**MetaInsight: COVID19** (Last data update: 13 May 2020)

Network Meta-Analysis of Pharmacological treatments for COVID 19: Tool for exploration, re-analysis, sensitivity analysis, and interrogation of data from living systematic reviews

**Why was this tool made and what does it do?**

MetaInsight is an interactive web-based tool that conducts network meta-analysis requiring no specialist software for the user to install but leveraging established analysis routines (specifically, but not exclusively, the [netmeta](https://cran.r-project.org/web/packages/netmeta/index.html) 1.2-1 , [gemtc](https://cran.r-project.org/web/packages/gemtc/index.html) 0.8-4 and the [BUGSnet](https://bmcmedresmethodol.biomedcentral.com/articles/10.1186/s12874-019-0829-2) 1.0.3 packages in R) ([Owen et al. 2019](https://onlinelibrary.wiley.com/doi/full/10.1002/jrsm.1373)). The regular version of the app can be found elsewhere (<https://crsu.shinyapps.io/metainsight_continuous2/)>

With the evidence on treating COVID19 rapidly evolving, we have created a special version of our app – MetaInsight: COVID19 - tailored specifically around the up-to-date evidence from randomised controlled trials on the effectiveness of pharmacological treatments for COVID19. It is our intention to update the data included in this app regularly (the hope is this can be done at least weekly) as it becomes available. As well as updating the data, we will be increasing the functionality of the tool as well periodically (see below on providing feedback into this process).

This tool is designed to act as a dynamic, and interactive tool for analysis of network meta-analysis with an emphasis on visualisation of data and analysis results. In every meta-analysis, subjective judgements have to be made including the studies and data included and the analysis method used. As others have noted ([Ahern et al. 2020](https://ebm.bmj.com/content/early/2020/04/09/bmjebm-2019-111308.info)), traditional static evidence summaries force the quality assessment criteria and analytical choices of the authors onto all stakeholders, some of whom may have different views on key features of the analysis. Through tools such as this, users can, with ease, take control of the evidence synthesis using their preferred analytic approach to ascertain how robust findings are to alternative analysis strategies and study inclusion criteria and assess the appropriateness of the modelling assumptions made etc.

**Where does the data come from?**

The authors of the MetaInsight:COVID19 tool are not involved in conducting a systematic review or meta-analysis of the COVID19 treatment evidence of their own, but several other groups around the world currently are carrying out living systematic reviews of this topic and frequently updating the evidence on their websites ([EPPI Center](http://eppi.ioe.ac.uk/cms/Projects/DepartmentofHealthandSocialCare/Publishedreviews/COVID-19Livingsystematicmapoftheevidence/tabid/3765/Default.aspx), [COVID19 – Living data](https://covid-nma.com/), [The LIVING Project](https://systematicreviewsjournal.biomedcentral.com/articles/10.1186/s13643-020-01371-0)). Presently, we include data from one of these (<https://covid-nma.com/>), though, depending on how each of these evolve, we may include data from other sources in the future.

Presently we are focusing solely on evidence from randomised controlled trials, but observational data may be considered in the future.

**How does the app work?**

The MetaInsight: COVID19 tool contains a first page titled ‘COVID19’ which includes functionality for outcome selection. Following this, the corresponding evidence table, network plot and results (shown as a summary forest plot) for this outcome are displayed. On subsequent pages the functionality of the pre-existing MetaInsight app is included to explore the data and do detailed re-analyses. For example, specific studies can be filtered and excluded from the analysis, the analysis model changed, and assessments of network coherence carried out. We hope much of the functionality is self-explanatory, but a full manual is available (add link).

The advanced section of the app allows the user to fit NMA models via Bayesian simulation methods using the external package [JAGS](https://en.wikipedia.org/wiki/Just_another_Gibbs_sampler). In addition to technical advantages, this also allows the checking of modelling assumptions via cross validation and the use of model fit statistics to choose between competing statistical models. The app also allows the user to download the R code used “under the hood” that carried out the analysis to ensure reproducibility of research.

**About us**

MetaInsight was developed by the UK National Institute for Health Research (NIHR) Complex Review Support Unit ([http://www.nihrcrsu.org/](http://www.nihrcrsu.org/guidance/apps/) ). We routinely support network meta-analyses and developed (peer reviewed) web-based software (including MetaInsight - <http://www.nihrcrsu.org/guidance/apps/>) to allow others, including [Cochrane Collaboration](https://www.cochrane.org/) groups, to conduct and critique network meta-analyses without the need for expert statistics programming.

We have received excellent feedback on MetaInsight and know it is getting 100s of hours use each month by researchers in many areas of the world, including those in low and middle income countries. In addition to its primary function of allowing non-statistical experts to do research using NMA, we get enthusiastic reports from statisticians who use it because of its ease and efficiency and educators who use it as a practical teaching tool in the classroom. The Cochrane Collaboration (www.cochrane.org), whose work is internationally recognised as a benchmark for high-quality information about the effectiveness of healthcare, promoted the use of MetaInsight recently via a webinar (<https://training.cochrane.org/resource/metainsight-complex-review-support-unit-crsu-network-meta-analysis-nma-web-based-app>).

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**Feedback**

This is a novel and evolving project. We hope similar tools can be made for other important living and completed network meta-analyses in the future. We would be very grateful to anyone who sends constructive feedback and suggestions on how the tool can be improved in the future and this will inform future versions of this and any subsequent tools. Please send any feedback to [yiqiao.xin@glasgow.ac.uk](mailto:yiqiao.xin@glasgow.ac.uk)