

Explanations for each step

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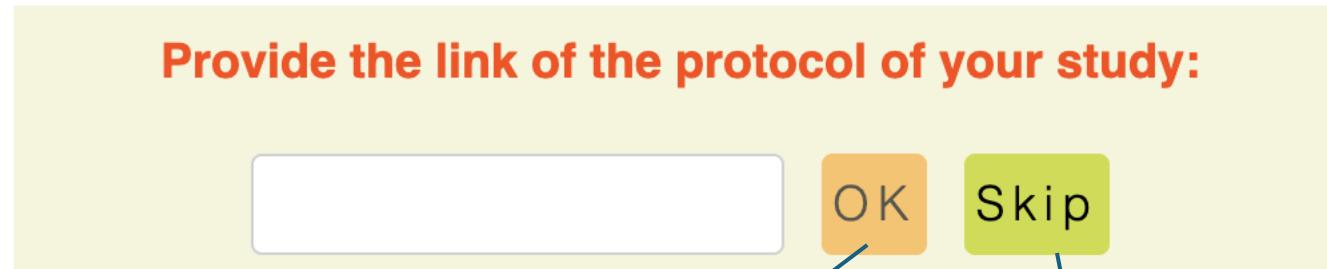
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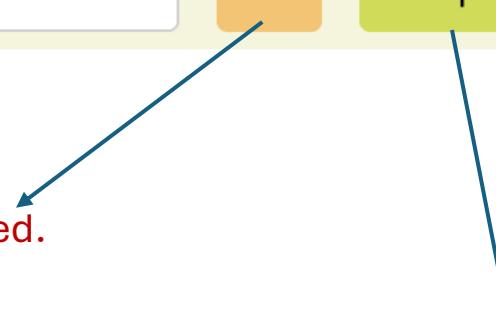
[**Step 9.** Select potential effect modifiers](#)

Step 1. Provide the protocol link

This step is optional, but we highly recommend users to provide the protocol link which improves the transparency of their researches.



It is triggered once the protocol link is provided.



Click it if no protocol is provided.

Note: If this step is skipped, a warning will appear on the results page.

Step 2. Upload the dataset file

Drag and Drop or [Select a File](#)

- Drag a file from your laptop or click “Select a File” to select one from your laptop.
- The file should be **csv** format.
- **Missing values** should be encoded as **'!', 'NA'** or left empty in the uploaded dataset.

Step 3. Select the format of your dataset

Long format: a study contributes as many rows as treatments present in the study. There is a single treatment per row. In this case, the user should provide the following:

Continuous outcome	Binary outcome
mean y (numeric)	number of events r (numeric)
standard deviation sd (numeric)	sample size n (numeric)
treatment $treat$ (string or numeric)	treatment $treat$ (string or numeric)

Select the format of your dataset:

long

wide

iv

NMAstudio allows three formats of the dataset: **long, wide and inverse-variance.**

Wide format: one data row per study. There is a single comparison per row, containing summary data for each treatment arm and corresponding standard errors. In this case, the user should provide the following:

Continuous outcome	Binary outcome
means in each arm y_1, y_2 (numeric)	number of events in each treatment arm r_1, r_2 (numeric)
standard deviation in each arm sd_1, sd_2 (numeric)	sample size in each treatment arm n_1, n_2 (numeric)
treatment in each arm $treat_1, treat_2$ (string or numeric)	treatment in each arm $treat_1, treat_2$ (string or numeric)

Wide inverse-variance (iv) format: one data row per study (as wide contrast), but instead of summary data for each treatment, only a comparison-specific estimate, assumed to be gaussian, of the relative treatment effect is available, alongside its standard error. In this case, the user should provide the following:

Continuous outcome	Binary outcome
treatment effect TE (numeric)	treatment effect TE (numeric)
effect standard deviation $seTE$ (numeric)	effect standard deviation $seTE$ (numeric)
treatment in each arm $treat_1, treat_2$ (string or numeric)	treatment in each arm $treat_1, treat_2$ (string or numeric)

Step 4. Select overall variables

-for long format dataset

Select overall variables

study ID:	<input type="text"/>
rob (optional):	<input type="text"/>
treat:	<input type="text"/>
year:	<input type="text"/>

Select the column that contains the name or the ID of a study. Each study should have a unique ID or name.

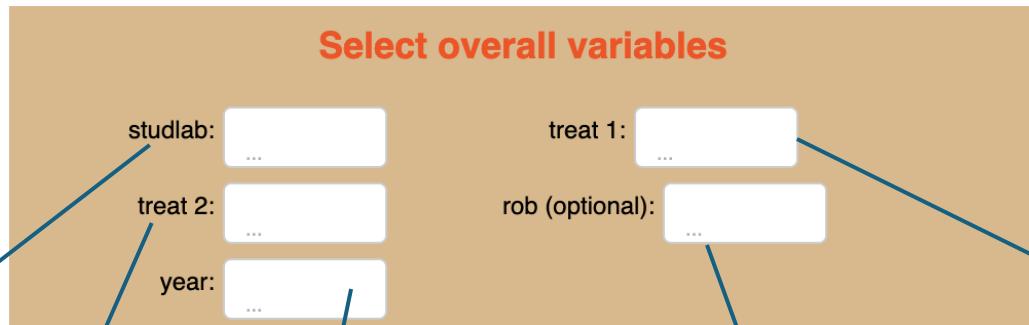
This is optional. Select the column that contains the risk of bias information of a study. risk of bias should be encoded in your data file as either **{1,2,3}, {l,m,h}** or **{L,M,H}**, the arms in the same study should have the same rob value.

Select the column that contains the intervention name of each arm within a study.

Select the column that contains the time information, such as the publication year or study completion year. If this information is not available, add a column to your dataset and enter '0'.

Step 4. Select overall variables

-for wide & iv format dataset



Select the column that contains the name or the ID of a study. Each study should have a unique ID or name.

Select the column that contains second intervention name for each comparison within a study.

Select the column that contains the time information, such as the publication year or study completion year. If this information is not available, add a column to your dataset and enter '0'.

Select the column that contains first intervention name for each comparison within a study.

This is optional. Select the column that contains the risk of bias information of a study. risk of bias should be encoded in your data file as either **{1,2,3}**, **{l,m,h}** or **{L,M,H}**, the arms in the same study should have the same rob value.

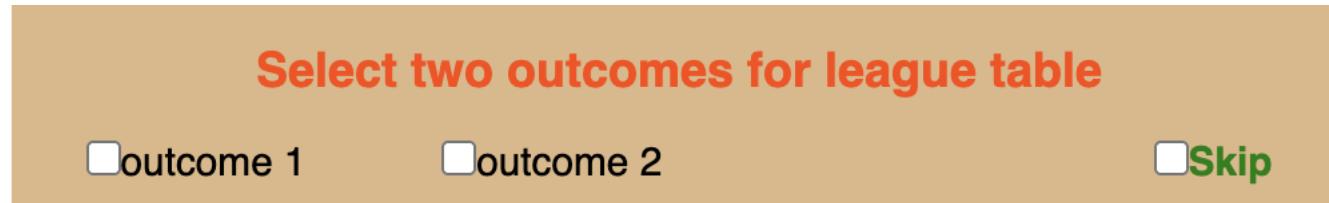
Step 5. Enter the number of outcomes

Enter the number of outcomes:

 OK

- NMAstudio supports running analyses for **multiple outcomes**.
- Please enter the number of outcomes you would like to analyze.
- The data for all outcomes should be included in the **same dataset file**, with information of **each outcome stored in different columns**.

Step 6. Select two outcomes for league tables



- **NMAstudio can generate two types of league tables:**
 - League table for a single outcome
 - League table for two outcomes
- **To generate a two-outcome league table:**
 - Select which two outcomes to include (especially when the dataset contains more than two outcomes).
- **Click 'Skip' if you do not want to generate a two-outcome league table.**

Step 7. Select outcome types & enter outcome names

Select the type of outcome 1:

continuous binary

outcome name

Select the type of outcome 2:

continuous binary

outcome name

- **Select the type for each outcome:**
 - **Binary**
 - **Continuous**
- **Survival data is not supported in NMastudio yet.**
- **Enter the outcome names.** If no names are provided, the results page will display default labels: “outcome 1”, “outcome 2”, etc.

Step 8. Select other variables

-for long format dataset

Binary outcome

Select effect size for outcome 1

OR

RR

Outcome direction for outcome 1

beneficial

harmful

Select variables for outcome 1

No. of events:

...

No. participants:

...

Previous

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Beneficial: A larger effect size indicates a **better** intervention (e.g., efficacy outcome).

Harmful: A larger effect size indicates a **worse** intervention (e.g., adverse event).

Select the column that contains the values for the outcome

Select the column that contains the standard deviation for the outcome

Select the column that contains the number of participants for the outcome

Continuous outcome

Select effect size for outcome 2

MD

SMD

Outcome direction for outcome 2

beneficial

harmful

Select variables for outcome 2

y: ...

sd: ...

n: ...

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- In this box, **each variable should refer to a unique column** in your dataset. For example, if you have two outcomes and the number of participants are the same in each study for two outcomes. The number of participants refer to column "N" in your dataset. **Do not select "N" for both outcome 1 and 2. In this case, you need to create another column "N2" for outcome 2.**

Step 8. Select other variables

-for wide format dataset

Binary outcome

Select effect size for outcome 1

OR RR

Outcome direction for outcome 1

beneficial harmful

Select variables for outcome 1

r1: ...	n1: ...
r2: ...	n2: ...

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Beneficial: A larger effect size indicates a **better** intervention (e.g., efficacy outcome).

Harmful : A larger effect size indicates a **worse** intervention (e.g., adverse event).

Select the columns that contains **the number of events** and **the number of participants** for the **first intervention** in each comparison.

Select the columns that contains **the number of events** and **the number of participants** for the **second intervention** in each comparison.

- In this box, **each variable should refer to a unique column** in your dataset. For example, if you have two outcomes and the number of participants are the same in each study for two outcomes. The number of participants refer to column "N" in your dataset. **Do not select "N" for both outcome 1 and 2. In this case, you need to create another column "N2" for outcome 2.**

Step 8. Select other variables

-for wide format dataset

Continuous outcome

Select effect size for outcome 2

MD SMD

Outcome direction for outcome 2

beneficial harmful

Select variables for outcome 2

y1: sd1:
y2: sd2:
n1: n2:

[Previous](#) [Next](#)

Beneficial: A larger effect size indicates a **better** intervention (e.g., efficacy outcome).

Harmful : A larger effect size indicates a **worse** intervention (e.g., adverse event).

Select the columns that contains **the value of the outcome** and **the standard deviation** for the **first intervention** in each comparison.

Select the columns that contains **the value of the outcome** and **the standard deviation** for the **second intervention** in each comparison.

Select the columns that contains **the number of participants** for the **first intervention** and the **second intervention** in each comparison.

- In this box, **each variable should refer to a unique column** in your dataset. For example, if you have two outcomes and the number of participants are the same in each study for two outcomes. The number of participants refer to column "N" in your dataset. **Do not select "N" for both outcome 1 and 2. In this case, you need to create another column "N2" for outcome 2.**

Step 8. Select other variables

-for iv format dataset

Binary outcome

Select effect size for outcome 1

OR

ORR

Outcome direction for outcome 1

beneficial

harmful

Select variables for outcome 1

TE: ...

seTE: ...

n1: ...

n2: ...

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Next

Beneficial: A larger effect size indicates a **better** intervention (e.g., efficacy outcome).

Harmful: A larger effect size indicates a **worse** intervention (e.g., adverse event).

Select the columns that contains **the treatment effect** and **the standard error of the treatment effect** for each comparison.

Select the columns that contains **the number of participants** for **each intervention** in each comparison.

Continuous outcome

Select effect size for outcome 2

MD

SMD

Outcome direction for outcome 2

beneficial

harmful

Select variables for outcome 2

TE: ...

seTE: ...

n1: ...

n2: ...

Previous

Next

- In this box, **each variable should refer to a unique column** in your dataset. For example, if you have two outcomes and the number of participants are the same in each study for two outcomes. The number of participants refer to column "N" in your dataset. **Do not select "N" for both outcome 1 and 2. In this case, you need to create another column "N2" for outcome 2.**

Step 9. Select potential effect modifiers

Select potential effect modifiers

<input type="checkbox"/> unique_id	<input type="checkbox"/> name	<input type="checkbox"/> year_publication	<input type="checkbox"/> Skip
<input type="checkbox"/> bias	<input type="checkbox"/> treat	<input type="checkbox"/> treat_class	
<input type="checkbox"/> sample_size	<input type="checkbox"/> nPASI90	<input type="checkbox"/> rPASI90	
<input type="checkbox"/> rSAE	<input type="checkbox"/> nSAE	<input type="checkbox"/> age	
<input type="checkbox"/> male_percentage	<input type="checkbox"/> weight	<input type="checkbox"/> bmi	

- Select the columns that contain the potential **effect modifier** values.
- Effect modifiers included in the box plots must be in **continuous format**.
 - For dichotomous variables, convert them into proportions (e.g., percentage of participants with a given characteristic).
 - For categorical variables, assign numerical codes to represent categories (e.g., 1, 2, 3).
- If you select ‘**Skip**’, a warning will appear on the results page.