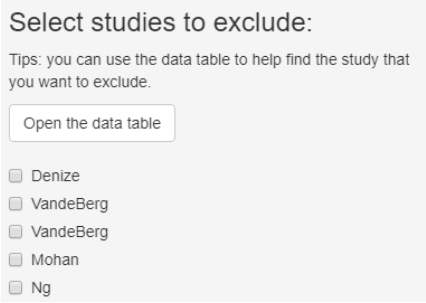**Troubleshooting**

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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 uses 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
1. Data		
1.1	Do your treatment names contain spaces or special characters (eg. /\&* etc.)?	Treatment names can only contain letters, digits, and underscore (_). Please remove any other characters.
1.2	Are your study names *exactly* the same between rows (long format)?	If the study names differ between rows, MetaInsight will think they are separate studies, even if they have the same study ID. An easy way to check this is to look at the 'excluded studies' list on the analysis page (example to the right):
1.3	Does a study only contain a single arm?	The app cannot synthesize the studies which only contains single arm. Please remove all single arm studies.

1.4	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)*.
1.5	Does the data contain "thousand separator" characters (. or ,) ?	Please remove any thousand separator characters from the data.
1.6	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 (without the need for continuity corrections). However, if all studies within a particular treatment contrast have 0 events 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 both arms of 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 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 is 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.

| 1.7 | 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 2.6 above. |

2. Analysis

| 2.1 | 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. |
| 2.2 | 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 (_). |

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.
    - if not, please check all the formatting requirement and advice above
    - 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.

1. Display

| 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 cours, 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. |

2. App is disconnected from the server

| 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: https://github.com/CRSU-Apps/MetaInsight. |
| 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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