

CodaReader Instructions

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Brief description:

CodaReader.exe is a free program, written for Microsoft Windows operating systems, supporting Bayesian analysis of dominance hierarchies, as described by Adams (2005).

The first steps are conducting using the freeware program “WinBUGS” (Spiegelhalter et al. 2002), which is now part of OpenBugs. See the companion document “Bayesian Hierarchies Manual.pdf” for instructions on obtaining WinBUGS and using it to analyze dominance hierarchies. The final steps described in that document are to generate and save a “CODA” file, which is then input by CodaReader, as described here.

CodaReader finds the rank orders that are best supported and reports their posterior probabilities. The user can use CodaReader to find the probability of any ordering (e.g., $\mathbf{d} > \mathbf{b} > \mathbf{a} > \mathbf{c} > \mathbf{e}$), the probability that any particular individual outranks any other particular individual (e.g., $\mathbf{b} > \mathbf{c}$), or that a set of individuals outranks a different set (e.g., $[\mathbf{a} \ \& \ \mathbf{b}] > [\mathbf{c} \ \& \ \mathbf{d}]$).

For example, consider the following data on the numbers of ‘wins’ and ‘losses’ in competitive encounters among five individuals (Bell and Gorton 1978). This table shows, for example, that individuals **a** and **b** met in 19 contests (9 + 10), and that individual **a** prevailed in 9 of these encounters, while individual **b** prevailed in the other 10.

	Loser :				
Winner ↓	a	b	c	d	e
a	--	9	12	6	27
b	10	--	9	12	12
c	2	5	--	0	2
d	3	3	0	--	2
e	2	3	0	4	--

Analysis of this data set, using WinBUGS and CodaReader, shows that the most probable ranking of these individuals is, from strongest to weakest, $\mathbf{a} > \mathbf{b} > \mathbf{c} > \mathbf{d} > \mathbf{e}$. This ranking has a posterior probability of 0.38, or 38%, which means that there is a 38% probability that this is the correct ranking, given the statistical model used in the analysis. CodaReader can be used to find the posterior probability for any other ranking involving some or all of the five individuals. Here are a few examples:

Ranking of individuals	Posterior probability
$\mathbf{b} > \mathbf{a} > \mathbf{c} > \mathbf{d} > \mathbf{e}$	14%
$\mathbf{a} > \mathbf{c}$	99.6%
$(\mathbf{a} \ \& \ \mathbf{b}) > (\mathbf{c}, \mathbf{d} \ \& \ \mathbf{e})$	98%

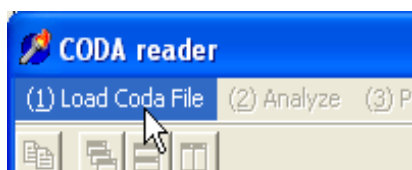
Instructions for using CODAReader.exe

These instructions assume that you have already used WinBUGS to produce a CODA file in the correct format.

Use of CODAReader is illustrated for a sample file “Example1.txt.”

1. Start the program CodaReader.exe

2. Read the disclaimer. Click “I accept” to agree to the terms listed. If you do not agree to these terms, the program will terminate.



3. Select ‘(1) Load Coda File’ from the menu bar to input the CODA file stored from your WinBUGS session. There may be a noticeable delay (perhaps of several minutes) while the program sorts information on the rank order of the $d[i]$ values. To follow the example, load the file “Example1.txt”

4. Adjust settings. When the CODA file is loaded, the “Settings” Window appears.

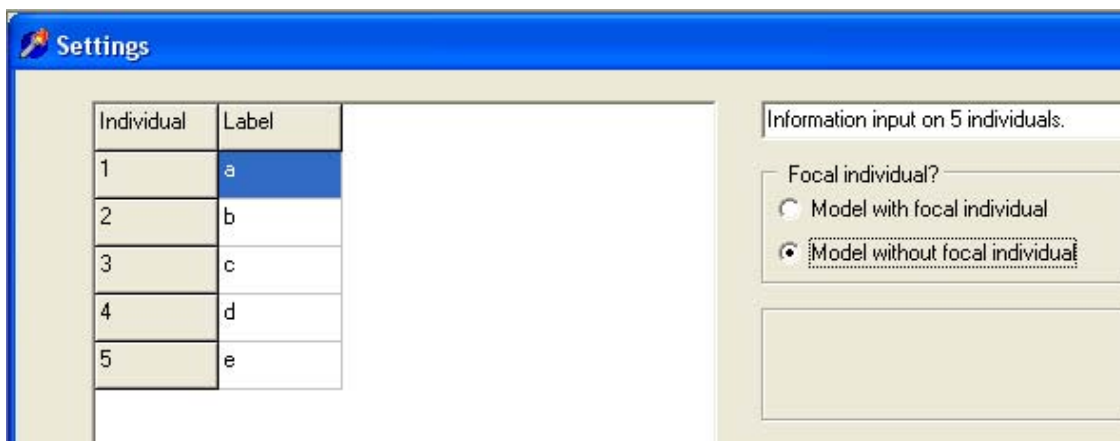
(a) If your WinBUGS model did not specify a focal individual, then click on the button indicating ‘Model without focal individual.’ If you followed the cockroach example in the companion document “Bayesian Hierarchies Manual.pdf,” the WinBUGS model did not specify a focal individual.

(b) If your WinBUGS model did specify a focal individual, click on the button ‘Model with focal individual.’ The model described by Adams (2005) specifies one individual as the focal individual.

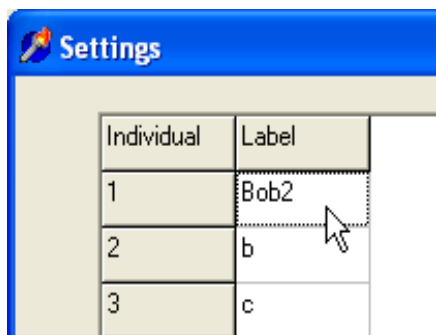
When this option is selected, an additional box appears asking:

“Which individual is the focal individual?”

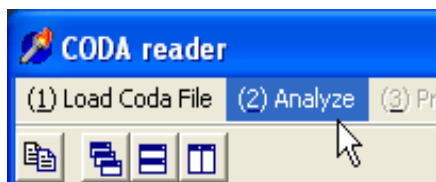
The default value is ‘1.’ Click on the up or down arrows to indicate which individual was the focal individual in your WinBUGS model.



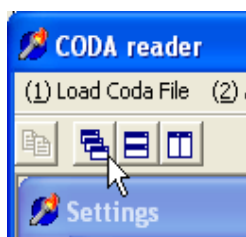
The model used to generate the file 'Example1.txt' did not specify a focal individual.



5. Edit labels. By default, consecutive lower case letters are assigned to each individual ('a', 'b', etc.). To edit a label, click on the cell containing the current label, then type the desired characters.



6. Once the settings and labels are correct, select '**(2) Analyze**' from the menu bar. Two new windows will open: the 'Analysis' window, and the 'Posterior Explorer.' To examine a different window, click on a visible part of the window to bring it to the top.



To arrange windows or to bring a different window into view, use the three buttons below the menu bar to arrange the open windows in a cascade, as horizontally arranged tiles, or as vertically arranged tiles. Windows can be resized and moved in the usual way.

7. The '**Analysis**' window shows...

a.up to 30 rank orderings and their posterior probabilities. These are the orderings with the highest posterior probabilities. For each ordering, the labels of the individuals are listed in order of decreasing rank. The posterior probability is shown as a value between 0 and 1. The cumulative posterior probability is the sum of the posterior probability for that ordering and all orderings listed above it. If more than 30 orderings tie for the highest posterior probability, then only 30 are shown. Running longer chains within WinBUGS may reduce the number of ties.

Part of the output for Example1.txt is shown here:

Columns:

1. Order of individuals (strongest to weakest)
2. Posterior probability
3. Cumulative probability

a b c d e	0.3805	0.3805
a b c e d	0.1614	0.5419
b a c d e	0.1382	0.6800

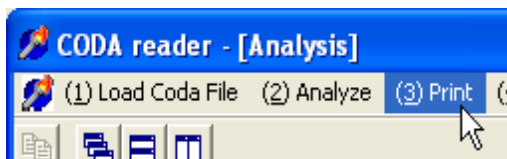
a	b	d	c	e	0.1308	0.8108
b	a	d	c	e	0.0517	0.8626
b	a	c	e	d	0.0461	0.9086
a	b	d	e	c	0.0278	0.9365
a	b	e	c	d	0.0165	0.9530

The ordering with the highest estimated posterior probability is **a > b > c > d > e**, which has a posterior probability of approximately 0.38, or 38%. Thus, there is a 38% probability that this is the true rank order of the individuals, given the data and the model. Other orderings follow. The eight orderings shown above have a cumulative posterior probability of more than 0.95; thus, there is a 95% probability that the true ordering is one of those in this set, given the statistical model. This is known as the 95% credibility set.

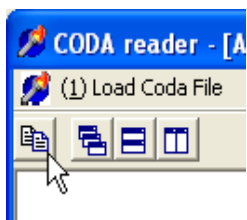
b.the number of orderings in the 95% credibility set. This is the smallest number of rank orderings with a cumulative posterior probability of at least 95%. For Example1.txt, there are 8 orderings in the 95% credibility set. In some cases, the size of the 95% credibility set is quite large, indicating great uncertainty as to the correct ranking of the individuals.

c.summary information on the number of individuals and the number of steps in the Markov chain. For Example1.txt, the following summary is shown:

There are 5 individuals.



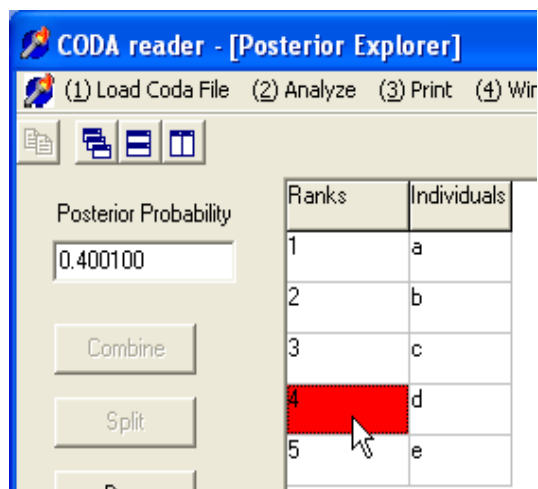
To print the contents of the 'Analysis' window, click on '**(3) Print**' on the menu bar.



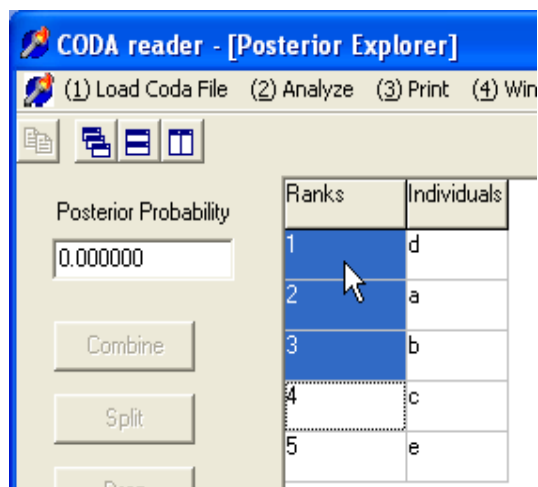
You can also select some or all of the text in the Analysis window and copy it to the clipboard either by clicking the left-most button below the menu bar, or by typing Control-C from the keyboard. (While holding the Control key down, press the 'C' key as well.) These options are activated only if text has been selected.

8. The 'Posterior Explorer' allows you to view the estimated posterior probability for any ordering of the individuals, or any subset of the individuals. You can also lump two or more individuals together. The individuals are displayed according to the ordering listed first in the Analysis. The box to the left show the estimated posterior probability of this ordering. You can now specify new rankings for some or all of the individuals to see the posterior probability.

To see the posterior probability for another ordering, you can rearrange the order of the individuals by dragging them to new rows using the mouse.



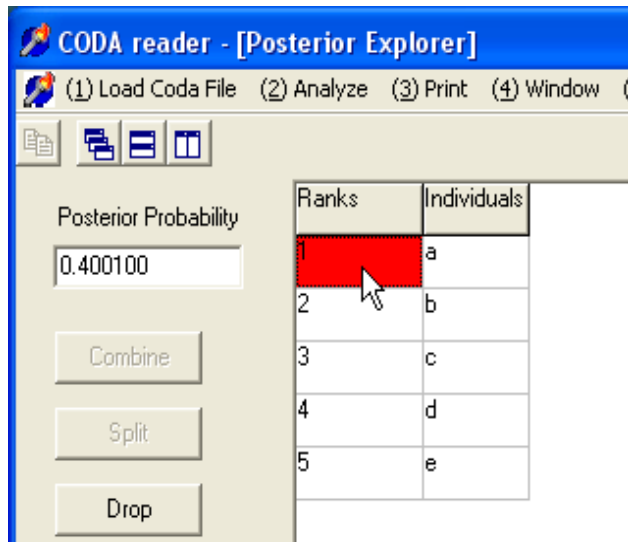
Using the left button of the mouse, click within the cell showing the rank of the individual that you would like to move. The cell will turn red.



Keep the mouse button depressed as you move the cursor to the position where you would like to move that individual. The start and end points of this dragging action should both be within the column titled “Ranks.” When you release the mouse button, the individual will be relocated within the listing and the posterior probability of the new ordering will be shown.

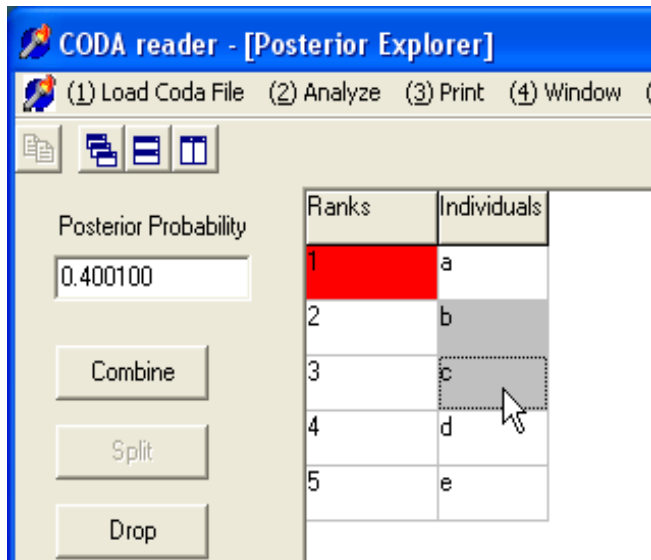
For the example shown here, **d** has been moved above individuals **a**, **b**, and **c**, to create the ordering **d > a > b > c > e**. The posterior probability for this ordering is near 0.

Two or more individuals can be combined within a single row to find the posterior probability of a simpler claim. For example, the Posterior Explorer can be used to find the probability that (**a & b & c**) outrank **d**, which outranks **e**, ignoring rankings within the top group. To combine two or more individuals within the same row:



(1) Select a cell in the 'Ranks' column

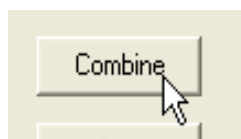
Click in the cell in the 'Ranks' column for one of the individuals. When the cell is selected, its background color turns red. If you make a mistake, a cell can be de-selected by clicking within it, in which case the background color reverts from red to white.



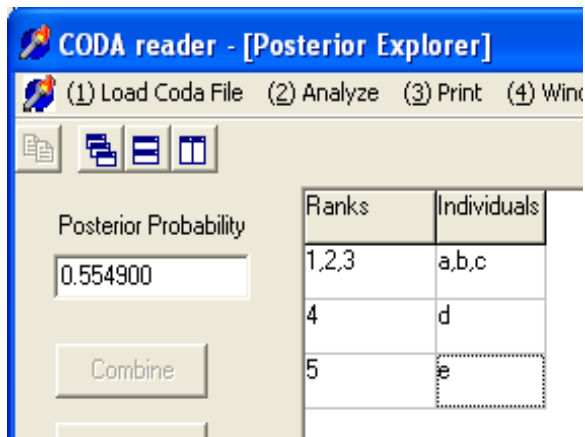
(2) Select cells in the 'Individuals' column

Click in the "Individuals" column for one or more other individuals to be combined with the individual selected in step 1. The background color of the selected cells will turn gray. To deselect a cell, click within it and the background reverts to white.

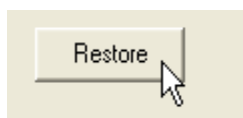
In the example shown on the left, the user has selected individuals **b** and **c** (highlighted in gray) to be combined within the first row (highlighted in red), which already contains individual **a**.



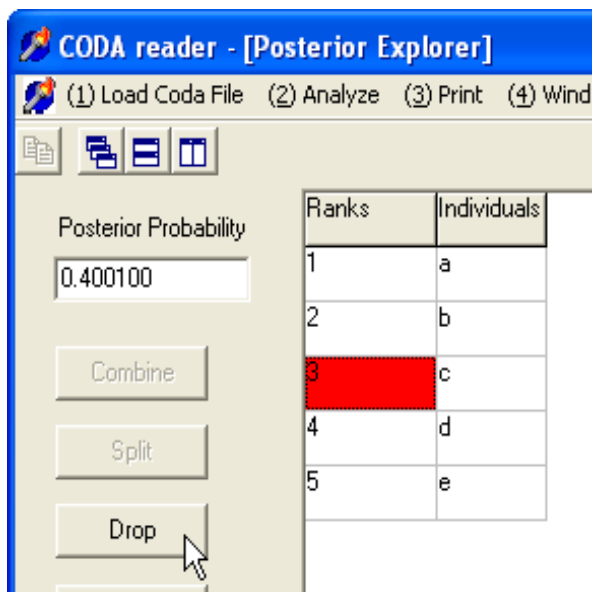
(3) Click the "Combine" button. When you have finished selecting individuals to combine, click on the "Combine" button. The selected individuals will be combined on a single row. To undo combinations, select the cell in the 'Ranks' column for the combined individuals, then click on the "Split" button.



Now **a**, **b**, and **c** have been combined in the top row. The Posterior Probability box shows that the ranking **(a, b & c) > d > e** has an estimated posterior probability of approximately 0.55, or 55%. (I haven't updated all of the screen shots, so the number that you see may be slightly different.)

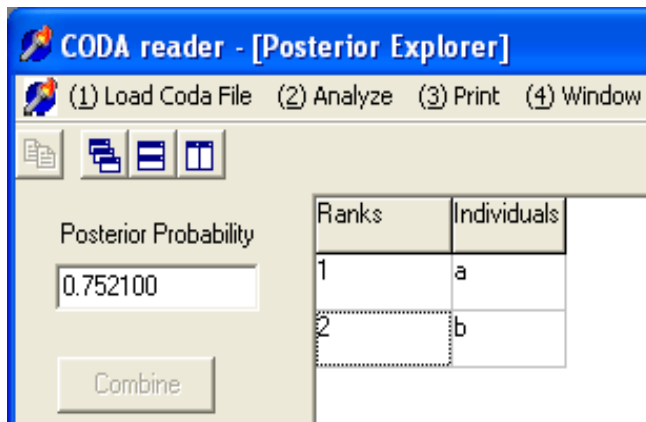


Click on the 'Restore' button to restore the original appearance of the Posterior Explorer.



To drop an individual from the listing, click on the cell within the 'Ranks' column for that individual. The background of the selected cell turns red. Then click on the 'Drop' button. The individual will be removed.

If all but two individuals are dropped, the 'Posterior Probability' box shows the posterior probability that the individual listed first outranks the other individual.



For this example, when individuals **c**, **d**, and **e** are dropped, you can see that the posterior probability that **a** outranks **b** is approximately 0.75, or 75%. Note that although individuals **c**, **d**, and **e** are dropped from the display, the records of their wins and losses in contests with individuals **a** and **b** affect the estimate of the probability that **a** outranks **b**.

References cited:

- Adams, E.S. (2005) Bayesian analysis of dominance hierarchies. *Animal Behaviour* 69:1191-1201.
- Bell, W.J. and Gorton, R.E., Jr. (1978) Informational analysis of agonistic behaviour and dominance hierarchy formation in a cockroach, *Nauphoeta cinerea*. *Behaviour* 67:217-235.
- Spiegelhalter, D., Thomas, A., Best, N. and Lunn, D. 2003. WinBUGS User Manual, Version 1.4. Cambridge, U.K.: MRC Biostatistics Unit.