

“Combining heterogeneous studies using the random-effects model is a mistake and leads to inconclusive meta-analyses”

Suhail A. R. Doi
Clinical Epidemiology Unit
SPH, UQ

What is a meta-analysis?

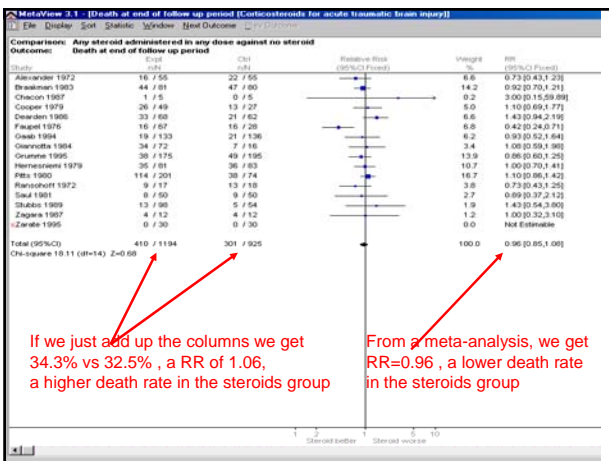
A weighted average of the effects in the trials under consideration
 This means that instead of each of the studies contributing equally to the final average, some studies contribute more than others
 Normalized weights are used (weights summing to 1)
 In a fixed effects approach this assumes of course that trials are exchangeable

The Inverse Variance Weight

Studies generally vary in size.
 An ES based on 100 subjects is assumed to be a more “precise” estimate of the population ES than is an ES based on 10 subjects.
 Therefore, larger studies should carry more “weight” in our analyses than smaller studies.
 Simple approach: weight each ES by its sample size.
 Better approach: weight by the inverse variance.

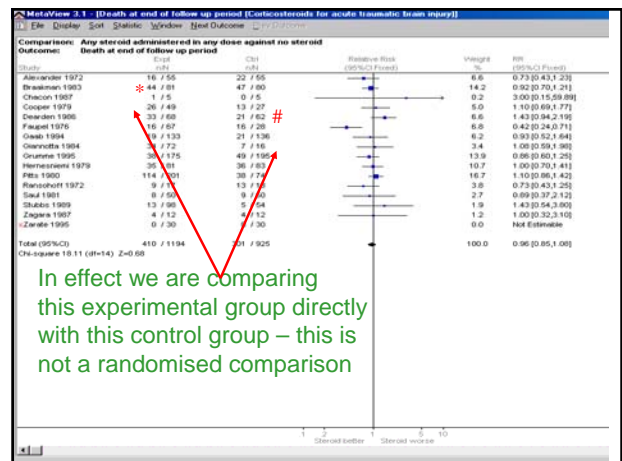
Could we just add the data from all the trials together?

One approach to combining trials would be to add all the treatment groups together, add all the control groups together, and compare the totals
 This is wrong for several reasons, and it can give the wrong answer
 This is because imbalances between trials may produce bias



If we just add up the columns we get 34.3% vs 32.5% , a RR of 1.06, a higher death rate in the steroids group

From a meta-analysis, we get RR=0.96 , a lower death rate in the steroids group



In effect we are comparing this experimental group directly with this control group – this is not a randomised comparison

Closer look at the Inverse Variance Weight

The standard error (SE) is a direct index of ES precision.
 SE is used to create confidence intervals.
 The smaller the SE, the more precise the ES.
 Hedges' showed that the optimal weights for meta-analysis are:

$$w = \frac{1}{SE^2}$$

Inverse Variance Weight for the Major Effect Sizes

Logged Odds-Ratio:

$$se = \sqrt{\frac{1}{a} + \frac{1}{b} + \frac{1}{c} + \frac{1}{d}} \quad w = \frac{1}{se^2}$$

Where a, b, c, and d are the cell frequencies of a 2 by 2 contingency table.

Logged RR:

$$se = \sqrt{\frac{(1-P_r)}{P_r n_r} + \frac{(1-P_c)}{P_c n_c}} \quad w = \frac{1}{se^2}$$

The Weighted Mean Effect Size

Start with the effect size (ES) and inverse variance weight (w) for 10 studies.

Study	ES	w
1	-0.33	11.91
2	0.32	28.57
3	0.39	58.82
4	0.31	29.41
5	0.17	13.89
6	0.64	8.55
7	-0.33	9.80
8	0.15	10.75
9	-0.02	83.33
10	0.00	14.93

$$\overline{ES} = \frac{\sum (w \times ES)}{\sum w}$$

The Standard Error of the Mean ES

The standard error of the mean is the square root of 1 divided by the sum of the weights.

Study	ES	w	w*ES
1	-0.33	11.91	-3.93
2	0.32	28.57	9.14
3	0.39	58.82	22.94
4	0.31	29.41	9.12
5	0.17	13.89	2.36
6	0.64	8.55	5.47
7	-0.33	9.80	-3.24
8	0.15	10.75	1.61
9	-0.02	83.33	-1.67
10	0.00	14.93	0.00
		269.96	41.82

$$se_{ES} = \sqrt{\frac{1}{\sum w}} = \sqrt{\frac{1}{269.96}} = 0.061$$

Homogeneity Analysis

Homogeneity analysis may test

- H0_a: treatment effect is zero AND identical in every trial.
- H0_b: treatment effect is identical to the weighted average in every trial

H0_a (according to Senn) is tested by the fixed effects analysis and requires the principle of exchangeability of trials

H0_b is tested using Cochran's Q statistic

H0_b can be rejected regardless of the FE results
 After such rejection:

- if FE is null this means that a large study was null and if not it means that the smaller studies were null.

Two options after H0_b is rejected:

- model between study differences
- fit a random effects model

Why fit a random model

We have rejected H0_b therefore we need to estimate the mean of the distribution of true effects that will tell us what is the likely result of a similar future trial of the type represented by the studies in the meta-analysis

H0_b is tested using

$$Q = \sum w_i (T_i - \bar{T})^2,$$

Where T is the treatment effect in each trial and \bar{T} is the fixed effect inverse variance weighted estimate.

Random Effects Models

Total Q is significant and you assume that the excess variability across effect sizes derives from random differences across studies (sources you **have not** identified or measured – this is different from sources you **cannot** identify or measure)

The Logic of a
Random Effects Model

Random effects model assumes that the variability between effect sizes is due to

sampling error **plus** variability in the population of effects (unique differences in the set of true population effect sizes)

In other words, instability in an effect size is due to subject-level “noise” and true unmeasured differences across studies (that is, each study is estimating a slightly different population effect size)

The Basic Procedure of a
Random Effects Model

Fixed effects model weights each study by the inverse of the sampling variance.

$$w_i = \frac{1}{se_i^2}$$

Random effects model weights each study by the inverse of the sampling variance **plus** a constant that represents the variability across the population effects.

$$w_i = \frac{1}{se_i^2 + \tau^2}$$

This is the random effects variance component.

How To Estimate the Random
Effects Variance Component

The random effects variance component is based on Q.

The formula is:

$$\tau^2 = \frac{Q_T - (k - 1)}{c}$$

Rerun Analysis with New
Inverse Variance Weight

Add the random effects variance component to the variance associated with each ES.

$$w_i = \frac{1}{se_i^2 + \tau^2}$$

Calculate a new weight.

Rerun analysis.

A very complex statistical analysis is done.

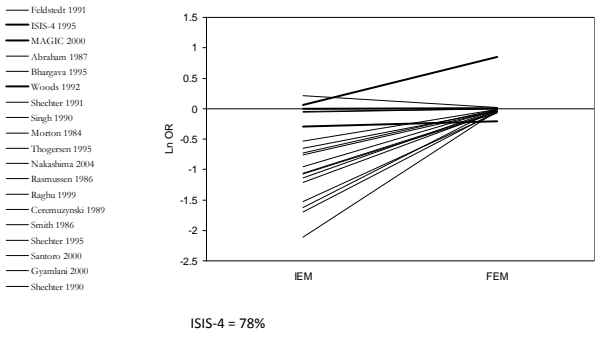
Comparison of Random Effect with Fixed Effect Results

The biggest difference you will notice is in the significance levels and confidence intervals.
 Confidence intervals will get bigger.
 Effects that were significant under a fixed effect model may no longer be significant.
 Random effects models are therefore more conservative **sometimes**.
 Unfortunately, because of the random nature of the random model, this may not necessarily be true

Example 1

Start off with a heterogenous group of studies and run a fixed effect analysis

OR 1.01 (95% CI 0.96-1.07)



Example 2

Start off with a homogenous group of studies and create heterogeneity

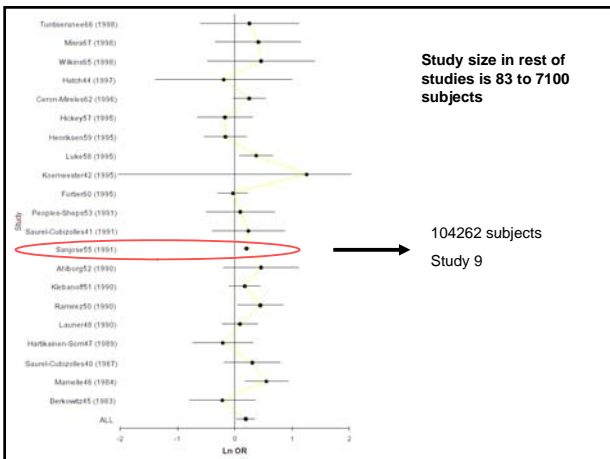


Figure 1

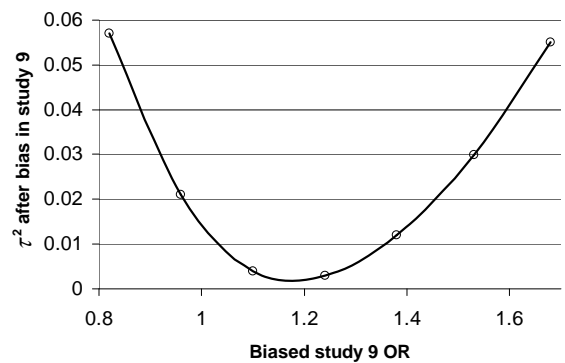


Figure 2

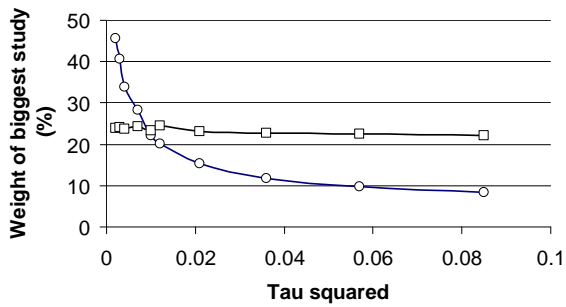


Figure 3

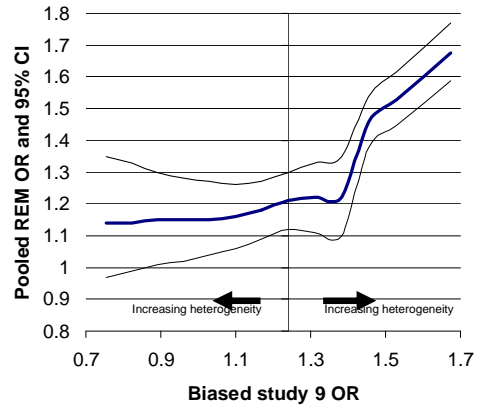


Figure 7

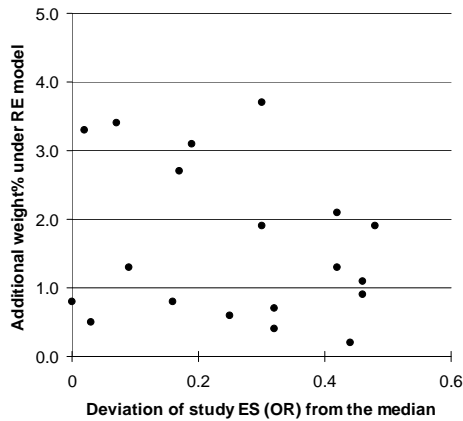
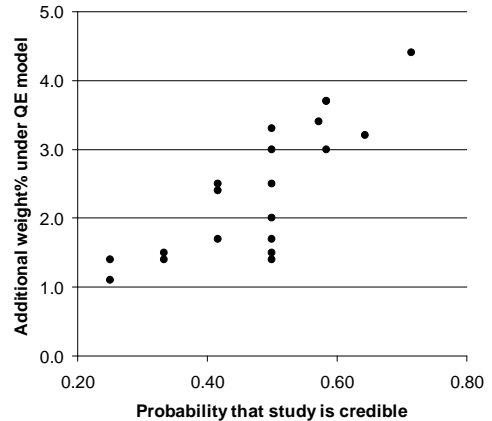


Figure 8



Comparison of Random Effect with Fixed Effect Results

Even the random effects method, when used in a meta-analysis of badly designed studies, will still result in bad statistics even though there is adjustment for heterogeneity.

Furthermore, such adjustments, based on an artificially inflated variance, lead to a widened confidence interval, supposedly to reflect heterogeneity, but do not have much clinical relevance.

Comparison of Random Effect with Fixed Effect Results

One of the reasons for inter-study differences is the quality of individual studies

If the quality of the primary material is inadequate, this may falsify the conclusions of the review, regardless of the random-effects model.

Clinical studies may become corrupted accidentally or deliberately,

- in the randomization process,
- in the masking to the allocated treatment,
- in the random generation of number sequences,
- in the analysis.

The need for analysis of the quality of these studies has become obvious and becomes more important than just inserting a random term based on heterogeneity.

Conclusion

Weighting studies: Random Effect

Choice of model entails a judgement of how much weight should be accorded to a trial by virtue of its numbers and effect size alone.

Random effects meta-analysis will award relatively more weight to smaller studies than such studies would receive in a fixed effect meta-analysis.

if results of smaller studies are systematically different from results of larger ones, (publication bias or low study quality bias) then a random effects meta-analysis will exacerbate the effects of the bias.

Alternatively if the large study is biased, then the random effects meta-analysis will exacerbate the effects of the bias.

If neither is biased, the random and fixed models will give the same results