

# The Software Comprehensive Meta-Analysis Needs to Be Upgraded Further: Letter to the Editors

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Dear editor,

The software comprehensive meta-analysis (CMA) is a good and easy to use software for researchers in order to perform their meta-analyses. This, is the beneficial point of this software in comparison to the others. But there are still some criticisms made us to write this letter.

Chi-square is a highly using statistical test in medical studies. Since a meta-analysis has 2 favours (positive and negative studies), the chi-square used in meta-analyses is always 2 by 2. Hence its low degree of freedom intend us to use Yate's correction. Other than the Yate's correction, some studies imported in a meta-analysis run into very low expected amounts for their contingency tables requiring us to use Fisher's exact test. Nevertheless, the software does not cover Yate's correction and Fisher's exact test even the latest version ([https://www.meta-analysis.com/pages/new\\_v3.php](https://www.meta-analysis.com/pages/new_v3.php)). Thus we were supposed to use for our previous meta-analyses [1, 2] the effect size format "chi-squared and total sample size" (figure 1) instead of "exposed and unexposed cases and controls" (figure 2). Figures 3 and 4 show that the formats "unmatched groups, retrospective" perform the analysis of chi-square without Yate's correction, and the worse, without any error for studies requiring Fisher's exact test. In another forest plot (figure 5) we compared a hypothetical study with a sample size of 100 in two conditions of with and without Yate's correction (studies B and C) with the significance level of a 100-populated study which is at significance level 0.05 (study A).

In spite of the high importance of Fisher's exact test [3], there is no format in CMA for calculation of effect size through it. Thus researchers are supposed to use the format "P value and sample size" in such cases (figure 6). This p value should be calculated through another software like SPSS. The new feature of CMA version 2 was that we could analyse studies having different statistical analyses in one meta-graph. Therefore in some cases needed both chi-square and Fisher's exact test, we can perform different formats. We suggest the options of Yate's correction and Fisher's exact test for the future versions of CMA.

FIGURE 1. Effect size formats of the software.

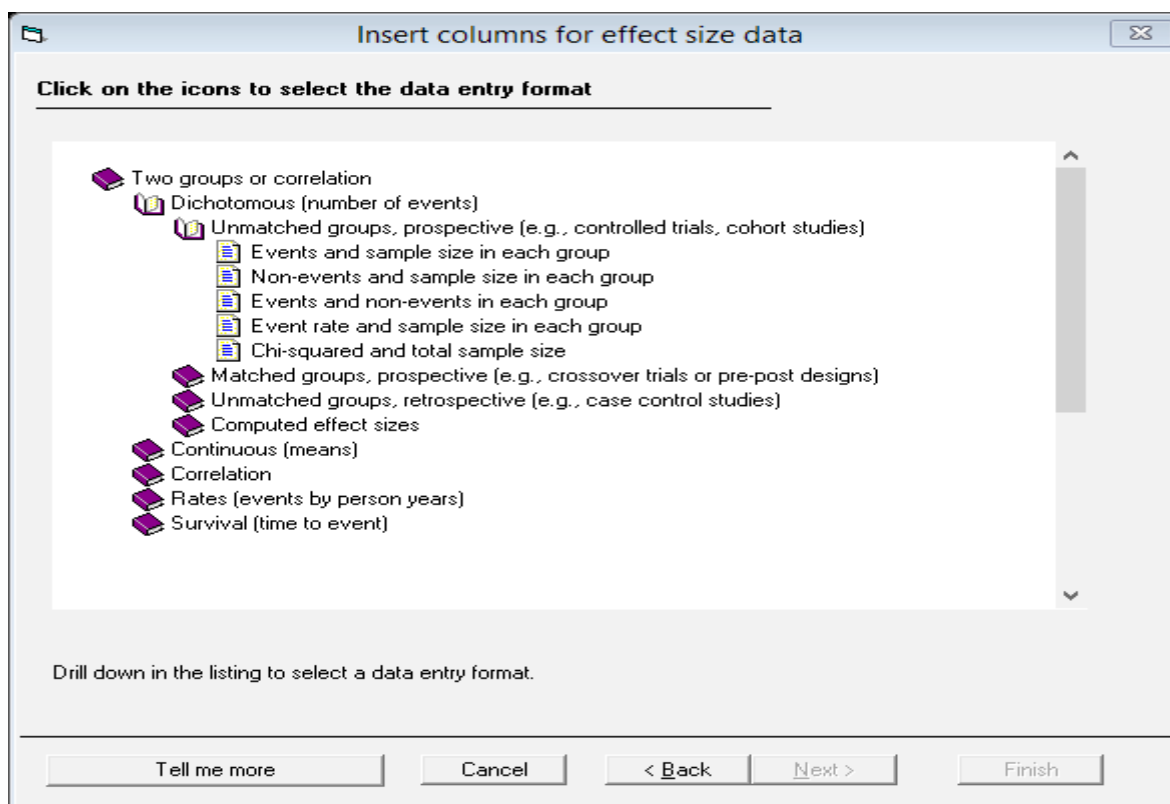


FIGURE 2. Effect size formats of the software.

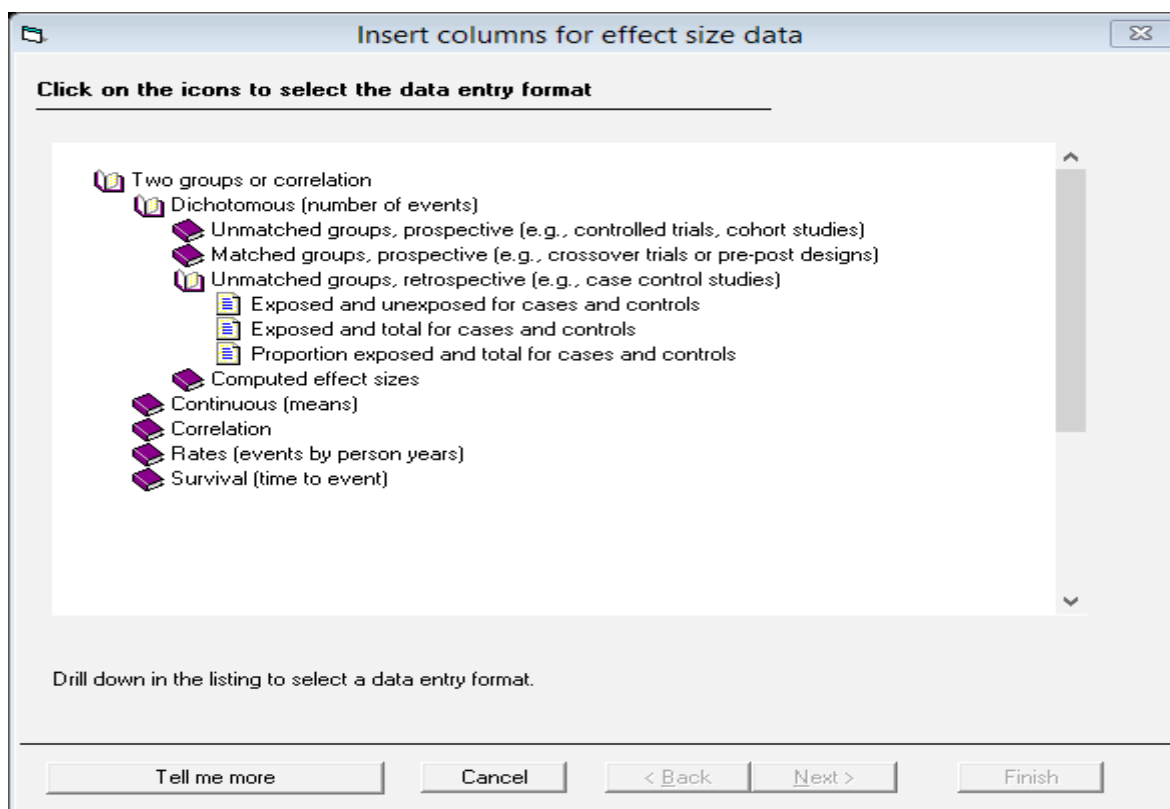


FIGURE 3. Studies A and C are the same; but Data formats are different.

Comprehensive meta								
File Edit Format View Insert Identify Tools Computational options Analyses Help								
Run analyses →								
	Study name	Data format	Chi Squared	Total N	Effect direction	Odds ratio	Log odds ratio	Std Err
1	A	Case control 2x2 (Exp/Total)				1/714	0/539	0/332
2	B	Case control 2x2 (Exp/Total)				0/778	0/251	0/318
3	C	Chi-squared for 2x2	2/160	100	Positive	1/714	0/539	0/372
4								
5								

FIGURE 4. Forest plot of figure 3. Lack of Yate's correction in study A results in a lower P value.

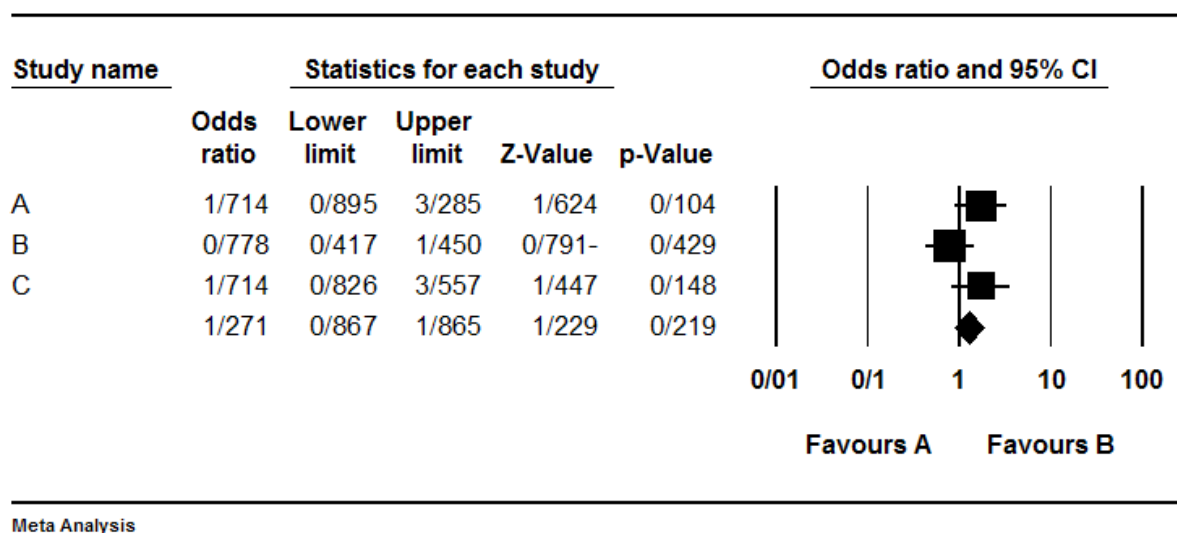
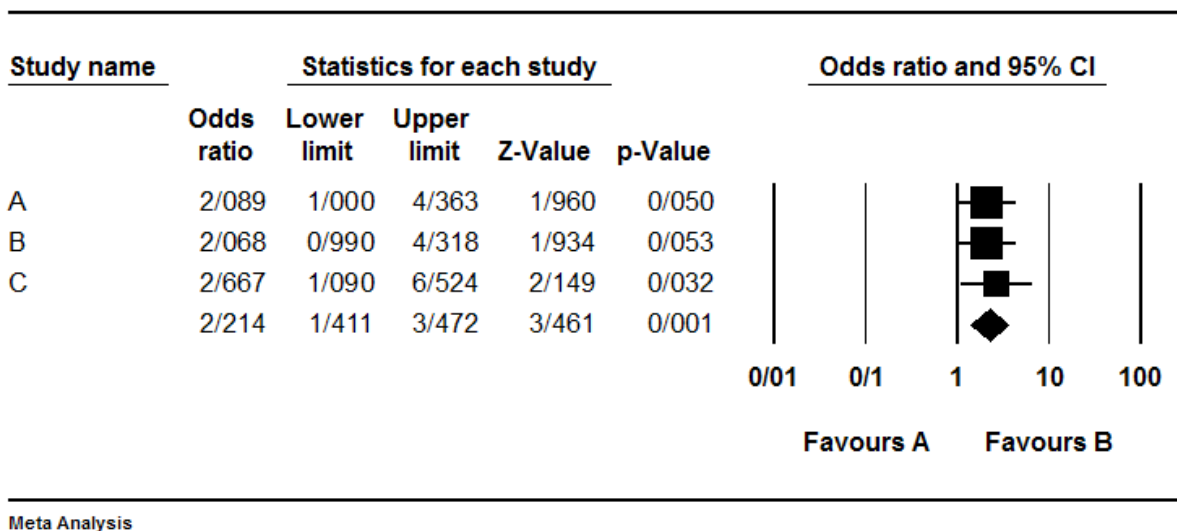
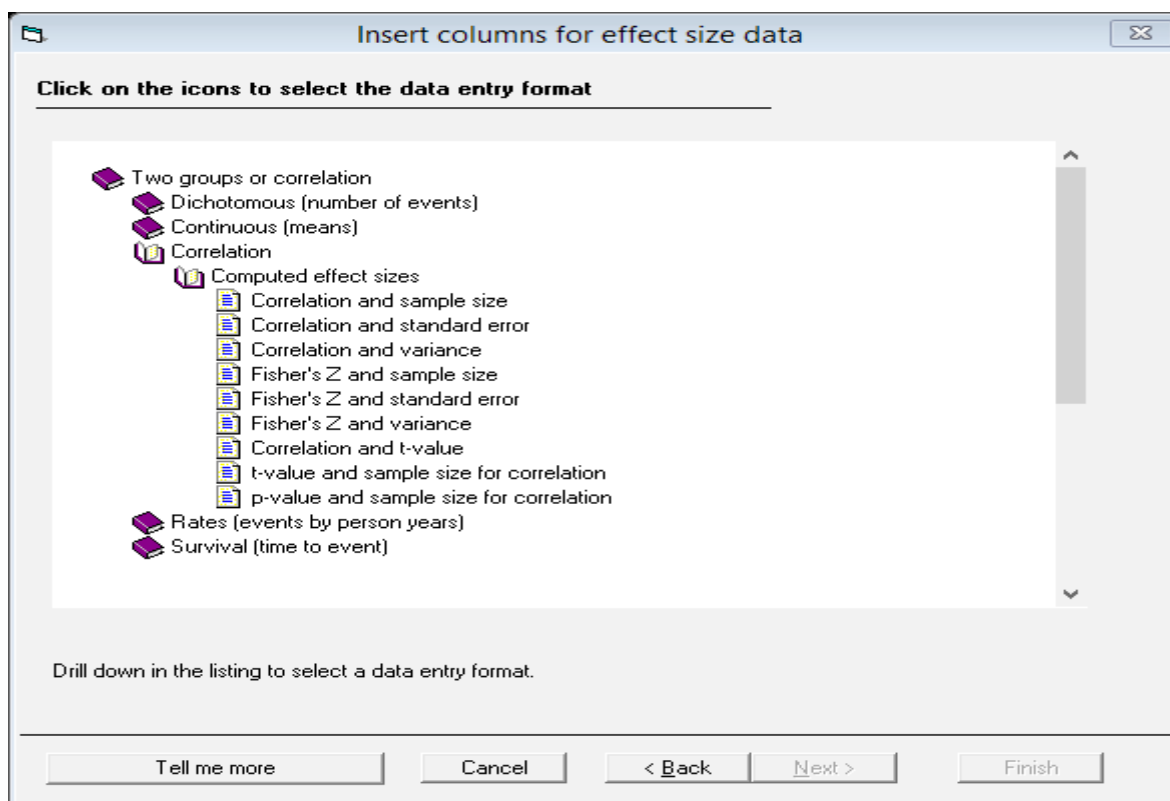


FIGURE 5. Although using Yate's correction does not impact on odds ratio, but the format "chi-squared and total sample size" requires a computed chi-square (effect size) computed by another software in which we used Yate's correction. So the different odds ratios in this figure is due to under-estimation of the software. Of course such under-estimated odds ratio are more reliable and a kind of statistical correction.



**FIGURE 6.** Although the format “P value and sample size for correlation” is usually for parametric tests, but odds ratio can be estimated automatically.



### References:

1. Ghanadi K, Shayanrad B, Ahmadi SAY, Shahsavari F, Eliasy H. Colorectal cancer and the KIR genes in the human genome: A meta-analysis. *Genomics Data*. 2016;10:118-26.
2. Shahsavari F, Mapar S, Ahmadi SAY. Multiple sclerosis is accompanied by lack of KIR2DS1 gene: A meta-analysis. *Genomics Data*. 2016;10:75-8.
3. Härmäläinen W. New upper bounds for tight and fast approximation of Fisher's exact test in dependency rule mining. *Computational Statistics & Data Analysis*. 2016;93:469-82.

