Compute Meta-analysis *Breakdown*

# Inputs

|  |  |
| --- | --- |
| Association Outputs | A screenshot of a cell phone  Description automatically generated |

(There are more than 4 features (columns), it continues on…)

The other two inputs are, 2. The name of the output RDS and 3. The name of the column (within model selected df) that is what we’re interested in researching about. In this example, the column is named “study\_condition” and is either a 1 or 0

# Code

All in all, this is a really simple script that shouldn’t be too hard to figure out.

run\_metaanalysis = "FALSE"

if(nrow(association\_outputs)>1){

run\_metaanalysis = "TRUE"

}

This code looks at the association\_outputs (our input file, see table above) and checks to see if there’s more than one line. If there’s just one line, we won’t have to do a meta-analysis because there’s only one dataset (cohort) that we’re looking at.

if (run\_metaanalysis == "TRUE") {

output <- compute\_metaanalysis(get\_metaanalysis\_dfs(association\_outputs,column\_of\_interest))

saveRDS(output,

outputname)

} else if (run\_metaanalysis == "FALSE") {

output <- get\_metaanalysis\_dfs(association\_outputs,column\_of\_interest)

saveRDS(output,

outputname)

}



This is the “main driver” of the code. Assuming we have more than one cohort, we will run the compute\_metaanlysis code which has get\_metaanlysis\_dfs nested inside of it.’

# Output

The output is a simple tibble where the columns refer to the features and there is just one row. For each feature, there has been a regression calculated that takes all the cohorts into account.

|  |  |
| --- | --- |
| CRC\_example\_meta\_analysis.rds |  |

This is what the cell looks like in row 1 (the only row) of column 1, “feature\_2”

SMD 95%-CI %W(random)

FengQ\_2015 -0.0792 [-0.5671; 0.4087] 6.5

HanniganGD\_2017 -0.0953 [-0.6494; 0.4589] 5.0

ThomasAM\_2018a 0.0833 [-0.2135; 0.3801] 17.5

ThomasAM\_2018b 0.1209 [-0.2934; 0.5353] 9.0

VogtmannE\_2016 0.1400 [-0.1375; 0.4175] 20.0

YuJ\_2015 -0.1543 [-0.3992; 0.0906] 25.7

ZellerG\_2014 -0.0695 [-0.3755; 0.2366] 16.4

Number of studies combined: k = 7

SMD 95%-CI z p-value

Random effects model -0.0075 [-0.1316; 0.1165] -0.12 0.9053

Prediction interval [-0.1702; 0.1552]

Quantifying heterogeneity:

tau^2 = 0 [0.0000; 0.0406]; tau = 0 [0.0000; 0.2015];

I^2 = 0.0% [0.0%; 50.4%]; H = 1.00 [1.00; 1.42]

Test of heterogeneity:

Q d.f. p-value

3.53 6 0.7397

Details on meta-analytical method:

- Inverse variance method

- Restricted maximum-likelihood estimator for tau^2

- Q-profile method for confidence interval of tau^2 and tau