NMAstudio web-application: A brief tutorial

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Abstract

For a given medical condition, network meta-analysis (NMA) compares multiple available treatments in a network of comparative studies and provides both direct and indirect estimates of the relative effects for all treatments at hand. Despite NMA is increasingly used to inform decision-making, the lack of user-friendly software is still limiting its usage within a restricted community of researchers and end-users. In this tutorial, we describe NMAstudio, a novel user-friendly tool aimed to produce and visualise network meta-analyses in a fully interactive way. NMAstudio enhances visualisation while simplifying the reporting and interpretation of findings. The main feature of the application is a direct visual connection between a customisable network diagram and the main NMA outputs. Specifically, users upload their data and interact with the network diagram by clicking one or more nodes-treatments or edges-comparisons; based on the selection made, tailored outputs and information are displayed. NMAstudio is written in Python and connected to the R package `netmeta` to produce the NMA estimates.

1   Introduction

Network meta-analysis (NMA) pools evidence from different studies on multiple treatments to estimate all relative treatment effects. Thus, the amount of evidence to be displayed and interpreted can be burdensome, especially when many treatments available. A comprehensive NMA assessment typically involves many graphical outputs, including forest plots for the network estimates, league tables reporting all possible two-by-two treatment comparisons, comparison-adjusted funnel plots, plots displaying ranking of treatments, and many more. However, available software so far do not provide satisfactory solutions to improve visualisation and screening of such large and complex results. Towards this end, we have developed NMAstudio, a new interactive web-application that simplifies the whole NMA process and enhances the visualisation of results. The key

feature of NMAstudio is that the users can directly interact with a customisable network diagram to produce tailored NMA outputs by clicking one or more nodes-treatments or edges-comparisons. For instance, the user clicks on a node in the network graph, say placebo, and an NMA forest plot of all network estimates against placebo will appear.

In the form of a tutorial, we will describe each step a user should undertake to perform a full NMA appraisal. To fix ideas, the web interface appearance is shown in Figure 1: on the left side of the screen, a network plot is displayed alongside with a dropdown menu for extra network settings; while on the right side of the screen the user may find seven different tabs. The first tab is used to upload and explore the uploaded data, while each of the subsequent tabs correspond to a key part of the NMA assessment. In the following, we will describe the general functionalities of the application, as well as specific features for each tab, i.e. each step of the NMA assessment. Throughout, we will assume the reader is familiar with the basic concepts of evidence synthesis and meta-analysis.
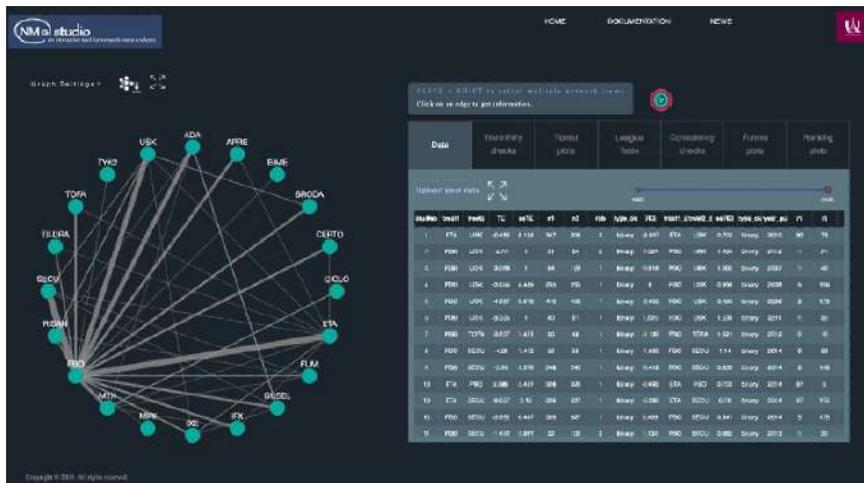
Figure 1: Browser illustration of the NMAstudio web interface.

2 Hosting and demo data

Hosting: NMAstudio is a Python web-application embedded into the Python Dash environment and further connected to the R package `netmeta`[1] to produce the network meta-analysis estimates. The NMA results are then imported in Python where interactive and downloadable visualisations are produced using 'Plotly' modules. No prior knowledge of these software is required to use NMAstudio. The application is open-source and can be freely accessed via any web browser at http://www.nmastudioapp.

`com`, although we recommend to use Firefox or Chrome browsers for optimal deployment. We also suggest the reader to follow both the guidelines provided in this tutorial and the full User Guide manual, downloadable from the web documentation page at http://www.nmastudioapp.com/doc. The latter provides additional advice and more detailed descriptions of available options for each plot and table included.

Data: To demonstrate our tool, we use a network of 158 RCTs comparing 20 pharmacological treatments for chronic plaque psoriasis which have been recently evaluated in a Cochrane systematic review[2−3]. Two outcomes will be analysed, namely a measure of efficacy and a measure of safety of treatment:

- Efficacy: proportion of participants achieving Psoriasis Area Severity Index ≥ 90 (PASI 90) (RR)

- Safety: serious adverse events (SAE) (RR)

This data set is permanently loaded as default project and we strongly encourage the users to explore and familiarise with NMAstudio through this running example before uploading their own data.

3 Uploading user data

NMAstudio allows two outcomes to be uploaded and analysed simultaneously, however the second outcome is optional and can be dismissed. For each outcome, a choice should be made about the type (continuous vs. binary) and the desired effect measure. The latter is to be chosen as mean difference (MD) or standardised mean difference (SMD) for continuous outcomes, and odds ratio (OR) or risk ratio (RR) for binary outcomes. To increase flexibility, different data formats are also allowed: a long format, a wide format and a wide inverse-variance format. The uploaded data are then automatically transformed into contrast-based format as expected by the package `netmeta`. Recall that:

Long format: a study contributes as many rows as treatments present in the study. There is a single treatment per row. In this case, the user should provide the following:

Continuous outcome	Binary outcome
mean y (numeric)	number of events r (numeric)
standard deviation sd (numeric)	sample size n (numeric)
treatment $treat$ (string or numeric)	treatment $treat$ (string or numeric)

Wide format: one data row per study. There is a single comparison per row, containing summary data for each treatment arm and corresponding standard errors. In this case, the user should provide the following:

Continuous outcome	Binary outcome
means in each arm $y1, y2$ (numeric)	number of events in each treatment arm $r1, r2$ (numeric)
standard deviation in each arm $sd1, sd2$ (numeric)	sample size in each treatment arm $n1, n2$ (numeric)
treatment in each arm $treat1, treat2$ (string or numeric)	treatment in each arm $treat1, treat2$ (string or numeric)

Wide inverse-variance (iv) format: one data row per study (as wide contrast), but instead of summary data for each treatment, only a comparison-specific estimate, assumed to be gaussian, of the relative treatment effect is available, alongside its standard error. In this case, the user should provide the following:

Continuous outcome	Binary outcome
treatment effect TE (numeric)	treatment effect TE (numeric)
effect standard deviation $seTE$ (numeric)	effect standard deviation $seTE$ (numeric)
treatment in each arm $treat1, treat2$ (string or numeric)	treatment in each arm $treat1, treat2$ (string or numeric)

Further, the user should provide the following additional variables:

1. **studlab**, study name or ID for each trial (numeric or string)
2. **year**, study-level year of publication (numeric),
3. **rob**, study-level risk of bias (RoB). RoB takes three possible values (low, medium, high) and should be encoded in your data file as either {1,2,3}, {l,m,h} or {L,M,H},
4. **treatment class (optional):** the user can provide information about the class of treatment. If such variable is present in the data, an option for colouring nodes of the network by class will be available. So far, the class variable should take the name of $treat\_class$ if data are uploaded in long format and $treat1\_class$ and $treat2\_class$ in case of wide format (numeric or string).

Except for treatment class (optional), custom field names are possible for each variable: the user will be prompted to fill a data selection form, as shown in an example in Figure 3. The user should first select the data format and the desired effect size. Based on the selection made, empty cells should be filled from a list of variable names that will appear (taken from the users data file).

During the results generation process, some warning messages may appear (such as presence of missing values etc.), however these do not prevent to proceed with the analysis. If any error occurs in the NMA process, the following alert will appear: "An error occurred during the NMA generation process: please check your data". In such cases, the user is recommended to double-check their data, looking specifically for network

Figure 2: Example of a data upload process, with uploaded data in long contrast, and binary outcomes. Note that the "Upload" button is activated only once all data selection fields are filled.

connectivity and any possible mistake in the reporting of multi-arm studies, as well as potential typos in the data fields. If the user wishes to perform a new analysis, the red "Reset" button on the right part of the screen should be used. However, we suggest the user to close and re-open the browser before uploading a new data set, as this will ensure that all variables and settings are cleared out of memory.

4 Presentation of the evidence

When the project set-up is completed, all NMA analyses are automatically produced, the corresponding network plot appears on the left part of the screen and the data table is displayed in the 'Data' tab (*cnf* Figure 1). By clicking one or multiple nodes and/or edges the user is now ready to:

- explore and filter their data in real time (the full or filtered data table can be expanded and exported in .csv via dedicated buttons),
- visualise the evolution of the network over time by using the time slider on the right-top of the 'Data' tab (this feature will be discussed in the next section),
- explore all NMA outputs produced within each of the remaining six tabs.

4.1 The network plot

The default network (*cnf.* Figure 1) has no node size and edge size proportional to the number of studies in that comparison. Node and edge size, as well as other settings and different layouts can be customised by the user using the 'Graph Settings' menu, as shown in Figure 4.1. We refer the reader to the User Guide documentation for detailed descriptions of all the available layouts. The most appropriate layout is to be chosen according to the data and network information that the user seeks to put more emphasis on. The network can also be expanded via the dedicated icon (see Figure 3) to minimise the risk of overlapping nodes in very large networks. In addition, it is possible to manually adjust the plot by dragging and zooming nodes to resize the network appearance. Note that NMAstudio allows to display both the network relating to the first outcome (default) as well as the second outcome, if present: the network for the second outcome automatically appears upon selection via the dedicated toggle-switches in the tabs.
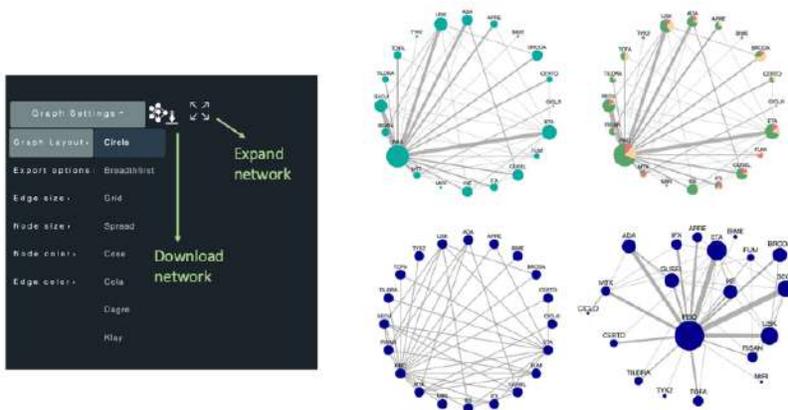
Figure 3: Graph Settings options (left) and examples of network plots, with circle layout, for PASI 90 outcome.

Finally, as mentioned above, the app contains a slider ('Data' Tab, upper-right side) to display the evolution of the evidence over time. The left marker corresponds to the year when the first trial was conducted (1963 in the psoriasis example reported here), while the right marker is the last year of available evidence (2020). The slider contains one marker for each point in time in which evidence was added. As a simple example, Figure 4.1 shows how the network of evidence has evolved over three timestamps: 1963, 2010, 2020. When the slider is used, note also that the data table will be filtered accordingly in real-time.
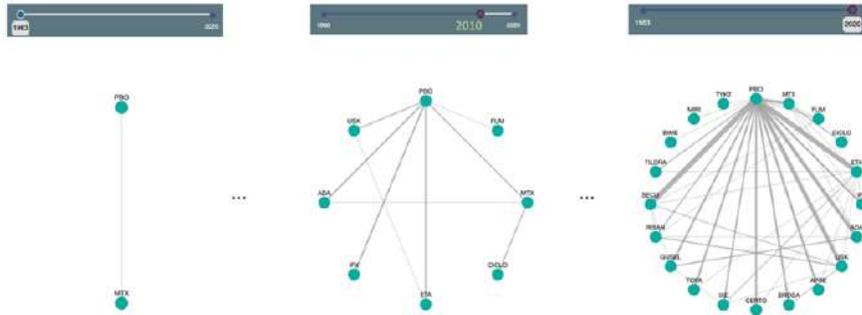
Figure 4: An example of the evolution of the network over three different timestamps alongside their corresponding slider marks.

4.2   The NMA assessment

Transitivity checks: Transitivity is the core assumption of network meta-analysis that makes the use of indirect evidence valid. Thus, evaluation of its plausibility is fundamental to ensure validity of the whole NMA process. However, transitivity is fundamentally a clinical assumption and so can only be checked graphically by looking at whether important differences in the distribution of the potential effect modifiers exist in the data. More detailed explanation of transitivity can be found elsewhere[4−5]. All the effect modifiers present in the data and suspected to differ in distribution should be checked. In NMAstudio, users can select the effect modifier they wish to investigate in the 'Transitivity' tab. As an example, in Figure 4.2 we have analysed the distribution of mean age of participants in each trial. The box-plots are fairly similarly distributed across comparisons, suggesting no intransitivity with respect to this variable. Users can highlight some box-plots of interest by clicking on the corresponding comparison-edge(s) in the network plot.

If data are uploaded in long format, the value of each effect modifier can differ between treatment arms: for example, the mean age or percentage of women in the treatment arm. In this situation, two variables instead of one variable will be included in the output dataset. The values "1" and "2" are added to the names for these variables, e.g. "mean.age" and "mean.age" for the mean age. More information at: https://rdrr.io/cran/netmeta/man/pairwise.html.

Forest plots: Three different forest plots are available: (i) forest plots of network estimates for the outcome of interest, (ii) forest plots of pairwise comparisons and (iii) bi-dimensional forest plots containing network estimates of the first and second outcome respectively on the x-axis and y-axis. Figure 4.2 shows how to produce forest plots
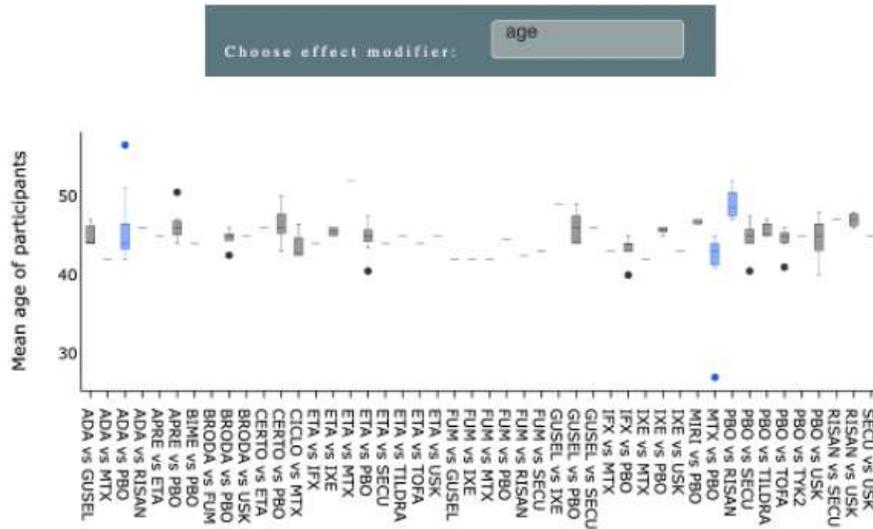
Figure 5: Transitivity box-plots with some comparisons highlighted in blue.

both for a single outcome or two outcomes together: the reference treatment (placebo here) is selected from the network and the corresponding plots appear in the 'NMA' or 'Bi-dimensional NMA' sub-tabs in the right part of the homepage. Information about heterogeneity is annotated to the NMA forest plot. The direction of the outcome (beneficial vs. harmful) can also be annotated to the plot. Although not shown here, standard pairwise forest plots for each direct comparison are also available, upon edge-click in the network. The standard meta-analysis estimates are calculated using the R library meta[6]. More information at: https://www.rdocumentation.org/packages/meta/versions/4.9-6/topics/metagen.

League tables: A league table typically contains all two-by-two estimated treatment effects from the network meta-analysis. NMAstudio allows for the full table to be displayed and saved, as well as a reduced league table containing a subset of selected treatments in the network. The ordering of selection corresponds to the order of appearance of treatments in the table. NMAstudio also allows to colour the table cells according to some criterion of interest. At the moment, two colouring options are available: first, by the average risk of bias in the comparison, and second, by the credibility in the full body of evidence from the CINeMA software[7−9] (Confidence in Network Meta-Analysis). To assess and summarise the level of concern for each comparison, CINeMA uses four
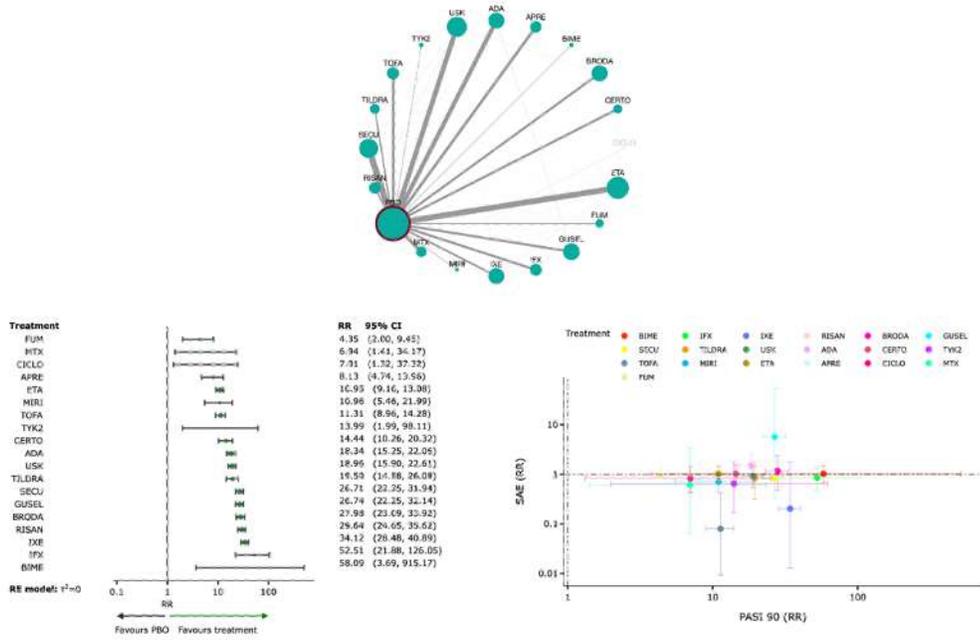
Figure 6: NMA and bi-dimensional forest plots for the efficacy outcome, alongside network plot with the selected node (placebo: PBO) used as reference treatment.

domains of confidence ("high", "moderate", "low", "very lo"), which result from an assessment of the confidence in each network meta-analysis estimate in terms of within-trial bias, reporting bias, indirectness, imprecision, heterogeneity, and incoherence. Some threshold values and evaluation rules need to be decided for carrying out some of the CINeMA steps: these are typically finalised through discussions between researchers and clinicians. After carrying out the CINeMA assessment following the principles above, in Figure 4.2 we report a table of relative treatment effects for both efficacy and safety, coloured according to overall confidence in the evidence and containing only a subset of nodes of interest.

Note: NMAstudio requires the user to upload the CINeMA report file in its original format, with mandatory columns "Comparison" and "Confidence rating", as shown below.

Comparison	Number of studies	Within-study bias	Reporting bias	Indirectness	Imprecision	Heterogeneity	Incoherence	Confidence rating
ADA:GUSEL	3	No concerns	Undetected	No concerns	No concerns	No concerns	No concerns	High
ADA:PBO	8	No concerns	Undetected	No concerns	No concerns	No concerns	No concerns	High
ADA:RISAN	1	No concerns	Undetected	No concerns	No concerns	No concerns	No concerns	High

Treatment	IFX	IXE	RISAN	BIME	MIRI	SECU	GUSEL	BRODA	ADA	ETA	PBO
IFX	IFX	1.45 (0.59, 3.53)	2.08 (0.88, 4.96)	0.14 (0.01, 2.35)	2.29 (0.49, 10.61)	1.46 (0.63, 3.39)	0.62 (0.25, 1.55)	0.69 (0.27, 1.79)	0.69 (0.30, 1.62)	0.56 (0.24, 1.27)	1.48 (0.71, 3.10)
IXE	1.54 (0.63, 3.74)	IXE	1.44 (0.74, 2.80)	0.20 (0.01, 3.23)	1.58 (0.38, 6.65)	1.01 (0.53, 1.91)	0.90 (0.51, 1.57)	1.01 (0.46, 2.18)	1.00 (0.55, 1.85)	0.81 (0.46, 1.41)	1.03 (0.62, 1.70)
RISAN	1.77 (0.73, 4.31)	1.15 (1.01, 1.31)	RISAN	0.28 (0.07, 4.67)	0.91 (0.22, 3.75)	0.70 (0.42, 1.18)	1.29 (0.66, 2.54)	1.45 (0.70, 2.99)	1.45 (0.84, 2.49)	1.16 (0.64, 2.09)	1.41 (0.89, 2.21)
BIME	1.11 (0.06, 19.96)	1.70 (0.11, 26.98)	1.96 (0.12, 31.07)	BIME	0.31 (0.01, 6.67)	0.20 (0.01, 3.21)	0.22 (0.01, 3.63)	0.20 (0.01, 3.27)	5.10 (0.32, 82.47)	0.24 (0.02, 3.95)	0.20 (0.01, 3.16)
MIRI	4.79 (1.57, 14.67)	3.11 (1.52, 6.39)	0.37 (0.18, 0.76)	5.30 (0.31, 91.07)	MIRI	0.64 (0.16, 2.59)	1.42 (0.33, 6.04)	1.59 (0.37, 6.91)	1.59 (0.39, 6.49)	1.28 (0.31, 5.18)	0.65 (0.17, 2.48)
SECU	1.97 (0.81, 4.78)	1.28 (1.12, 1.45)	1.11 (1.00, 1.23)	0.41 (0.14, 34.45)	0.41 (0.20, 0.84)	SECU	0.90 (0.46, 1.76)	1.01 (0.50, 2.03)	1.01 (0.58, 1.78)	0.81 (0.47, 1.41)	0.98 (0.65, 1.48)
GUSEL	0.51 (0.21, 1.24)	0.78 (0.72, 0.85)	0.90 (0.79, 1.02)	2.17 (0.14, 34.43)	2.44 (1.19, 5.01)	1.00 (0.88, 1.14)	GUSEL	1.12 (0.50, 2.50)	1.12 (0.63, 1.98)	0.90 (0.48, 1.70)	0.92 (0.53, 1.58)
BRODA	0.53 (0.22, 1.30)	0.82 (0.71, 0.95)	0.94 (0.83, 1.08)	2.08 (0.13, 32.92)	2.55 (1.24, 5.26)	1.05 (0.94, 1.17)	1.05 (0.90, 1.22)	BRODA	1.00 (0.49, 2.05)	1.25 (0.61, 2.54)	1.03 (0.57, 1.87)
ADA	0.35 (0.14, 0.85)	0.54 (0.48, 0.60)	0.62 (0.55, 0.69)	0.32 (0.02, 5.00)	1.67 (0.81, 3.44)	0.69 (0.60, 0.78)	0.69 (0.63, 0.75)	0.66 (0.56, 0.77)	ADA	1.25 (0.71, 2.19)	1.03 (0.68, 1.56)
ETA	0.21 (0.09, 0.51)	0.32 (0.29, 0.36)	0.37 (0.32, 0.43)	5.31 (0.33, 84.05)	1.00 (0.49, 2.05)	0.41 (0.36, 0.47)	0.41 (0.36, 0.47)	2.56 (2.19, 2.99)	1.67 (1.45, 1.94)	ETA	0.83 (0.55, 1.23)
PBO	52.51 (21.88, 126.05)	34.12 (28.48, 40.89)	0.03 (0.03, 0.04)	58.09 (3.69, 915.12)	10.96 (5.46, 21.99)	0.04 (0.03, 0.04)	26.74 (22.25, 32.14)	27.98 (23.09, 33.92)	18.34 (15.25, 22.06)	10.95 (9.16, 13.08)	PBO

Figure 7: League table for a subset of treatments containing RRs for efficacy (lower triangle) and safety (upper triangle) with their 95%CIs coloured by certainty of evidence assessed in CINeMA: high (green), moderate (blue), low (yellow) and very-low (red) confidence in the evidence. RRs larger than 1 favour the treatment on the left for the lower triangle and smaller than 1 for the upper triangle.

Consistency checks: Inconsistency expresses statistical disagreement of direct and indirect evidence, and can sometimes reflect the presence of intransitivity or heterogeneity in the network. NMAstudio reports results from two statistical tests assessing the presence of inconsistency i.e. local inconsistency in parts of the network and global inconsistency in the whole network[10]. An example of both tests produced via NMAstudio is reported in Table 1 and Table 2. Table 1 suggests that no overall inconsistency is present while Table 2 (where we have selected a subset of comparisons clicking edges in the network) suggests that two comparisons, tofacitinib (TOFA) vs. etanercept (ETA) and tofacitinib vs. placebo, have some concerns of intransitivity. Information about the number of studies can be found in the dedicated box (*cnf* Figure 1) when clicking the comparison of interest.

Outcome	Q	df(Q)	p-value
PASI 90	22.9497	27	0.6877
SAE	32.348	26	0.1819

Table 1: Design-by-treatment interaction tests for efficacy and safety, alongside Q statistic and degrees of freedom.

Comparison	direct	indirect	p-value
ADA vs GUSEL	0.678	0.737	0.5124
ETA vs TOFA	0.8968	1.3581	0.0989
IXE vs PBO	39.5201	33.6765	0.6337
IXE vs USK	1.7263	1.8419	0.6201
PBO vs TOFA	0.1125	0.0777	0.1367

Table 2: Node-splitting local tests for inconsistency: p-value <0.10 in red and 0.10<p-value<0.15 in yellow.

Small-study effects assessment: To evaluate the presence of small-study effects, we use comparison-adjusted funnel plots[11]. These plots report each study's effect estimates centred at the comparison-specific effect against their reversed standard error and so they allow to further investigate the distribution of the effect sizes: An asymmetry in the plot might suggest that larger effects tend to be systematically found in smaller studies. In this case, the effects are suspect to have been inflated for publication[12−13]. An ordering of the treatments is necessary for a meaningful interpretation of this plot, and when this is not possible only the studies compared to the same reference treatment should be included in the plot. At present, NMAstudio allows for the second option only. In our example, we report the funnel plot for efficacy for all active treatments against placebo. The plot is shown in Figure 4.2 and was produced clicking on the node PBO in the network plot, which was thus used as reference.
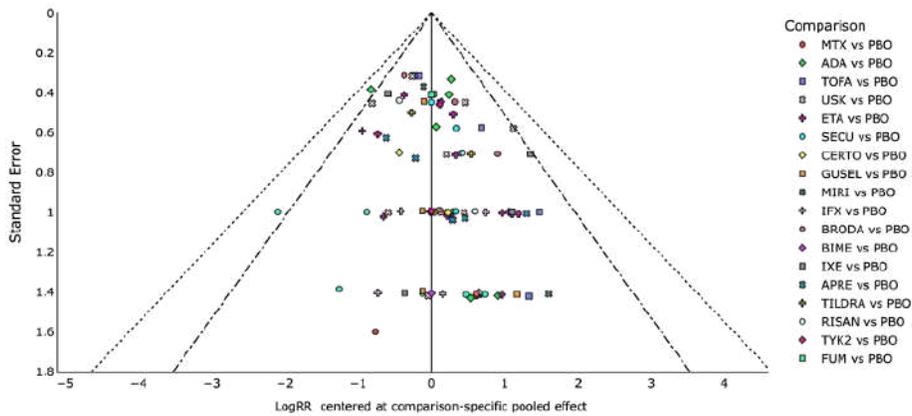
Figure 8: Comparison-adjusted funnel plot for efficacy, showing logRRs for studies compared to Placebo (PBO). The plot is automatically produced upon clicking on the node PBO in the network plot.

Treatment ranking: Network meta-analyses usually provide a final ranking of treatments. NMAstudio uses P-scores[14] to rank treatments, as these are provided in `netmeta`. P-scores range from 0 to 1, and can be interpreted as an average degree of certainty for a treatment to be better than the other treatments in the network. The following ranking plots are available in NMAstudio: first, a heatmap of treatments sorted by P-scores and then, a scatterplot of P-scores for the two outcomes, if both are present. In the heatmap, treatments are sorted and coloured from best to worse P-score, however when both outcomes are present, the sorting is made according to the first (main) outcome of interest. The scatterplot displays instead P-scores of the first outcome on the x-axis and P-scores for the second outcome on the y-axis. Clearly, optimal treatment(s) should have high values in both outcomes. However, when uncertainty is high, rankings may be not very informative and looking at the relative treatment effects may be clinically more relevant and appropriate[15]. Thus, we encourage the users to always evaluate ranking also in light of the uncertainty found in the estimates. In Figure 4.2, we report the two plots hereby described alongside the fundamental toggle switch to drive the direction of the ranking, i.e. to choose whether the outcomes are beneficial or harmful.
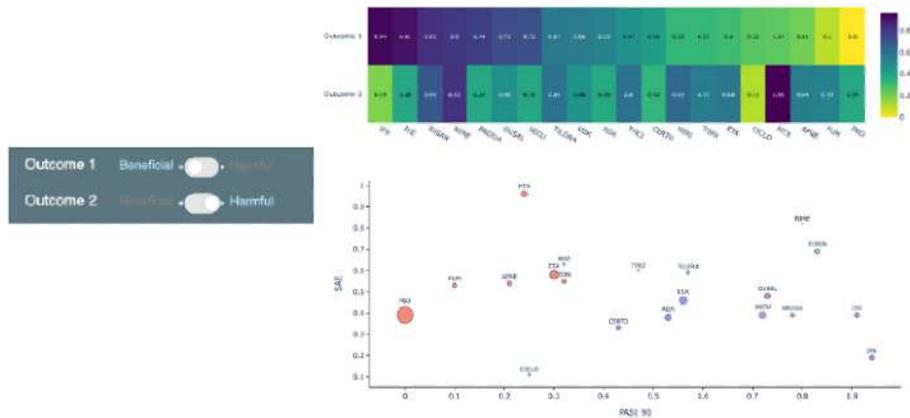
Figure 9: P-scores heatmap and P-scores scatter plot for both outcomes. In the scatterplot, the size of the bubble is proportional to the number of people randomised in that treatment and each colour correspond to treatments placed in the same cluster of treatments (via simple K-means clustering).

5   Short summary

In this tutorial, we have introduced NMAstudio, a novel web application to perform network meta-analyses through easy "point and click" interactions. NMAstudio is the first web interface in the field of network meta-analysis to provide full interactivity between the network plot and all the most relevant NMA outputs. Navigating through large and complex outputs can be time-consuming and sometimes confusing, thus we believe interactivity is an essential feature, especially when having large networks with many treatments. Further software updates will be available soon. First, we seek to include Bayesian analyses by connecting Python to R-Jags or the Stan environment. This can enable a number of additional settings under which frequentist analysis is not possible or poorly performant. In addition, we wish to allow users to directly upload their results and use the application for visualisation purposes only. To this end, we plan to partner NMAstudio with a corresponding Python package. Finally, we intend to add options for performing sensitivity analyses and to strengthen our current system of warnings and alerts. Further options in the customisation of the network plot are also foreseen. Examples include colouring of edges by risk of bias and edge size by study precision. All forthcoming and future features are listed in the app at the page `http://www.nmastudioapp.com/news`. In conclusion, we hope that NMAstudio will prove a useful resource for researchers and end-users undertaking network meta-analyses, and that it will help to communicate meta-analytic results more clearly to diverse audience. All detailed options for customising the graphical displays are summarised in details in the software accompanying User Guide, while the full software code is currently available at `https://github.com/silviametelli/network-meta-analysis`.

Acknowledgments

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