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# A Simple Guide to R-PsiMLE

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This guide is intended for R-PsiMLE version 2.0 (2015)

For the latest version, visit [panamath.org/psimle/](http://panamath.org/psimle/)

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# 1 Introduction

Researchers in psychophysics, cognitive, developmental, and comparative psychology, as well as neuroscience and computational modelling have long been interested in the relationship between physical sensation and our subjective experience of it. For example, how well can people estimate how many things are in a collection, or how long a sound lasted for, or how salty some food was?

The most popular methods for measuring the relationship between physical sensation and our perception of it are the magnitude estimation, magnitude production, and magnitude reproduction tasks. For example, a magnitude estimation task might present the participant with some target value (e.g., a tone that lasted three seconds) and ask them to estimate it (e.g., say how long the tone was).

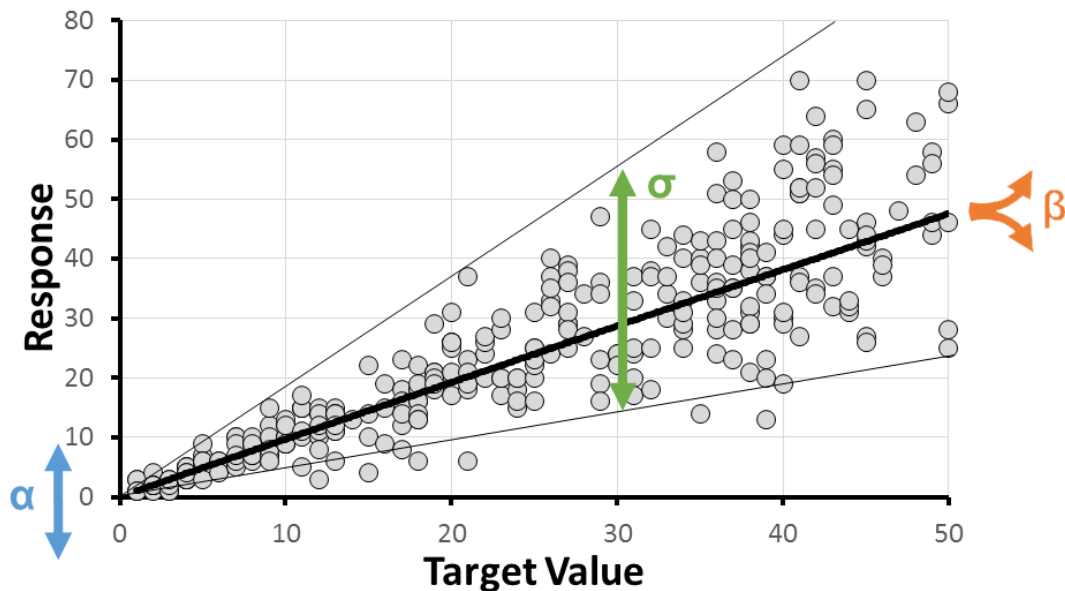


Figure 1: Traditional magnitude estimation, production and reproduction data looks like this and is captured by three parameters:  $\alpha$ , in blue, indexes the intercept or up-down shift;  $\beta$ , in orange, indexes the expansion or compression of the responses as target value increase, and  $\sigma$ , in green, is the growing scalar variability.

As illustrated in Figure 1, these tasks estimate three parameters of interest:  $\alpha$  (or intercept), measuring the constant amount of under- or over-estimation in our perception,  $\beta$  (or exponent/slope), measuring whether our perception compresses

or expands the physical sensation, and  $\sigma$ s (also measured as the coefficient of variance), measuring the amount of noise or uncertainty in our perception.

R-PsiMLE provides researchers with a straightforward and simple way of measuring  $\alpha$ ,  $\beta$ , and  $\sigma$  through a maximum-likelihood estimator (MLE) procedure without any previous experience. Additionally, R-PsiMLE permits Bayesian data analysis where information on priors is known. R-PsiMLE provides estimates that are valid and more reliable and efficient compared to traditional linear regression on log-log plots and measures of coefficients of variance (for details, see Odic et al., under review but available upon request, [1]).

This guide explains how R-PsiMLE should be installed, how it can be used to analyse data, and provides a guide for the optional and advanced settings it can be used for (e.g., to check if observers counted time or number).

## 1.1 Bayesian Data Analysis

Although the MLE method is a significant improvement over the traditional methods (see [1]), there are additional advantages that could be gained from Bayesian data analysis. In the Bayesian approach, further information is provided about the prior expectations about the distributions of  $\beta$  and  $\sigma$ , allowing for more efficient and accurate estimation. Furthermore, the logic of Bayesian data analysis is substantially more sound and not reliant on traditional frequentist analysis, which carries a number of serious issues (see Kruschke, 2012).

At the same time, where Bayesian data analysis gains sophistication, it also increases in complexity. We cannot assume that most of our readers are familiar with these methods. As a result, the bulk of R-PsiMLE and this guide focus entirely on MLE methods. However, the R-PsiMLE application does allow for (simplistic) Bayesian data analysis (see 5.1). We emphasize, however, that users really interested in this option should use the R and JAGS code provided online once they understand the logic of Bayesian parameter estimation. JAGS code is also available in the published manuscript.

## 2 Installing R-PsiMLE

You can download R-PsiMLE for free from [panamath.org/psimle/](http://panamath.org/psimle/). R-PsiMLE runs through Java and the R Statistical package, both of which are free and available for Windows, MacOS, or Linux platforms, allowing R-PsiMLE to work on all of them. Both Java and R must be installed prior to running R-PsiMLE.

### 2.1 Installing Java and R

Most computers have Java already installed. The latest version can be downloaded from [java.com/en/download/](http://java.com/en/download/). The latest version of R can be downloaded from [r-project.org](http://r-project.org). Once Java and R are installed, installing R-PsiMLE is extremely straightforward.

### 2.2 Installing R-PsiMLE on Windows

On any version of Windows, installing R-PsiMLE is simply a matter of unzipping the file downloaded from [panamath.org/psimle/](http://panamath.org/psimle/) into a folder and double clicking on the `r-psimle.jar` file.

Because R-PsiMLE requires a copy of R to run, you will be asked to specify where you installed R on your computer the first time you run R-PsiMLE (see Section 3.1). By default, this folder is located in `C:/Program Files/R/` or in `C:/Program Files (x86)/R/`. It is sufficient for you to select the R folder, though you may also select the `RScript.exe` file in the Bin folder.

### 2.3 Installing R-PsiMLE on Mac OS

On any version of Mac OS, installing R-PsiMLE is a matter of unzipping the file downloaded from [panamath.org/psimle/](http://panamath.org/psimle/) into a folder (preferably into the Application folder, but any folder will do) and double clicking on the `r-psimle.jar` file.

Because R-PsiMLE requires a copy of R to run, you will be asked to specify where you installed R on your computer the first time you run R-PsiMLE (see Section 3.1). By default, this folder is located in your `/usr` folder. It is sufficient for you to select the `/usr` or `/bin` folders, though you may also select the `RScript` script file within the bin folder.

## 2.4 Bayesian Option: Installing JAGS and rJAGS

For users interested in extending R-PsiMLE and using Bayesian parameter estimation, two additional packages are required. First, users should download JAGS - a freely available Gibbs sampler application compatible with Windows, Mac, and Linux, and one of the most popular solutions for Bayesian data analysis today: [mcmc-jags.sourceforge.net](http://mcmc-jags.sourceforge.net).

Second, users should install rJAGS - the library in R that connects R to JAGS and allows for effortless use between the two applications. By installing rJAGS, users can also use the R-PsiMLE application for Bayesian estimation (though we stress that advanced users familiar with JAGS should just download our free code online, as it allows much more control and flexibility compared to R-PsiMLE). To install rJAGS, open R and type `install.packages('rjags')`. The CODA package should be automatically installed, as well.

### 3 Using R-PsiMLE in Four Steps

Once R-PsiMLE is installed, you can double click on the r-psimle.jar file every time you need to estimate parameters from your data. If on a Mac, the first time you open the file you may have to hold the CONTROL button to override a permission error not allowing you to open downloaded applications. To actually estimate parameters, you go through four steps (one which you only need to do once, and one of which is optional). Note that this section assumes that the Bayesian option is not being used; for further information on it, please see 5.1.

#### 3.1 Step One: Check Dependencies

This step is required for R-PsiMLE to know where you installed R. This step is only required the first time you run R-PsiMLE or if you update your version of R. On Windows, By default, this folder is located in C:/Program Files/R/ or in C:/Program Files (x86)/R/, and on Mac OS this folder is located in your /usr/ folder. Press **Browse** to locate the folder (see Figure 2 below). On Windows, it is sufficient to select the R folder in Program Files and press Open; on Mac OS, you can select the bin folder within /usr and press Open.

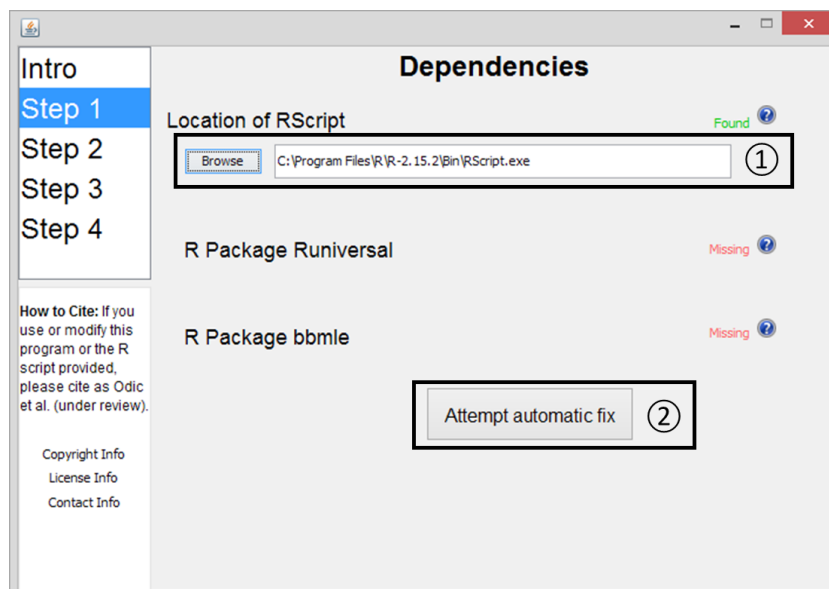


Figure 2: Screenshot of Step 1. (1) Press Browse and locate your R folder. (2) If any of the packages are missing, press Automatic Fix to install them.

Once R is located by the program, it will check whether two R packages are installed that allow R to interface with the R-PsiMLE software. The two packages are *RUniversal* and *bbmle*. If the packages are not found, press **Automatic Fix**, as shown in Figure 2. In almost all situations, this will install the packages and you can proceed to the next step.

If the Automatic Fix does not install the required packages, open R itself, and type in two commands: `install.packages("RUniversal")` and `install.packages("bbmle")`. Restart R-PsiMLE once you run these commands. See Figure 3 for an example.

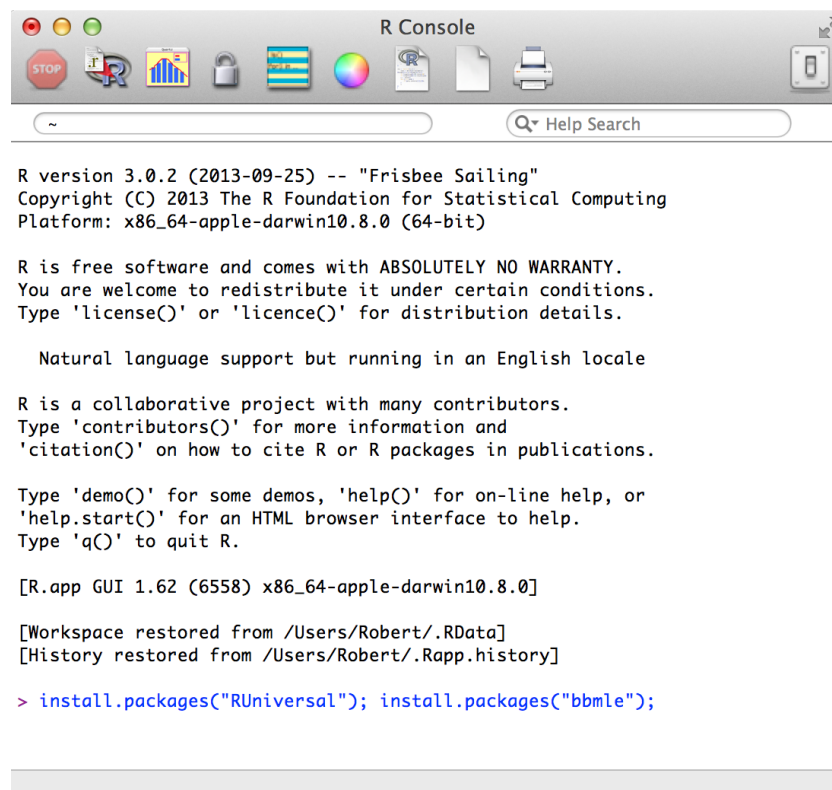


Figure 3: A screenshot of typing the manual commands. *Do this only if the Automatic Fix does not work.*

## 3.2 Step Two: Upload Data

Select the data file or folder that contains multiple data files that should be analyzed (see Figure 4). The data files can be in csv, xls, xlsx, xlsxm, or txt format. The selected folder should **only contain the data files**. If other files exist in the



folder, R-PsiMLE will attempt to analyze them, as well, often producing an error.

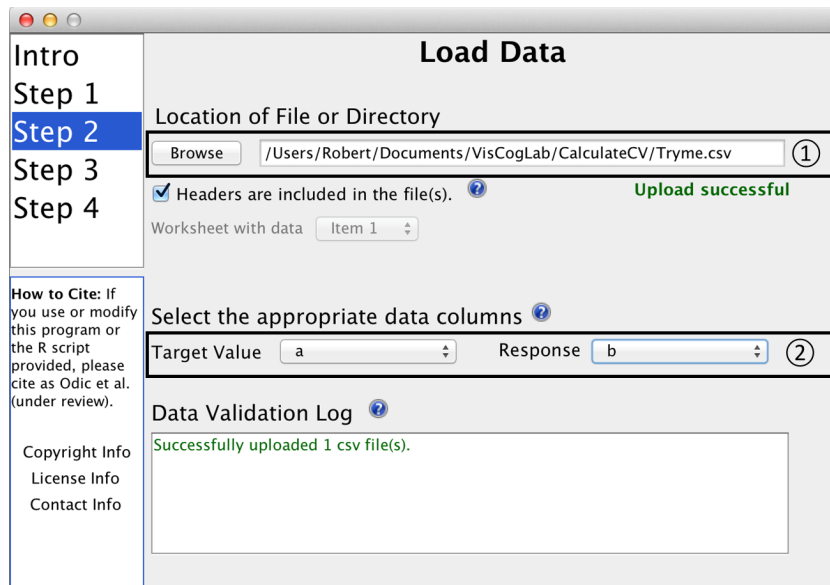


Figure 4: Screenshot of Step 2. (1) Press Browse to locate the data file or folder (the folder can only contain data files). (2) Select the column that contains target values and the column that contains responses.

Once the data is uploaded, you need to select which column corresponds to the **Target Values** (e.g., the number of dots presented, or the actual weight, or the amount of salt), and which column corresponds to the **Responses** (e.g., what the subject actually said or produced). If your data files contain a header (a row that names each column), you should make sure that **Header Row** is checked. If your data does not have a header, columns are named alphabetically. See Figure 5 for an example of data files with and without a header.

	A	B	C	D
①	1 Subject	Trial	Target Value	Response
2	1	1	100	81
3	1	2	60	55
4	1	3	100	105
5	1	4	60	53
6	1	5	40	50
7	1	6	40	46

	A	B	C	D
②	1	1	100	81
2	1	2	60	55
3	1	3	100	105
4	1	4	60	53
5	1	5	40	50
6	1	6	40	46
7	1	7	100	124

Figure 5: (1) An example of a data file that contains a header. (2) An example of a data file that does not contain a header.

### 3.3 Step Three: Optional Settings

This step is entirely optional, and you can skip it and let R-PsiMLE analyze the data in Step Four. But, R-PsiMLE also offers a host of optional settings that you can apply (see Figure 6). For example, you can choose to remove outliers, or to check if observers guessed.

The optional settings allow you to apply different models to your data. A thorough review of these options is explained in [1].

#### 3.3.1 Outliers

If you wish to remove outliers from your data, select this option and input how many standard deviations from the expected Target Value you would consider an outlier (we recommend values around 2.5).

#### 3.3.2 Confidence Intervals

One advantage of R-PsiMLE, is that it simplifies the construction of confidence intervals and allows them to be computed for each individual observer. Although there is continued discussion about how confidence intervals should be interpreted (Hoekstra, Morey, Rouder, & Wagenmakers, 2014; Whitener, 1990), they complement traditional p-values (Colegrave & Ruxton, 2003; Gardner & Altman, 1986). Furthermore, many statisticians urge researchers to use confidence intervals for power and effect size calculations, for aiding in interpreting null results, and for broader statistical inference (Hoenig & Heisey, 2001). In the case of Bayesian statistics, the credibility intervals provide us with an estimate of the range in which the true parameter value is likely to be, and are also calculated with ease.

The confidence interval in the maximum-likelihood method is constructed by first taking each estimates standard error (i.e., observed Fisher information), and multiplying it by the desired z-value (e.g., 1.96 for 95% intervals). For example, if our  $\theta$  is estimated at 0.20, and the SE of this estimate is 0.015, our 95% confidence interval would be  $[0.20 - (0.015*1.96), 0.20 + (0.015*1.96)] = [0.17, 0.23]$ .

In the R-PsiMLE application, 95% confidence intervals are automatically reported in the output file.

### 3.3.3 Alternative Models

Not all researchers use power-law models. Here, you can select to use either power-, linear- or log-based model (or all of the above). Selecting multiple models will also automatically include information on whether one of them was a better fit in the output (see Section 4.1).

### 3.3.4 Significance Test

If you wish to test whether any of your parameters (e.g.,  $\alpha$ ,  $\beta$ , or  $\sigma$ ) exceed a certain value, or if a model with different parameter values is a better fit to your data, you can select the options here.

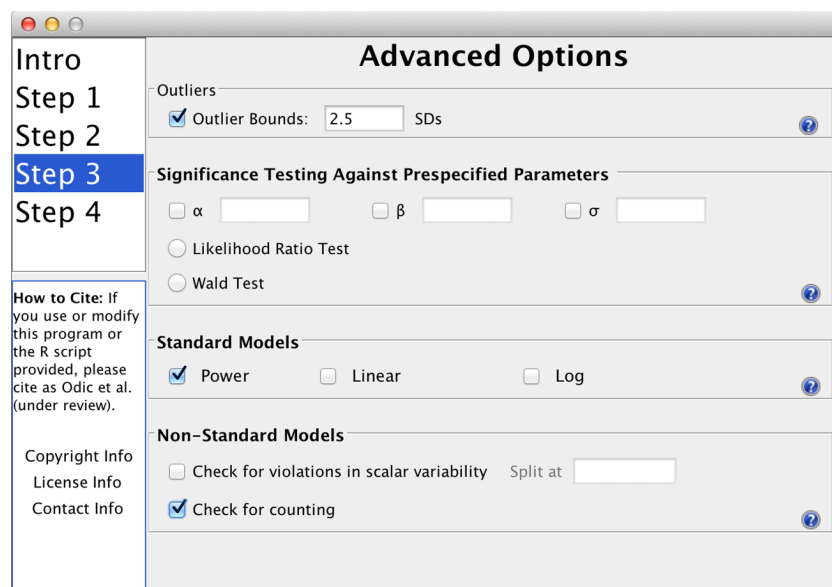


Figure 6: Screenshot of Step 3. These settings are entirely optional. See [1] for details.

Significance testing is easily accomplished in MLE frameworks through either the Wald test (analogical to a t-test) or the Likelihood Ratio tests (analogical to an ANOVA). In general, results from these two inferential statistics will produce near-identical results (Buse, 1982; Engle, 1984). The Wald test can be used on individual parameters, and computes the squared difference between the observed parameter value (e.g.,  $\beta$  of 0.80) and the null hypothesis value (e.g.,  $\beta$  of 0), and divides this difference by the parameter estimates variance (the estimates squared

SE); we can compute a p-value by comparing this ratio against the Chi-squared distribution with one degree of freedom.

Likelihood Ratio tests compare the likelihood values of two models (e.g., the maximum-likelihood model and the null model) where some number of parameters are fixed to a specific value. For instance, the log-likelihood value of the standard psychophysical model may be 100, while the log-likelihood of a model applied over the same data but with  $\sigma$  fixed at 0.20 may be 50. The difference of these two log likelihoods obeys a Chi-squared distribution (with the number of degrees of freedom equivalent to the difference in the number of free parameters in these models), and returns a p-value that one model is a significantly better fit than the other.

### 3.3.5 Non-Standard Models

In some situations, researchers are interested if the standard model (i.e., scalar variability) is violated. For example, observers might have counted time or number, or the  $\sigma$  value might be different for low- versus high-intensities (e.g., below 1 second and above 1 second durations). For an in-depth overview of non-standard models, please see [1].

If there are theoretically motivated reasons for you to suspect that either of these non-standard models may apply to the data, check of these boxes. R-PsiMLE will automatically test whether the standard or non-standard model is a better fit to the data (see Section 4.1).

### 3.3.6 Model Comparison via AIC

Researchers are often interested in examining whether the data is better fit by the standard psychophysical model or some different model (e.g., one where observers counted, or where scalar variability was violated). In these cases, the models are not nested and may differ in the number of free parameters they have, making the Likelihood Ratio test inappropriate. A more appropriate test for model comparison is to compute each models Akaike Information Criterion (AIC) value, which adjusts the likelihood value with respect to the number of free parameters (Myung, 2003). As the number of parameters grows, models will naturally fit the data better, but at the price of overfitting; AIC protects against this, penalizing the likelihood by

the number of parameters the model has.

In the Bayesian version, one can either use the DIC or Bayes Factor for model comparison. Each has its own disadvantage: while DICs are easy to compute, they generally like AIC values overstate the evidence against the null hypothesis; Bayes Factor, on the other hand, can be difficult to calculate.

To use AIC for model selection, we first compute the AIC value for each model, and then take the difference between these values (absolute AIC values are meaningless, and we only care about the difference). As a rule of thumb, differences below 2.0 suggest that the two models fit the data equivalently well, values above 3.0 suggest that one model fits the data better, and values above 10.0 suggest a substantial preference for one model (Burnham & Anderson, 2002, 2004; Myung, 2003). Additionally, we can compute AIC weights, which give us a rough probability that one model is better than the other; by dividing two weights, we can get an estimate of approximately how many times one model is better than the other. Note that the AIC method does not produce p-values.

In R-PsiMLE, the AIC method is used whenever the standard model is compared to a non-standard one (see 3.3.5). The output returns whether either of the models is a better fit (sometimes there is no evidence that either is better), as well as the AIC difference.

### 3.4 Step Four: Estimation and Graphs

Once all the data is uploaded and optional settings selected, select the folder where you want to save the output and press **GO** (see Figure 7). The output will be in an xlsx format and will contain names of files, the parameters, and the confidence intervals for them. See Section 4.1 for any additional details about the output.

You can also select to output plots of the fit data and the applied models in PDF format. As stressed in Section 4.2, we strongly recommend visually inspecting the output to make sure the fit models are appropriate for the data. See Section 4.2 for any additional details about the plots.

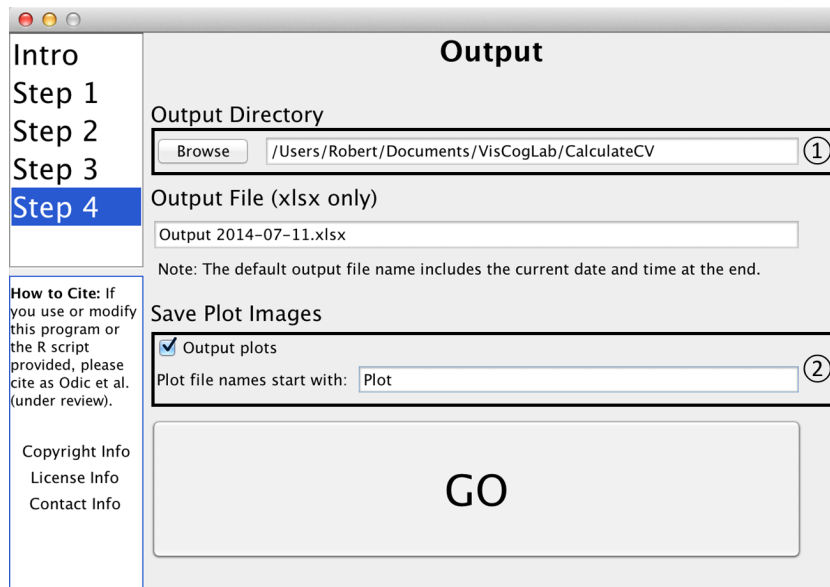


Figure 7: Screenshot of Step 4. (1) Press Browse to select the folder where you would like the output file saved. (2) Select whether you want the plots to be saved and, if so, what name should be appended to them. When done, press GO to perform the estimation procedure.

## 4 Understanding the R-PsiMLE's Output

R-PsiMLE outputs both an xlsx file (called the output file) that contains all the estimated parameters, confidence intervals, and any optional settings, as well as a set of plot files.

### 4.1 Understanding the Output File

An example of the default output file (i.e., output file without any optional settings) is shown in Figure 8. The basic output file is simple and contains the subject file read, the estimated  $\alpha$ ,  $\beta$ , and  $\sigma$ , and their confidence intervals (which give a numerical sense of the certainty of the estimate).

	①			②									
	A	B	C	D	E	F	G	H	I	J	K	L	M
1	subject	alpha	beta	sigma	alpha_ci-	alpha_ci+	beta_ci-	beta_ci+	sigma_ci-	sigma_ci+	num_trials	num_outliers	
2	subject1.csv	8.18213	0.60887	0.21826	5.2341528	11.1301072	0.5497956	0.6679444	0.177394	0.259126	60	0	
3	subject10.csv	0.35279	1.13958	0.28289	0.1575544	0.5480256	1.0507332	1.2284268	0.2283628	0.3374172	60	0	
4	subject2.csv	1.67651	0.90146	0.29986	0.5990392	2.7539808	0.7937776	1.0091424	0.2410992	0.3586208	60	0	
5	subject3.csv	0.38429	1.10378	0.33874	0.1263344	0.6422456	0.9942748	1.2132852	0.271512	0.405968	60	0	
6	subject4.csv	7.44424	0.67742	0.21542	4.5835416	10.3049384	0.6152292	0.7396108	0.1747892	0.2560508	59	1	
7	subject5.csv	0.3191	1.18261	0.3133	0.0761776	0.5620224	1.0567976	1.3084224	0.2519324	0.3746676	60	0	
8	subject6.csv	7.16815	0.66212	0.45107	-0.19508	14.53138	0.4982444	0.8259956	0.3541872	0.5479528	59	1	
9	subject7.csv	1.30849	0.9339	0.27495	0.5452856	2.0716944	0.8390752	1.0287248	0.2221084	0.3277916	60	0	
10	subject8.csv	4.67113	0.7001	0.2909	2.3188556	7.0234044	0.618858	0.781342	0.2346088	0.3471912	60	0	
11	subject9.csv	1.02191	0.93262	0.35451	0.259666	1.784154	0.8120408	1.0531992	0.2833816	0.4256384	60	0	

Figure 8: An example of a basic output file. (1) The estimated parameters for each subject. (2) The 95% confidence intervals for each parameter, calculated by taking the standard error of each parameter and multiplying it by 1.96.

When optional settings are selected, the output file contains two additional things (see Figure 9):

- For each statistical test run (e.g., Wald's Test), R-PsiMLE will add a column with the corresponding p-value. If this value is lower than a set alpha value (e.g., 0.05), then the parameter or model tested was different from the tested value. For further details on interpreting these tests, see [1].
- For each additional model run (e.g., linear-model, counting model, etc.) there is a separate Excel sheet (see Figure 9). Each sheet contains the parameter estimates for that model. For each model, there is also an AIC (or AICc)

value that tests whether one model is a superior fit. AIC values over 3.0 are usually seen as sufficient evidence, and R-PsiMLE will report which model exceeded that value (if any). For further details on interpreting alternative models and AIC values, see [1].

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	subject	alpha	beta	sigmaint	alpha_ci-	alpha_ci+	beta_ci-	beta_ci+	sigma_ci-	sigma_ci+	num_trials	num_outliers	power_counting_AICbetter	power_counting_AICDiff
2	1.csv	8.18	0.61	0.22	7.91	8.44	0.60	0.62	0.21	0.22	60	0	power	17.01
3	2.csv	0.35	1.14	0.28	0.35	0.36	1.12	1.15	0.28	0.29	60	0	count	3.54
4	3.csv	1.68	0.90	0.30	1.64	1.75	0.87	0.92	0.29	0.30	60	0	power	10.90
5	4.csv	0.38	1.10	0.34	0.37	0.40	1.08	1.15	0.34	0.34	60	0	power	11.24
6	5.csv	7.44	0.68	0.22	7.24	7.69	0.65	0.69	0.21	0.23	59	1	power	10.45
7	7.csv	0.32	1.18	0.31	0.31	0.32	1.18	1.22	0.30	0.32	60	0	power	31.19
8	8.csv	7.17	0.66	0.45	6.93	7.22	0.64	0.67	0.45	0.46	59	1	power	7.79
9	9.csv	1.31	0.93	0.27	1.27	1.35	0.91	0.98	0.26	0.29	60	0	power	30.29
10	10.csv	4.67	0.70	0.29	4.60	4.81	0.69	0.73	0.29	0.29	60	0	power	7.14
11	11.csv	1.02	0.93	0.35	1.02	1.07	0.90	0.94	0.35	0.37	60	0	power	20.34

Figure 9: An example of an advanced output file. Like the basic file, it contains parameter estimates and confidence intervals. But, in addition, it has additional details (1) For each non-standard model, there is an additional sheet with the estimated parameters and confidence intervals given that model (2) If significance of model testing is turned on, the relevant AIC and p values will be reported in these columns. When possible, we also report which model was the better fit (in this simulated data set, all observers but one were better fit by the power model compared to the counting model).

## 4.2 Understanding the Plot Files

We strongly urge users to visualize data both before and after using R-PsiMLE. Because scientific models almost always have multiple free parameters, R-PsiMLE will return parameter estimates even when the model applied is entirely inappropriate (e.g., when observers responded entirely randomly; see Section 5.2).

R-PsiMLE provides data visualization by outputting the raw data and the modelled data in its output. If selected, a plot file (in PDF format) will be outputted for each subject. See Figure 10 for an example of a plot file.

In regular situations, the plot file will include a graph of the raw data (that may include outliers) and a plot of the fit model. The blue line corresponds to the expected means (determined from  $\alpha$  and  $\beta$ ), and the upper and lower “fan lines” correspond to the growing variability (determined from  $\sigma$ ). The fan lines diagram 2.5 standard deviations from the mean and, hence, capture the majority of the



expected spread of responses.

If additional models are selected, each will be outputted in a separate panel within the same plot file (see Figure 9).

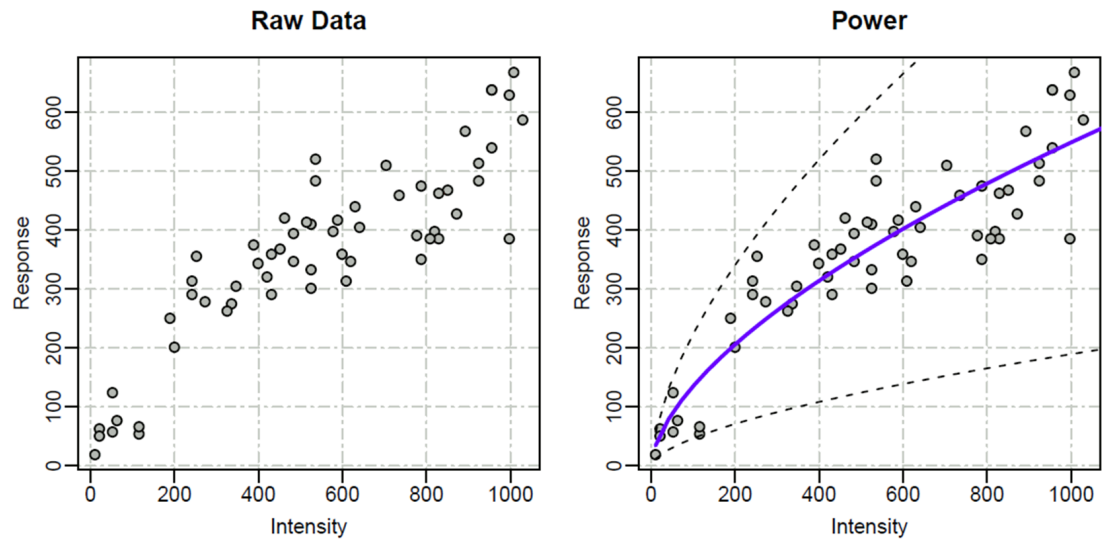


Figure 10: An example of the basic plot output. On the left is the raw data. On the right is the standard power-model with the estimated  $\alpha$ ,  $\beta$ , and  $\sigma$ . The fanning lines illustrate the expected spread given 2.5 standard deviations given the estimated  $\sigma$ . This plot will also not include any data points that were removed as outliers.

## 5 Further Information

Here, we briefly outline a few things that researchers should keep in mind when using R-PsiMLE.

### 5.1 The Bayesian Option

Underneath Step 4, you will notice an additional tab permitting the use of Bayesian parameter estimation through JAGS. Unfortunately, time and space does not permit us to give a full tutorial on Bayesian data analysis, and this section assumes familiarity with it, the logic of Gibbs sampling, and JAGS.

If interested in using the Bayesian option, follow these steps to use it:

1. Make sure that JAGS and rJAGS are properly installed. See section 2.4 for details.
2. Select the "Bayesian" tab underneath Step 4.
3. Specify the priors over  $\alpha$ ,  $\beta$ , and  $\sigma$ . For details on what we believe to be typical priors, see [1]. Please note that JAGS codes precision -  $1/\text{variance}$  - rather than SD. As a result, the default values for precision are uninformative priors.
4. Specify the JAGS parameters, including the number of MCMC chains. In most situations, the default values specified will be the correct ones.
5. Choose whether or not chain plots will be outputted. If yes, these plots will have the estimated posterior distributions for each parameter. Note that these plots do not overwrite or otherwise alter the output of plots specified in Step 4.
6. Estimate. Note that estimation will take substantially longer than the MLE version. The output file will contain both the regular MLE estimates and brand new tabs for the Bayesian estimates.

For users interested in going beyond the R-PsiMLE interface, code for JAGS and rJAGS that can be custom tailored is available online and in the Appendix to [1].

## 5.2 Guessing Data

Suppose that one of your participants guesses randomly on every trial (such scenarios are especially likely if you work with children). R-PsiMLE would still be able to analyze this data, and it would return parameter values. However, these parameter values would not be an appropriate description of how the participant actually represented the target values.

One way of catching participants who guessed is to examine their  $\alpha$  and  $\beta$  values. If the participant truly guessed, their data should look similar to Figure 10 and their responses should have no relationship to the target values presented. Hence, their  $\alpha$  should be very high, and their  $\beta$  should be close to 0.

You can attempt to statistically catch counters by applying a Likelihood Ratio Test or Wald's Test to test whether the  $\beta$  value is significant from 0. If it is, there is evidence that the participant did not guess.

## 5.3 Having Enough Data

Statistical models need as much data as possible. This is especially true when you are interested in comparing whether one model is better than another (e.g., by AIC). As a general rule of thumb, you want at least 40 trials per parameter, meaning that the standard models should have around 120 trials for reliable estimates and for comparing AIC values to another model.

In cases where there are fewer than 120 trials, R-PsiMLE will automatically use AICc values, which correct for a bias present with low number of trials.

## 5.4 Getting Additional Support

On [panamath.org/psimle/](http://panamath.org/psimle/) users can find a support forum where users can assist one another with any issues that come up.

## References

- [1] Darko Odic, Hee Yeon Im, Robert Eisinger, Ryan Ly, and Justin Halberda, *PsiMLE: A maximum-likelihood approach to estimating psychophysical scaling and variability more reliably, efficiently, and flexibly.* under review