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:

Auranofin	Cell viability	Agents
0.075	0.758	Mino
0.150	0.576	Mino
0.300	0.357	Mino
0.600	0.128	Mino
1.250	0.002	Mino
2.500	0.002	Mino

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:

$$\log \frac{E}{1 - E} = \beta_0 + \beta_1 \log d$$

where β_0 and β_1 are the intercept and slope parameters that determine a sigmoid dose-response relationship with respect to the effect E at the dose level d.

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

$$\log \frac{E}{1 - E} = \beta_0 + \beta_1 d$$

2. 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).
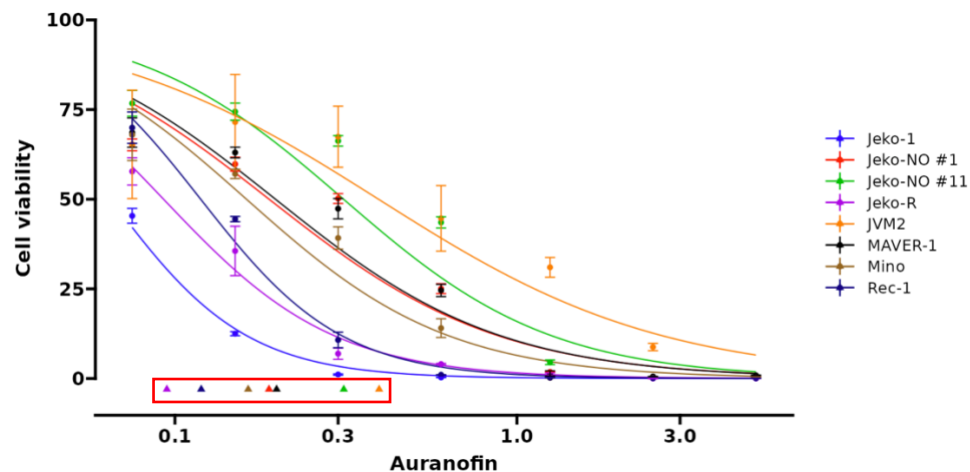

Figure 1 Dose-response curve plot. Triangles in the red box show IC50 values for each dose-response curve.

Model comparison

1. Potency estimations

   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.
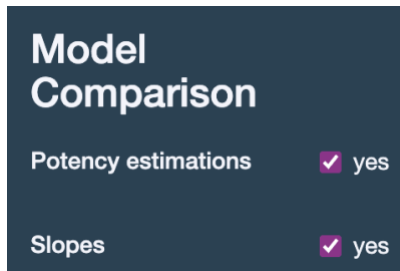
2. Slopes

   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.

3. Models

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.

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

3. 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.