META-ANALYSIS USING METAL

Guides can be found here: [*METAL Documentation - Genome Analysis Wiki (umich.edu)*](https://genome.sph.umich.edu/wiki/METAL_Documentation)

**STEP 1**

**Run the following command:**

/emc/cbmr/METAL/generic-metal> /emc/cbmr/METAL/generic-metal/metal

**STEP2  
The following script can be used to meta-analyse 2 studies that have been previously curated.**

* Note that the curated files are separated by commas.
  + If other separator has been used change the 1st line to WHITESPACE or TAB.
* Describe and process input file:
  + Requires that you change the names on the right to your column names
* Process
  + You need to process as many files as you want to meta-analyse (in this example 2)
  + If the files have different column names you will need to describe the second file column names before processing it. In this case, both files have the same column names so that describing the columns for file 2 is not needed
* Indicate your output file
* Type ANALYZE
* Quit the program once it has run

#THIS SCRIPT EXECUTES AN ANALYSIS OF TWO STUDIES

SEPARATOR COMMA

# UNCOMMENT THE NEXT LINE TO ENABLE GenomicControl CORRECTION

# GENOMICCONTROL ON

# === DESCRIBE AND PROCESS THE FIRST INPUT FILE ===

MARKER variant

ALLELE effect\_allele other\_allele

EFFECT beta

PVALUE p\_value

WEIGHT sample\_size

PROCESS /emc/cbmr/users/wfs758/smoking\_project/data/curated\_data/estradiol\_female.txt

# === THE SECOND INPUT FILE HAS THE SAME FORMAT AND CAN BE PROCESSED IMMEDIATELY ===

PROCESS /emc/cbmr/users/wfs758/smoking\_project/data/curated\_data/estradiol\_male.txt

# === CARRY OUT AN INTERIM ANALYSIS OF THE TWO FILES ===

OUTFILE /emc/cbmr/users/wfs758/smoking\_project/data/metaanalysis\_data/METAANALYSIS\_estradiol\_ .tbl

ANALYZE

QUIT

**STEP3 – extra settings  
These are some “extras” you can add while computing your meta-analysis**

* See link on top

**NOTES – FILE OUTPUT INFO**

# This file contains a short description of the columns in the

# meta-analysis summary file, named '/emc/cbmr/users/wfs758/smoking\_project/data/metaanalysis\_data/METAANALYSIS\_estradiol\_1.tbl'

# Marker - this is the marker name

# Allele1 - the first allele for this marker in the first file where it occurs

# Allele2 - the second allele for this marker in the first file where it occurs

# Weight - the sum of the individual study weights (typically, N) for this marker

# Z-score - the combined z-statistic for this marker

# P-value - meta-analysis p-value

# Direction - summary of effect direction for each study, with one '+' or '-' per study

# Input for this meta-analysis was stored in the files:

# --> Input File 1 : /emc/cbmr/users/wfs758/smoking\_project/data/curated\_data/estradiol\_female.txt

# --> Input File 2 : /emc/cbmr/users/wfs758/smoking\_project/data/curated\_data/estradiol\_male.txt

(base) wfs758@porus03:/emc/cbmr/users/wfs758/smoking\_project/data/metaanalysis\_data> cat METAANALYSIS\_estradiol\_1.tbl | head

MarkerName Allele1 Allele2 Weight Zscore P-value Direction

rs2326918 a g 311675.00 -1.350 0.177 -+

rs56252526 a g 311675.00 1.093 0.2744 ++

rs977590 a g 311675.00 0.368 0.7127 +-

rs66941928 t c 311675.00 -0.166 0.8678 +-

rs17278013 t g 311675.00 -1.233 0.2177 --

rs62234673 t c 311675.00 0.760 0.4472 ++

rs7190157 a c 311675.00 -1.030 0.3031 -+

rs12364336 a g 311675.00 0.818 0.4134 ++

rs6977693 t c 311675.00 0.845 0.398 +-