Practical 4 Solutions: Detecting inconsistency in network meta-analysis

Course on network meta-analysis, Kea, Greece

## R packages

We will use the package **readxl** to import excel data and the packages **netmeta** to run network meta-analyses.

library(readxl)  
library(netmeta)

## Datasets

We will use the Acute mania and Schizophrenia datasets. Load the data by running the following commands.

AcuteMania = read\_excel("AcuteMania.xls")  
AcuteMania = as.data.frame(AcuteMania)

Leucht = read\_excel("Leucht.xls")  
Leucht = as.data.frame(Leucht)

## Network meta-analyses

Run the following R commands to fit a network meta-analysis model to each dataset.

AcuteManiaPair = pairwise(treat = treatment, event = r, n = n,  
 data = AcuteMania, studlab = studyid, sm = "OR")  
net1 = netmeta(AcuteManiaPair, ref = "PLA", comb.fixed = FALSE, comb.random = TRUE)

net3 = netmeta(effect, se, treat1, treat2, study, data = Leucht,  
 sm = "SMD", ref = "PBO", comb.fixed = FALSE, comb.random = TRUE,  
 tol.multiarm = 0.075)

## Inconsistency evaluation in acute mania dataset

First, you can print the number of designs:

net1$d

## [1] 30

and the list of all designs:

designs1 = as.character(decomp.design(net1)$Q.het.design$design)  
designs1

## [1] "ARI:HAL" "CARB:DIV" "CARB:HAL" "DIV:LITH"   
## [5] "DIV:OLA" "HAL:OLA" "LAM:LITH" "LITH:OLA"   
## [9] "LITH:QUE" "OLA:RIS" "PLA:ARI" "PLA:CARB"   
## [13] "PLA:DIV" "PLA:OLA" "PLA:PAL" "PLA:QUE"   
## [17] "PLA:RIS" "PLA:TOP" "PLA:ZIP" "PLA:ARI:HAL"   
## [21] "PLA:ARI:LITH" "PLA:ASE:OLA" "PLA:DIV:LITH" "PLA:DIV:OLA"   
## [25] "PLA:HAL:OLA" "PLA:HAL:QUE" "PLA:HAL:RIS" "PLA:HAL:ZIP"   
## [29] "PLA:LITH:QUE" "PLA:PAL:QUE"

Are there any multi-arm studies in the networks?

We see that the acute mania dataset contains 30 designs of which 11 are three-arm designs.

Next, we apply the back-calculation method for assessing local inconsistency. Run the following code to print the results for the random effects model.

split1 = netsplit(net1)   
print(split1, showall = FALSE, digits = 2)

## Random effects model:   
##   
## comparison k prop nma direct indir. RoR z p-value  
## ARI:HAL 2 0.46 0.88 1.16 0.70 1.65 1.48 0.1398  
## ARI:LITH 1 0.34 1.13 1.09 1.15 0.95 -0.12 0.9044  
## ARI:PLA 6 0.83 1.99 1.77 3.55 0.50 -1.93 0.0534  
## ASE:OLA 1 0.82 0.78 0.69 1.37 0.50 -0.85 0.3938  
## ASE:PLA 1 0.67 1.69 2.04 1.15 1.78 0.85 0.3938  
## CARB:DIV 1 0.16 1.25 0.42 1.55 0.27 -1.46 0.1455  
## CARB:HAL 1 0.11 1.10 0.80 1.14 0.70 -0.33 0.7415  
## CARB:PLA 1 0.78 2.47 3.10 1.10 2.83 1.41 0.1579  
## DIV:LITH 2 0.25 1.12 0.78 1.25 0.62 -0.90 0.3704  
## DIV:OLA 2 0.48 0.91 0.77 1.06 0.73 -0.89 0.3712  
## DIV:PLA 5 0.70 1.98 2.16 1.60 1.35 0.85 0.3955  
## HAL:OLA 2 0.31 1.03 1.21 0.97 1.25 0.62 0.5363  
## HAL:PLA 5 0.57 2.25 2.26 2.24 1.01 0.03 0.9753  
## HAL:QUE 1 0.23 1.16 1.72 1.03 1.66 1.12 0.2612  
## HAL:RIS 1 0.31 0.95 0.95 0.96 0.99 -0.01 0.9902  
## HAL:ZIP 1 0.32 1.64 2.05 1.48 1.38 0.76 0.4468  
## LITH:OLA 2 0.20 0.81 0.62 0.87 0.72 -0.67 0.5050  
## LITH:PLA 3 0.56 1.77 2.28 1.28 1.78 1.60 0.1100  
## LITH:QUE 2 0.47 0.91 0.70 1.15 0.61 -1.22 0.2242  
## OLA:PLA 8 0.67 2.18 1.90 2.89 0.66 -1.66 0.0971  
## OLA:RIS 1 0.28 0.92 1.20 0.83 1.45 0.89 0.3750  
## PAL:PLA 2 0.85 1.72 1.57 2.85 0.55 -0.92 0.3601  
## PAL:QUE 1 0.53 0.89 1.25 0.60 2.08 1.47 0.1426  
## QUE:PLA 6 0.83 1.94 1.98 1.77 1.12 0.29 0.7724  
## RIS:PLA 4 0.74 2.36 2.51 1.99 1.26 0.60 0.5503  
## ZIP:PLA 5 0.91 1.37 1.48 0.63 2.33 1.46 0.1447  
##   
## Legend:  
## comparison - Treatment comparison  
## k - Number of studies providing direct evidence  
## prop - Direct evidence proportion  
## nma - Estimated treatment effect (OR) in network meta-analysis  
## direct - Estimated treatment effect (OR) derived from direct evidence  
## indir. - Estimated treatment effect (OR) derived from indirect evidence  
## RoR - Ratio of Ratios (direct versus indirect)  
## z - z-value of test for disagreement (direct versus indirect)  
## p-value - p-value of test for disagreement (direct versus indirect)

How do you interpret the results? Are there any significant discrepancies between the direct and indirect estimates? Are there any treatment comparisons that are particularly inconsistent?

The column ‘RoR’ shows the ratio of odds ratios between direct and indirect. The columns ‘z’, and ‘p-value’ give the results of the corresponding test. Based on the results, there is no pairwise comparison showing large inconsisteny between direct and indirect evidence.

Finally, let us look at the design-by-treatment interaction model.

decomp.design(net1)

## Q statistics to assess homogeneity / consistency  
##   
## Q df p-value  
## Total 88.39 45 0.0001  
## Within designs 33.62 17 0.0094  
## Between designs 54.77 28 0.0018  
##   
## Design-specific decomposition of within-designs Q statistic  
##   
## Design Q df p-value  
## LITH:OLA 2.71 1 0.0995  
## PLA:ARI 7.32 3 0.0623  
## PLA:DIV 3.38 2 0.1842  
## PLA:OLA 6.88 4 0.1426  
## PLA:QUE 1.66 2 0.4350  
## PLA:RIS 6.73 2 0.0345  
## PLA:ZIP 4.93 3 0.1771  
##   
## Between-designs Q statistic after detaching of single designs  
##   
## Detached design Q df p-value  
## ARI:HAL 48.70 27 0.0064  
## CARB:DIV 51.94 27 0.0027  
## CARB:HAL 54.51 27 0.0013  
## DIV:LITH 51.82 27 0.0028  
## DIV:OLA 51.67 27 0.0029  
## HAL:OLA 54.68 27 0.0013  
## LITH:OLA 54.11 27 0.0015  
## LITH:QUE 49.78 27 0.0048  
## OLA:RIS 52.71 27 0.0022  
## PLA:ARI 54.23 27 0.0014  
## PLA:CARB 51.97 27 0.0027  
## PLA:DIV 54.18 27 0.0014  
## PLA:OLA 54.27 27 0.0014  
## PLA:PAL 48.07 27 0.0075  
## PLA:QUE 54.33 27 0.0014  
## PLA:RIS 51.38 27 0.0031  
## PLA:ZIP 54.77 27 0.0012  
## PLA:ARI:HAL 51.92 26 0.0018  
## PLA:ARI:LITH 54.34 26 0.0009  
## PLA:ASE:OLA 53.23 27 0.0019  
## PLA:DIV:LITH 51.82 26 0.0019  
## PLA:DIV:OLA 52.20 26 0.0017  
## PLA:HAL:OLA 50.78 26 0.0025  
## PLA:HAL:QUE 52.09 26 0.0018  
## PLA:HAL:RIS 53.82 26 0.0011  
## PLA:HAL:ZIP 47.87 26 0.0056  
## PLA:LITH:QUE 49.80 26 0.0033  
## PLA:PAL:QUE 47.93 26 0.0055  
##   
## Q statistic to assess consistency under the assumption of  
## a full design-by-treatment interaction random effects model  
##   
## Q df p-value tau.within tau2.within  
## Between designs 28.27 28 0.4503 0.2861 0.0819

The first piece of information in the output regards Q statistics about the total heterogeneity/inconsistency in the network, using a fixed-effects NMA model. Is there evidence of heterogeneity within designs?

The overall Q statistics shows evidence of within-design heterogeneity.

Now look at the second piece of information in the output. Which individual comparison contributes most to the within-design heterogeneity?

The comparison ‘PLA:OLA’ contributes most to the within-design heterogenity.

The third piece of information shows the inconsistency of the network after detaching each design. Based on this information, which designs do you think contribute the most to the between-design inconsistency?

The designs ‘ARI:HAL’ and ‘PLA:PAL’ have the largest p-values for the between-designs Q statistic after detaching a single design. This implies that after detaching these designs, the remaining network is more consistent. Accordingly, these two designs contribute the most to the inconsistency in the network.

Based on the last piece of information in the output, is there any residual inconsistency left in the network after allowing for a full design by treatment interaction model?

No residual inconsistency remains after allowing for a full design by treatment interaction model.

## Inconsistency evaluation in schizophrenia dataset

Again, we print the number of designs

net3$d

## [1] 63

and the list of all designs

designs3 = as.character(decomp.design(net3)$Q.het.design$design)  
designs3

## [1] "AMI:HAL" "AMI:OLA" "AMI:RIS"   
## [4] "ARI:HAL" "ARI:OLA" "ARI:RIS"   
## [7] "ARI:ZIP" "ASE:OLA" "CLO:CPZ"   
## [10] "CLO:HAL" "CLO:OLA" "CLO:RIS"   
## [13] "CLO:ZOT" "CPZ:QUE" "HAL:ILO"   
## [16] "HAL:OLA" "HAL:QUE" "HAL:RIS"   
## [19] "HAL:SER" "HAL:ZIP" "HAL:ZOT"   
## [22] "OLA:QUE" "OLA:RIS" "OLA:SER"   
## [25] "OLA:ZIP" "PBO:ARI" "PBO:CPZ"   
## [28] "PBO:HAL" "PBO:LURA" "PBO:OLA"   
## [31] "PBO:pal" "PBO:QUE" "PBO:RIS"   
## [34] "PBO:SER" "PBO:ZIP" "PBO:ZOT"   
## [37] "QUE:RIS" "RIS:SER" "RIS:ZIP"   
## [40] "ARI:OLA:QUE:RIS" "CLO:HAL:OLA" "CLO:HAL:RIS"   
## [43] "OLA:QUE:RIS" "OLA:QUE:RIS:ZIP" "PBO:ARI:HAL"   
## [46] "PBO:ARI:RIS" "PBO:ASE:HAL" "PBO:ASE:OLA"   
## [49] "PBO:ASE:RIS" "PBO:CLO:CPZ" "PBO:CPZ:HAL"   
## [52] "PBO:CPZ:ZOT" "PBO:HAL:ILO" "PBO:HAL:LURA"   
## [55] "PBO:HAL:QUE" "PBO:HAL:RIS" "PBO:HAL:SER"   
## [58] "PBO:HAL:ZIP" "PBO:ILO:RIS" "PBO:ILO:ZIP"   
## [61] "PBO:LURA:OLA" "PBO:LURA:QUE" "PBO:OLA:pal"

We see that the schizophrenia dataset contains 63 designs of which 22 are three-arm designs and 2 are four-arm designs.

Next, we apply the back-calculation method to print the results for the random effects model.

split3 = netsplit(net3)   
print(split3, showall = FALSE, digits = 2)

## Random effects model:   
##   
## comparison k prop nma direct indir. Diff z p-value  
## AMI:HAL 6 0.40 -0.21 -0.30 -0.14 -0.16 -1.33 0.1827  
## AMI:OLA 5 0.37 -0.07 -0.01 -0.10 0.09 0.75 0.4558  
## AMI:RIS 4 0.35 -0.10 -0.05 -0.13 0.08 0.64 0.5253  
## ARI:HAL 4 0.34 0.02 -0.01 0.04 -0.05 -0.48 0.6278  
## ARI:OLA 4 0.36 0.16 0.23 0.11 0.12 1.17 0.2418  
## ARI:PBO 6 0.42 -0.43 -0.44 -0.42 -0.03 -0.28 0.7825  
## ARI:QUE 1 0.03 0.00 0.38 -0.01 0.39 1.14 0.2530  
## ARI:RIS 3 0.17 0.13 0.10 0.13 -0.04 -0.25 0.7990  
## ARI:ZIP 1 0.14 -0.04 -0.16 -0.02 -0.14 -0.80 0.4244  
## ASE:HAL 1 0.18 0.07 -0.02 0.09 -0.11 -0.64 0.5205  
## ASE:OLA 3 0.57 0.21 0.13 0.32 -0.19 -1.43 0.1538  
## ASE:PBO 4 0.58 -0.37 -0.18 -0.64 0.46 3.43 0.0006  
## ASE:RIS 1 0.10 0.18 -0.15 0.22 -0.37 -1.61 0.1078  
## CLO:CPZ 5 0.49 -0.48 -0.42 -0.53 0.11 0.61 0.5421  
## CLO:HAL 8 0.51 -0.40 -0.48 -0.32 -0.16 -1.02 0.3057  
## CLO:OLA 2 0.15 -0.26 0.07 -0.32 0.39 1.71 0.0879  
## CLO:PBO 1 0.02 -0.85 -1.64 -0.83 -0.81 -1.51 0.1299  
## CLO:RIS 2 0.13 -0.29 -0.36 -0.28 -0.08 -0.33 0.7401  
## CLO:ZOT 2 0.27 -0.36 -0.43 -0.33 -0.10 -0.40 0.6868  
## CPZ:HAL 1 0.04 0.08 -0.29 0.09 -0.39 -0.91 0.3640  
## CPZ:PBO 11 0.53 -0.37 -0.39 -0.34 -0.04 -0.26 0.7945  
## CPZ:QUE 1 0.24 0.06 0.05 0.07 -0.02 -0.08 0.9380  
## CPZ:ZOT 1 0.25 0.12 0.76 -0.09 0.85 3.28 0.0011  
## HAL:ILO 4 0.51 -0.12 -0.08 -0.18 0.10 0.94 0.3494  
## HAL:LURA 1 0.13 -0.12 -0.28 -0.10 -0.18 -0.94 0.3468  
## HAL:OLA 11 0.31 0.14 0.14 0.14 0.00 0.04 0.9679  
## HAL:PBO 21 0.42 -0.45 -0.50 -0.41 -0.09 -1.44 0.1491  
## HAL:QUE 4 0.22 -0.02 -0.07 -0.00 -0.07 -0.63 0.5302  
## HAL:RIS 17 0.37 0.11 0.16 0.07 0.09 1.25 0.2111  
## HAL:SER 3 0.53 -0.06 -0.12 0.01 -0.13 -0.95 0.3396  
## HAL:ZIP 3 0.23 -0.05 -0.13 -0.03 -0.09 -0.77 0.4413  
## HAL:ZOT 4 0.45 0.04 -0.09 0.15 -0.24 -1.31 0.1892  
## ILO:PBO 4 0.51 -0.32 -0.26 -0.39 0.13 1.15 0.2493  
## ILO:RIS 2 0.29 0.23 0.29 0.21 0.09 0.69 0.4932  
## ILO:ZIP 1 0.21 0.07 0.02 0.08 -0.06 -0.38 0.7004  
## LURA:OLA 1 0.19 0.26 0.16 0.28 -0.12 -0.71 0.4758  
## LURA:PBO 6 0.82 -0.33 -0.34 -0.29 -0.05 -0.30 0.7621  
## LURA:QUE 1 0.22 0.10 0.17 0.08 0.09 0.50 0.6145  
## OLA:pal 4 0.51 -0.09 -0.06 -0.13 0.07 0.60 0.5514  
## OLA:PBO 14 0.40 -0.58 -0.58 -0.59 0.01 0.16 0.8728  
## OLA:QUE 7 0.29 -0.15 -0.08 -0.19 0.10 1.00 0.3164  
## OLA:RIS 10 0.31 -0.03 -0.05 -0.02 -0.04 -0.44 0.6591  
## OLA:SER 1 0.22 -0.20 -0.23 -0.19 -0.04 -0.26 0.7928  
## OLA:ZIP 5 0.42 -0.19 -0.14 -0.23 0.09 0.84 0.3988  
## pal:PBO 8 0.85 -0.49 -0.50 -0.46 -0.04 -0.25 0.7990  
## QUE:PBO 7 0.44 -0.43 -0.42 -0.43 0.01 0.14 0.8874  
## RIS:PBO 12 0.42 -0.55 -0.58 -0.53 -0.05 -0.76 0.4483  
## SER:PBO 3 0.39 -0.39 -0.35 -0.41 0.06 0.43 0.6704  
## ZIP:PBO 4 0.30 -0.39 -0.40 -0.39 -0.01 -0.10 0.9212  
## ZOT:PBO 2 0.37 -0.49 -0.54 -0.46 -0.08 -0.42 0.6737  
## QUE:RIS 6 0.39 0.12 0.06 0.17 -0.11 -1.13 0.2586  
## QUE:ZIP 1 0.19 -0.04 -0.02 -0.04 0.02 0.14 0.8876  
## RIS:SER 1 0.15 -0.17 0.15 -0.22 0.37 1.87 0.0612  
## RIS:ZIP 2 0.26 -0.16 -0.09 -0.19 0.10 0.85 0.3941  
##   
## Legend:  
## comparison - Treatment comparison  
## k - Number of studies providing direct evidence  
## prop - Direct evidence proportion  
## nma - Estimated treatment effect (SMD) in network meta-analysis  
## direct - Estimated treatment effect (SMD) derived from direct evidence  
## indir. - Estimated treatment effect (SMD) derived from indirect evidence  
## Diff - Difference between direct and indirect treatment estimates  
## z - z-value of test for disagreement (direct versus indirect)  
## p-value - p-value of test for disagreement (direct versus indirect)

How do you interpret the results? Are there any large discrepancies between the direct and indirect estimates?

There are many comparisons for which the p-values for inconsistency are low. But, we need to also note the large number of comparisons we have (54 comparisons in total). Thus, these findings might be just due to chance. A simple Bonferroni correction for multiple testing would suggest that only the comparison ‘ASE:PBO’ has evidence that direct and indirect evidence differs substantially (p = 0.0006 < 0.05 / 54).

Finally, we look at the design-by-treatment interaction model.

decomp.design(net3)

## Q statistics to assess homogeneity / consistency  
##   
## Q df p-value  
## Total 279.59 192 < 0.0001  
## Within designs 139.67 118 0.0846  
## Between designs 139.93 74 < 0.0001  
##   
## Design-specific decomposition of within-designs Q statistic  
##   
## Design Q df p-value  
## AMI:HAL 2.15 5 0.8287  
## AMI:OLA 14.48 4 0.0059  
## AMI:RIS 1.92 3 0.5897  
## ARI:OLA 0.14 2 0.9320  
## CLO:CPZ 5.93 3 0.1151  
## CLO:HAL 8.03 5 0.1549  
## CLO:ZOT 3.06 1 0.0804  
## HAL:ILO 0.19 2 0.9109  
## HAL:OLA 8.85 9 0.4510  
## HAL:QUE 0.76 2 0.6844  
## HAL:RIS 24.26 12 0.0187  
## HAL:ZIP 0.03 1 0.8619  
## HAL:ZOT 6.39 3 0.0942  
## OLA:QUE 0.31 1 0.5781  
## OLA:RIS 0.04 4 0.9998  
## OLA:ZIP 2.23 3 0.5269  
## PBO:ARI 0.27 1 0.6027  
## PBO:CPZ 2.87 7 0.8968  
## PBO:HAL 8.52 6 0.2025  
## PBO:LURA 3.89 2 0.1432  
## PBO:OLA 13.24 6 0.0394  
## PBO:pal 2.86 3 0.4136  
## PBO:QUE 5.03 4 0.2844  
## PBO:RIS 3.27 4 0.5143  
## PBO:ZIP 0.02 1 0.8806  
## OLA:QUE:RIS 2.69 4 0.6102  
## PBO:ARI:HAL 3.66 4 0.4537  
## PBO:ASE:OLA 4.44 2 0.1087  
## PBO:HAL:RIS 4.16 4 0.3850  
## PBO:HAL:SER 1.24 2 0.5377  
## PBO:ILO:RIS 0.77 2 0.6796  
## PBO:OLA:pal 3.99 6 0.6774  
##   
## Between-designs Q statistic after detaching of single designs  
##   
## Detached design Q df p-value  
## AMI:HAL 137.90 73 < 0.0001  
## AMI:OLA 139.51 73 < 0.0001  
## AMI:RIS 139.32 73 < 0.0001  
## ARI:HAL 139.35 73 < 0.0001  
## ARI:OLA 138.16 73 < 0.0001  
## ARI:RIS 139.89 73 < 0.0001  
## ARI:ZIP 138.79 73 < 0.0001  
## ASE:OLA 134.81 73 < 0.0001  
## CLO:CPZ 137.81 73 < 0.0001  
## CLO:HAL 138.95 73 < 0.0001  
## CLO:OLA 139.93 73 < 0.0001  
## CLO:RIS 139.79 73 < 0.0001  
## CLO:ZOT 139.50 73 < 0.0001  
## CPZ:QUE 139.89 73 < 0.0001  
## HAL:ILO 137.71 73 < 0.0001  
## HAL:OLA 139.75 73 < 0.0001  
## HAL:QUE 138.57 73 < 0.0001  
## HAL:RIS 139.74 73 < 0.0001  
## HAL:SER 139.86 73 < 0.0001  
## HAL:ZIP 139.92 73 < 0.0001  
## HAL:ZOT 137.86 73 < 0.0001  
## OLA:QUE 139.36 73 < 0.0001  
## OLA:RIS 139.69 73 < 0.0001  
## OLA:SER 139.85 73 < 0.0001  
## OLA:ZIP 139.91 73 < 0.0001  
## PBO:ARI 139.83 73 < 0.0001  
## PBO:CPZ 138.83 73 < 0.0001  
## PBO:HAL 136.40 73 < 0.0001  
## PBO:LURA 139.93 73 < 0.0001  
## PBO:OLA 137.62 73 < 0.0001  
## PBO:pal 133.19 73 < 0.0001  
## PBO:QUE 134.12 73 < 0.0001  
## PBO:RIS 139.50 73 < 0.0001  
## PBO:SER 139.52 73 < 0.0001  
## PBO:ZIP 139.07 73 < 0.0001  
## PBO:ZOT 139.05 73 < 0.0001  
## QUE:RIS 139.93 73 < 0.0001  
## RIS:SER 134.82 73 < 0.0001  
## RIS:ZIP 139.72 73 < 0.0001  
## ARI:OLA:QUE:RIS 137.29 71 < 0.0001  
## CLO:HAL:OLA 135.71 72 < 0.0001  
## CLO:HAL:RIS 132.96 72 < 0.0001  
## OLA:QUE:RIS 139.58 72 < 0.0001  
## OLA:QUE:RIS:ZIP 133.26 71 < 0.0001  
## PBO:ARI:HAL 139.18 72 < 0.0001  
## PBO:ARI:RIS 139.62 72 < 0.0001  
## PBO:ASE:HAL 138.94 72 < 0.0001  
## PBO:ASE:OLA 116.83 72 0.0007  
## PBO:ASE:RIS 137.26 72 < 0.0001  
## PBO:CLO:CPZ 137.10 72 < 0.0001  
## PBO:CPZ:HAL 136.48 72 < 0.0001  
## PBO:CPZ:ZOT 124.04 72 0.0001  
## PBO:HAL:ILO 139.08 72 < 0.0001  
## PBO:HAL:LURA 131.62 72 < 0.0001  
## PBO:HAL:QUE 138.66 72 < 0.0001  
## PBO:HAL:RIS 131.06 72 < 0.0001  
## PBO:HAL:SER 137.11 72 < 0.0001  
## PBO:HAL:ZIP 138.36 72 < 0.0001  
## PBO:ILO:RIS 138.59 72 < 0.0001  
## PBO:ILO:ZIP 139.30 72 < 0.0001  
## PBO:LURA:OLA 138.41 72 < 0.0001  
## PBO:LURA:QUE 124.26 72 0.0001  
## PBO:OLA:pal 130.89 72 < 0.0001  
##   
## Q statistic to assess consistency under the assumption of  
## a full design-by-treatment interaction random effects model  
##   
## Q df p-value tau.within tau2.within  
## Between designs 113.70 74 0.0021 0.0728 0.0053

How do you interpret the overall results (Q statistics)?

The within design Q-statistic shows no substantial heterogeneity within designs.

Which individual comparisons contribute most to the within-design heterogeneity?

The comparisons ‘AMI:OLA’ and ‘HAL:RIS’ contribute most to the (non-significant) within-study heterogeneity.

Which designs contribute the most to between-design inconsistency?

Looking at the Q statistics and noticing that the degrees of freedom are very similar, we see that the designs ‘PBO:ASE:OLA’, ‘PBO:CPZ:ZOT’, and ‘PBO:LURA:QUE’ contribute most to the between-study inconsistency.

Is any residual inconsistency left after allowing for a full design by treatment interaction model?

Substantial residual inconsistency remains in a full design by treatment interaction model.