

Meta-analysis is a method of evidence synthesis using data from independent primary studies on the same subject. In simplest terms, it is a quantitative assessment of a given phenomenon, such as the effectiveness of an intervention on a given outcome.

The main two steps in the analysis include data extraction through title and abstract screening followed by the main analysis using statistical programs such as R and Stata. Here is a quick demonstration of the method using the 'meta' package in R. R has several other packages for the same purpose e.g. rmeta and metafor, but I prefer to use 'meta' as it best suits the type of data I have.

Here is a hypothetical example using studies on the impact of drinking honey on low back pain:

Step 1: load the library:

```
library("meta")
```

Step 2: Importing the results to R:



```
summary(df)
```

Study	event.e	n.e
Length:9	Min. : 5.00	Min. : 54.0
Class :character	1st Qu.:12.00	1st Qu.:125.0
Mode :character	Median :23.00	Median :230.0
	Mean :27.44	Mean :252.7
	3rd Qu.:34.00	3rd Qu.:365.0
	Max. :56.00	Max. :425.0

Step 3: Preparing the dataset for analysis using the `metaprop` function that performs the necessary calculations to carry out the meta-analysis and also storing the outcome to a new object 'me.ta' :

```
me.ta <- metaprop(event = event.e,  
                  n= n.e,  
                  data=df,  
                  studlab = Study,  
                  sm="Plogit",  
                  level = 0.95,  
                  comb.fixed=TRUE, comb.random=TRUE,  
                  hakn=F,  
                  method.tau="DL")
```

Notes: `sm` refers to summary measures, which is logit transformation in this case;

Level refers to confidence level which is set to the default of 95%;

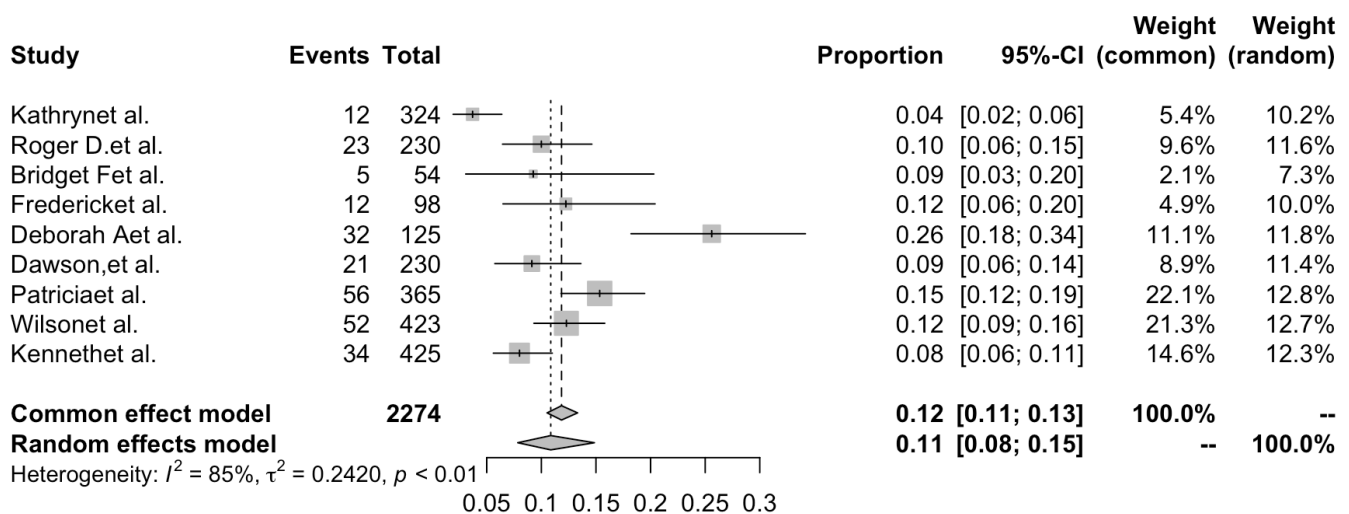
`comb.fixed`: fixed-effects meta-analysis;

comb.random: random effects meta-analysis.

method.tau: method used to calculate between-study variance (DL= DerSimonian-Laird estimator)

Step 4: plotting the results:

```
forest(me.ta)
```



Step 5: Interpretation of the plot:

The forest plot provides a visual representation of the analysis and conclusions that illustrates the estimates of effect size and confidence intervals for each study. It is an effective method for 1) assessing the relevant diagnostic information such as the level of heterogeneity and 2) comparing the effect sizes of the included studies.

Estimation of the heterogeneity: Heterogeneity is present in all meta-analyses that arise due to clinical (population or study settings, study design, measurement of the indicators) and statistical factors. It indicates whether the differences between studies are not due to chance and whether the level of the heterogeneity is too high for the conclusion to be accepted as valid. There are two different statistics to assess heterogeneity on the chart: I and tau-squared.

The tau-squared ( $\tau^2$ ) is an estimation of the heterogeneity of the effect sizes across the individual studies which is also known as a between-study variance. The cut-off values are defined as: might not be important when ranging from 0-25%; may represent moderate heterogeneity when 30% to 60%; may represent substantial heterogeneity when >50%.

In general, when I-squared is  $\leq 50\%$  then the studies are considered to be homogeneous for which a fixed effect model is recommended. In this study, the value of I-squared is above the threshold which requires using a random effect model due to high heterogeneity. Here we have asked for both of the estimates and found a slight difference between the two with the effect size being 0.12 [0.11; 0.13] for the fixed-effect model and 0.11 [0.08; 0.15] for the random effect model, both of which indicate a statistically significant association as the CI for none of them overlaps with the line of no effect. This HYPOTHETICAL meta-analysis concludes that drinking honey can be an effective remedy for low back pain.

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