

## Troubleshooting

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We have received a large number of emails over the years from the users and thus summarized the frequently identified issues as below. Users are requested to check this trouble shooting page before contacting us regarding issues with using the app. The data formatting requirements for the app are exacting and the majority of problems are when users deviate from the required format (see below).

- A. If you receive an error message in the app (as below), please check the following aspects of your data:

**Error: An error has occurred. Check your logs or contact the app author for clarification.**

Possible actions that may cause the error		Guidance and solutions
<b>1. Data label formatting</b>		
1.1	Does your treatment names contain space, slashes (/), &, * or other special characters?	Treatment names can only contain letters, digits, and underscore (_). Please remove any other characters.
1.2	Did you directly type into the box of treatment labels?	Please format the labels and copy and paste the labels from a tab separated file. <b>We recommend inputting treatment labels into Excel (csv, comma delimited format) first, and then copy and paste into the label box.</b> This makes sure the two columns 'Number' and 'Label' are separated by tabspace.
<b>2. Data</b>		
2.1	Does the column names contain space or any other characters that are not as permitted in the instructions?	Please check all the column names according to the instructions for uploading long or wide format data
2.2	Does a study only contain a single arm?	The app cannot synthesize the studies which only contains single arm. Please remove the single arm study(ies).

2.3 Is the data saved in *CSV (comma delimited)* format ?

Please note, only this format can be recognised by the app. A common mistake is saving the data with the format of *CSV UTF-8 (comma delimited)*.

2.4 Does the data contain thousand separators (. or ,) ?

Please remove any thousand separators from the data.

2.5 If your data are binary outcomes, does the outcome column(s) ('R' in long format, or 'R.1', 'R.2' etc. in wide format) contain(s) 0s?

Bayesian analysis allows the inclusion of studies with 0 events in one or more arms. However, if all studies in a particular treatment contrast network connection for one or both treatments, you may run into problems and we recommend you consider this not to be a valid network connection edge. If all arms of a study have 0 event then we recommend removing such studies from the dataset prior to analysis (others may disagree with this recommendation). Furthermore, when there are very few events for certain treatments, the credible intervals may be very wide and so please be cautious when you interpret the results.

Frequentist analysis may run into problems depending on where the 0s located in the data:

- If 0s are contained in the pairwise studies (i.e. studies that contain only 2 arms): unless both arms have 0 outcome, the analysis will automatically include a "continuity correction" (i.e. adding 0.5 events to all arms of the studies with one or more arms with 0 events and 1 to the total number of people in each arm) and the result will show as normal. If both arms have 0 outcome, the entire study will be removed from the frequentist analysis.
- If the 0s are contained in the multi-arm studies: the arms that contain 0 outcomes will be removed first, leaving the arms that do not contain 0 outcome in the analysis. If only one arm left after removing the 0 outcome arms, the app will run into an error due to missing treatment effect. In this case, users will need to apply a "continuity correction" manually in the data before uploading or exclude the study.

2.6 Have you included continuity corrections to your (binary) data?

Unfortunately, for Bayesian analysis the *gemtc* package only takes integer values when working with binary data. For most cases, if you remove the corrections, the Bayesian analysis should cope with the zero cells, however, if this is not the case, please refer to point 2.5 above.

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### 3. Analysis

3.1 Is the error shown in the sections displaying sensitivity analysis (analysis after excluding studies) but not for the primary analysis?

There are two most likely reasons for this error:

- a) the network is disconnected, and therefore the analysis cannot be performed. Please check the remaining studies and continue removing studies until only one network remains, or add studies back until network reconnected.
- b) the reference treatment is removed from the analysis. Please recode the treatment to assign another treatment to be reference treatment.

3.2 Frequentist results runs okay but Bayesian results show an error.

This is usually caused by the format of treatment labels, which may contain characters other than letters, digits, and underscore (\_).

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Data checking advice:

- please start with only including two studies from your data, making sure the network is connected, and see if the result will show.
  - o if not, please check all the formatting requirement and advice above
  - o if yes, please add more studies gradually to identify the error.

B. If you have other questions, please check the following list of suggestions. If none of them resolves your issue, please feel free to contact us.

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## 1. Display

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| 1.1 | Forest plot on the '1b. Study Results' tab looks very crowded.   | This is usually caused by the large number of studies included. A possible work-around is to try to load approximately 1/2 your data into the app at a time to produce this plot over 2 figures. A key thing is to make sure you don't split data for the same comparisons over different plots. It is only a summary of the entered data so this may work to produce a 2-page summary plot. You, of course, would then load all the data for analysis afterwards etc. |
| 1.2 | Plot results cannot be displayed fully                           | We haven't got any have better solutions at the moment other than suggesting users to adjust the browser resolution to 75% or less and check if the problem improves.  |
| 1.3 | Frequentist/Bayesian forest plots are not showing all treatments | This is likely due to there being too many treatments included in the network. When this happens, two forest plots are created, but only the latter is presented in MetaInsight. To obtain the entire forest plot, either consider reducing the number of treatments in your network, or download the plot in PDF format (exporting as PDF has functionality to show both plots).  |

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## 2. App is disconnected from the server


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| 2.1 | Are you running node-splitting model when the app is disconnected?        | This is caused by the memory demanding computing process of the node splitting process in the app server on the web. If you use R/RStudio, this problem could be solved by downloading our codes for the app on Github and running the app from your RStudio console. Link to the Github repository: <a href="https://github.com/CRSU-Apps/MetaInsight">https://github.com/CRSU-Apps/MetaInsight</a> . |
| 2.2 | Does the app keep disconnected from the server when you upload your data? | Please check all the formatting requirement of the app, and all the formatting advice on this trouble shooting page section A.   |
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## Contact details

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[UK NIHR Complex Review Support Unit](#)

 <p>The logo for the NIHR Complex Reviews Support Unit (CRSU) is displayed. It features the text "NIHR CRSU" in a large, bold, blue font at the top. Below this, "COMPLEX REVIEWS SUPPORT UNIT" is written in a smaller, bold, blue font. At the bottom, there are five logos: the University of Glasgow crest, the University of Leicester crest, the London School of Hygiene &amp; Tropical Medicine crest, a circular logo with a horse, and the NIHR logo with the text "National Institute for Health Research".</p>	<p><b>Funding Acknowledgement:</b> The Complex Reviews Support Unit is funded by the National Institute for Health Research (project number 14/178/29).</p> <p><b>Department of Health Disclaimer:</b> The views and opinions expressed herein are those of the authors and do not necessarily reflect those of the NIHR, NHS or the Department of Health.</p> <p>Please click <a href="#">here</a> for more information about the UK NIHR Complex Reviews Support Unit (CRSU).</p>
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