# Package 'metacor'

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Type Package
<b>Title</b> Meta-Analytic Effect Size Calculation for Pre-Post Designs with Correlation Imputation
Version 1.1.1
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<b>Description</b> Tools for the calculation of effect sizes (standardised mean difference) and mean difference in pre-post controlled studies, including robust imputation of missing variances (standard deviation of changes) and correlations (Pearson correlation coefficient). The main function metacor_dual() implements several methods for imputing missing standard deviation of changes or Pearson correlation coefficient, and generates transparent imputation reports. Designed for meta-analyses with incomplete summary statistics. For more details on the methods, see Higgins et al. (2023) and Fu et al. (2013).
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Encoding UTF-8
RoxygenNote 7.3.2
Imports officer, stringr, stats
Suggests knitr, rmarkdown
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metacor_dual	Effect Sizes and Imputation for Meta-Analysis of Pre-Post Studies and
	Pre-Post intervention and control groups studies (metacor_dual)

## Description

Calculates effect sizes (i.e., SMDpre, SMDchange, ScMDpooled, ScMDpre) and allows for various imputation methods (i.e., none, cv, direct, mean) for missing SDdiff and correlation coefficients in pre-post meta-analyses, with or without a control group. Generates a detailed imputation report in Word format.

## Usage

```
metacor_dual(
    df,
    digits = NULL,
    add_to_df = TRUE,
    method = "both",
    apply_hedges = TRUE,
    SMD_method = "SMDpre",
    MeanDifferences = FALSE,
    impute_method = "none",
    verbose = TRUE,
    report_imputations = FALSE,
    custom_sd_diff_int = NULL,
    custom_sd_diff_con = NULL,
    single_group = FALSE
)
```

### Arguments

df	Data frame with the necessary columns for intervention and (optionally) control groups.	
digits	Number of decimal places to round results (default: NULL).	
add_to_df	Logical. If TRUE, results are added to the original data frame.	
method	Method for SDdiff calculation (i.e., 'p_value', 'ci', 'both').	
apply_hedges	Logical. Apply Hedges' g correction? (default: TRUE)	
SMD_method	Method for effect size (i.e., 'SMDpre', 'SMDchange', 'ScMDpooled', 'ScMDpre').	
MeanDifferences		
	Logical. Calculate mean differences and variances? (default: FALSE)	
<pre>impute_method</pre>	Imputation method for missing SDdiff (i.e., 'none', 'direct', 'mean', 'cv').	
verbose	Logical. Print messages during processing? (default: TRUE)	
report_imputations		
	Logical. Generate Word imputation report? (default: FALSE)	

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```
custom_sd_diff_int
List with elements 'row' and 'value' for manual sd_diff_int values.

custom_sd_diff_con
List with elements 'row' and 'value' for manual sd_diff_con values.

single_group Logical. Is the design single-group only? (default: FALSE)
```

#### Value

Data frame with calculated variables. Optionally, a Word report ('imputation\_report.docx') is generated.

#### References

Higgins, J. P. T., Thomas, J., Chandler, J., Cumpston, M., Li, T., Page, M. J., & Welch, V. A. (Eds.). (2023). Cochrane handbook for systematic reviews of interventions (Version 6.3). Cochrane. https://training.cochrane.org/handbook Fu, R., Vandermeer, B.W., Shamliyan, T.A., ONeil, M.E., Yazdi, F., Fox, S.H., & Morton, S.C. (2013). Handling Continuous Outcomes in Quantitative Synthesis. Methods Guide for Comparative Effectiveness Reviews. AHRQ Publication No. 13-EHC103-EF. https://effectivehealthcare.ahrq.gov/reports/final.cfm

#### **Examples**

```
df <- data.frame(
    study_name = c("Study1", "Study2", "Study3", "Study4",
    "Study5", "Study6", "Study7", "Study8", "Study9"),
    p_value_Int = c(1.038814e-07, NA, NA, NA, NA, 2.100000e-02, NA, NA, NA),
    n_Int = c(10, 10, 10, 10, 15, 15, 10, 10, 10),
    meanPre_Int = c(8.17, 10.09, 10.18, 9.85, 9.51, 7.70, 10.00, 11.53, 11.20),
    meanPost_Int = c(10.12, 12.50, 12.56, 10.41, 10.88, 9.20, 10.80, 13.42, 12.00),
    sd_pre_Int = c(1.83, 0.67, 0.66, 0.90, 0.62, 0.90, 0.70, 0.60, 1.90),
    sd_post_Int = c(1.85, 0.72, 0.97, 0.67, 0.76, 1.10, 0.70, 0.80, 1.80),
    upperCI_Int = c(NA, NA, NA, NA, NA, NA, NA, NA, NA),
    lowerCI_Int = c(NA, NA, NA, NA, NA, NA, NA, NA, NA))
    result <- metacor_dual(df)
    print(result)</pre>
```

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