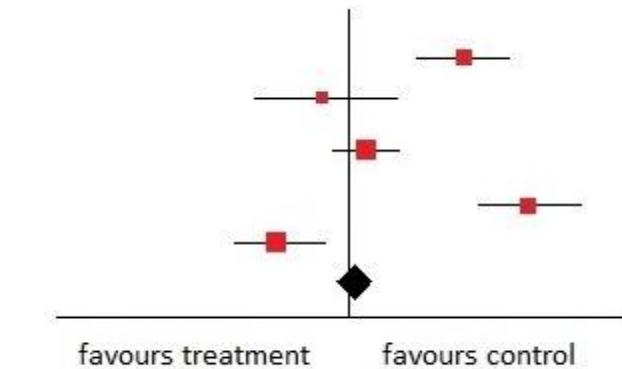
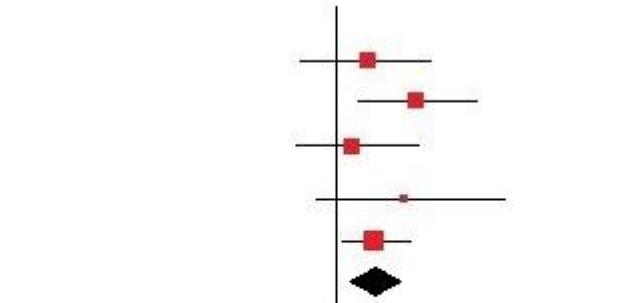
Value	Interpretation
0% to 30%	Low heterogeneity
30% to 50%	Moderate heterogeneity
50% to 75%	Substantial heterogeneity
75% to 100%	Considerable heterogeneity

# META-ANALYSIS

## HETEROGENEITY

Strategies for addressing heterogeneity :

1. Check again that the data are correct
2. Do not do a meta-analysis
3. Explore heterogeneity
4. Ignore heterogeneity
5. Perform a random-effects meta-analysis
6. Reconsider the effect measure
7. Exclude studies



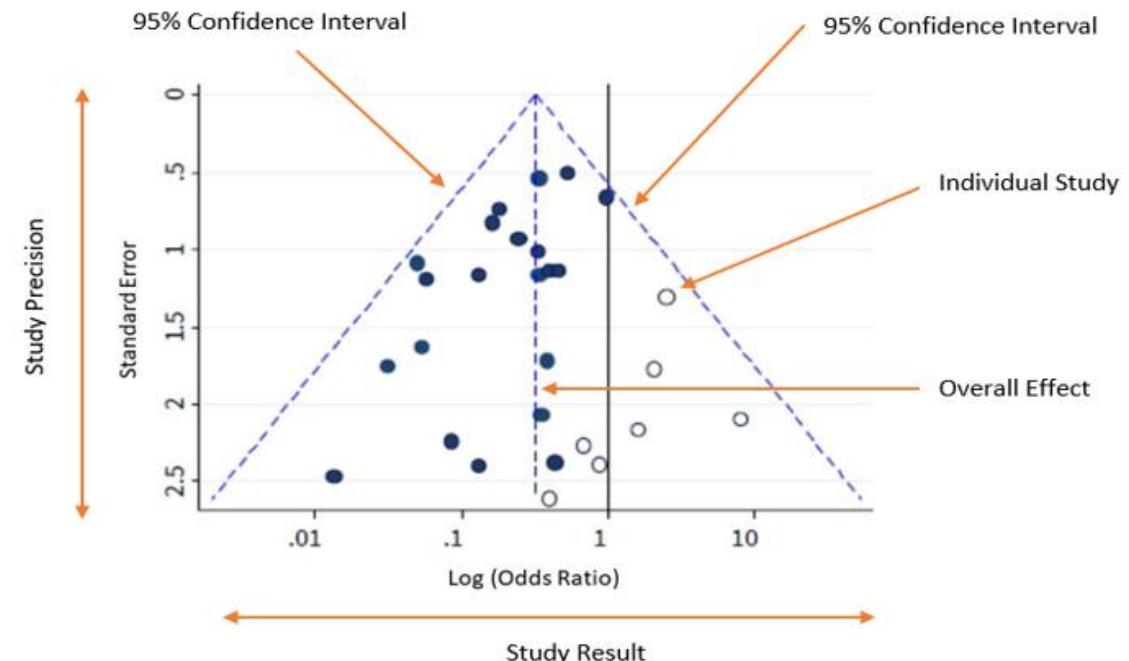
# META-ANALYSIS

## HETEROGENEITY PLOTS : FUNNEL PLOT

Plots for studying heterogeneity :

Funnel plot :

- Studies are represented with dots
- The maximum number of studies should be located **inside the pyramid**
- Studies must be **symmetrically distributed** around the overall effect
- A study with high impact on **heterogeneity** can be identified outside the triangle.



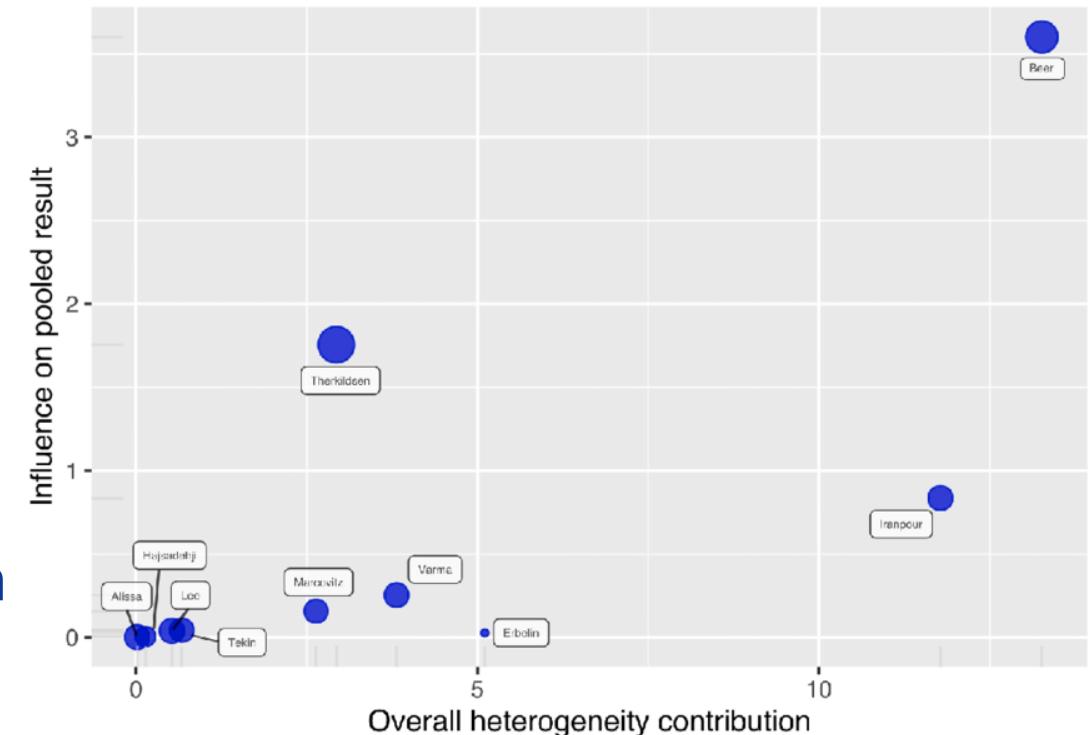
# META-ANALYSIS

## HETEROGENEITY PLOTS : BAUJAT PLOT

Plots for studying heterogeneity :

Baujat plot :

- Studies are represented with **dots** (size is related to the weight of each study)
- X-axis : overall **heterogeneity contribution** of each study
- Y-axis : influence on **pooled results** of each study
- Removing a study with high levels in both parameters will have a **great impact on results** as well as on heterogeneity of the meta-analysis.

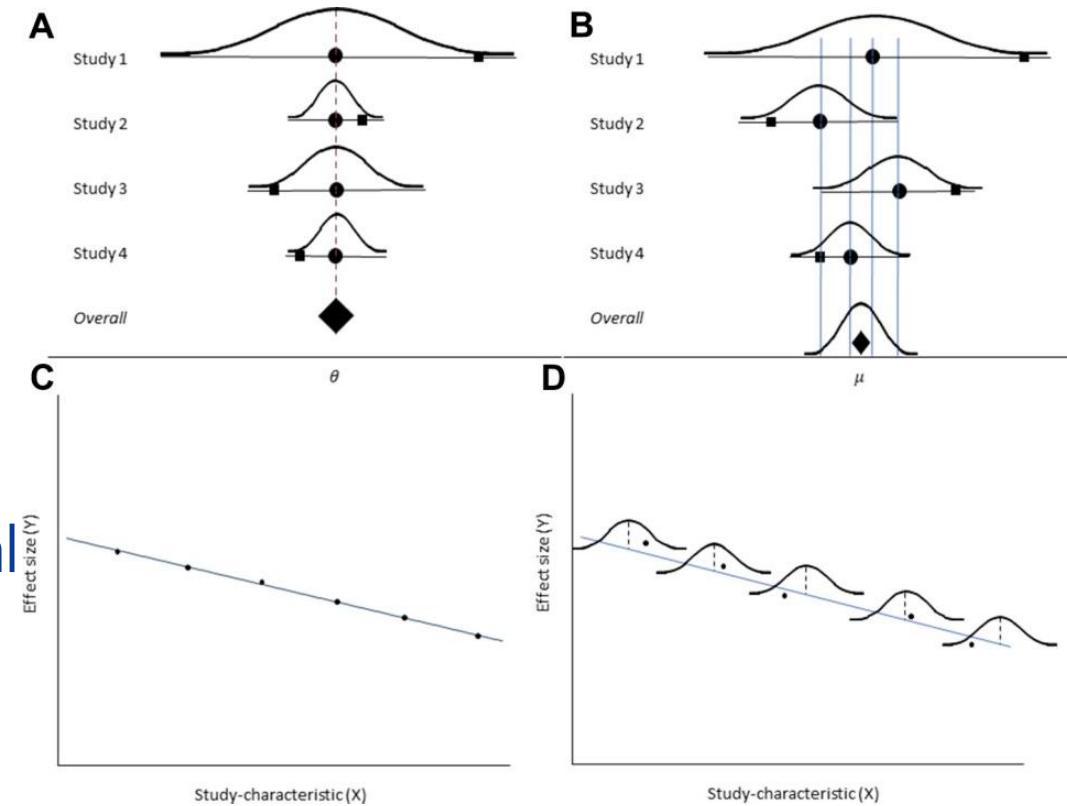


# META-ANALYSIS

## FIXED VS RANDOM EFFECTS MODELS

Two models available:

- **Fixed effects model** : true effect size across all studies, and estimation of a **common effect size** (known as summary effect size) (plots A and C)
- **Random effects model** : assuming a **normal distribution** of true effect sizes and estimate the mean (also known as summary effect size) and the variance (known as heterogeneity) of this distribution (plots B and D)



# META-ANALYSIS

## META-REGRESSION

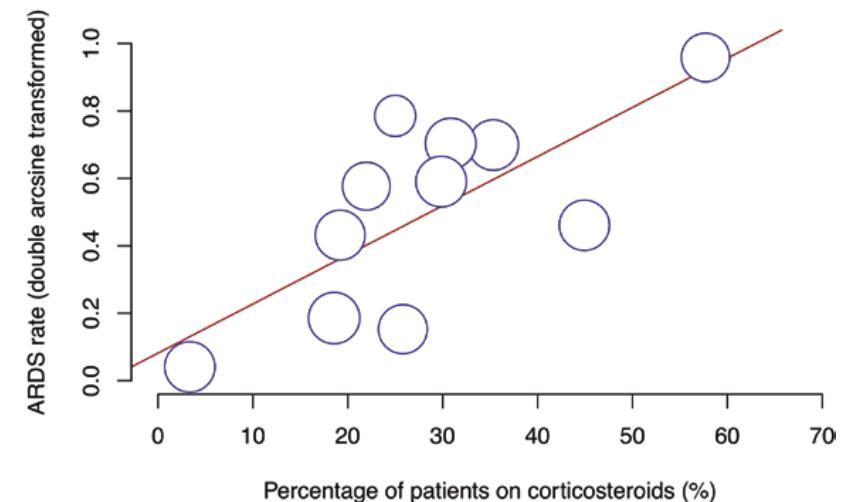
Definition : statistical model built on results of a meta-analysis in order to study impact of covariates (also called “*moderators*”) on effect-sizes.

Goal : identify covariates which can bring heterogeneity in a meta-analysis

Prerequisites : availability of covariates values  
(often baseline characteristics : Men/Women ratio, mean age, mean BMI...)

Results can be visualized with a **bubble plot**

A pvalue is provided by the model



# META-ANALYSIS

## APPLICATION WITH

Package **meta** allows to run meta-analysis :

- Function **metacont** for Y = continuous variable
- Function **metabin** for Y = binary variable
- Function **metacor** for single correlation
- Function **metameans** for single mean
- Function **metaprop** for single proportions
- Function **metarate** for single incidence rates

Parameters : **n, n.e, n.c** = sample size of studies (e = experimental group ; c = control group)

(example for **metacont**) **mean, mean.e, mean.c** = means of outcome of studies

**sd, sd.e, sd.c** = standard-deviation of outcome of studies

**studlab** = names of studies

**subgroup** = variable for subgroups analysis

# META-ANALYSIS

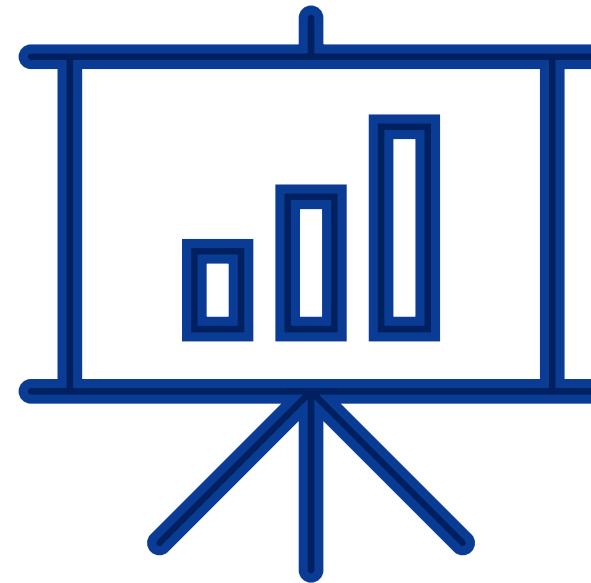
## APPLICATION WITH

Other functions are available in *meta* package :

- *funnel* : funnel plot
- *baujat* : baujat plot

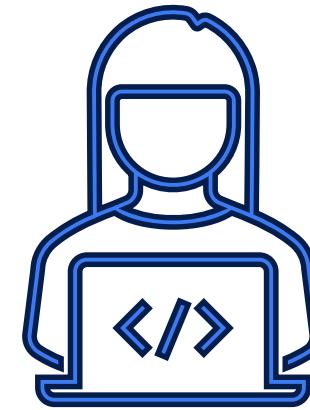
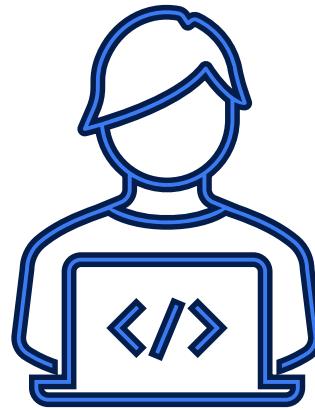
Meta-regressions with *metareg* function and *bubble.metareg* function for bubble plot

# META-ANALYSIS



Live demo

# META-ANALYSIS



Time to play !  
(10 minutes)

CLINICAL  
TRIAL  
DATA

04

# CLINICAL TRIAL DATA

## DATA COLLECTION HISTORY

- Census of population exists since Ancient Egypt and aims for a government to evaluate the size, composition, structure and evolution of a population across time for management of public policies.
- Data collection on individuals exists since Humans were able to write and store information in **physical documents** : papyrus, sheets, books, registers...
- With the rising of **computers, datacenters, Internet** and **numerical supports** (databases, datalakes, clouds, Excel sheets...), data collection, monitoring and storage saw an **exponential increase**.
- With this rise, new challenges and **ethical questions** raised : **data privacy, spying on social networks and medias, phishing, data hacking...**

# CLINICAL TRIAL DATA

## CLINICAL DATA MANAGEMENT

- Clinical Data Management (CDM) : process of collecting, cleaning, analyzing and managing study data in clinical research.
- Main goal : gather as much quality study data as possible.
- CDM applies across all three main stages of clinical trials and even occurs in pre-clinical phases.
- In the pursuit to speed up the drug development process, CDM has become particularly important for achieving faster development times. With better data quality comes better reliability. This lets evaluators make quicker decisions with improved efficiency.

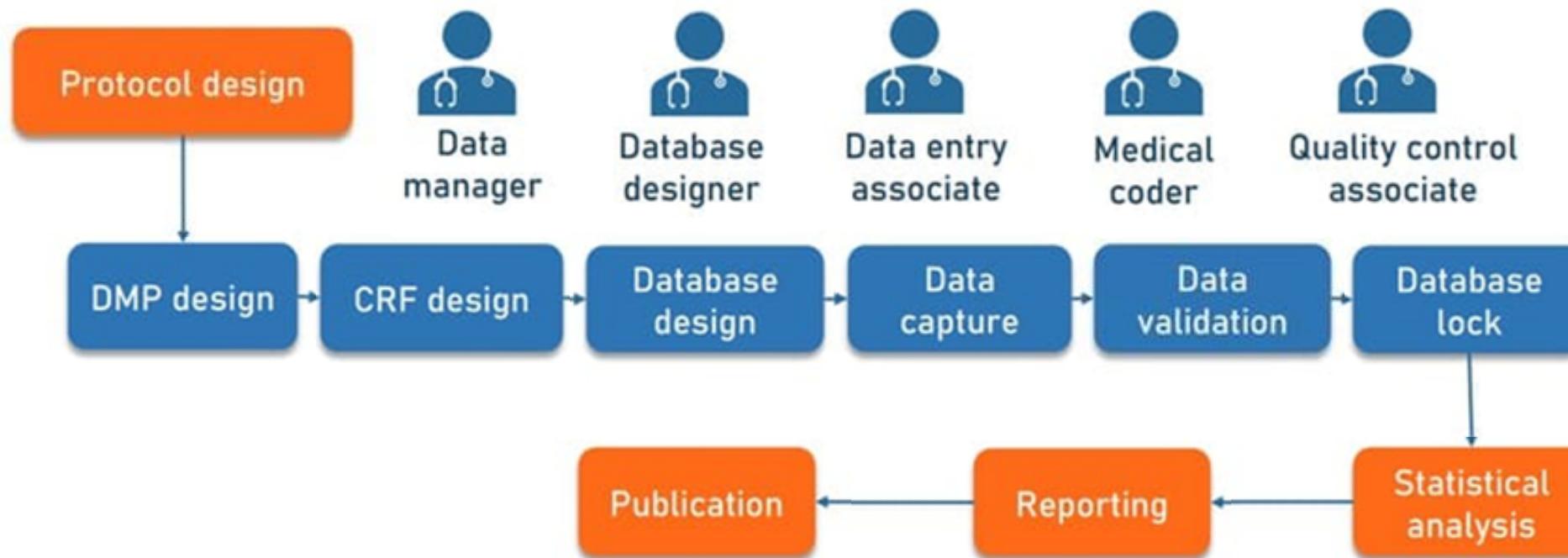
# **CLINICAL TRIAL DATA**

## CLINICAL DATA MANAGEMENT

- CDM ensures :
  - ✓ Quality data collection
  - ✓ Compliance with regulatory standards
  - ✓ Data security
  - ✓ Efficient clinical research process
- Three main pillars of data quality that clinical data management processes aim to achieve:
  - ✓ Accuracy : data that is true to life and error free.
  - ✓ Completeness : datasets that contain the full-extent of the required data.
  - ✓ Consistency : data entries that follow consistent formatting throughout.

# CLINICAL TRIAL DATA

## CLINICAL DATA MANAGEMENT WORKFLOW



Procedures beyond clinical data management cycle

# CLINICAL TRIAL DATA

## DATA MANAGEMENT PLAN

DMP describes the following aspects :

- Data to be gathered from trial participants,
- Existing data that can be integrated,
- Data formats,
- Metadata and its standards,
- Storage and backup methods,
- Security measures to protect confidential information,
- Data quality procedures,
- Responsibility assignments across team members,
- Access and sharing mechanisms and limitations,
- Long-time archiving and preservation procedures,
- The cost of data preparation and archiving, and
- Compliance with relevant regulations and requirements.



# **CLINICAL TRIAL DATA**

## CASE REPORT FORM

CRFs collect only data necessary for the clinical study, avoiding any redundancy.  
The fields to be filled in may include :

- Demographics (age, gender)
- Basic measurements (height, weight)
- Vital signs (blood pressure, temperature, etc.) captured at various time points
- Lab exams
- Medical history
- Adverse events
- Other parameters, based on the research requirements.

CRF can be **physical** (printed documents) and/or **electronic** (eCRF).

# CLINICAL TRIAL DATA

## CLINICAL DATA INTERCHANGE STANDARDS CONSORTIUM

- Clinical Data Interchange Standards Consortium (CDISC) is the official international organization dedicated to the development and maintenance of standards in clinical data collection, storage and sharing.
- Founded in 1997 and hosted in Austin, Texas (USA).
- Since 2016, CDISC standards are mandatory for FDA submission.
- Study Data Tabulation Model (SDTM) : harmonize data structure in human clinical trial for an easy data re-use.



# **CLINICAL TRIAL DATA**

## CASE REPORT FORMS REVIEW



10 minutes

# LONGITUDINAL DATA ANALYSIS

05

# LONGITUDINAL DATA ANALYSIS

## ARTICLE REVIEW



10 minutes

# LONGITUDINAL DATA ANALYSIS

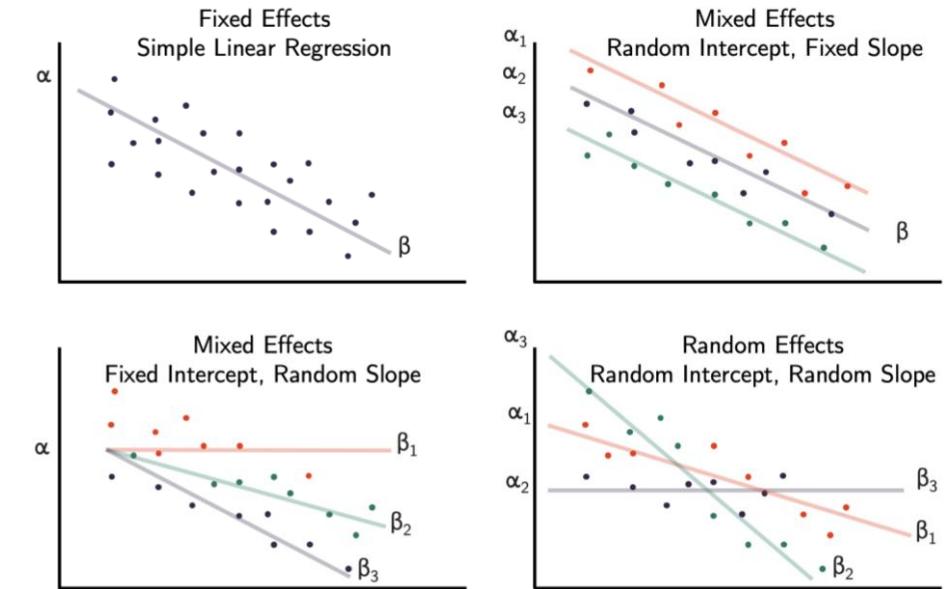
## LONGITUDINAL DATA OVERVIEW

- Longitudinal data : collection of data for an individual across time.
- During clinical trials (except retrospective trials), data is collected, monitored and stored in secured database for each patient included in the trial.
- This data can have various forms : biomarkers (in blood, urine, stool...), electronic health records (heart rate, respiratory rate, temperature...), quality of life questionnaires...
- Each patient is anonymized with a unique Patient ID.
- Data collection, treatment and storage is strictly controlled during a clinical trial.

# LONGITUDINAL DATA ANALYSIS

## FIXED EFFECTS VS MIXED EFFECTS

- Fixed effect :
  - Estimate separate levels with no relationship assumed between the levels.
  - Easily interpretable effect (p-value)
  - Most common in a linear model.



- Random effect :
  - Each level can be thought of as a **random variable** from an underlying process or distribution
  - Complex interpretable effect (often not studied)
  - Less common in a linear model.

# LONGITUDINAL DATA ANALYSIS

## LINEAR MIXED MODEL DEFINITION

- Linear model which contains **fixed** and **random effects**

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \boldsymbol{\varepsilon}$$

With

$\mathbf{Y}$ : vector of observations (continuous)

$\mathbf{X}$  : design matrix of fixed effects

$\boldsymbol{\beta}$  : unknow vector a fixed effects

$\mathbf{Z}$  : design matrix of random effects

$\mathbf{u}$  : unknow vector a random effects

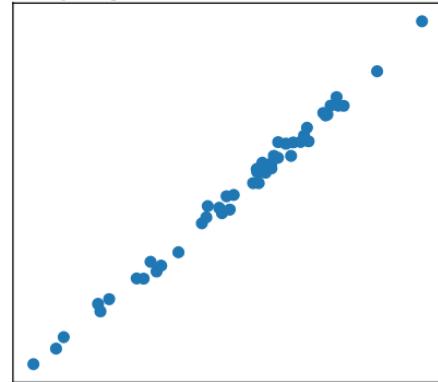
$\boldsymbol{\varepsilon}$  : residuals

- Often used for analysis of **longitudinal clinical data** : many timepoints / patient

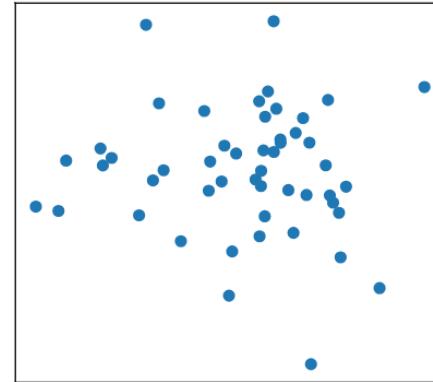
# LONGITUDINAL DATA ANALYSIS

## COVARIANCE STRUCTURES

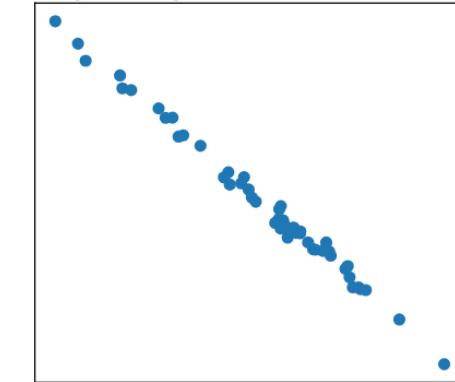
large positive covariance



covariance of zero



large negative covariance



- Introducing random effect implies to use a specific **covariance matrix**.
- Overall shape :  
(example of a matrix for 3 patients evaluated each at 3 timepoints)

$$\begin{bmatrix} R_1 & 0 & 0 \\ 0 & R_2 & 0 \\ 0 & 0 & R_3 \end{bmatrix}$$

# LONGITUDINAL DATA ANALYSIS

## COVARIANCE STRUCTURES

- Many designs for R :

- General form :

matrix of **variances** of each timepoint on the diagonal and covariances of timepoints elsewhere

$$R_i = \begin{bmatrix} \sigma_1^2 & \sigma_{1,2} & \sigma_{1,3} \\ \sigma_{1,2} & \sigma_2^2 & \sigma_{2,3} \\ \sigma_{1,3} & \sigma_{2,3} & \sigma_2^2 \end{bmatrix}$$

- Compound symmetry :

matrix of random term variances with the same **total variance** of the diagonal (default matrix in *lme* function)

$$R_i = \begin{bmatrix} \sigma^2 & \theta & \theta \\ \theta & \sigma^2 & \theta \\ \theta & \theta & \sigma^2 \end{bmatrix}$$

# LONGITUDINAL DATA ANALYSIS

## COVARIANCE STRUCTURES

- Many designs for R :

- First order autoregressive :

matrix with global variance on the diagonal and correlations between timepoints with an index

$$R_i = \sigma^2 \begin{bmatrix} 1 & \rho & \rho^2 \\ \rho & 1 & \rho \\ \rho^2 & \rho & 1 \end{bmatrix}$$

- Toeplitz :

matrix of random term variances with the same total variance of the diagonal

$$R_i = \begin{bmatrix} \sigma^2 & \sigma_1 & \sigma_2 \\ \sigma_1 & \sigma^2 & \sigma_1 \\ \sigma_2 & \sigma_1 & \sigma^2 \end{bmatrix}$$

# LONGITUDINAL DATA ANALYSIS

## APPLICATION WITH

*lme* function (*nlme* package)

Parameters :

- formula* =  $Y \sim$  fixed effects
- random* =  $\sim$  random effects
- data* = dataset
- subset* = subset of the rows of the dataset to keep
- method* = « REML » (for Restricted Log-Likelihood method)

Outputs :

- lme* object which contains results :
- Coefficients of the equation
- Residuals
- Fitted values
- Covariance matrix
- REML value

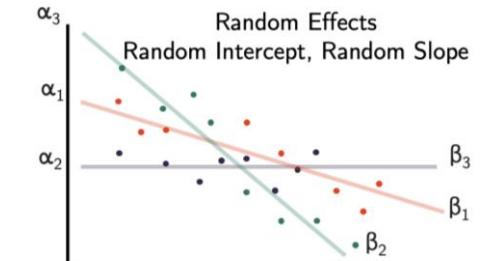
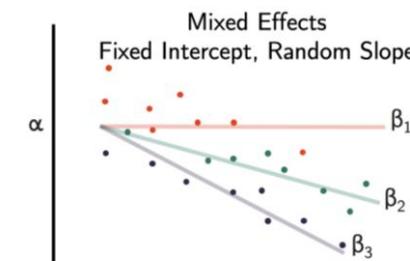
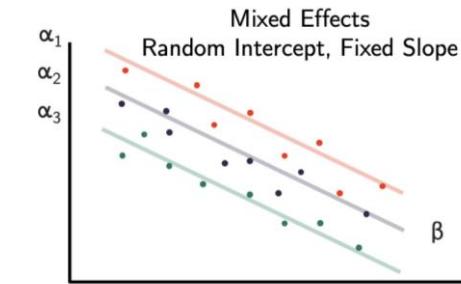
# LONGITUDINAL DATA ANALYSIS

## APPLICATION WITH

`getVarCov` function (`nlme` package) : variance and correlation components from a random-effect model

How to write a random effect in `lme` :

- `~ 1 | Patient_ID` : random intercept
- `~ Time | Patient_ID` : random slope
- `~ (1 + Time) | Patient_ID` :  
random intercept + random slope



# LONGITUDINAL DATA ANALYSIS

## APPLICATION WITH

`r2` function (*performance* package) : get the  $R^2$  of mixed models (also called *Nakagawa's R<sup>2</sup>*)

Two  $R^2$  are computed :

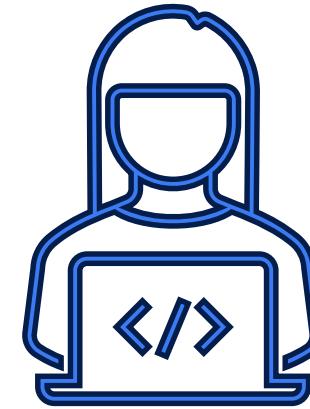
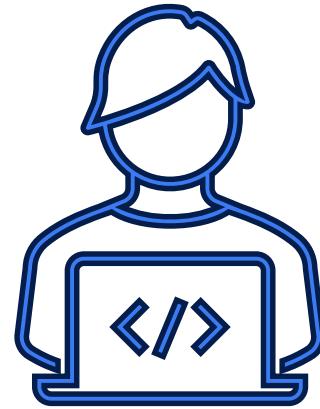
- Conditional  $R^2$  :  $R^2$  of the overall model (fixed + random effects)
- Marginal  $R^2$  :  $R^2$  of fixed effects

# LONGITUDINAL DATA ANALYSIS



Live demo

# LONGITUDINAL DATA ANALYSIS



Time to play !  
(15 minutes)

# SURVIVAL ANALYSIS

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# SURVIVAL ANALYSIS

## ARTICLE REVIEW



10 minutes

# SURVIVAL ANALYSIS

## BRIEF HISTORY

- Survival analysis emerged during the 17<sup>th</sup> century with the **rising of statistics in medicine**.
- John GRAUNT (1620 – 1674), English founder of demography and epidemiology.



CAPTAIN JOHN GRAUNT

He produced a **life table** which shows, for each age, the probability that a person of that age will die before their next birthday ("probability of death").

He used it during the **bubonic plague** in London in 1665-1666 (100.000 deaths in 18 months, almost  $\frac{1}{4}$  of the city population)

A historical document titled "A TABLE of the CHRISTENINGS and MORTALITY for the Year 1603 and 1666." The table is organized by month and includes columns for weeks, days, christenings, burials, and mortality rates. The document also contains a note about the bubonic plague in London.

Month	Weeks	Days	Christ. Bur.	Per cent.
January	1	1	115	1.00
February	2	177	121	0.80
March	3	121	118	0.95
April	4	121	118	0.95
May	5	149	138	0.93
June	6	169	158	0.93
July	7	133	121	0.90
August	8	121	118	0.95
September	9	133	121	0.90
October	10	121	118	0.95
November	11	121	118	0.95
December	12	121	118	0.95
Total		1809	1612	0.90

# SURVIVAL ANALYSIS

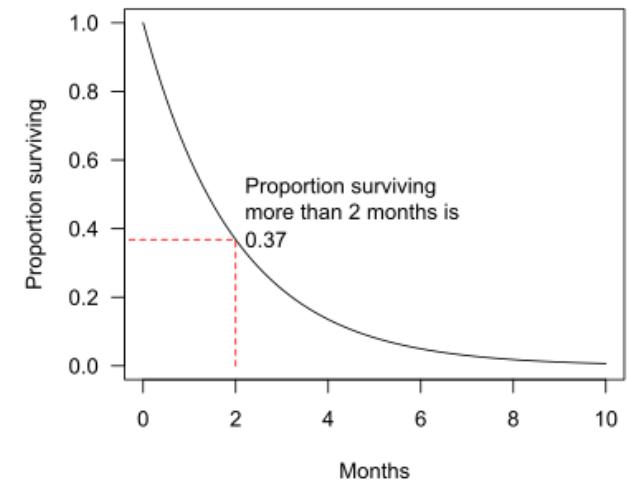
## OVERVIEW

- Definition : branch of statistics dedicated to the analysis of expected duration of time **until one event occurs**
- Many **events** to model : death, cancer remission, heart attack...
- Also used in **economics / sociology** fields
- Used in several ways :
  - **Describe** the survival times of members of a group
  - **Compare survival** time of two or more groups
  - **Describe the effect of categorical or quantitative variables** on survival

# SURVIVAL ANALYSIS

## KAPLAN-MEIER ESTIMATOR

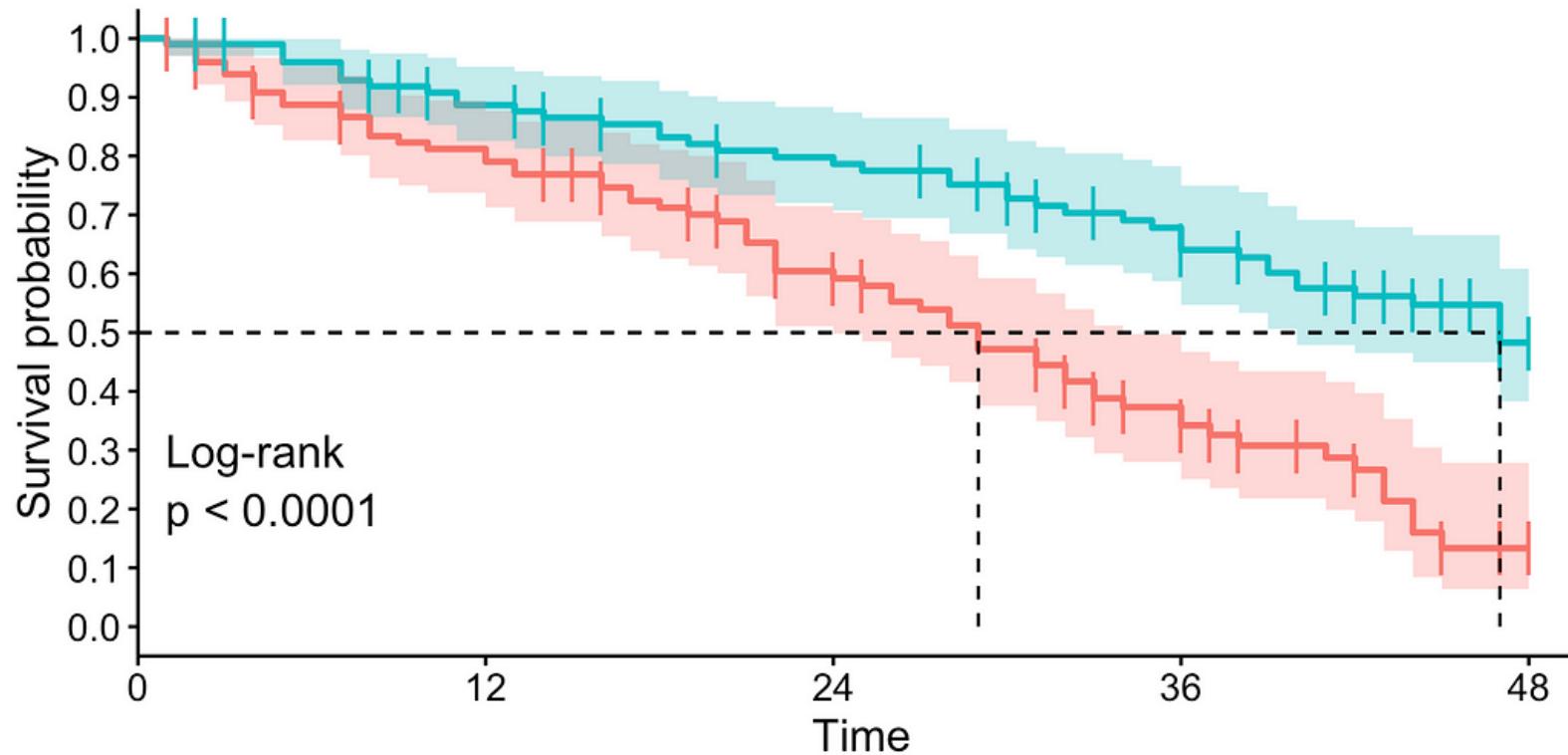
- Definition : Non-parametric statistic used to estimate the **survival function** from lifetime data.
- Invented by **Edward L. KAPLAN** (1920 – 2006) and **Paul MEIER** (1924 – 2011), two American statisticians
- Survival function : 
$$S(t) = P(T > t)$$
- Kaplan-Meier plot : illustrates the evolution of **overall survival** or within groups across time.
- Log-rank test : compare the **survival of two groups** with a pvalue (also called Cochran-Mantel-Haenszel test).



# SURVIVAL ANALYSIS

## KAPLAN-MEIER PLOT

 Treatment=A  Treatment=B

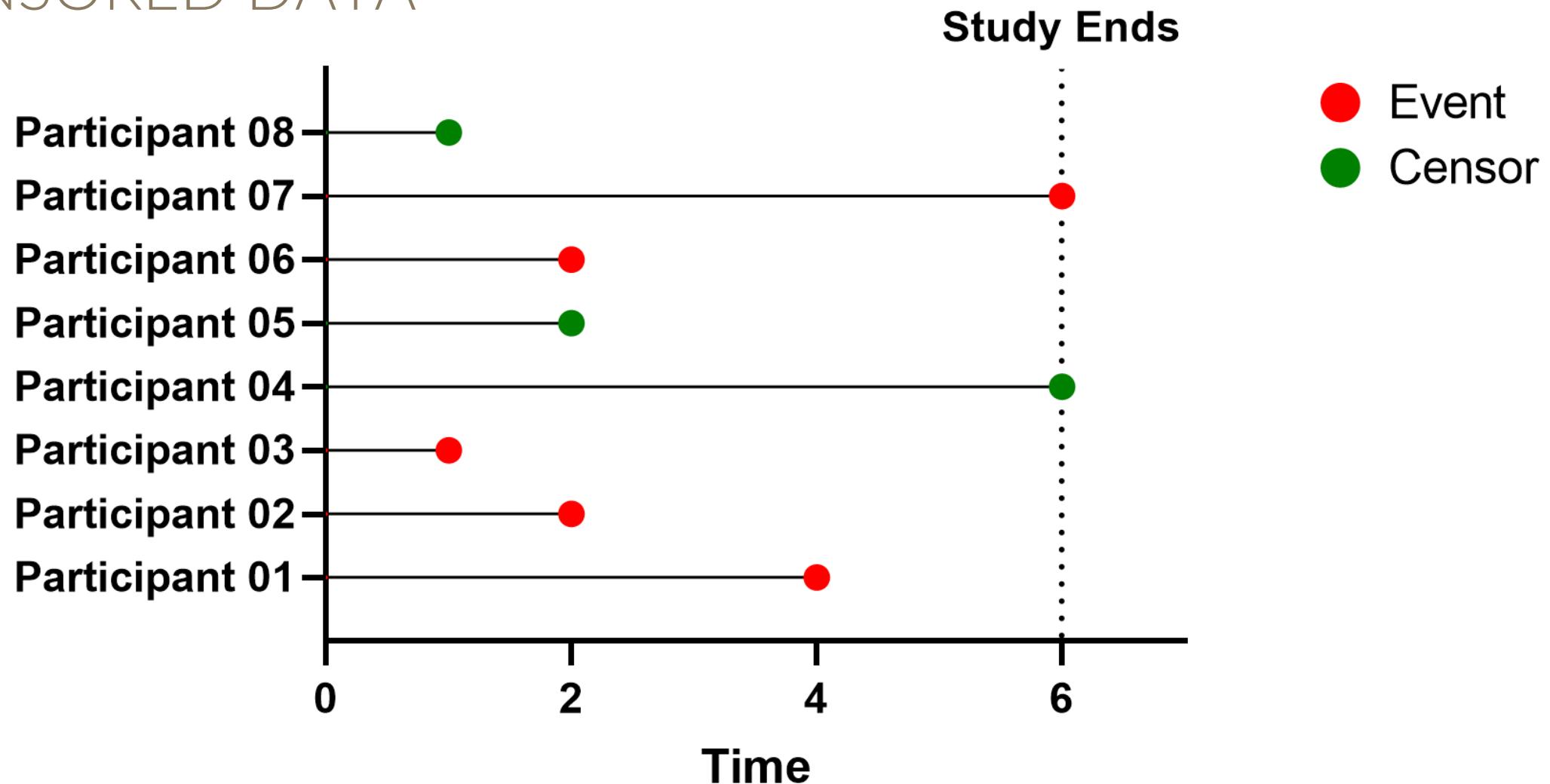


Number at risk (number censored)

100 (0)	75 (7)	49 (16)	24 (24)	3 (36)
100 (0)	83 (6)	70 (11)	54 (18)	29 (57)

# SURVIVAL ANALYSIS

## CENSORED DATA



# SURVIVAL ANALYSIS

## PROPORTIONAL HAZARDS MODEL (COX MODEL)

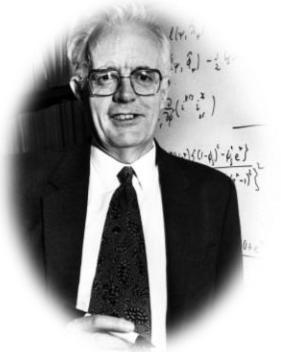
- Invented by Sir David COX (1924 – 2022), British statistician in 1972. He is also the inventor of logistic regression in 1958.
- Goal : study the impact of one or more parameters (continuous or categorical) on the survival.
- Uses hazard-function :

$$\lambda(t|X_i) = \lambda_0(t) \exp(\beta_1 X_{i1} + \dots + \beta_p X_{ip})$$

with :  $t$  : time

$\lambda_0(t)$  : baseline risk at time  $t$

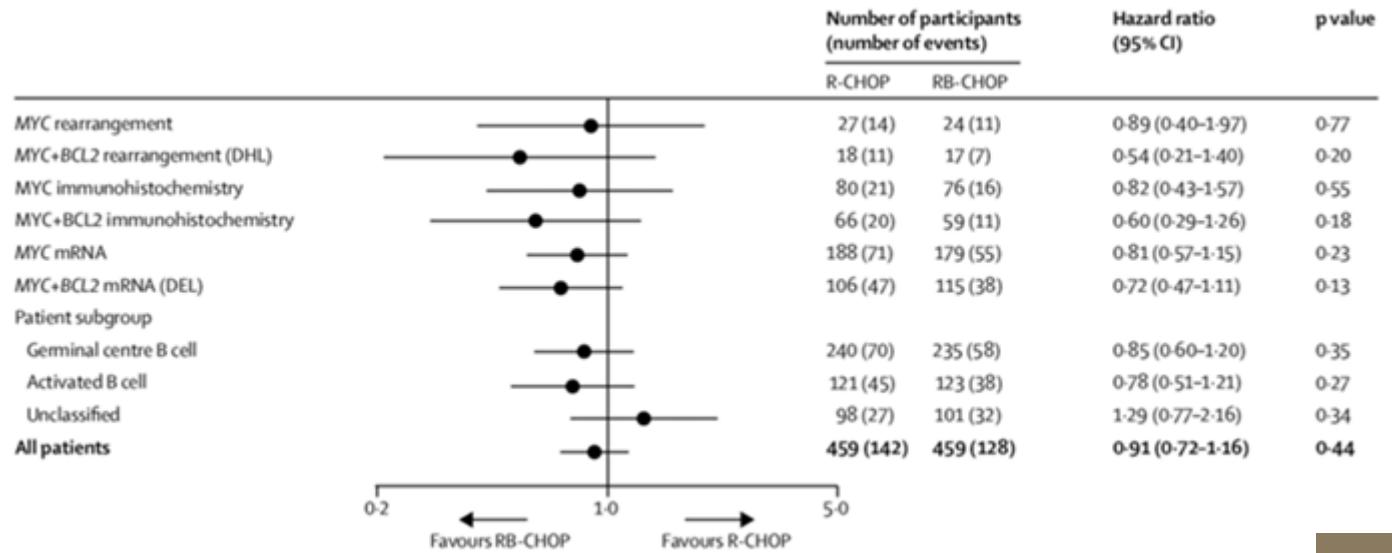
$X_{ip}$  : covariate  $p$  value for individual  $i$



# SURVIVAL ANALYSIS

## HAZARDS RATIOS

- Hazard-ratio : 
$$HR = \frac{\lambda(t|x+1)}{\lambda(t|x)}$$
 (values : 0 to  $+\infty$ )
- Assumption : assumes the hazards for any two individuals have the same proportion at all times
- Illustration with forest-plot
- $HR = \exp(\beta)$



# SURVIVAL ANALYSIS

## APPLICATION WITH

*survfit* function (*survival* package) : Kaplan-Meier curve

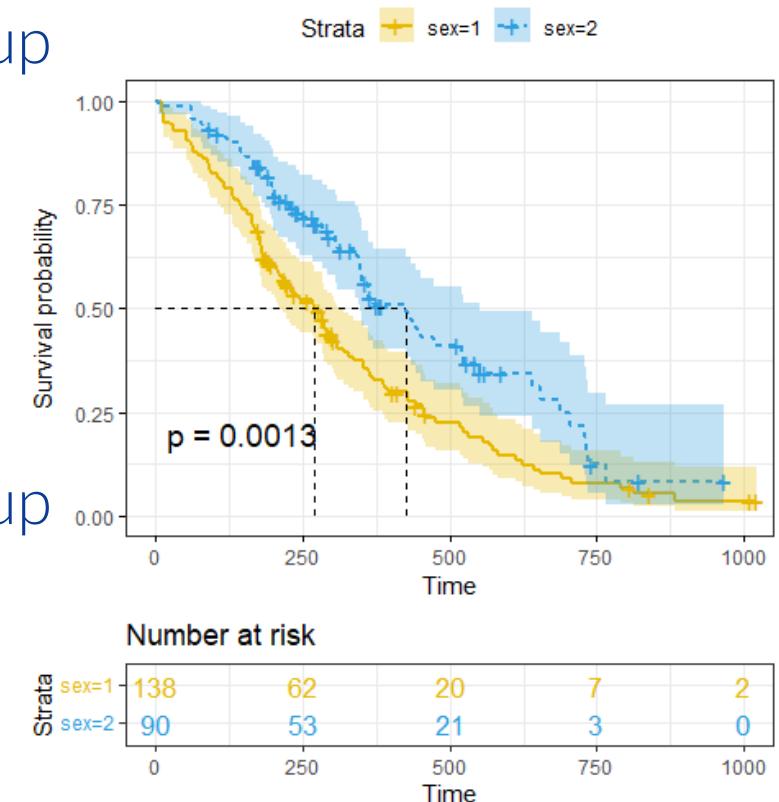
Parameters :   
*formula* = Surv(time, outcome) ~ group  
*data* = dataset

Outputs :   
*Kaplan-Meier curve*

*survdiff* function (*survival* package) : log-rank test

Parameters :   
*formula* = Surv(time, outcome) ~ group  
*data* = dataset

Outputs :   
*log-rank test*



*ggsurvplot* function (*survminer* package) : customized plots

# SURVIVAL ANALYSIS

## APPLICATION WITH

*coxph* function (*survival* package) : Cox model

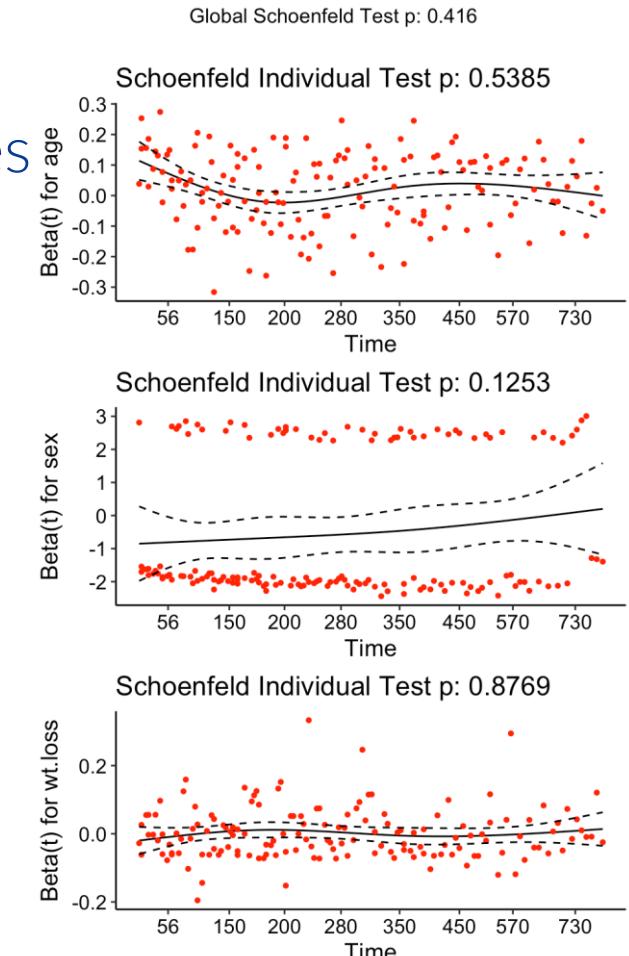
Parameters : *formula* = Surv(time, outcome) ~ covariates  
*data* = dataset

Outputs : Cox model

*cox.zph* function (*survival* package) : test for proportional hazard assumption

Parameters : *model* = Cox model object

Outputs : pvalues  
plots

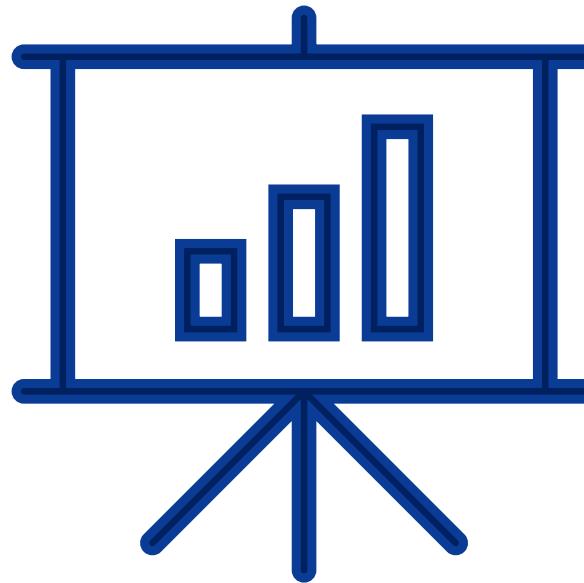


# SURVIVAL ANALYSIS

## APPLICATION WITH

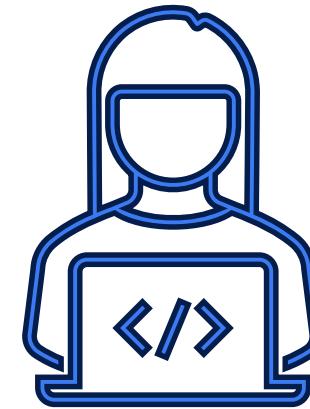
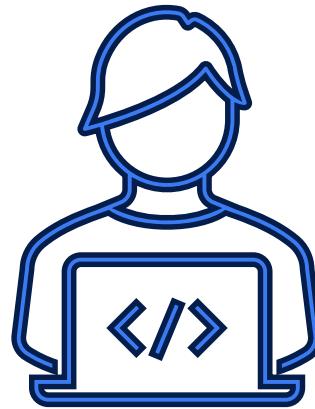
*ggforest* function (*surminer* package) : Forest-plot of Hazard-ratios

# SURVIVAL ANALYSIS



Live demo

# SURVIVAL ANALYSIS



Time to play !  
(15 minutes)

QUESTIONS

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THANK  
YOU  
FOR  
YOUR  
ATTENTION

NOVEMBER 2025

