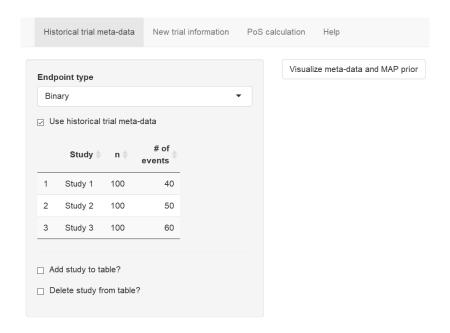# Probability of Success Using RBesT
RShiny App Walkthrough

James Normington

July 8, 2019

In this document, I briefly walk through a Shiny App to compute a trial's probability of success (PoS) using Sebastian Weber's RBesT package.
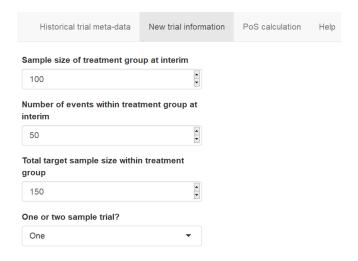
Historical trial meta-data

Use the first tab to specify the type of endpoint and whether or not your analysis should utilize historical trials' meta-data. If the *Use historical trial meta-data* box is checked, you can directly edit the table. If there are more than three trials of meta-data available, add a study using the *Add study to table?* checkbox. To delete a row of meta-data, use the *Delete study from table?* checkbox. To create a forest plot to visualize the meta-data and MAP prior, click the *Visualize meta-data and MAP prior* button; it should take around 10 seconds for the plot to appear. To change the priors for τ^2 and β, do so on the *Model specification* section of the "PoS calculation" tab.

New trial information

Use the second tab to specify the sample size and observed statistics at interim, as well as the total target sample size at the end of the trial. For two arm studies (i.e., treatment vs. control), select "Two" from the *One or two sample trial?* field and add the information underneath.
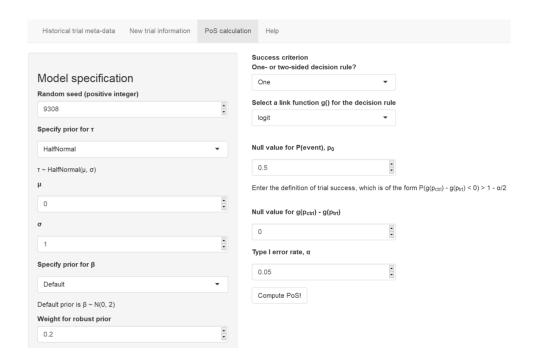

PoS calculation

Use the third tab to specify the remaining hyperpriors, define the criterion for trial success, and compute the PoS.

Model specification

Use this section to select a random seed (for reproducibility) and specify priors for τ and β. The default prior for β (for a given endpoint) is listed; select *Specify* to change it. The code also automatically adds a robust component (e.g., a Uniform(0,1) for binary endpoints, a diffuse Gaussian distribution for Normal endpoints) to the prior mixture distributions. The default value is 0.2. To protect against an overly informative MAP prior, enter in a higher weight (say, 0.4). To allow the MAP prior to be more informative, enter in a lower weight (say, 0.1). It is not recommended to enter in a weight higher than 0.7.

Success criterion

Use this section to specify the definition of trial success. Your decision rule can be specified as one or two-sided. If the trial is two sample, you can select a link function for the decision rule. For example, with binary endpoints, you can make a decision based on absolute difference in proportions (identity link), relative difference in odds (logit link),

Historical trial meta-data   New trial information   PoS calculation   Help

Model specification

Random seed (positive integer)

9308

Specify prior for τ

HalfNormal

$\tau \sim \text{HalfNormal}(\mu, \sigma)$

μ

0

σ

1

Specify prior for β

Default

Default prior is $\beta \sim N(0, 2)$

Weight for robust prior

0.2

Success criterion

One- or two-sided decision rule?

One

Select a link function g() for the decision rule

logit

Null value for P(event), p_0

0.5

Enter the definition of trial success, which is of the form $P(g(p_{ctrl}) - g(p_{trt}) < 0) > 1 - \alpha/2$

Null value for $g(p_{ctrl}) - g(p_{trt})$

0

Type I error rate, α

0.05

Compute PoS!

or relative difference in proportion (log link). If the trial is one sample, you can specify its sidedness with the *Lower or upper tail?* field. The text underneath should update as you switch between one or two samples, one or two sided decision rules, and (if one sample) lower/upper tail. Then, enter in the null hypothesized value and desired type I error rate. Finally, click the *Compute PoS* button to compute the probability of trial success. If you are not using historical data, this should compute in less than a second. If you are using historical data, this could take several seconds (though usually not more than one minute).