** Minor feature changes on 24 March 2022 (v3.1.12) **

- Size of forest plots (UI and downloads) are now reactive to the size of the network.
- Ranking tab has been rearranged and sizing editing to help with large networks regarding readability.

** Minor feature change on 14 February 2022 (v3.1.11) **

- When downloading forest plots after running frequentist of Bayesian analyses, the PDF outputs are larger, giving more space to larger networks/treatment names

** New feature added on 15 December 2021 (v3.1.10) **

- The user can now adjust the size of the labels on the network plots.

** Bug fixed on 6 December 2021 (v3.1.9) **

- It was discovered that the new feature added in v3.1.8 was not implemented for downloading forest plots and so caused errors. This has now been resolved, and the new formatting options follow through when downloading forest plots.

** New feature added on 24 November 2021 (v3.1.8) **

- The forest plots of results for both frequentist and Bayesian analyses now have additional formatting options regarding the width of the x-axis. If the user decided to shorten the x-axis such that a confidence interval would 'run-off' the page, the respective confidence interval will have an arrowhead instead.

** Bug fixed on 7 October 2021 (v3.1.7) **

- It was discovered that within tab '3f. Deviance report', the residual deviance from NMA model and UME inconsistency model plot for studies within the sensitivity analyses was not rendering. This has now been resolved.

** New feature added on 8 April 2021 (v3.1.6) **

- For the forest plot of individual studies on '1b. Study results' tab, formatting functionality has been added. Users can now alter the text size for the main text, group headers, and text when downloading forest plots.

** Minor feature changes on 13 March 2021 (v3.1.5) **

- Minor text alterations to provide extra clarity to some plots and statistics that users had reported confusion over.

- When analysing the default datasets, the default ranking options have been selected such that analysis results are interpretable in the first instance.

** Version history implemented with GitHub **

- As of 19 February 2021, the complete code for MetaInsight is available on GitHub [https://github.com/CRSU-Apps/MetaInsight] with active version control to see detailed update history.

** New link for MetaInsight from 12 Aug 2020 (v3.1.4) **

- Please note that MetaInsight has a new web address now: https://crsu.shinyapps.io/MetaInsight/. This is because we combined the binary and continuous app together into one app in March 2020. Hence, to eliminate confusion, we thought it would be good to give it a new link. This will replace the previous links, including https://crsu.shinyapps.io/MetaInsight_continuous2/ and https://crsu.shinyapps.io/MetaInsight_binary2/. For the time being, the previous links will still be working but will automatically redirect to the new link.

** Bug fixed on 2 July 2020 (v3.1.3) **

- All users: a bug was fixed associated with the estimate of confidence intervals in the grouped forest plot on the '1. Data summary' – '1b. Study results' tab. This bug caused inflation of the confidence intervals within said plot. Please note that this bug does not affect any of the results of the network meta-analysis, but only the descriptive forest plot of individual studies. If you have used this grouped forest plot before or your interpretation was based on this plot, please re-upload the studies and re-check the plot using the most recent version of the app. We apologise for any inconvenience caused. If you have any questions, please feel free to contact us.

** Bugs fixed on 15 June 2020 (v3.1.2) **

- A bug was fixed associated with the display of median rank chart of sensitivity analysis on '3c. Ranking table' tab and the display of between-study standard deviation of sensitivity analysis on the '3a. Forest plot' tab.

** Bugs fixed on 14 June 2020 (v3.1.1) **

- We fixed a bug associated with copying and pasting the labels on the 'Load data' page on 14th June 2020. If you experiences disconnection problems or cursor not selecting problems when using the version 3.10 (released on 10th June 2020), please try again with the current version 3.11.

** New features updated on 10 June 2020 (v3.1.0) **

- We added a User Guide tab where users can find a complete manual for using the MetaInsight app (including Bayesian functionality), and webinar videos recorded as part of Cochrane network meta-analysis training series which included a demonstration of the app.

- We added a Trouble shooting page based on the queries that we received over the years. The frequently identified issues and their solutions are summarised.

- A data table has been added to the 'Data analysis' tab which facilitates the identification of studies for exclusion in the sensitivity analysis.

- 'Data characteristics' tables are now added to '1. Data summary' page to provide a summary of characteristics of all studies, and in sensitivity analysis.

- The app will provide a notification to the users when the network is disconnected.

- Users can now choose between two styles of network structure to view: one with number of trials shown on the line, and the other with number of people indicated by size of node etc.

** New features updated on 25 March 2020 (v3.0.0) **

- The binary and continuous app are now combined into one app. The users just need to select the outcome option at the 'Home' page based on the outcome in their study.

- The deviance plots of the Bayesian analysis on the 'Data analysis' tab – '3f. Deviance report' are not interactive. User can hover their cursor on the data points to identify the corresponding study.

** New features updated on 15 Nov 2019 (v2.1) **

- Network connectivity information is now shown on the '1b. Network Plot' tab.

- A plot of residual deviance from NMA model and UME inconsistency model is now displayed on the '3f. Deviance report' tab to assist users to determine the model fit.

** New features updated on 19 August 2019 (v2) **

Long and wide format data uploading:

- This version now allows uploading data in 'long' format (1 study arm per row), in addition to the 'wide' format (1 whole study per row). The app will automatically detect the data format and prepare the data for analysis accordingly. Instructions for uploading data are on the 'Load data' tab with subtabs for formatting 'long' and 'wide' data, respectively.

- Example datasets with associated treatment label files can now be downloaded which users can adapt to create files of their data in the correct format for the app.

- Preparing the 'wide' format data is now more flexible: when there are less than 6 treatment arms, the users just need to input the headings up to their maximum number of arms, i.e., you do not need to add the empty columns with headings in the data anymore.

- **For existing users (breaking change):** Please note that the **required heading names have been changed** slightly compared to the last version so you will need to change the names of

the headings in your existing data files accordingly. Please see instructions on the 'Load data' page.

2. Bayesian analysis:

- This app now allows Bayesian network meta-analysis, in addition to the existing frequentist network meta-analysis.

- The Bayesian network meta-analysis uses the R gemtc package, which can generate forest plots of the results; generate comparisons of relative treatment effects for all possible treatment pairs from the NMA; provide a ranking table and a median rank chart based on the probability for each treatment to be the best; perform node-split models to compare direct estimates and indirect estimates; check the model convergence using the Gelman-Rubin convergence assessment plot; check model fit by producing the deviance reports; and provide model details including model code, initial values and simulations ready for download.