** New features updated on 25 March 2020 (v3) ** :

- 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 now interactive. User can hover their curser 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 nodesplit 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, and initial values and simulations ready for download.