

# High-throughput Sequencing Analysis

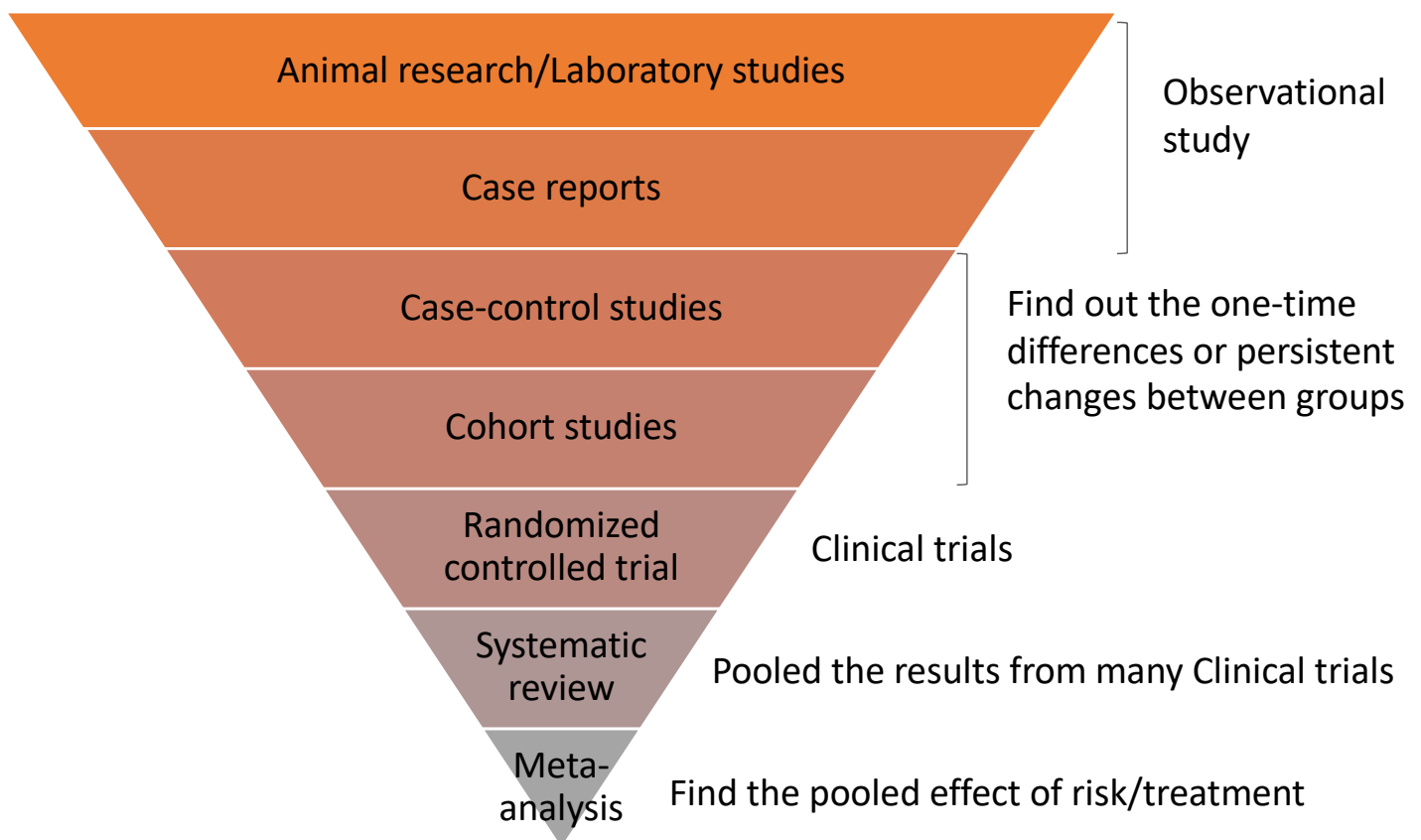
## **Meta-Analysis**

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2019-05-31

# Meta-analysis

- Meta-analysis is a quantitative and epidemiological study design to conduct a systematic reviews of previous research studies.
- The outcome of meta-analysis represents the 'pooled' results of the studies and therefore could provide a more precise estimate of the effect of risk (or treatment) for disease.



- Compare to a single study, meta-analysis
  - has greater study power (bigger sample size, greater diversity)
  - provides more reliable results
  - helps to find out the effects from studies that have conflicting results
  - helps to discover the effects across different populations
  - can pool the results from studies with smaller sample size that are not statistically significant

# Meta-analysis

- The limitations of meta-analysis including
  - Time consuming and difficult to find appropriate studies
  - Details provided by each study might not be adequate for analysis
  - Requires advanced statistical analysis
  - There might be a publication bias – only publications with positive/significant findings were reported
- To perform the meta-analysis, the first step is to perform a systematic review.
- Usually we aim to find as many publications as possible, and prefer studies with bigger sample size.
- Ideally, the selected studies shall be
  - Studies with large diversity
  - Study results were generated using similar statistical methods (and adjust for similar covariates)
  - Studies with same “effects”.
  - Studies with both positive/negative, significant/insignificant results
  - Studies with comparable information
  - For genetic studies, sometimes we need to consider the ‘molecular meanings’ before analysis
- The “effects” can be used for meta-analysis including:
  - Mean, mean difference
  - Risk ratio, odds ratio
  - Proportion, rate change
  - Coefficients (beta coefficients, correlation coefficients)

# Searching the literature with Pubmed

- What do you usually do for literature reviewing? Pubmed?

## No filter

Search results: Items: 1 to 20 of 794

Sort by: Best match | Most recent

Results by year

PMC Images search for Floaters

## Different filters

## With filter (year range)

Search results: Items: 1 to 20 of 281

Filters activated: Publication date from 2015/01/01 to 2019/12/31. Clear all to show 692 items.

Sort by: Best match | Most recent

Results by year

Download CSV

## Year filter

- Can we do text mining easily using Pubmed?
- Probably not.

	A	B
1	pubmed - Floaters	
2	year	count
3	2019	33
4	2018	71
5	2017	55
6	2016	50
7	2015	41

# Searching the literature with R

- Alternatively, we can use a package “RISmed” to make things easier

```
# Install and use the package
```

```
> install.packages("RISmed")
```

```
> library(RISmed)
```

```
# Let's see how it works
```

```
> fit <- EUtilsSummary("Floaters", type="esearch", db="pubmed",  
datetype='pdat', mindate=2015, maxdate=2019)
```

```
# "Floaters": this is the keyword you are interested in. Try to  
replace it with other character
```

```
# db: database, we search publications on pubmed
```

```
# mindate: publication year (min)
```

```
# maxdate: publication year (max)
```

```
# Check how many references you found
```

```
> fetch <- EUtilsGet(fit)
```

```
> QueryCount(fetch)
```

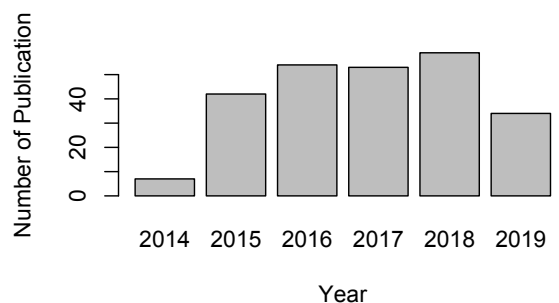
```
[1] 250
```

```
# Check how it distributed during 2015 and 2019
```

```
> y <- YearPubmed(fetch)
```

```
> table(y)
```

```
2014 2015 2016 2017 2018 2019  
    7   42   54   53   59   34
```



```
# The results are 'slightly' different  
from what we've got using Pubmed...
```

```
> barplot(table(y),ylab="Number of Publication",xlab="Year")
```

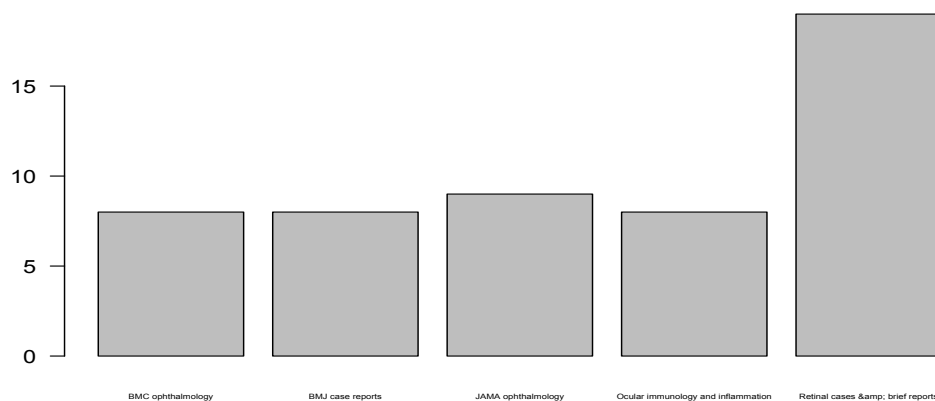
# Searching the literature with R

```
# We can get all kind of information from these publications
> alllist <- EUtilsGet(fetch)
> slotNames(alllist)
[1] "Query"                "PMID"                "YearReceived"
[4] "MonthReceived"        "DayReceived"         "HourReceived"
...
[58] "CollectiveName"      "Mesh"

# Alternatively, just select the information you are interested in
> data <- data.frame(pmid=PMID(fetch),year=YearPubmed(fetch),
title=ArticleTitle(fetch),journal=Title(fetch),country=Country(fetch))

# Check the dimension now, we got 5 columns listing the pmid, year,
title, journal, and country information
> dim(data)
[1] 249  5

# You can get some interesting information from the fetch results
# For example, check which journal potentially wants to take a related
articles in the future
> journal1 <- table(data$journal)
> barplot(journal1[journal1>7],horiz=F,las=1.5,cex.names=0.4)
```



```
# Or check who are interested in this topic
> sort(table(data$country),decreasing=T)
```

United States	England	Switzerland
112	70	21

# Searching the literature with R

```
# And next, let's check if there is a popular word (or words) in the
publication title
# Let's check with the first publication, which list on the first row of your
data
> a<- data$title[1]
> a
[1] "Ocular and orbital side effects of ALK inhibitors: a review article"

# We can remove all the punctuations at the beginning
> a <- gsub("[:]", "", a)
> a <- gsub("[;]", "", a)
> a <- gsub("[.]", "", a)
# Now, split the string into single characters
> a1 <- strsplit(as.character(a), " ")
> a1
[[1]]
 [1] "Ocular"      "and"          "orbital"      "side"         "effects"
 [6] "of"          "ALK"          "inhibitors"  "a"            "review"
[11] "article"

# Let's try to do it altogether
> a <- data$title
> a <- gsub("[:]", "", a)
> a <- gsub("[;]", "", a)
> a <- gsub("[.]", "", a)
> a1 <- strsplit(as.character(a), " ")

# a1 is a "list"
# You need to "unlist" it before counting it

> a2 <- unlist(a1)
> sort(table(a2), decreasing=T)[1:20]
a2
      of      and      in      the      a      for      with
159      96      92      59      55      49      40
  A  Floaters floaters Vitreous vitreous to      an
 36      28      27      27      24      23      22
Retinal Vitrectomy      after      case      retinal      as
 20      14      13      13      13      12
```

# Example of Meta-analysis: OR

```
# After fetching the publications of interests, you can select the
publications for the meta-analysis
# Let's use an simple example here, please download R package "meta"
> install.packages("meta")
> library(meta)
```

```
# We will use a dataset 'Fleiss93' in meta package
# The use of aspirin in preventing death after myocardial infarction
> data(Fleiss93)
> Fleiss93
```

	study	year	event.e	n.e	event.c	n.c
1	MRC-1	1974	49	615	67	624
2	CDP	1976	44	758	64	771
3	MRC-2	1979	102	832	126	850
4	GASP	1979	32	317	38	309
5	PARIS	1980	85	810	52	406
6	AMIS	1980	246	2267	219	2257
7	ISIS-2	1988	1570	8587	1720	8600

	Aspirin	Placebo
Death #	49	67
Alive #	566	557

```
# Study: study label
# year: year of publication
# event.e: number of deaths in aspirin group
# n.e: number of observations in aspirin group
# event.c: number of deaths in placebo group
# n.c: number of observations in placebo group
```

```
# Basically we will compare the odds ratio for each study
```

	Aspirin	Placebo
Death number		
Alive number		
Total number		



# Example of Meta-analysis: outcome

```
# metabin function helps you to calculate odds ratio first
> result <- metabin(event.e, n.e,event.c,n.c,data=Fleiss93,sm="OR")
> result
```

**1.**

	OR	95%-CI	%W(fixed)	%W(random)	Weight of individual studies
1	0.7197	[0.4890; 1.0593]	3.2	8.2	<ul style="list-style-type: none"> <li>• Fixed effect</li> <li>• Same mean, zero bt study variance</li> <li>• Random effect</li> <li>• Different mean, with bt study variance</li> </ul>
2	0.6808	[0.4574; 1.0132]	3.1	7.8	
3	0.8029	[0.6065; 1.0629]	5.7	13.2	
4	0.8007	[0.4863; 1.3186]	1.8	5.4	
5	0.7981	[0.5526; 1.1529]	3.2	8.9	
6	1.1327	[0.9347; 1.3728]	10.2	20.7	
7	0.8950	[0.8294; 0.9657]	72.9	35.8	

Number of studies combined: k = 7

**4.**

	OR	95%-CI	z	p-value
Fixed effect model	0.8969	[0.8405; 0.9570]	-3.29	0.0010
Random effects model	0.8763	[0.7743; 0.9917]	-2.09	0.0365

Quantifying heterogeneity:

$\tau^2 = 0.0096$ ;  $H = 1.29$  [1.00; 1.99];  $I^2 = 39.7\%$  [0.0%; 74.6%]  
 variance of the true effect sizes

Test of heterogeneity:

Q	d.f.	p-value	<b>2.</b>
9.95	6	0.1269	—

- 3.**  $I^2$  ranged between 0% and 100%
- <25% : low
  - 25%-75%: middle
  - >75%: high

- If  $P < 0.1$ , there is a significant heterogeneity problem (that means the studies have great variability)
- You need to find out the reasons for heterogeneity, and use random-effect result instead.

Details on meta-analytical method:

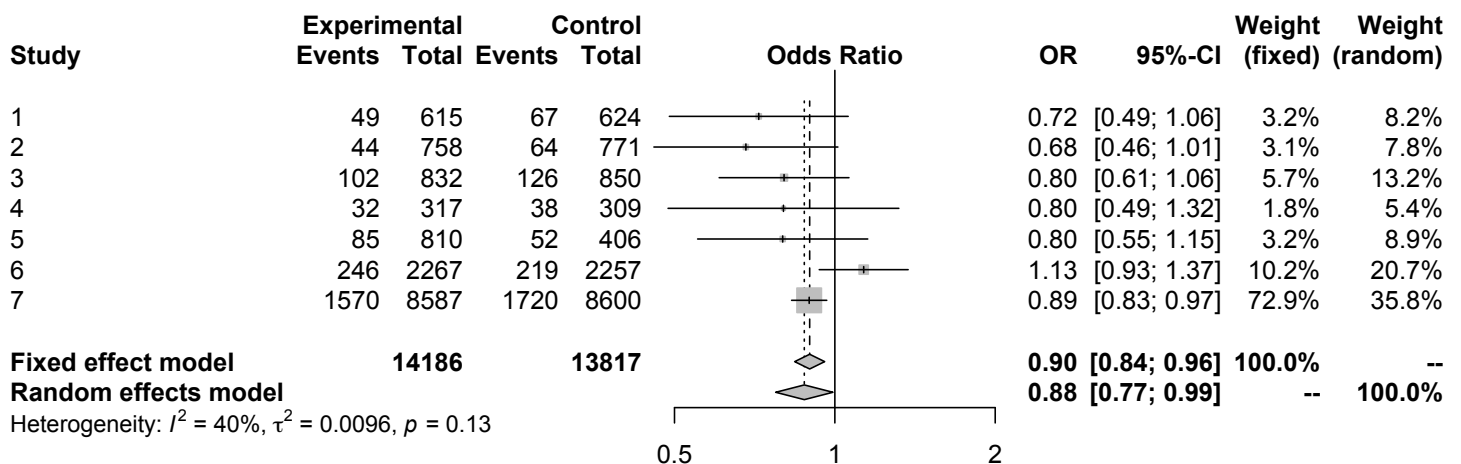
- Mantel-Haenszel method
- DerSimonian-Laird estimator for  $\tau^2$

# Example of Meta-analysis: forest plot

# Now we can generate the famous forest plot to visual our result  
 > forest(result)

# We can see Aspirin seems to help preventing death after myocardial infarction in most of the studies

# Therefore, the overall effect is significant (but most likely, the results were highly influenced by the study result of Study 7.



# For the next step, let's consider the potential publication bias in this meta-analysis

# We will use 'Funnel Plot' to visual the bias

# A funnel plot is a scatter plot of intervention effect estimates against a measure of study precision.

# Asymmetry in the funnel plot suggest there might be a publication bias for the study

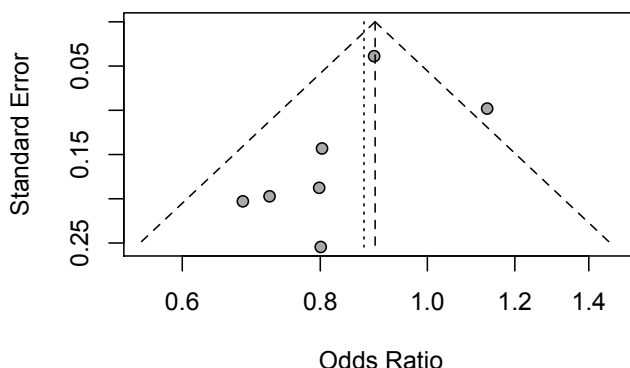
# The bias could be due to

- Reporting bias or selective reporting
- Poor methodological quality (e.g. sample size too small)
- Heterogeneity among studies
- Simply by chance

# When you have studies < 10, funnel plot is not suggested for judging the publication bias (lack of power)

# Example of Meta-analysis: asymmetry analysis

```
# Asymmetry analysis
> funnel(result)
```



```
# If you have studies > 10, you can use this function to test your
publication bias
```

```
> metabias(result,method.bias="peters")
```

Warning message:

```
In print.metabias(x) :
```

```
Number of studies (k=7) too small to test for small study effects
(k.min=10). Change argument 'k.min' if appropriate.
```

```
# We do see Asymmetry in the funnel plot, we can adjust our results using
either trim and filled or copas model.
```

```
> tf1 <- trimfill(result, comb.fixed=TRUE)
```

```
> summary(tf1)
```

```
Number of studies combined: k = 10 (with 3 added studies)
```

	OR	95%-CI	z	p-value
Fixed effect model	0.9140	[0.8587; 0.9727]	-2.83	0.0047
Random effects model	0.9231	[0.8252; 1.0327]	-1.40	0.1622

```
Quantifying heterogeneity:
```

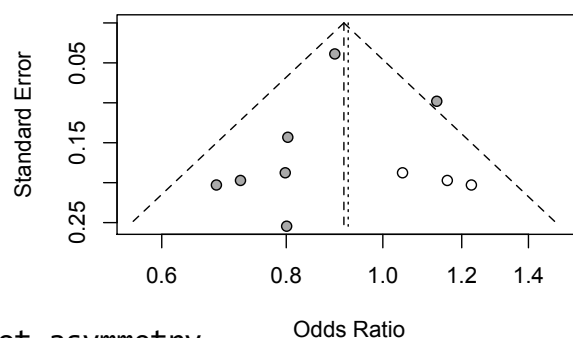
```
tau^2 = 0.0102; H = 1.26 [1.00; 1.83]; I^2 = 37.4% [0.0%; 70.1%]
```

```
Test of heterogeneity:
```

Q	d.f.	p-value
14.37	9	0.1099

```
Details on meta-analytical method:
```

- Inverse variance method
- DerSimonian-Laird estimator for tau^2



- Trim-and-fill method to adjust for funnel plot asymmetry
- ```
> funnel(tf1)
```

# Example of Meta-analysis: sensitivity test

# We can exclude 1 study a time to check the meta-analysis results each time

```
> metainf(result, pooled="fixed")
```

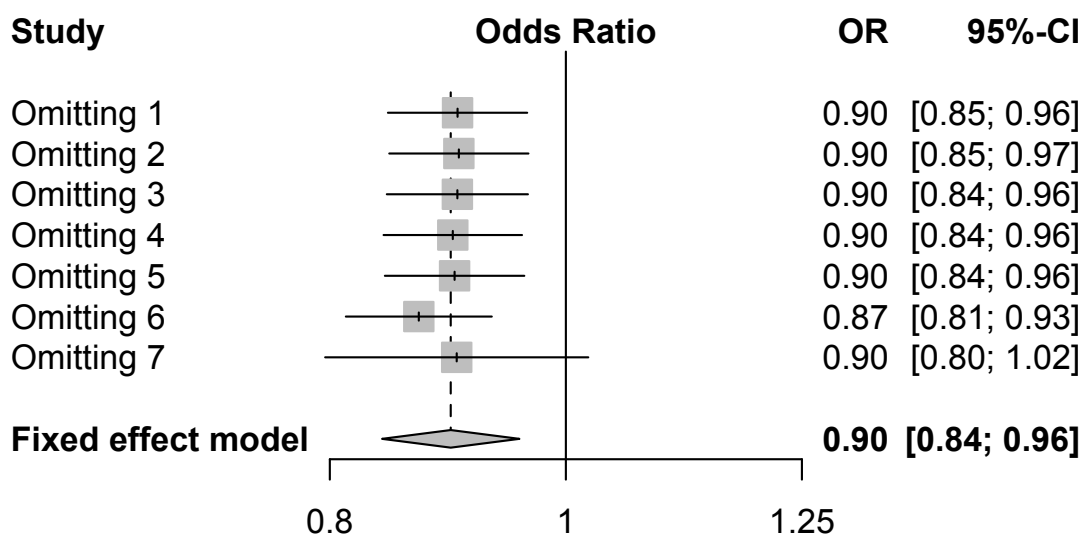
Influential analysis (Fixed effect model)

|                 | OR     | 95%-CI           | p-value  | tau^2  | I^2   |
|-----------------|--------|------------------|----------|--------|-------|
| Omitting 1      | 0.9027 | [0.8452; 0.9641] | 0.0023   | 0.0099 | 42.3% |
| Omitting 2      | 0.9038 | [0.8462; 0.9652] | 0.0026   | 0.0082 | 37.9% |
| Omitting 3      | 0.9025 | [0.8443; 0.9648] | 0.0026   | 0.0129 | 46.3% |
| Omitting 4      | 0.8986 | [0.8417; 0.9594] | 0.0014   | 0.0123 | 48.7% |
| Omitting 5      | 0.9001 | [0.8427; 0.9615] | 0.0018   | 0.0124 | 47.6% |
| Omitting 6      | 0.8702 | [0.8122; 0.9324] | < 0.0001 | 0.0000 | 0.0%  |
| Omitting 7      | 0.9020 | [0.7965; 1.0214] | 0.1040   | 0.0268 | 49.7% |
| Pooled estimate | 0.8969 | [0.8405; 0.9570] | 0.0010   | 0.0096 | 39.7% |

Details on meta-analytical method:

- Mantel-Haenszel method

```
> forest(metainf(result), comb.fixed=TRUE)
```



- The result again suggest that the overall results were highly influenced by the study result of Study 7.