

# Meta\_analysis

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```
# Set your file path (update if necessary)
data_path <- "C:/Users/HomePC/OneDrive/Desktop/new statya/icg_meta_analysis_ready.csv"

# Load data
df <- read_csv(data_path)
```

```
## Rows: 5 Columns: 10
## -- Column specification -----
## Delimiter: ","
## chr (2): file, title
## dbl (8): year, sample_size_icg, sample_size_control, ln_mean_icg, ln_sd_icg,...
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
# View a quick summary (optional)
print(head(df))
```

```
## # A tibble: 5 x 10
##   file      title  year sample_size_icg sample_size_control ln_mean_icg ln_sd_icg
##   <chr>    <chr> <dbl>         <dbl>             <dbl>      <dbl>
## 1 1_cjcr~ Adva~  2022             30                NA         NA
## 2 1_curre~ and ~  2024             0                0         NA
## 3 1_jgc-1~ 145   2017             NA                NA        55.9
## 4 1_jgc-2~ 290   2020             2                 2        239.
## 5 1_s4146~ Arti~  2023            258            258        50.5
## # i 3 more variables: ln_mean_control <dbl>, ln_sd_control <dbl>, p_value <dbl>
```

```
# Perform meta-analysis using metacont (mean difference of lymph nodes retrieved)
meta_ln <- metacont(
  n.e = sample_size_icg,
  mean.e = ln_mean_icg,
  sd.e = ln_sd_icg,
  n.c = sample_size_control,
  mean.c = ln_mean_control,
  sd.c = ln_sd_control,
  data = df,
  studlab = file,
  sm = "MD", # MD = Mean Difference
  method.tau = "DL", # DerSimonian-Laird (random effects)
```

```

hahn = TRUE          # Use Hartung-Knapp adjustment
)

## Warning: Use argument 'method.random.ci' instead of 'hahn' (deprecated).

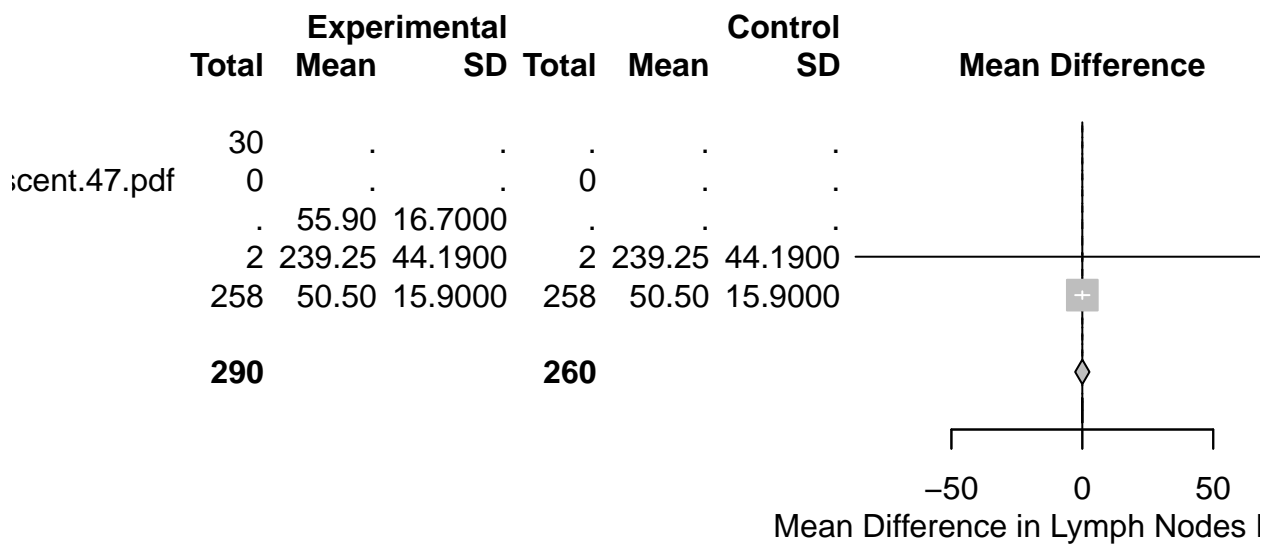
## Warning in metacont(n.e = sample_size_icg, mean.e = ln_mean_icg, sd.e =
## ln_sd_icg, : Note, studies with non-positive values for n.e and / or n.c get no
## weight in meta-analysis.

# Summary of meta-analysis
summary(meta_ln)

##
##
## MD
## 1_cjcr-34-6-587.pdf NA
## 1_current_status_of_indocyanine_green_fluorescent.47.pdf NA
## 1_jgc-17-145.pdf NA
## 1_jgc-20-290.pdf 0.0000
## 1_s41467-023-42712-6.pdf 0.0000
##
## 95%-CI
## 1_cjcr-34-6-587.pdf
## 1_current_status_of_indocyanine_green_fluorescent.47.pdf
## 1_jgc-17-145.pdf
## 1_jgc-20-290.pdf [-86.6108; 86.6108]
## 1_s41467-023-42712-6.pdf [-2.7438; 2.7438]
##
## %W(common) %W(random)
## 1_cjcr-34-6-587.pdf 0.0 0.0
## 1_current_status_of_indocyanine_green_fluorescent.47.pdf 0.0 0.0
## 1_jgc-17-145.pdf 0.0 0.0
## 1_jgc-20-290.pdf 0.1 0.1
## 1_s41467-023-42712-6.pdf 99.9 99.9
##
## Number of studies: k = 2
## Number of observations: o = 550 (o.e = 290, o.c = 260)
##
## MD 95%-CI z|t p-value
## Common effect model 0.0000 [-2.7424; 2.7424] 0.00 1.0000
## Random effects model 0.0000 [ 0.0000; 0.0000] -- --
##
## Quantifying heterogeneity:
## tau^2 = 0; tau = 0; I^2 = 0.0%; H = 1.00
##
## Test of heterogeneity:
## Q d.f. p-value
## 0.00 1 1.0000
##
## Details of meta-analysis methods:
## - Inverse variance method
## - DerSimonian-Laird estimator for tau^2
## - Calculation of I^2 based on Q
## - Hartung-Knapp adjustment for random effects model (df = 1)

```

```
# Forest plot
forest(meta_ln,
  xlab = "Mean Difference in Lymph Nodes Retrieved",
  leftlabs = c("Study", "ICG (n)", "Control (n)"),
  rightlabs = c("Mean Diff", "95% CI"),
  colgap.forest.left = "2mm",
  digits = 2)
```



```
# Funnel plot to assess publication bias
funnel(meta_ln,
  xlab = "Mean Difference",
  ylab = "Standard Error",
  main = "Funnel Plot")
```

# Funnel Plot

