REAP-2 User Guide

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# Input data

## Dataset input requirements:

* The input dataset can be in csv, tsv and txt format
* The input dataset contains three columns: Concentration, Effect and Agent
* Columns in the input dataset should follow the order of Concentration, Effect and Agent

## Truncation strategy:

It is recommended that users normalize the response variable to the range of (0,1) by themselves. Otherwise, REAP will automatically truncate the values exceeding the boundaries to (0,1) using a truncation algorithm.

## Example dataset:

The example dataset can be downloaded through the following link:

<https://github.com/vivid225/REAP/blob/main/REAP/31780660_F1B_exampledata.csv>

Here is a screenshot of the dataset:

Table

Description automatically generated

# Parameter selection

## Choosing model feature

1. Log transform dose

The dose-response curve in REAP-2 is based on the median-effect equation. For statistical modeling, the dose-response curve is formulated as:

where and are the intercept and slope parameters that determine a sigmoid dose-response relationship with respect to the effect at the dose level .

By unchecking the *log transform dose* option, the dose-response curve will be re-formulated as:

1. Add potency estimation

The input value of the potency estimation is within (0, 100). By specifying the interested drug potency, REAP-2 will provide point estimation and standard deviation of the potency along with triangle signs specified in the dose-response curve plot (Red box in Fig. 1).

Line chart

Description automatically generated with low confidence

Figure 1 Dose-response curve plot. Triangles in the red box show IC50 values for each dose-response curve.

## Model comparison

1. Potency estimations

Graphical user interface, application

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By checking the *Potency estimations* option, REAP-2 will provide hypothesis testing on whether the **potency estimations** are the same for all the agents in the Summary tab.

1. Slopes

Graphical user interface, application

Description automatically generated

By checking the *Slopes* option, REAP-2 will provide hypothesis testing on whether the **slope estimations** are the same for all the agents in the Summary tab.

1. Models

Graphical user interface, application

Description automatically generated

By checking both the *Potency estimations* option and the *Slopes* option, REAP-2 will provide hypothesis testing on whether the **fitted models** are the same for all the agents in the Summary tab.

## Plot specifics

1. Show values: points, means and StdDev

In the Curve tab, users can choose what to include in the dose-response curve plot. *Points* represent the original raw data. *Means* provide mean estimations of the input dataset under each dose level. *StdDev* provide standard deviations of the response under each dose level. The default setting is a curve plot with mean and standard deviation of each dose level as in Fig. 1.

1. Log10(dose)

*Log10(dose)* determines whether to log transform the dose level (x-axis) in the curve plot.

1. X-axis and y-axis names

The default x-axis and y-axis names are based on the input dataset. Users can specify the names to change the axis labels of the curve plot.

## Download report

There are three sections in the downloaded plot:

1. Setting includes all the parameter selections in REAP-2 for all the results in the report.
2. Dose-response curve plot saves the results under the Curve tab.
3. The tables in the report are saved from the results under the Summary tab.