

Conjoint Recognition Tutorial

In this tutorial, we explain how to analyze data from investigations employing the conjoint recognition paradigm, which can measure true and false memory processes. Section I provides a brief overview of conjoint recognition models. In Section II, we demonstrate how to calculate parameter estimates and goodness-of-fit statistics using an in-depth example.

Section I: Conjoint Recognition Models

Dual-process accounts of recognition define two memory operations: familiarity and recollection. If a test probe isn't recognized as familiar, then recollection is employed, accepting a probe if it was on a studied verbatim list and rejecting it if it was not. However, this dual-process accounts of recognition tend to produce false alarms by recognizing probes that are semantically related to actual targets. Another two-process model, called Conjoint Recognition, was introduced to account for this phenomenon (Brainerd et al. 2001). This model covers not only an inclusion-exclusion procedure but also a third instructional condition -- verbatim, gist, verbatim-gist -- and two distinct classes of distractors --unrelated and related--. With these three instructional conditions and three probes, nine empirical probabilities exist (Brainerd et al. 1999).

The model testing false memory begins when a participant enters the study portion. During the study portion, a participant studies the Deese-Roediger-McDermott (DRM) list. The DRM list is composed of multiple related words called targets (e.g. doctor, disease, bed, patients). Although not shown with the targets, there is a critical distractor which is related to the targets (e.g. hospital) (Brainerd et al. 1999).

After studying the DRM list, the participant moves onto the test portion. During this test portion, conjoint recognition examines the participant's accept-reject decisions about targets, related distractors, and unrelated distractors under three instructional conditions: verbatim (accepting targets and rejecting both related and unrelated distractors), gist (accepting related distractors and rejecting both targets and unrelated distractors), and verbatim-gist (accepting both targets and related distractors and rejecting unrelated distractors) (Brainerd et al. 1999). This model has six different recognition processes: three involved in true recognition and three in false recognition. True recognition, that is, correctly identifying targets, includes identity judgment, erroneous recollection rejection, and similarity judgment. On the other hand, false recognition happens when a past item is incorrectly recognized. False recognition in this model includes phantom recollection, second similarity judgment, and recollection rejection (Brainerd et al. 2001).

Each parameter represents different processes. First, I, Identity judgement, parameter accepts a target based on verbatim traces of that target. E, erroneous recollection rejection, is a parameter that rejects a target based on gist-cued verbatim traces of a different target. While parameter B1,2,3 are the probabilities of accepting a distractor due to response bias in the respective conditions, parameter R is the probability of rejecting a distractor based on gist-cued verbatim traces of a target. Parameter P, is the probability of distractor acceptance due to phantom recollection of its presentation. While S1 parameter measures and accepts similarity judgment for target, S2 parameter measures and accepts similarity judgment for related distractor.

Section II: Example

The following example uses a database of 80 subjects who were given a recognition test after studying 12 DRM lists. The experiment followed an between-subjects design with participants falling into arbitrary conditions “A” or “B”. The recognition test follows the design described in Section I.

1. Database Structure

When designing a database, the goal is to calculate and organize the appropriate response frequencies for each instructional condition and probe type. This can be accomplished in many ways. The database (figure 1) contains information such as gender, age, and subject id. Following these demographic variables are test probes.

Subject ID	Age	Gender	Condition	V																															
				FLU	SHIVER	MEDICINE	FAUCET	THIRSTY	LAKE	STUPID	QUICK	KNOWLEDGE	NOTE	READ	PENCIL	COLD	WATER	SMART	WRITE	WEATHER	AIR	NERD	WORD	FAKE	SQUARE	TERRIBLE	BILL	FRAUD	CUBE	ROTTEN	PAYMENT				
1	20	Male	A	1	1	1	1	0	0	1	1	1	1	1	1	0	1	1	1	0	0	0	1	0	0	0	0	0	1	0	1	0	1		
2	20	Male	A	1	1	1	1	0	1	0	0	0	1	1	0	0	1	1	1	0	0	0	0	0	0	1	0	0	1	1	0	1	0		
3	20	Male	A	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1	1	1	0	0	0	0	1	0	1	0		
4	20	Male	A	0	1	1	0	0	0	1	1	1	1	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5	20	Male	A	1	1	0	1	1	0	1	1	1	1	1	1	0	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	
6	20	Male	A	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
7	20	Male	A	0	0	1	0	1	0	1	0	1	1	1	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
8	20	Male	A	0	1	0	1	1	1	0	1	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
9	20	Male	A	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	
10	20	Male	A	1	1	0	1	1	1	1	1	0	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
11	20	Male	A	0	1	0	1	1	1	1	1	1	0	0	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	
12	20	Male	A	1	1	1	1	0	0	0	0	0	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	
13	20	Male	A	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	
14	20	Male	A	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	0	0	1	0	1	0	0	0	0	0	
15	20	Male	A	0	1	1	1	1	1	1	1	0	0	1	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	
16	20	Male	A	0	1	0	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
17	20	Male	A	0	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	0	0	1	0	1	0	0	1	0	0	0	1	0	1	0	
18	20	Male	A	0	1	0	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
19	20	Male	A	1	1	1	1	1	1	0	1	1	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
20	20	Female	A	1	1	1	0	0	1	0	1	1	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
21	20	Female	A	1	1	0	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	
22	20	Female	A	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
23	20	Female	A	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	
24	20	Female	A	1	1	1	1	0	1	0	1	0	1	1	0	1	1	0	1	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	
25	20	Female	A	1	1	0	1	0	0	0	0	0	1	0	1	1	1	1	1	1	1	1	0	1	0	1	1	0	0	1	0	1	0	1	
26	20	Female	A	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	20	Female	A	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	
28	20	Female	A	1	0	1	1	1	1	1	1	1	1	1	1	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	0	
29	20	Female	A	0	0	1	1	1	1	0	1	1	1	1	1	1	0	0	1	1	0	0	0	1	0	0	1	1	0	0	1	0	1	0	
30	20	Female	A	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	
31	20	Female	A	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
32	20	Female	A	0	0	1	1	1	1	1	1	0	1	1	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
33	20	Female	A	0	0	0	1	1	1	0	1	0	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
34	20	Female	A	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	
35	20	Female	A	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0	
36	20	Female	A	1	0	1	0	1	0	1	0	1	1	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0	0	1	1	0	0	0	
37	20	Female	A	1	1	0	0	1	0	1	0	1	0	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
38	20	Female	A	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	1	0	0	1	0	0	1	0	
39	20	Female	A	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	
40	20	Female	A	1	1	0	1	1	1	1	1	0	1	0	0	1	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	1	0	
41	20	Male	B	1	1	1	0	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	0	1	0	0	0	0	0	0	0	1	0	
42	20	Male	B	0	0	1	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	1	0	
43	20	Male	B	1	1	1	0	1	1	1	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
44	20	Male	B	1	1	0	1	1	1	1	1	0	1	1	1	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	
45	20	Male	B	1	1	1	0	1	0	1	0	1	0	1	1	0	0	1	1	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0
46	20	Male	B	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
47	20	Male	B	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	0	0	1	1	0	1	0	1	0	0	0	1	1	0	0	0	
48	20	Male	B	0	1	1	1	1	1	1	1	0	1	1	0	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 1.

Within each instructional condition (verbatim, gist, and verbatim-gist) there are a total of 12 targets (green), 4 critical distractors (dark orange), 4 related distractors (light orange), 4 type 1 unrelated distractors (dark blue), and 4 type 2 unrelated distractors (light blue). Only the verbatim instructional condition is shown below.

Response frequencies for each type of probe within each instructional condition should be calculated in the following order, copied into a separate excel sheet, and saved a .csv file:

VT_1	VT_0	GT_1	GT_0	VGT_1	VGT_0	VR_1	VR_0	GR_1	GR_0	VGR_1	VGR_0	VU_1	VU_0	GU_1	GU_0	VGU_1	VGU_0
355	125	177	303	421	59	107	53	88	72	145	15	38	122	45	115	46	74

VT_1 represents acceptances for verbatim condition targets, VT_0 represents rejections for verbatim condition targets, GT_1 represents acceptances for gist condition targets, etc.

Within this example, there are two sets of response data (A and B), so each set is saved to a different .csv file. Additionally, a joint frequency .csv file is created:

A_VT_1	A_VT_0	A_GT_1	A_GT_0	A_VGT_1	A_VGT_0	A_VR_1	A_VR_0	A_GR_1	A_GR_0	A_VGR_1	A_VGR_0	A_VU_1	A_VU_0	A_GU_1	A_GU_0	A_VGU_1	A_VGU_0	B_VT_1	B_VT_0	B_GT_1	B_GT_0	B_VGT_1	B_VGT_0
337	119	164	292	397	59	101	51	83	69	137	15	38	114	41	111	43	71	337	143	173	307	431	

2. Conjoint Recognition Model EQN File

The order of these frequencies must reflect the order in which they will be interpreted by the conjoint recognition model EQN file (see Figure 2).

```

36
1 1 I
1 2 (1-I)*E
1 1 (1-I)*(1-E)*S1
1 1 (1-I)*(1-E)*(1-S1)*B1
1 2 (1-I)*(1-E)*(1-S1)*(1-B1)
2 4 I
2 3 (1-I)*E
2 3 (1-I)*(1-E)*S1
2 3 (1-I)*(1-E)*(1-S1)*B2
2 4 (1-I)*(1-E)*(1-S1)*(1-B2)
3 5 I
3 5 (1-I)*E
3 5 (1-I)*(1-E)*S1
3 5 (1-I)*(1-E)*(1-S1)*B3
3 6 (1-I)*(1-E)*(1-S1)*(1-B3)
4 8 R
4 7 (1-R)*P
4 7 (1-R)*(1-P)*S2
4 7 (1-R)*(1-P)*(1-S2)*B1
4 8 (1-R)*(1-P)*(1-S2)*(1-B1)
5 9 R
5 10 (1-R)*P
5 9 (1-R)*(1-P)*S2
5 9 (1-R)*(1-P)*(1-S2)*B2
5 10 (1-R)*(1-P)*(1-S2)*(1-B2)
6 11 R
6 11 (1-R)*P
6 11 (1-R)*(1-P)*S2
6 11 (1-R)*(1-P)*(1-S2)*B3
6 12 (1-R)*(1-P)*(1-S2)*(1-B3)
7 13 B1
7 14 (1-B1)
8 15 B2
8 16 (1-B2)
9 17 B3
9 18 (1-B3)

```

```

72
1 1 I_A
1 2 (1-I_A)*E_A
1 1 (1-I_A)*(1-E_A)*S1_A
1 1 (1-I_A)*(1-E_A)*(1-S1_A)*B1_A
1 2 (1-I_A)*(1-E_A)*(1-S1_A)*(1-B1_A)
2 4 I_A
2 3 (1-I_A)*E_A
2 3 (1-I_A)*(1-E_A)*S1_A
2 3 (1-I_A)*(1-E_A)*(1-S1_A)*B2_A
2 4 (1-I_A)*(1-E_A)*(1-S1_A)*(1-B2_A)
3 5 I_A
3 5 (1-I_A)*E_A
3 5 (1-I_A)*(1-E_A)*S1_A
3 5 (1-I_A)*(1-E_A)*(1-S1_A)*B3_A
3 6 (1-I_A)*(1-E_A)*(1-S1_A)*(1-B3_A)
4 8 R_A
4 7 (1-R_A)*P_A
4 7 (1-R_A)*(1-P_A)*S2_A
4 7 (1-R_A)*(1-P_A)*(1-S2_A)*B1_A
4 8 (1-R_A)*(1-P_A)*(1-S2_A)*(1-B1_A)
5 9 R_A
5 10 (1-R_A)*P_A
5 9 (1-R_A)*(1-P_A)*S2_A
5 9 (1-R_A)*(1-P_A)*(1-S2_A)*B2_A
5 10 (1-R_A)*(1-P_A)*(1-S2_A)*(1-B2_A)
6 11 R_A
6 11 (1-R_A)*P_A
6 11 (1-R_A)*(1-P_A)*S2_A
6 11 (1-R_A)*(1-P_A)*(1-S2_A)*B3_A
6 12 (1-R_A)*(1-P_A)*(1-S2_A)*(1-B3_A)
7 13 B1_A
7 14 (1-B1_A)
8 15 B2_A
8 16 (1-B2_A)
9 17 B3_A
9 18 (1-B3_A)
10 19 I_B
10 20 (1-I_B)*E_B
10 19 (1-I_B)*(1-E_B)*S1_B
10 19 (1-I_B)*(1-E_B)*(1-S1_B)*B1_B
10 20 (1-I_B)*(1-E_B)*(1-S1_B)*(1-B1_B)
11 22 I_B
11 21 (1-I_B)*E_B
11 21 (1-I_B)*(1-E_B)*S1_B
11 21 (1-I_B)*(1-E_B)*(1-S1_B)*B2_B
11 22 (1-I_B)*(1-E_B)*(1-S1_B)*(1-B2_B)
12 23 I_B
12 23 (1-I_B)*E_B
12 23 (1-I_B)*(1-E_B)*S1_B
12 23 (1-I_B)*(1-E_B)*(1-S1_B)*B3_B
12 24 (1-I_B)*(1-E_B)*(1-S1_B)*(1-B3_B)
13 26 R_B
13 25 (1-R_B)*P_B
13 25 (1-R_B)*(1-P_B)*S2_B
13 25 (1-R_B)*(1-P_B)*(1-S2_B)*B1_B
13 26 (1-R_B)*(1-P_B)*(1-S2_B)*(1-B1_B)
14 27 R_B
14 28 (1-R_B)*P_B
14 27 (1-R_B)*(1-P_B)*S2_B
14 27 (1-R_B)*(1-P_B)*(1-S2_B)*B2_B
14 28 (1-R_B)*(1-P_B)*(1-S2_B)*(1-B2_B)
15 29 R_B
15 29 (1-R_B)*P_B
15 29 (1-R_B)*(1-P_B)*S2_B
15 29 (1-R_B)*(1-P_B)*(1-S2_B)*B3_B
15 30 (1-R_B)*(1-P_B)*(1-S2_B)*(1-B3_B)
16 31 B1_B
16 32 (1-B1_B)
17 33 B2_B
17 34 (1-B2_B)
18 35 B3_B
18 36 (1-B3_B)

```

Figure 2. Equation file for a processing tree for a single set of data

This file (CR model.eqn) is available for download on the Memory and Neuroscience Research [website](#).

This file describes a multinomial processing tree model. Each letter variable (I, E, R, P, S1, S2, B1, B3, B3) represents a different memory process, and different lines represent the probabilities of acceptance or rejection rates which are mapped onto acceptance and rejection frequency data.

The order of this tree determines the order in which frequencies need to be organized in the .csv file. For example, the probability of using the sole process of I (identity judgement) should lead to the acceptance of verbatim targets, and the probability of not using I (I-1) times using the independent process of E (erroneous recollection rejection) should lead to the rejection of verbatim targets.

In addition, both sets of response frequencies (A and B) can be modeled jointly in order to determine important differences between the two sets of responses. Figure 3 shows example of a joint conjoint recognition EQN file which has been modified to fit our example data.

Figure 3. Equation file for a processing tree for two sets of data

3. Running Model Fits

In this tutorial, we will be using **R** ([download link](#)), a free statistical software package, and **R Studio** ([download link](#)), an integrated development environment for R. The module **MPTinR** is also required – this can be downloaded using the packages tab underneath the ‘Global Environment’ window in R Studio.

Conjoint recognition data is evaluated using a G-test of goodness of fit between the data and frequencies predicted by the model.

```

1 #header=T if there is a header row
2 A_freq <- read.csv("C:/Users/Nico/Desktop/CR Tutorial/A_data.csv", header = T, sep = ",")
3 B_freq <- read.csv("C:/Users/Nico/Desktop/CR Tutorial/B_data.csv", header = T, sep = ",")
4 joint_freq <- read.csv("C:/Users/Nico/Desktop/CR Tutorial/A_B_data.csv", header = T, sep = ",")
5
6 #loading MPTinR library
7 library(MPTinR)
8
9 #important <- defining model equation file as 'cr' and joint model at 'cr_joint'
10 cr <- "C:/Users/Nico/Desktop/CR Tutorial/CR model.eqn"
11 cr_joint <- "C:/Users/Nico/Desktop/CR Tutorial/CR joint model AB.eqn"
12
13
14 #model equation - all conditions - A
15 full_a <- fit.mpt(A_freq, model.filename = cr)
16
17 #model equation - all conditions - B
18 full_b <- fit.mpt(B_freq, model.filename = cr)
19
20 #model equation, restricted - all conditions - A
21 full_a_r <- fit.mpt(A_freq, model.filename = cr, restrictions.filename = list("B1=B2"))
22
23 #model equation, restricted - all conditions - B
24 full_b_r <- fit.mpt(B_freq, model.filename = cr, restrictions.filename = list("B1=B2"))
25
26 #model equation - all conditions - joint
27 full_joint <- fit.mpt(joint_freq, model.filename = cr_joint)
28
29 #model equation, restricted - all conditions - joint
30 full_joint_r <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B"))
31
32 # equality constraints for parameters comparisons - all conditions
33 full_joint_R_E <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B", "E_A=E_B"))
34
35 full_joint_R_I <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B", "I_A=I_B"))
36
37 full_joint_R_P <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B", "P_A=P_B"))
38
39 full_joint_R_R <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B", "R_A=R_B"))
40
41 full_joint_R_S1 <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B", "S1_A=S1_B"))
42
43 full_joint_R_S2 <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B", "S2_A=S2_B"))
44
45 full_joint_R_B3 <- fit.mpt(joint_freq, model.filename = cr_joint, restrictions.filename = list("B1_A=B2_A", "B1_B=B2_B", "B3_A=B3_B"))

```

Figure 4. Example of script that will run a G-test of goodness of fit on the example data.

Remember that the directories accessed will change from machine to machine depending where you keep your data and CR model files.

Figure 4 shows all the code required to run the relevant statistical tests on the data from our example database. The following bullet points explain key elements of this code:

- In lines 21, 24, and 30 the restriction B1=B2 is imposed. This is done to meaningfully contrast the two different sets of frequencies (A and B). These restrictions may change, depending on the nature of the experiment.
- Running full_a and full_b grants outputs for unrestricted models which can help illuminate which parameters may be restricted, or why certain restrictions do not produce acceptable model fits. The decision to restrict a parameter should be justified based on particular aspects of the experimental design.
- Running full_a_r and full_b_r produces an output which demonstrates whether the restriction imposed produces an acceptable model fit ($p > 0.05$).

Running `full_joint_r` (line 30) should produce the following output in the console window of R Studio:

```

Console ~/ / 
> full_joint_r
$goodness.of.fit
  Log.Likelihood G.Squared df    p.value
1      -2482.686 0.3516332  2 0.8387718

$information.criteria
      AIC      BIC
1 32.35163 135.2996

$model.info
  rank.fisher n.parameters n.independent.categories
1          16           16                   18

$parameters
  estimates lower.conf upper.conf restricted.parameter
B1_A 0.2598684 0.21056892 0.3091679          B2_A
B1_B 0.1718750 0.13053910 0.2132109          B2_B
B2_A 0.2598684 0.21056892 0.3091679
B2_B 0.1718750 0.13053910 0.2132109
B3_A 0.3771930 0.28822081 0.4661652
B3_B 0.2666667 0.18754553 0.3457878
E_A  0.2088105 0.07777536 0.3398457
E_B  0.3839387 0.24937758 0.5184999
I_A  0.4865911 0.42440066 0.5487816
I_B  0.5243046 0.46982411 0.5787850
P_A  0.4306669 0.27659646 0.5847373
P_B  0.6011285 0.40726319 0.7949939
R_A  0.2182519 0.12259207 0.3139118
R_B  0.3832475 0.29164090 0.4748541
S1_A 0.4885657 0.40192643 0.5752050
S1_B 0.5249924 0.42284359 0.6271413
S2_A 0.6439910 0.52195113 0.7660310
S2_B 0.5496211 0.33971482 0.7595273

$data
$data$observed
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16] [,17] [,18]
[1,]  337  119  164  292  397   59  101   51   83   69  137   15   38  114   41  111   43   71
  [,19] [,20] [,21] [,22] [,23] [,24] [,25] [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33] [,34]
[1,]   337   143   173   307   431   49   84   76   86   74  147   13   26  134   29  131
  [,35] [,36]
[1,]    32    88

$data$predicted
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16] [,17] [,18]
[1,]  337  119  164  292  397   59  101   51   83   69  137   15 39.5 112.5 39.5 112.5   43   71
  [,19] [,20] [,21] [,22] [,23] [,24] [,25] [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33] [,34]
[1,]   337   143   173   307   431   49   84   76   86   74  147   13 27.5 132.5 27.5 132.5
  [,35] [,36]
[1,]    32    88

```

Figure 5. Full output for `full_joint_r`

The test statistics for the G-test are first shown (`$goodness.of.fit`), followed by penalized likelihood criteria (`$information.criteria`) (these values assess the penalization to fit a model should receive based on the number parameters the model estimates – [more here](#))

Next is information on degrees of freedom parameter value estimates (`$parameters`). Finally, the frequencies observed and frequencies predicted are shown (`$data`).

To compare differences across models, equality constraints on each individual parameter need to be imposed (see lines 33-45 in figure 4). If the new model doesn't fit well (i.e. p is below or near 0.05), then we know that the parameter made equal was responsible for the lack of fit.

To evaluate the true fit of the equality constraint, one must compare the joint restricted model (full_joint_r in our example) and the joint equality constrained model (full_joint_r_PARAMETER in our example, PARAMETER = P, I, E, etc.). This can be accomplished through the following steps:

1. Subtract G^2 value of full_joint_r from the G^2 value of full_joint__R_PARAMETER (call ΔG^2)
2. Subtract the degrees of freedom of full_joint_r from the degrees of freedom of full_joint_R_PARAMETER (call Δdf)
3. Determine the X^2 critical value at Δdf for the appropriate α of your given study (in this example $\alpha = 0.05$).
4. If $\Delta G^2 > \text{critical value}$, then the parameter in question is statistically different between the sets of data within the joint model

These steps are illustrated below for all parameters in our example:

```
> full_joint_r
$goodness.of.fit
Log.Likelihood G.Squared df p.value
1 -2482.686 0.3516332 2 0.8387718
```

```
> full_joint_R_E
$goodness.of.fit
Log.Likelihood G.Squared df p.value
1 -2484.363 3.705434 3 0.295079
```

$$\Delta G^2 = 3.705434 - 0.3516332 = 3.3538008$$

$$\Delta df = 3 - 2 = 1$$

$p = 0.067$, FAIL to reject null (i.e. E is not significantly different between A and B)

```
> full_joint_r
$goodness.of.fit
Log.Likelihood G.Squared df p.value
1 -2482.686 0.3516332 2 0.8387718
```

```
> full_joint_R_I
$goodness.of.fit
Log.Likelihood G.Squared df p.value
1 -2483.089 1.158265 3 0.7630305
```

$$\Delta G^2 = 1.158265 - 0.351622 = 0.8066318$$

$$\Delta df = 3 - 2 = 1$$

$P = 0.369$, FAIL to reject null (i.e. I is not significantly different between A and B)

```
> full_joint_r
$goodness.of.fit
  Log.Likelihood G.Squared df    p.value
1      -2482.686  0.3516332  2  0.8387718
```

```
full_joint_R_P
goodness.of.fit
  Log.Likelihood G.Squared df    p.value
1      -2483.618  2.214483  3  0.5291014
```

$$\Delta G^2 = 2.214483 - 0.351622 = 1.8628498$$

$$\Delta df = 3 - 2 = 1$$

$p = 0.172$, FAIL to reject null (i.e. P is not significantly different between A and B)

```
> full_joint_r
$goodness.of.fit
  Log.Likelihood G.Squared df    p.value
1      -2482.686  0.3516332  2  0.8387718
```

```
> full_joint_R_R
$goodness.of.fit
  Log.Likelihood G.Squared df    p.value
1      -2485.649  6.278177  3  0.09883338
```

$$\Delta G^2 = 6.278177 - 0.351622 = 5.926555$$

$$\Delta df = 3 - 2 = 1$$

$p = 0.0149$, REJECT null (i.e. R is significantly different between A and B)

```
> full_joint_r
$goodness.of.fit
  Log.Likelihood G.Squared df    p.value
1      -2482.686  0.3516332  2  0.8387718
```

```
full_joint_R_S1
goodness.of.fit
  Log.Likelihood G.Squared df    p.value
1      -2482.824  0.6281921  3  0.8899492
```

$$\Delta G^2 = 0.6281921 - 0.351622 = 0.2765589$$

$$\Delta df = 3 - 2 = 1$$

$p = 0.599$, FAIL to reject null (i.e. S1 is not significantly different between A and B)

<pre>> full_joint_r \$goodness.of.fit Log.Likelihood G.Squared df p.value 1 -2482.686 0.3516332 2 0.8387718</pre>	<pre>full_joint_R_S2 goodness.of.fit Log.Likelihood G.Squared df p.value 1 -2483.016 1.01122 3 0.7985371</pre>
---	---

$$\Delta G^2 = 1.01122 - 0.351622 = 0.6595868$$

$$\Delta df = 3 - 2 = 1$$

p = 0.417, FAIL to reject null (i.e. S1 is not significantly different between A and B)

From this, we conclude that recollection rejection (parameter R) differs significantly between groups A and B.

References

- Brainerd, C. J., Wright, R., Reyna, V. F. (2001). Conjoint Recognition and Phantom Recollection. *Journal of Experimental Psychology: Learning Memory and Cognition*, 27 (2): 307-327.
- Brainerd, C. J., Reyna, V. F., Mojardin, A. H. (1999). Conjoint Recognition. *Psychological Review*, 106 (1): 160-179.