BATS 1.1.0 Documentation

Introduction

BATS (Bayesian Adaptive Trial Simulator) is a simulation tool for designing Bayesian Multi-Arm Multi-Stage trials.

Requirements

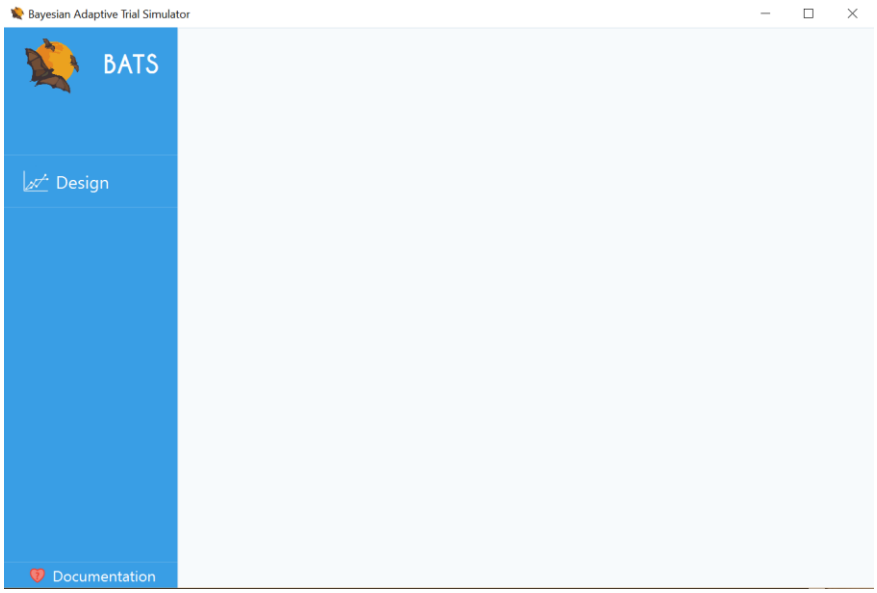
The BATS binary installer runs in Windows 7 or newer. No other dependencies are required to run the software.

License

Using BATS

Initialization

To open the tool, double-click on the ‘BATS’ under the folder. The interface of BATS will display after a few seconds.



The main window is shown as above. It contains a title bar on the top and a menu bar on the left (I need to use number to indicate the area). Users can find two menus in the menu bar:

- **‘Design’**, where users can perform a simulation for a specific type of Bayesian trial design

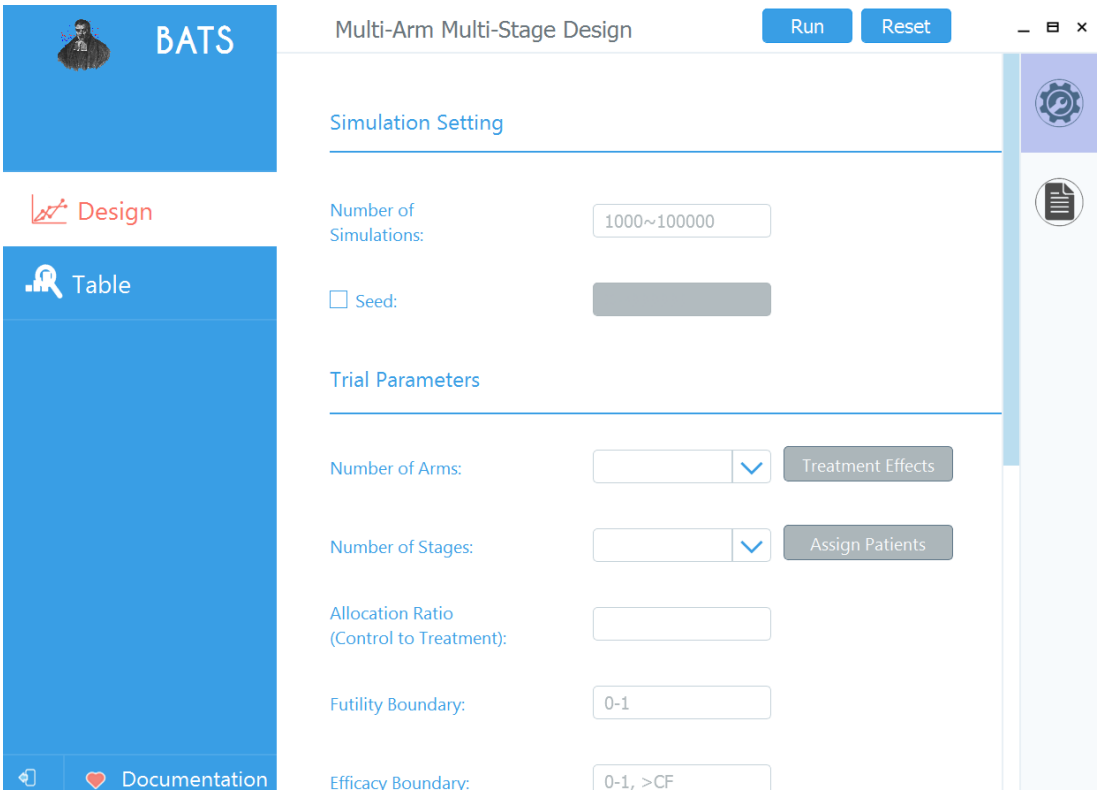
Current supported functions are shown in the following table.

Menu	**Supported Functions**
Design	Multi-Arm Multi-Stage (MAMS) Design

Open Documentation

The users can open the documentation by clicking on the **'Documentation'** button on the bottom of the menu bar

Select a Task



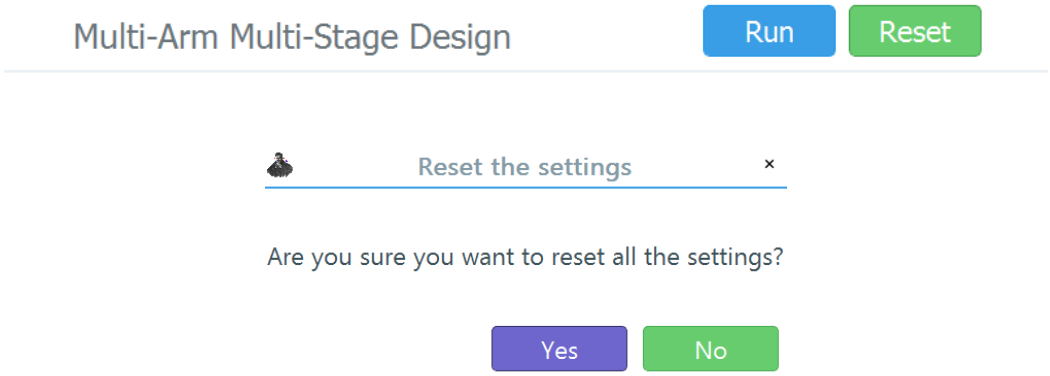
The users can start a task by selecting one of the menus, the corresponding interface for the task directly shows up in the right area of the main window.

The interface has a control panel at the top, a sub menu at the rightmost. Users can switch between settings interface and log interface by clicking on the tabs of sub menu

Run a Task

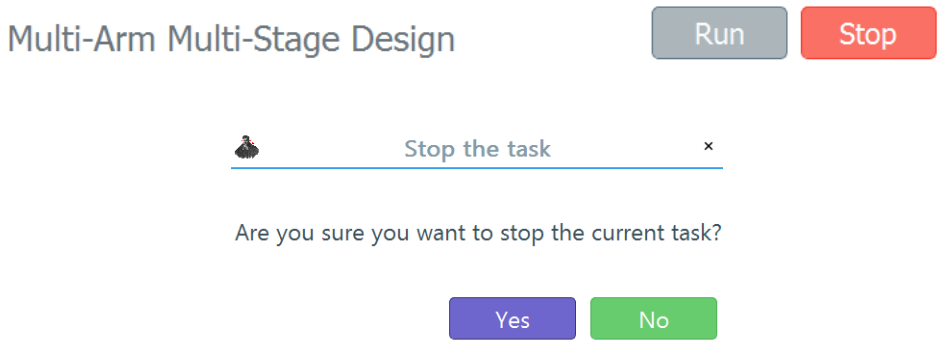
After selecting the specific task to perform and finishing the setting, users can start to run the task by clicking on the **'Run'** button on the top.

Reset a Task



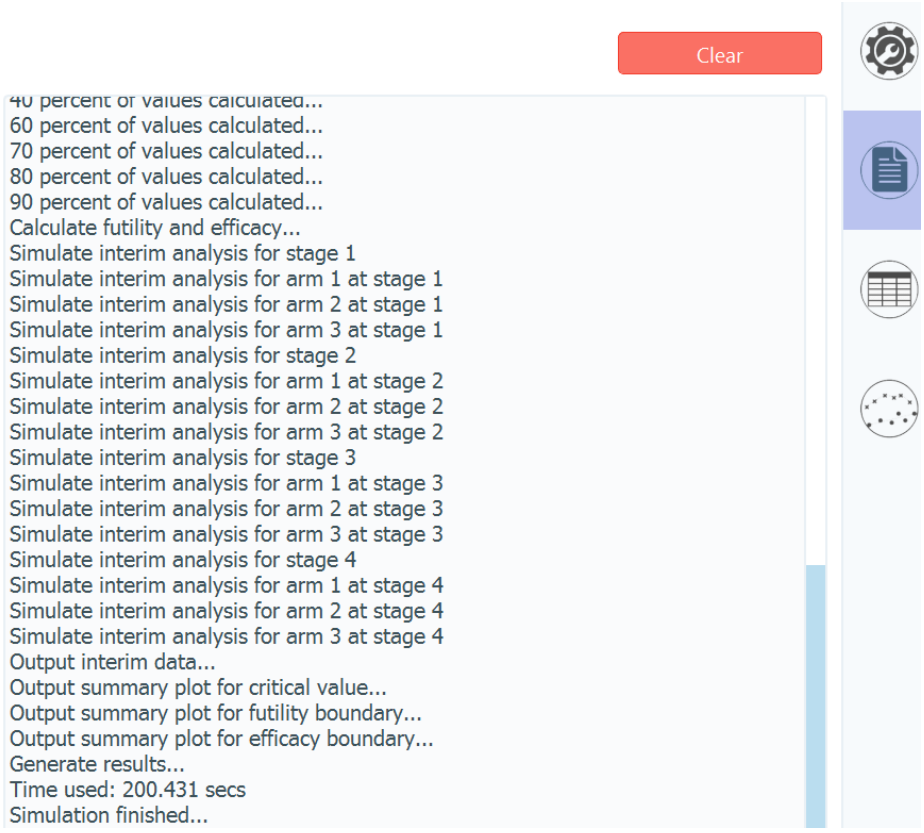
When setting up parameters of the design, users can clear all inputs by clicking on the **'Reset'** button and answering **'Yes'** to the dialog popped up. The input will not be cleared if users response **'No'** or close the dialog.

Stop a Task



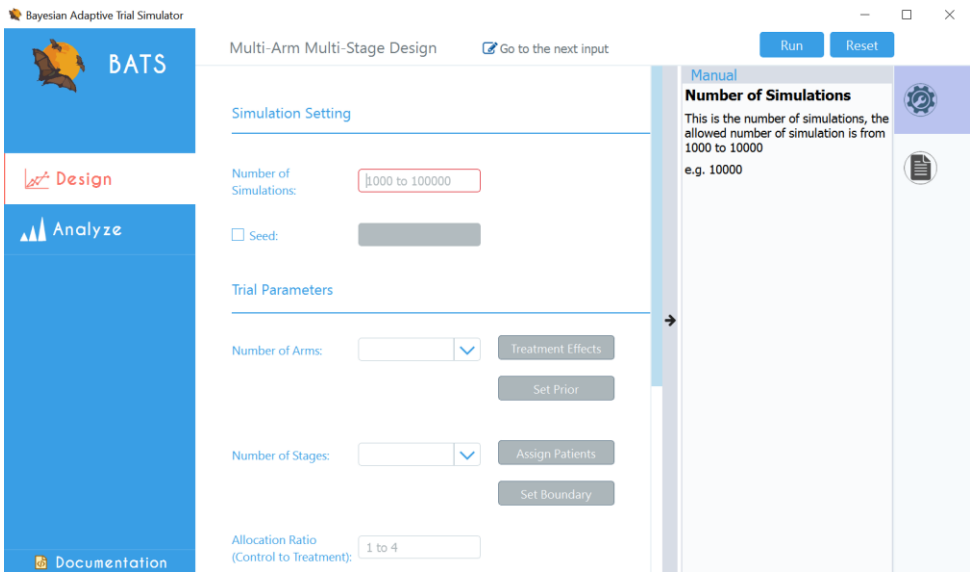
The task could also be stopped by clicking on the **'Stop'** button and response **'Yes'** during running. The task would not be stopped if users response **'No'** or close the dialog. During the task progress, users cannot click on the **'Run'** button or change any input in the setting tab.

Log System



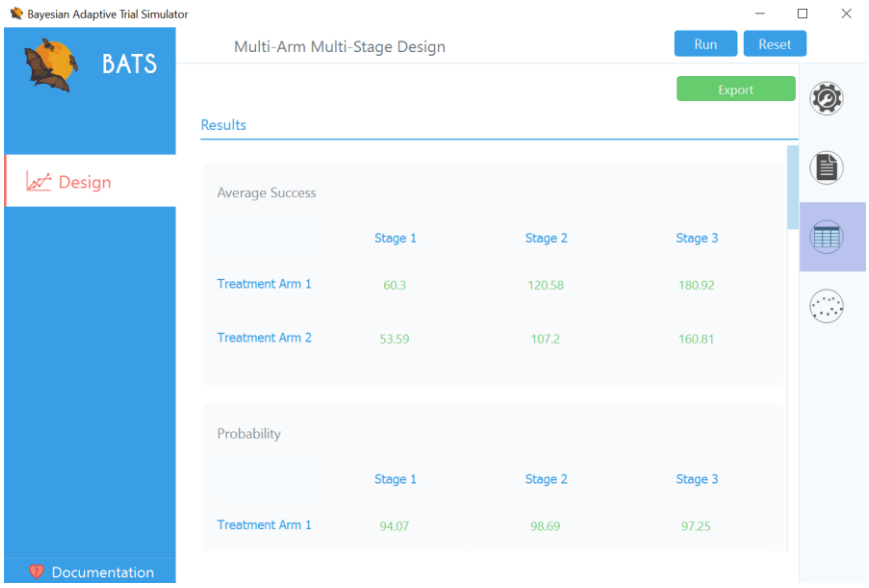
When the task starts, the interface will automatically switch from **'Setting'** tab to **'Log'** tab. The log system will record and show the process of the task. It is useful for users to track the settings for previous tasks. The information for settings will be displayed in red color and the error information will be displayed in green. Users can clear all the log information by clicking on the **'Clear'** button on the top

View Manual

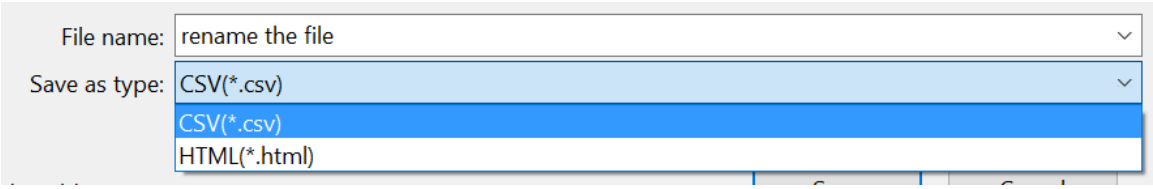


When user hover or focus on the input, a helper will appear in the right panel. It basically tells what the input means for the users. User can hide the manual by clicking on the ‘left arrow’ button.

View Results



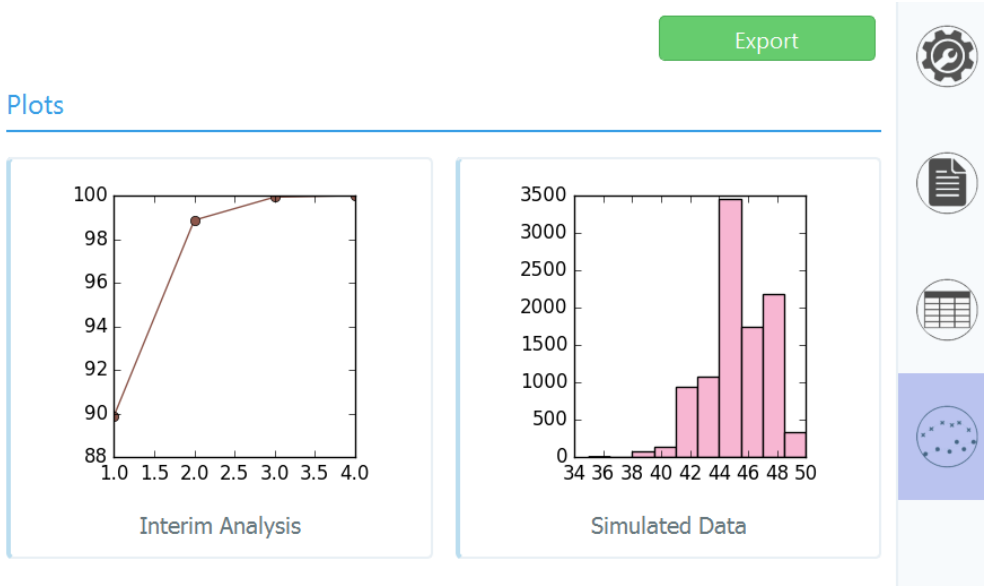
The **'Table'** tab is immediately available when a task is finished and it has summary results to output. Users can view the summary results or export them to the local disk by clicking on the **'Export'** button.



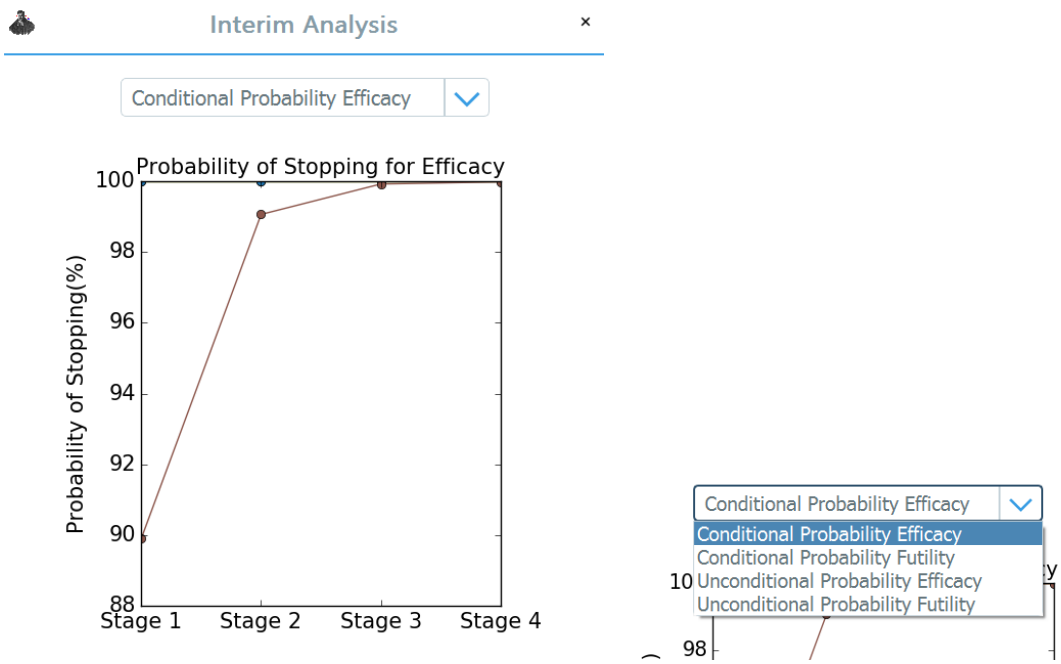
Currently, two file types (.csv and .html) are supported for the exported results and users can specify the output file name in the 'File name:' input.

View Plots

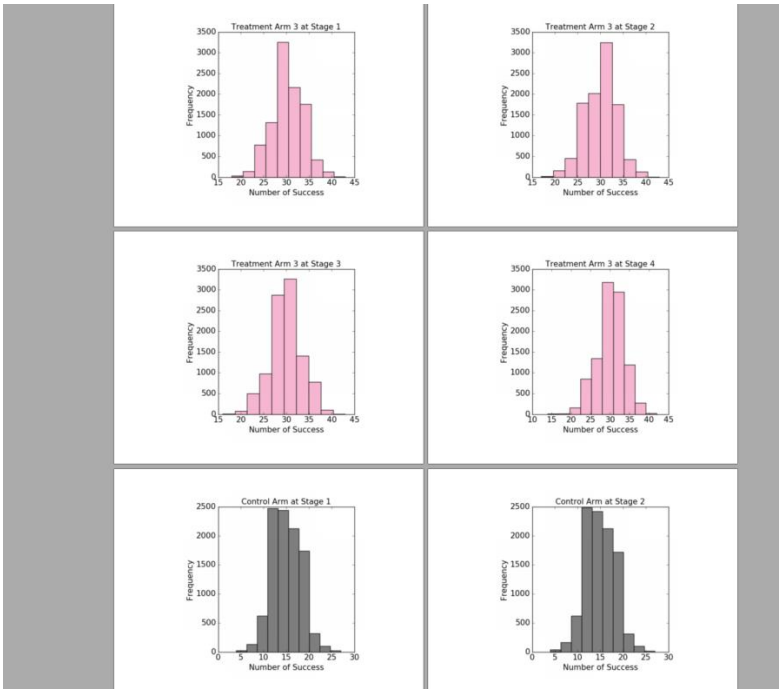
If the results include plots, the **'Plot'** tab will also be available once the task is finished.



The **'Plot'** tab will display modules that corresponding specific type of plots. For example, the tab above contains plots related to interim analysis and the simulated outcomes.



Users can click on each module to open a graph viewer and select a plot to look at through the drop-down box. The graph viewer could be closed by clicking on the close button or press on place outside the viewer. Similar to the tables, the plots can be exported by clicking on the **'Export'** button, in a single pdf file. Each page of the file will contain one plot.



MAMS Design

Introduction

The multi-arm multi-stage (MAMS) design was proposed as a novel adaptive Phase II/III clinical trial design (Royston et al, 2011) in which multiple therapeutic treatments are simultaneously compared to a pooled control. Similar, to a two-arm group sequential design, the trial can be stopped early for overwhelming efficacy, or one or more treatment arms can be stopped early for futility. By simultaneously investigating multiple candidate agents, the design can potentially reduce the cost and time of drug development, particularly in cases where there are a large number of candidate treatments in the pipeline. In addition, this design requires significantly fewer patients compared to separately testing each agent against individual control groups.

Statistical Properties

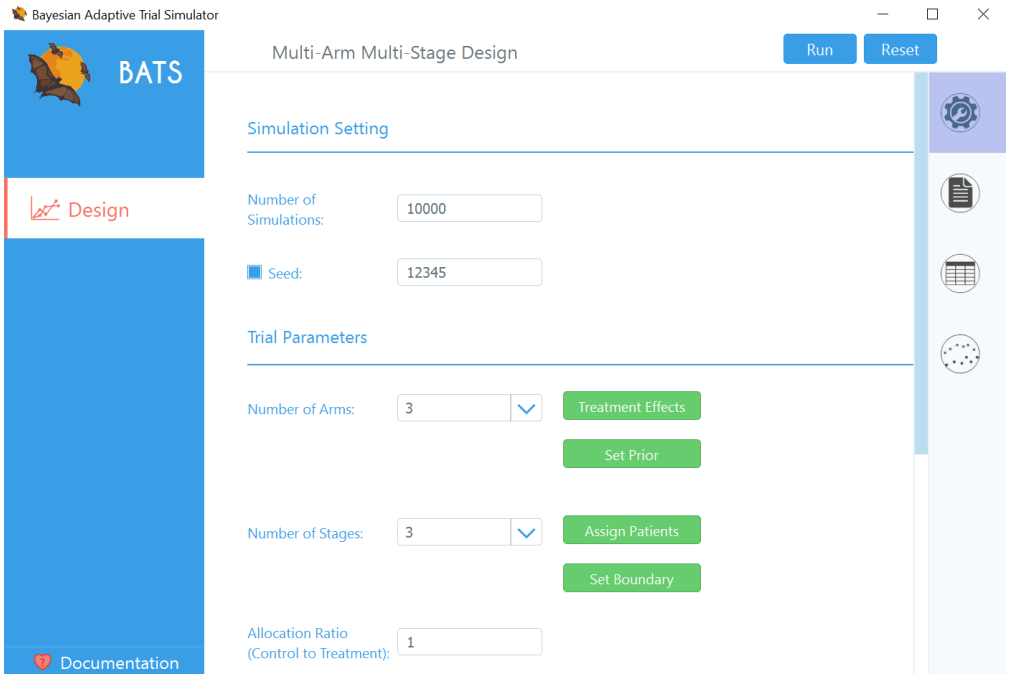
In the general Bayesian MAMS design, subjects may be randomized to a control treatment $(j=0)$ or one of $j=1,\ldots,J$ experimental treatments and the primary outcome Y_{ij} for subjects, $i=1,\ldots,n_j$ are independently Bernoulli distributed with probability p_j, $0 \le p_j \le 1$. Suppose the trial is partitioned in to k stages $(k=1,\ldots,K)$, each terminating in an interim or final analysis respectively. That is, at stage k, a total of n_{jk} subjects have been randomized to each treatment arm, and $Y_{.jk}=\sum_{i=1}^{n_{jk}} Y_{ijk}$ positive outcomes have been observed, where $Y_{.j1} \le \ldots \le Y_{.jK}$ and $Y_{.jk} \le n_{jk}$. At the end of each stage, it might be of interest to calculate the posterior probability that each active treatment is superior to the control treatment. That is, for each treatment arm we calculate the posterior probability of

treatment success assuming a uniform prior and binomial likelihood yielding: $\left(p_j \mid Y_{.jk}, n_{jk}\right) \sim Beta\left(1+Y_{.jk}, 1+n_{jk}-Y_{.jk}\right)$. At each interim analysis we use the respective posterior distributions to calculate the probability that each treatment is superior to control by a pre-specified margin, δ. That is, to test the null hypothesis $H_0 : p_{jk} - p_{0k} \le \delta$, we define the following quantity of interest $P\left(\hat{p}_{jk} - p_{0k} > \delta\right)$. If the probability exceed boundary for efficacy ($C_{E,jk}$) or futility ($C_{F,jk}$) of continued evaluation, randomization to that active treatment is terminated. Similarly, at the end of the trial, we may want to calculate the posterior probability, or alternatively, we may want to calculate the predictive probability (i.e. the probability that we will reject the null hypothesis given additional patients are randomized to each arm). Here, the probability of observing s_j future successes given an additional m_j subjects is calculated from the pmf of the $Beta - Binomial\left(m_j, 1+Y_{.jK}, 1+n_{jK}-Y_{.jK}\right)$ distribution. The predictive probability of success comparing active arm j to control is then defined as

$$\sum_{s_0=Y_{.0K}}^{s_{0,MAX}} \sum_{s_j=Y_{.jK}}^{m_j} P\left(s_j\right) I\left[P\left(\tilde{p}_{jK} - \tilde{p}_{0K} > \Delta\right) > C_P\right], \text{ where}$$

$\tilde{p}_{jK} \sim Beta\left(1+\left(Y_{.jK}+s_j\right), 1+\left(n_{jK}+m_j\right)-\left(Y_{.jK}+s_j\right)\right)$ and C_P is the threshold to reject the null hypothesis $H_0 : \tilde{p}_{jK} - \tilde{p}_{0K} \le \Delta$.

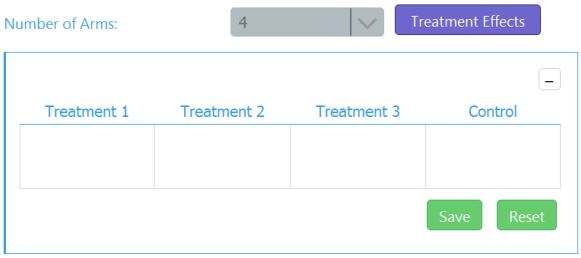
Setting



Number of Simulations: The number of simulations is restricted from 1,000 times to 100,000 times.

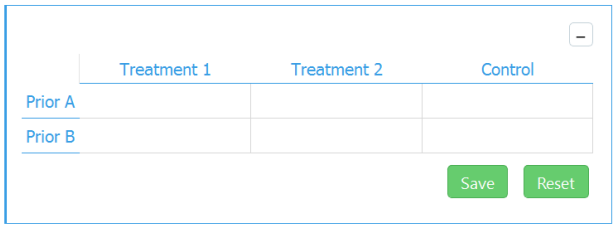
Seed: The seed to generate the look-up table. With the same seed the same table will be generated.

Number of Arms: The number of treatment arms in the trial, including one control arm. The minimum number of arms is 3 and the maximum is 10.



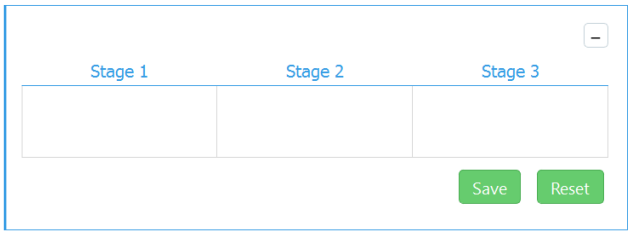
Treatment Effects: The true treatment effect of each arm. Users can specify them after selecting the number of arms and clicking on the **'Treatment Effects'** button. Click on **'Save'** to save the

treatment effects, click on **'Reset'** to reset all the entries. Once the number of arms is changed, all entered treatment effects will be reset.

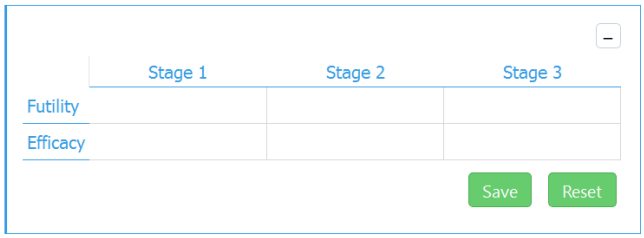


Prior Distribution: The prior distribution of each arm. The prior has a Beta(a, b) distribution, users can input the prior distribution for each arm. The first row is for the first parameter, a in beta distribution, while the second is for the second parameter, b.

Number of Stages: The number of stages in the trial, ranging from 2 to 6.



Patient at Each Stage: The number of total patients at each stage. Users can specify them after selecting the number of arms and stages and clicking on the **'Assign Patients'** button. Click on **'Save'** to save the assignments, click on **'Reset'** to reset all the entries. Once the number of stages is changed, all entered numbers will be reset.

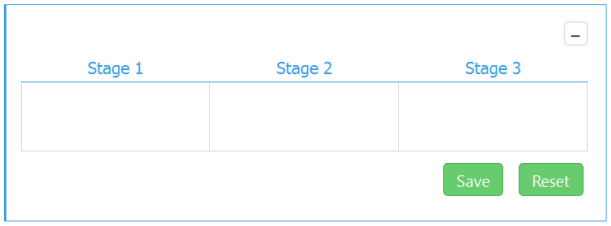


Stopping Boundaries: The users can specify the stopping boundary C_F and C_E. The boundaries can change over stages, however, the efficacy boundary should always be greater than or equal the futility boundary.

Allocation Ratio: The allocation ratio of control to treatment. In MAMS design, we assume the allocation ratio is fixed and all treatment arm has the same number of patients.

Clinically Significant Difference: The clinically significant difference δ to be detected in the trial.

Predictive Probability: If this box is checked, the simulation will include calculating predictive probabilities. If not, the simulation will finish after simulating interim analysis.



Number of New Patients: The number of total patients planned to add to calculate the predictive probabilities at each stage. Users can enter a number at each stage, which means the predictive probability will be used to compare to the stopping boundaries. If users enter 0 to that, only posterior probability will be calculated to evaluate the stopping boundaries.

Success Boundary: C_P. We will conclude the observed pair will succeed if greater than this boundary.

Use Same Clinically Significant Difference or Specify a New Value: Sometimes users may want to use a different clinically significant difference value for the predictive probability, that is, $\Delta \neq \delta$. If the box is checked, then the same value as in the interim analysis will be used, otherwise a new value must be entered.

Results

Average Success: The average cumulative count of patients with success outcomes for each treatment arm at each stage.

Probability: If the posterior probability is calculated, that will be the posterior probability $P\left(\hat{p}_{jk} - \hat{p}_{0k} > \delta\right)$. Otherwise, it is the predictive probability.

Conditional Futility: The conditional probability of stopping a treatment arm for futility at each stage. For each arm each stage, that is calculated from dividing the cumulative number of stops for futility by number of simulations.

Unconditional Futility: The unconditional probability of stopping a treatment arm for futility at each stage. For each arm each stage, that is calculated from dividing the number of stops for futility at that stage by number of simulations.

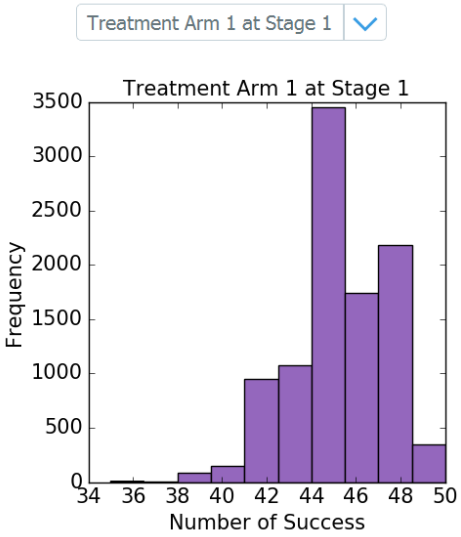
Conditional Efficacy: The conditional probability of stopping a treatment arm for efficacy at each stage. For each arm each stage, that is calculated from dividing the cumulative number of stops for efficacy by number of simulations.

Unconditional Efficacy: The unconditional probability of stopping a treatment arm for efficacy at each stage. For each arm each stage, that is calculated from dividing the number of stops for efficacy at that stage by number of simulations.

Predictive Probability: The posterior predictive probability of each treatment arm. This measures how likely the trial will reach a successful outcome given a number of future patients.

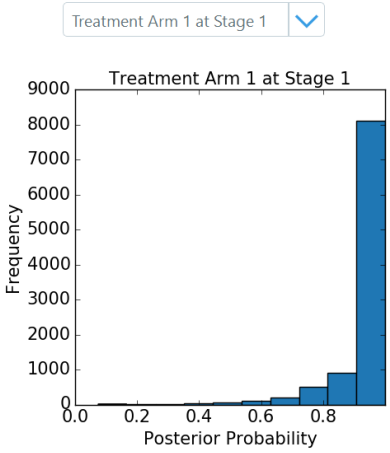
Plots

Simulated Data



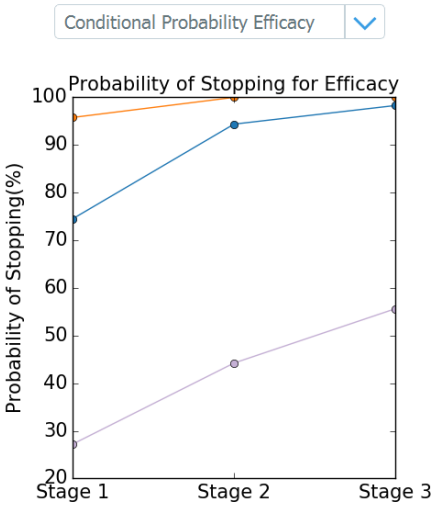
The histograms of the simulated outcome for each arm at each stage. The data comes from the same arm will be plotted in the same color.

Predictive Probability/ Posterior Probability



The histograms of the posterior probability/predictive probability calculated during the simulation.

Interim Analysis



The plots for conditional/unconditional futility and efficacy. Each line represents a treatment arm.

Reference

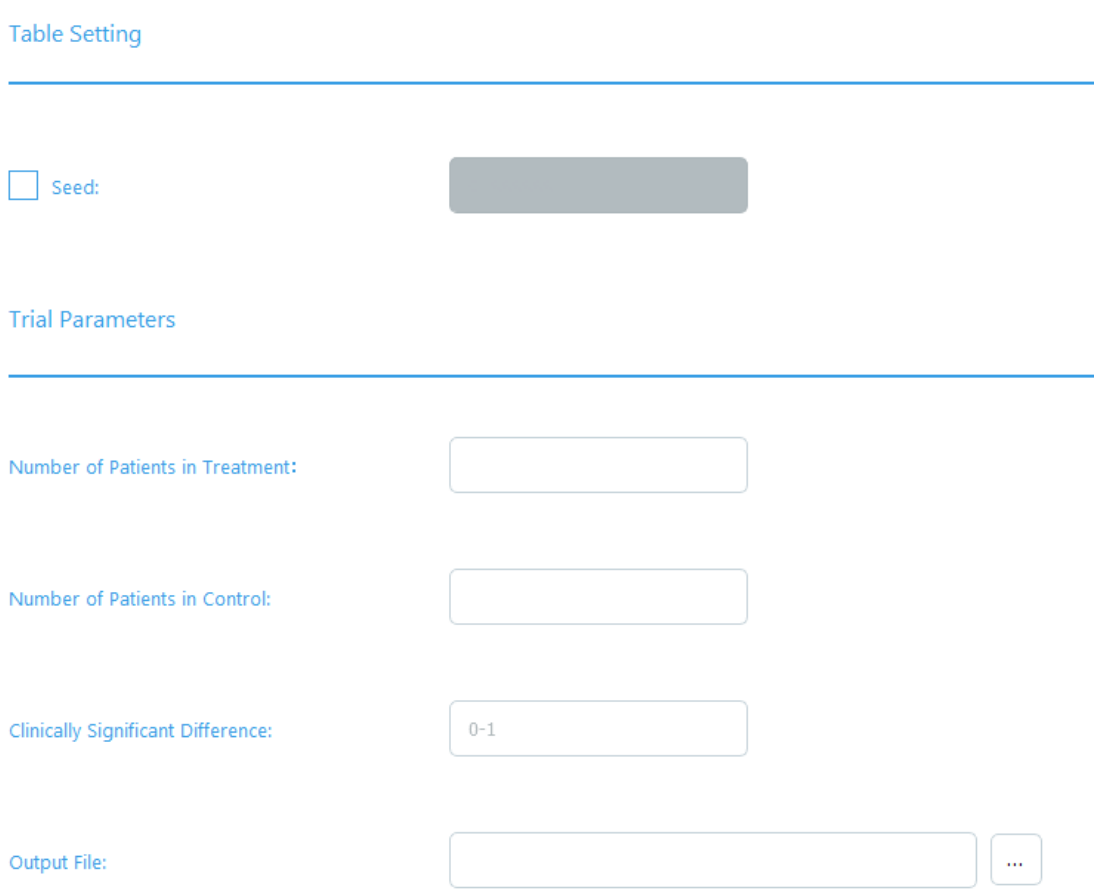
Royston, P., Barthel, F. M.-S., Parmar, M. K. B., Choodari-Oskooei, B., & Isham, V. (2011). Designs for clinical trials with time-to-event outcomes based on stopping guidelines for lack of benefit. *Trials*, *12*(1), 81. http://doi.org/10.1186/1745-6215-12-81

Critical Value Look-up Table

Introduction

It is useful to generate a look-up table to store critical values for all possible outcomes that could be observed at each analysis, to avoid redundant calculations.

Setting



Users can specify the followings in creating critical value look-up table:

Seed: The seed to generate the look-up table. With the same seed the same table will be generated.

Number of Patients in the Treatment: The number of patients in the treatment arm.

Number of Patients in the Control: The number of patients in the control.

Clinically Significant Difference: The clinically significant difference.

Output File: Specify the output directory for the generated table.

Results

The output file will be in csv format. The first column is the number of success in the treatment, the second column is the number of success in the control and third column is the critical value calculated from the observed outcome.