

A computational way station for reporting network meta-analyses

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1 Network meta-analysis reporting

Pairwise analyses between treatment and control, exposed and unexposed, intervention and no intervention, are conventionally undertaken with meta-analysis in fields such as ecology, medicine, and the social sciences [1]. Network meta-analysis provides a means of comparing three or more treatments or interventions, including control or placebo [5]. The question answered by a network meta-analysis is not *if* a treatment works, but *which* treatments perform better, comparatively [4]. A particularly useful aspect of network meta-analysis is combining the results of more than one pairwise analysis and constructing indirect comparisons, where pairwise evidence is unavailable, from a network of direct comparisons. An example of direct comparisons provided by existing evidence is shown in Figure 1. Network meta-analysis

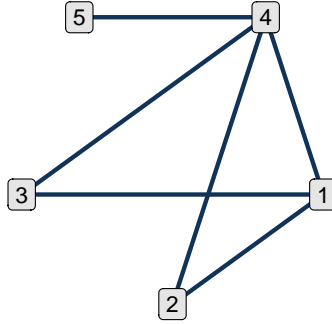


Figure 1: This network shows the direct evidence provided by pairwise comparisons in seven studies on treatments for Parkinson’s disease [11]. Each node represents a treatment, including one placebo, represented by the fourth node. Where there is an edge connecting two treatment nodes, there exists a pairwise comparison in the literature between these two treatments. Where there is no edge connecting the nodes of the network, there is no direct evidence.

17 converts the network to a complete graph, where all treatments are compared
 18 with all other treatments, that is, every node connects to every other node
 19 via direct or indirect comparison.

20 Software to implement network meta-analyses are relatively new and do
 21 not provide complete toolchains for specific protocols, such as reporting re-
 22 sults according to Cochrane’s handbook [5]. For example, the handbook
 23 recommends reporting the network of direct evidence, for which the R pack-
 24 age `multinma::` includes a tool [11], an example of which is shown in Figure
 25 1. However, the handbook also recommends reporting a **contribution ma-**
 26 **trix** of the percentage of each study’s contribution to the estimated overall

27 effect, and this is not provided as a visualisation tool with `multinma::`.

28 Furthermore, open source scientific software is shifting from all-purpose
29 packages for an entire analysis, such as `metafor::`, to smaller task-specific
30 software packages. One method of aggregation of tools is a **metapackage**,
31 such as `tidyverse::` [16], for data engineering, which comprises a number of
32 packages that each pertain to different problems, such as `ggplot2::` for data
33 visualisation, and `dplyr::` for Boolean data manipulation. Here we explore
34 another way of aggregating resources, for the specific purpose of network
35 meta-analysis reporting: a computational **way station**, a temporary resting
36 place between two points of travel, of toolchains and tool development. Since
37 protocols and tools are are still being developed, this is a way station between
38 a single person’s analysis, and a resource that is definitive for all practitioners
39 to follow.

40 1.1 A snapshot of a living resource

41 In this manuscript, we next describe the gaps in the toolchain for implement-
42 ing network meta-analysis via R according to Cochrane’s reporting standards.
43 Standards for network meta-analysis are not, however, fixed, but in devel-
44 opment, and Cochrane’s reporting standards may not be appropriate for,
45 say, ecological network meta-analyses. Thus, instead of aiming to provide
46 a complete toolchain for network meta-analysis, we instead propose a com-
47 putational way station as a meeting place for stakeholders with different
48 priorities to provide perspective and collaborate. This way station is a **liv-**

49 **ing resource**, in anticipation of future updates following stakeholder input
50 and computational development, comprising multiple points of access:

51 **website** A website with vignettes of toolchains. Currently the existing solu-
52 tions for Cochrane’s reporting standards are provided, however there is
53 scope for future vignettes for network meta-analyses according to other
54 discipline or organisational protocols.

55 **open source code repository** Source code is provided for toolchains and
56 software extensions.

57 **contributing** Detailed instructions for different stakeholders with varying
58 levels of mathematical and computational training to contribute.

59 **issues** In addition to the source code, the issues associated with the code
60 repository provide a public record for discussions.

61 Living resources provide a solution to the problem of overabundance of
62 systematic reviews, flooding literature to the point that decision makers are
63 unsure of where to look [3, 7, 8, 13]. Consider Covid-19, where in the first 88
64 days after naming the disease, there already existed 88 systematic reviews,
65 one for every day since the disease was named [10]. Cochrane’s COVID-NMA
66 initiative (<https://covid-nma.com/>) is a living synthesis solution to this prob-
67 lem, via network meta-analysis of regularly updated Covid-19 research [2].

68 **nmareporting::** is also a living resource, but to solve a different problem.
69 How to bring people together for open scientific collaboration when not all

70 the solutions exist. As a package it is not ready for CRAN, and may never be
71 intended for CRAN. In some ways similar to the `rethinking::` package the
72 accompanies the canonical¹ text, *Statistical Rethinking*, the intention of this
73 software is not to ship a polished piece of software to CRAN, or a publish a
74 manuscript with a definitive toolchain [6]. Rather, this manuscript provides a
75 snapshot of a living resource for open collaboration on network meta-analysis
76 reporting.

77 2 Toolchain gaps in Cochrane reporting stan- 78 dards

79 There exist several software packages for conduction network meta-analysis in
80 R; for example, `gemtc::` [15], `multinma::` [11], and `netmeta::` [14]. Different
81 tools will no doubt have unique advantages and disadvantages, however, there
82 is no one tool for all reporting standards for a Cochrane network meta-
83 analysis. Furthermore, visualisations and reporting for meta-analysis are
84 still being developed.

85 2.1 Missing tables and improved visualisations

86 Cochrane recommends reporting the percentage each study contributes to
87 the overall estimated effect via a **contribution matrix**, shown in Figure 2.

¹At the time of writing *Statistical Rethinking* has 1243 citations.

Figure 11.6.b Contribution matrix for the network on interventions for heavy menstrual bleeding presented in Figure 11.4.a. Four direct comparisons in the network are presented in the columns, and their contributions to the combined treatment effect are presented in the rows. The entries of the matrix are the percentage weights attributed to each direct comparison. The intervention labels are: A, first generation hysteroscopic techniques; B, hysterectomy; C, second generation non-hysteroscopic techniques; D, Mirena

		Direct comparisons in the network (% contribution)			
		A-B	A-C	A-D	C-D
Network meta-analysis estimates	Mixed estimates				
	A-B	100.0			
	A-C		97.8	1.1	1.1
	A-D		34.5	34.1	34.5
	C-D		14.4	14.4	71.2
	Indirect estimates				
	B-C	49.6	48.9	0.7	0.7
	B-D	38.5	28.0	15.5	28.0
Entire network		34.4	36.4	10.5	21.7
Included studies		5	11	1	3

Figure 2: A contribution matrix shows what percentage each study contributes to the overall estimated effect in a network meta-analysis. This is the example given in the Cochrane Handbook [5].

88 The `netmeta::` package has tools for contribution matrices, but if one
89 is performing the analysis with, say, `multinma::`, it is unclear how to piece
90 together the tools to produce a complete set of Cochrane reporting.

91 Visualisations, too, are still in development. A recent improvement on
92 standard forest plots are orchard plots which contain not only credible in-
93 tervals, but prediction intervals, and group studies categorically, particularly
94 useful for large meta-analyses [9]. `nmareporting::` is a place where imple-
95 mentation of orchard plots for network meta-analysis can be developed.

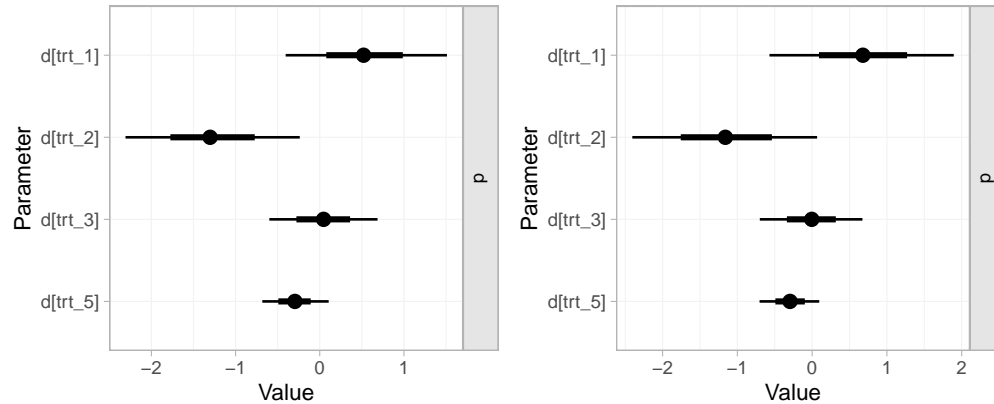


Figure 3: On the left is a forest plot of all analyses. On the right is a forest plot of the analysis with a randomly selected study omitted.

2.2 Sensitivity

Sensitivity in network meta-analysis measures how much the studies agree in results. A standard approach to measuring this is a ‘leave one out analysis’ [1], shown in Figure 3, where a study is randomly selected to be omitted, and the meta-analysis is rerun to see if the results differ. We randomly select

```
## [1] "study_1"
```

to remove from the analysis.

In this case, there is little disagreement between the studies. However, it does raise the question of what the analysis would report if another study

²This manuscript is fully reproducible, with all analyses and code embedded in the document. The source for this manuscript can be found here: <https://github.com/softloud/nmareporting/blob/master/manuscript/draft/nmarep-ms.Rnw>.

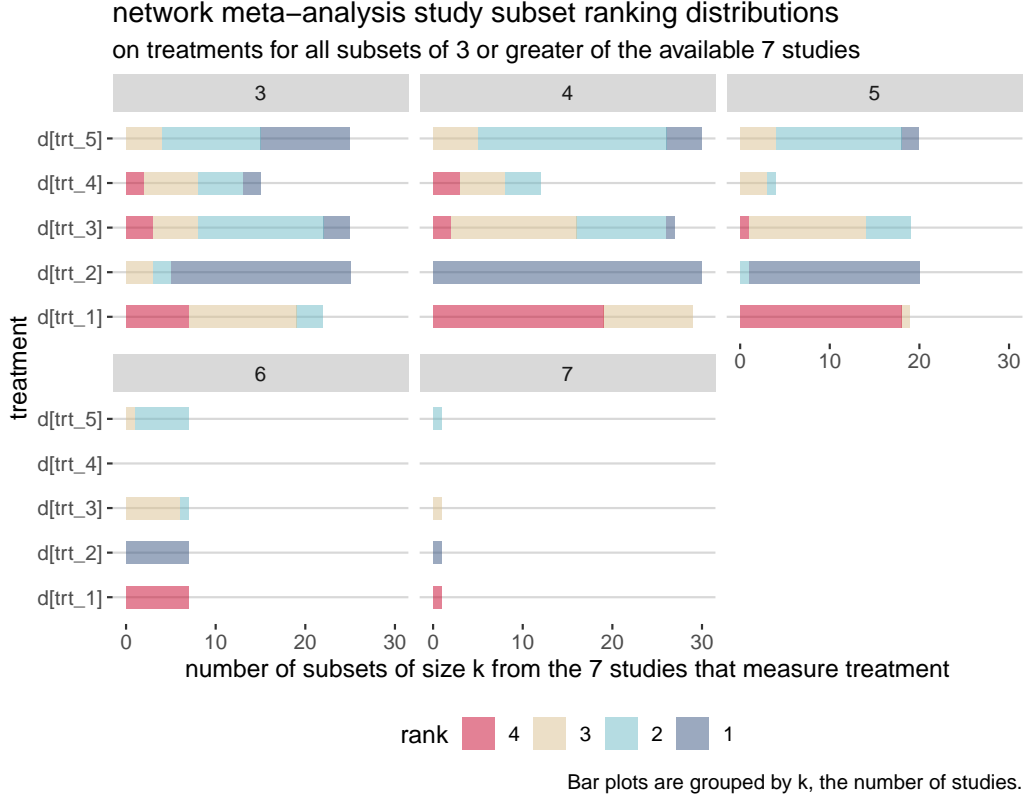


Figure 4: Rankings for leave m out analyses, where $m = 0, \dots, 4$ studies omitted from the total 7 studies available.

105 were omitted, and, indeed, what if more than one study were omitted? In
 106 Figure 4, we provide aggregation of rankings of network meta-analyses run
 107 on all subsets, of size three or greater, of the studies.

108 Unsurprisingly, the ranking are in agreement when including all seven
 109 studies, with treatment 2 predicted to have the greatest reduction in the
 110 measure of interest, the mean off-time reduction in patients given dopamine
 111 agonists as adjunct therapy in Parkinson’s disease [11]. And as treatment
 112 2 dominates in all subgroups, we surmise that there is confidence in the

113 meta-analytic recommendation of treatment 2.

114 However, other possible inferences do exist in these rankings, supposing
115 we did not have all seven studies, and it is easy to see how a different conclu-
116 sion might be drawn. Furthermore, another drawback is that whilst leave m
117 studies (for $m \leq k$ studies) works for seven studies, this analysis is not prac-
118 tical for meta-analyses that aggregate a larger number of studies. Indeed,
119 the number of network meta-analyses performed in this analysis is

```
## [1] 99
```

120 from seven studies. Clearly this type of analysis would become computa-
121 tionally intractable for larger meta-analyses.

122 A more robust approach would be threshold analysis, where an **invariant**
123 **interval** is provided for each study, showing the interval in which the study's
124 results will not change the ranking [12]. However, this solution is challenging,
125 involving mathematics and **stan** syntax, so providing toolchains, guides, and
126 support for practitioners will surely be helpful.

127 **3 Computational way station for open and** 128 **inclusive scientific method development**

129 Stakeholders engage with meta-analyses in multiple ways. A lead researcher
130 may not be interested in interacting with code repositories, but may well have
131 thoughts about how to improve reporting for inference. A computational

132 collaborator may wish to contribute tools for related analyses, even if not
133 directly involved in the project.

134 In this section, we consider developing a toolchain for reporting a Cochrane
135 network meta-analysis, considering how different researchers may wish to
136 provide feedback on the implemented protocol. With increasing levels of
137 computational complexity, we step through how researchers in various roles
138 might contribute.

139 **3.1 Domain-specific principal investigator**

140 Consider a study where the principal investigator (PI) is a psychologist who
141 delegates statistical analysis to other members of the team: a lead statis-
142 tician, and a postdoctoral scholar under their supervision. The PI will in-
143 terpret the meta-analytic findings, but will not wish to interact with code
144 repositories. In this case, an email address of the primary maintainer (the
145 postdoctoral scholar) of the living resource is provided for comments that can
146 then be converted to issues by the maintainer on the repository for discussion
147 amongst the community.

148 **3.2 Lead statistician**

149 The lead statistician will be comfortable with code, but will be time poor in
150 comparison to the maintainer of the living resource, the postdoctoral scholar
151 under their supervision. Whilst they may not have time to contribute they

will likely have comments for the maintainer. They will likely have a GitHub account, and thus can contribute to the discussion via issues, where not only the maintainer, but any interested party can consider and add to the suggestions.

3.3 Computational collaborators

Now consider a computational ecologist, interested in developing tools and protocols for their own network meta-analyses. In this case, they may wish to contribute new vignettes to the website, with new toolchains, as well as develop new tools to fill the toolchain gaps.

The R package `usethis::` includes a workflow for contributing to someone else's package³ [17].

In Figure 5 is a sketch of the workflow for contributing to `nmareporting::`, the underlying code base of the site and development. Let us suppose the ecologist is contributing an ecology-specific vignette for network meta-analysis.

4 Conclusion

In the era of big data and rapid-fire advances in statistical software, research is still adapting to what, in fact, constitutes a useful research artifact. Mathematical algorithms are conventionally implemented via software. Computa-

³Workflow documentation available here: <https://usethis.r-lib.org/articles/articles/pr-functions.html>

```

library(usethis)
# create a fork and clone
create_from_github("softcloud/nmareporting")
# create a branch for the specific contribution
pr_init("ecovignette")
#
# ecologist then writes vignette
#
# contribute the vignette to the code repository
pr_push()
#
# waits for maintainer to merge
#
# once the maintainer has merged
pr_finish()

```

Figure 5: A workflow for contributing to the `nmareporting::` computational way station.

171 tional way stations provide a meeting point, between a scholar's inception of
 172 an analysis technique, and it's formalisation in scientific protocol.

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