Manual OneForAll to analyze individual hypotheses and evaluate whether individuals are homogeneous

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This manual describes how the Shiny Application 'OneForAll' can be used. A stable link to the app can be found on http://github.com/fayetteklaassen/OneForAll. The application can be run on any computer with an internet connection. By using the application, you agree to the Terms of Usage, as displayed on the starting screen of the app. This application allows you to evaluate informative hypotheses for multiple N=1 studies of your own data. If you want to execute a simulation study (like presented in the paper), please contact the author at klaassen.fayette@gmail.com for R code or a Shiny application you can run locally on your own computer.

1 Analyze own data

This section describes each of the steps required to analyze own data in the tab *Analyze own data* within the Shiny Application OneForAll. This item consists of three options from the menu: *Settings and load data*, *Individual Bayes factors*, and *GPBF output*. The first will be discussed in detail, while the other two can be used to view the results.

1.1 Step 1: Data and hypotheses

Step 1 is to select the data file to be used for analysis. You can choose to use the example data from Zedelius, Veling, and Aarts (2011) (as described in the paper One for all or some for all? Evaluting informative hypotheses for multiple N=1 studies (Klaassen, Zedelius, Veling, Aarts, & Hoijtink, 2017)). Alternatively, you can upload your own data file to be analyzed. This file should be a *.txt* with as many rows as persons or cases, and per row the entries for each condition, separated by a space or tab (white space). Each entry in the file should be an integer, describing the number of successes in each condition. The rows and columns should not be numbered or labeled. SPSS data can be saved as a Tab delimited .dat file (without row and column names), and the .dat extension must be manually changed to .txt . When the file is selected, a preview of the data is visible, together with a description of

the number of conditions and the number of participants. If these numbers are correct, you can continue. If not, the data file was not in the right format. Common problems are that the first row contains column names (you can just delete this row), or strange symbols in the first entry, which can also be deleted. Next, the number of replications used in the experiment should be given.

1.2 Step 2: Number of conditions and hypotheses

Step 2 is to define the constraints of the hypotheses considered. Three options are available. Below examples are provided on how to use this option, using the hypotheses specified in Table 1.

- *Option 1: Using >.* This option requires that for each hypothesis you want to consider, you specify each constraint using $>$ and separate constraints with a comma. Each hypothesis is specified on its own line. The parameters of interest are the success probabilities in the experimental conditions. They can be referred to by a number that corresponds to the column number of that condition in the data. Two types of constraints can be specified: a constraint between two parameters (e.g. "1>2"), or a constraint between two combinations of two parameters, separated by a $'+'$ (e.g. "1+2>3+4"). Note that one parameter cannot be on both sides of the constraint (e.g. "1+2 > 2+3" is not allowed). Figure 1 specifies all hypotheses from Table 1 that can be specified using this option.

- *Option 2: Using constraint matrix.* This options allows the user to specify a constraint matrix for each hypothesis. For more details on a constraint matrix, see Mulder, Hoijtink, and de Leeuw (2012) for example. The first line should specify how many hypotheses M are specified, and each hypothesis $m = 1, ..., M$ should start with a line specifying the number of constraints (rows) in R_m. Each constraint matrix contains $J + 1$ columns, where J is the number of conditions. The first J columns specify the constraint matrix, and the last additional column should contain the contrast vector r. With this option

Table 1: Possible specifications for 6 hypotheses.

Hypothesis	Using $>$	Using R	Default
$H_1^i : \pi_1^i > \pi_2^i > \pi_3^i > \pi_4^i > \pi_5^i > \pi_6^i$	✓	✓	✓
$H_2^i : \pi_1^i + \pi_2^i > \pi_3^i + \pi_4^i > \pi_5^i + \pi_6^i$	✓	✓	✓
$H_3^i : \pi_1^i + \pi_2^i + \pi_3^i > \pi_4^i + \pi_5^i + \pi_6^i$	x	✓	x
$H_4^i : \pi_1^i > \pi_2^i > \pi_3^i > \pi_4^i > \pi_6^i > \pi_5^i$	✓	✓	✓
$H_5^i : \pi_1^i > \pi_3^i > \pi_2^i > \pi_4^i > \pi_6^i > \pi_5^i$	✓	✓	x

more complex hypotheses can be specified. Figure 2 shows how H_1^i and H_3^i could be specified using R, Option 2. Option 2 is more flexible than Option 1, but as can be seen in Figures 1 and 2, Option 1 is more straightforward to specify, if the hypotheses allow for this option.

- *Option 3: Default.* This option is only available for an even number of conditions, and specifies automatically three hypotheses: $H_1^i : \pi_1^i > \pi_2^i > ... > \pi_J^i$, a full ordered hypothesis, where $J \geq 4$, $H_2^i : \pi_1^i > \pi_2^i > ... > \pi_J^i > \pi_{J-1}^i$, that only deviates from H_1^i because the last two parameters are reversed in the ordering, and finally $H_3^i : \pi_1^i + \pi_2^i > ... > \pi_{J-1}^i + \pi_J^i$, a full ordered hypothesis of each adjoining pair of parameters.

When the constraints are submitted, the third step is to specify which Bayes factors should be computed. The options available are all combinations of the hypotheses specified, and each hypothesis against its complement and the unconstrained hypothesis. By pressing the button 'Check constraints' the constraints are checked, and a textbox is returned with the hypothesis as processed by the app. If something is incorrect here, please re-enter your constraints.

1.3   Step 3: Computation details

The number of iterations required for the computation of the Bayes factor. By default, this value is $10,000$. Decreasing this value will increase the speed of computation, but particularly for larger number of conditions (say 8), decrease the precision of the Bayes factor computation. You can enter and adjust the computation seed, for reproducibility of your results.

By then pressing the button 'Execute analysis' (appears if the constraints are filled in and checked), the computation will start. A pop-up will appear in the bottom right corner to indicate that the computation is busy, and a notification 'Analysis finished' will appear under the button when ready. Then, you can access the other two tabs to view the results

Figure 1: Option 1: Using >

Step 2: Constraints

How define constraints?

◉ Using >

○ Using R

○ Default(only for even number of conditions)

Specify your constraints. Use one line per hypothesis and use > as a constraint. To the left and right of > can be either one number specifying the condition of interest, or two separated by a +. Separate constraints by a comma.

```
1>2, 2>3, 3>4, 4>5, 5>6
1+2>3+4, 3+4>5+6
1>2, 2>3, 3>4, 4>6, 6>5
1>3, 3>2, 2>4, 4>6, 6>5
```

Submit constraints for checking

Figure 2: Option 2: Using R

Step 2: Constraints
How define constraints?

◯ Using >

⦿ Using R

◯ Default(only for even number of
conditions)

Specify your constraintmatrices. Start with
one line specifying the number of
hypotheses. Start each hypothesis with a line
stating the number of constraints. Use as
many columns as J + 1 (r)

```
2
5
1 -1 0 0 0 0 0
0 1 -1 0 0 0 0
0 0 1 -1 0 0 0
0 0 0 1 -1 0 0
0 0 0 0 1 -1 0
1
1 1 1 -1 -1 -1 0
```

Submit constraints for checking

References

Klaassen, F., Zedelius, C., Veling, H., Aarts, H., & Hoijtink, H. (2017). All for one or some for all? Evaluating informative hypotheses for multiple N=1 studies. *Behavior Research Methods*, 1-16. doi: 10.3758/s13428-017-0992-5

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Zedelius, C. M., Veling, H., & Aarts, H. (2011). Boosting or choking – How conscious and unconscious reward processing modulate the active maintenane of goal-relevant information. *Consciousness and Cognition*, *20*, 355-362. doi: 10.1016/j.concog.2010.05.001