

#Rstats

# Statistical Inference in R

Jacob O. Wobbrock, Ph.D.

The Information School | DUB Group

University of Washington

wobbrock@uw.edu

# Table of Analyses

## Proportions & Association

Samples	Categories	Tests
1	2	One-sample chi-squared test, binomial test
1	≥2	One-sample chi-squared test, multinomial test
2	≥2	Two-sample chi-squared test, <i>G</i> -test, Fisher’s exact test
2 <sup>†</sup>	≥2	Symmetry test

### Assumptions

- Normality:  
Shapiro-Wilk test
- Homoscedasticity:  
Levene’s test
- Sphericity:  
Mauchly’s test

### Distributions

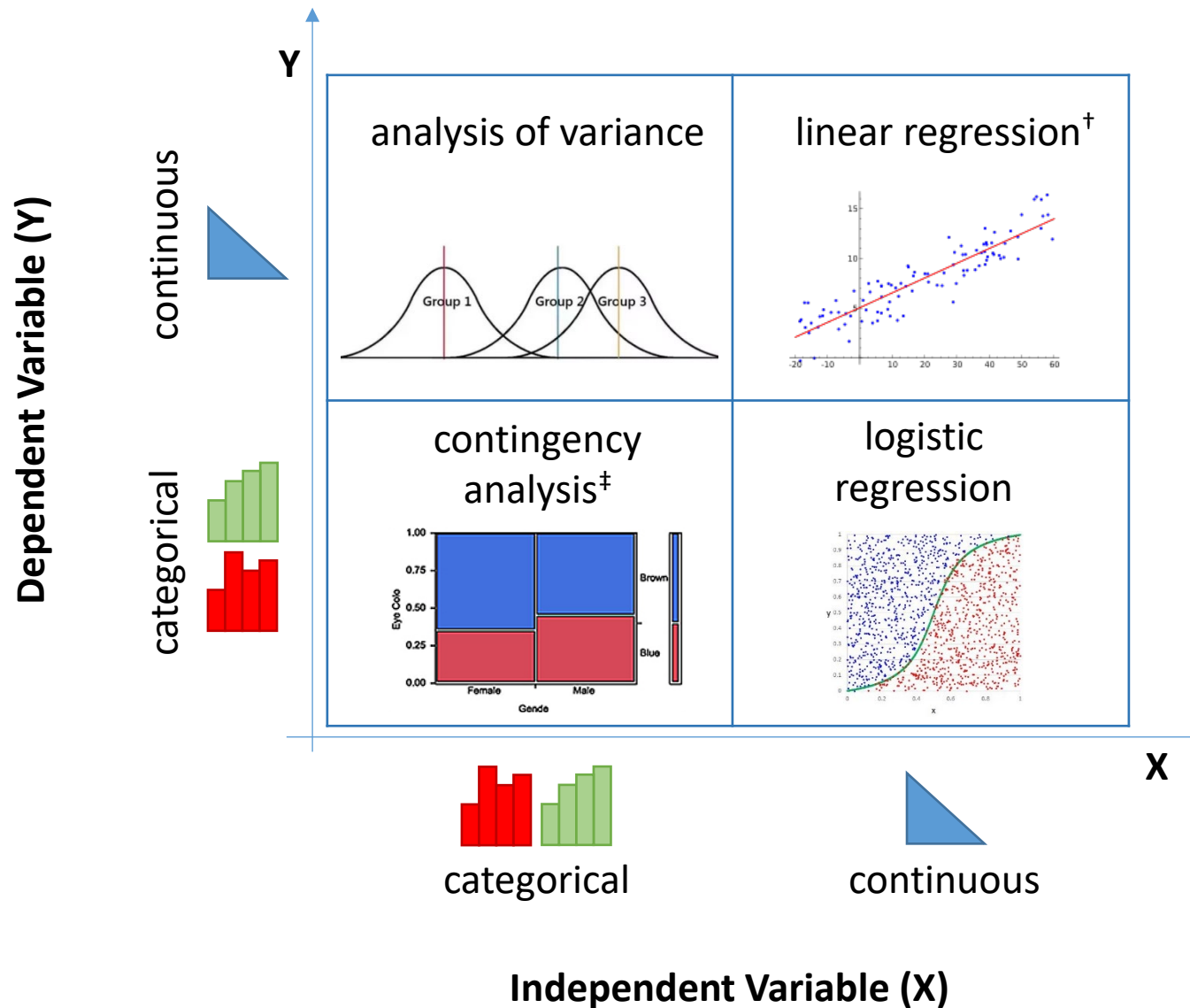
- Shapiro-Wilk test
- Chi-squared GOF test

<sup>†</sup>Dependent samples

## Analyses of Variance

Factors	Levels	Between or Within	Parametric Tests	Nonparametric Tests	
			Linear Models	Generalized Models	
1	2	B	Independent-samples <i>t</i> -test	Median test	Mann-Whitney <i>U</i> test
1	2	W	Paired-samples <i>t</i> -test	Sign test	Wilcoxon signed-rank test
1	≥2	B	One-way ANOVA	Kruskal-Wallis test	
1	≥2	W	One-way repeated measures ANOVA	Friedman test	
≥2	≥2	B	Factorial ANOVA	Aligned Rank Transform (ART)	
			Linear Model (LM)	Generalized Linear Model (GLM)	
≥2	≥2	W	Factorial repeated measures ANOVA	Aligned Rank Transform (ART)	
			Linear Mixed Model (LMM)	Generalized Linear Mixed Model (GLMM)	

# Analysis Categories



Credit: This table is adapted from the “Fit Y by X” dialog in SAS® JMP™. <http://jmp.com/>

<sup>†</sup>All of the parametric tests in the previous table are forms of linear regression.

<sup>‡</sup>See the tests of proportion in the previous table.

# Proportions & Association

# Proportions

## One sample

Samples	Response Categories	Test Name	Exact Test?	R Code
1	2	Binomial test	Yes, use with $N < 200$	<pre># df is a long-format data table w/columns for participant (PIId) and 2-category outcome (Y) df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$Y = factor(df\$Y) # Y is an outcome of 2 categories xt = xtabs( ~ Y, data=df) # make counts binom.test(xt, p=0.5, alternative="two.sided")</pre>
1	$\geq 2$	Multinomial test	Yes, use with $N < 200$	<pre># df is a long-format data table w/columns for participant (PIId) and N-category outcome (Y) library(XNomial) # for xmulti df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$Y = factor(df\$Y) # Y is an outcome of ≥2 categories xt = xtabs( ~ Y, data=df) # make counts xmulti(xt, rep(1/length(xt), length(xt)), statName="Prob")  # or, equivalently library(RVAideMemoire) # for multinomial.test multinomial.test(df\$Y)</pre>
		One-sample chi-squared test	No, use with $N \geq 200$	<pre># df is a long-format data table w/columns for participant (PIId) and N-category outcome (Y) df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$Y = factor(df\$Y) # Y is an outcome of ≥2 categories xt = xtabs( ~ Y, data=df) # make counts chisq.test(xt)</pre>

# Proportions

## One sample

Samples	Response Categories	Test Name	Exact Test?	Report
1	2	Binomial test	Yes, use with $N < 200$	“Out of 60 responses, 42 were ‘yes’ and 18 were ‘no’. A two-sided exact binomial test indicated that these proportions were significantly different from chance ( $p = .003$ ).”
1	$\geq 2$	Multinomial test	Yes, use with $N < 200$	“Out of 60 outcomes, 17 were ‘yes’, 12 were ‘no’, and 31 were ‘maybe’. An exact multinomial test indicated that these proportions were statistically significantly different from chance ( $p = .009$ ).”
		One-sample chi-squared test	No, use with $N \geq 200$	“Out of 60 outcomes, 17 were ‘yes’, 12 were ‘no’, and 31 were ‘maybe’. A one-sample Pearson chi-squared test indicated that these proportions were significantly different from chance ( $\chi^2(2, N=60) = 9.70, p = .008$ ).”

# Association

## Two samples

Samples	Response Categories	Test Name	Exact Test?	R Code
2	$\geq 2$	Fisher's exact test	Yes, use with $N < 200$	<pre># df is a long-format data table w/participant (PIId), factor (X), and N-category outcome (Y) df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$X = factor(df\$X) # X is a factor of m ≥ 2 levels df\$Y = factor(df\$Y) # Y is an outcome of n ≥ 2 categories xt = xtabs( ~ X + Y, data=df) # make m×n crosstabs fisher.test(xt)</pre>
		G-test	No, use with $N < 200$	<pre># df is a long-format data table w/participant (PIId), factor (X), and N-category outcome (Y) library(RVAideMemoire) # for G.test df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$X = factor(df\$X) # X is a factor of m ≥ 2 levels df\$Y = factor(df\$Y) # Y is an outcome of n ≥ 2 categories xt = xtabs( ~ X + Y, data=df) # make m×n crosstabs G.test(xt)</pre>
		Two-sample chi-squared test	No, use with $N \geq 200$	<pre># df is a long-format data table w/participant (PIId), factor (X), and N-category outcome (Y) df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$X = factor(df\$X) # X is a factor of m ≥ 2 levels df\$Y = factor(df\$Y) # Y is an outcome of n ≥ 2 categories xt = xtabs( ~ X + Y, data=df) # make m×n crosstabs chisq.test(xt)</pre>

# Association

## Two samples

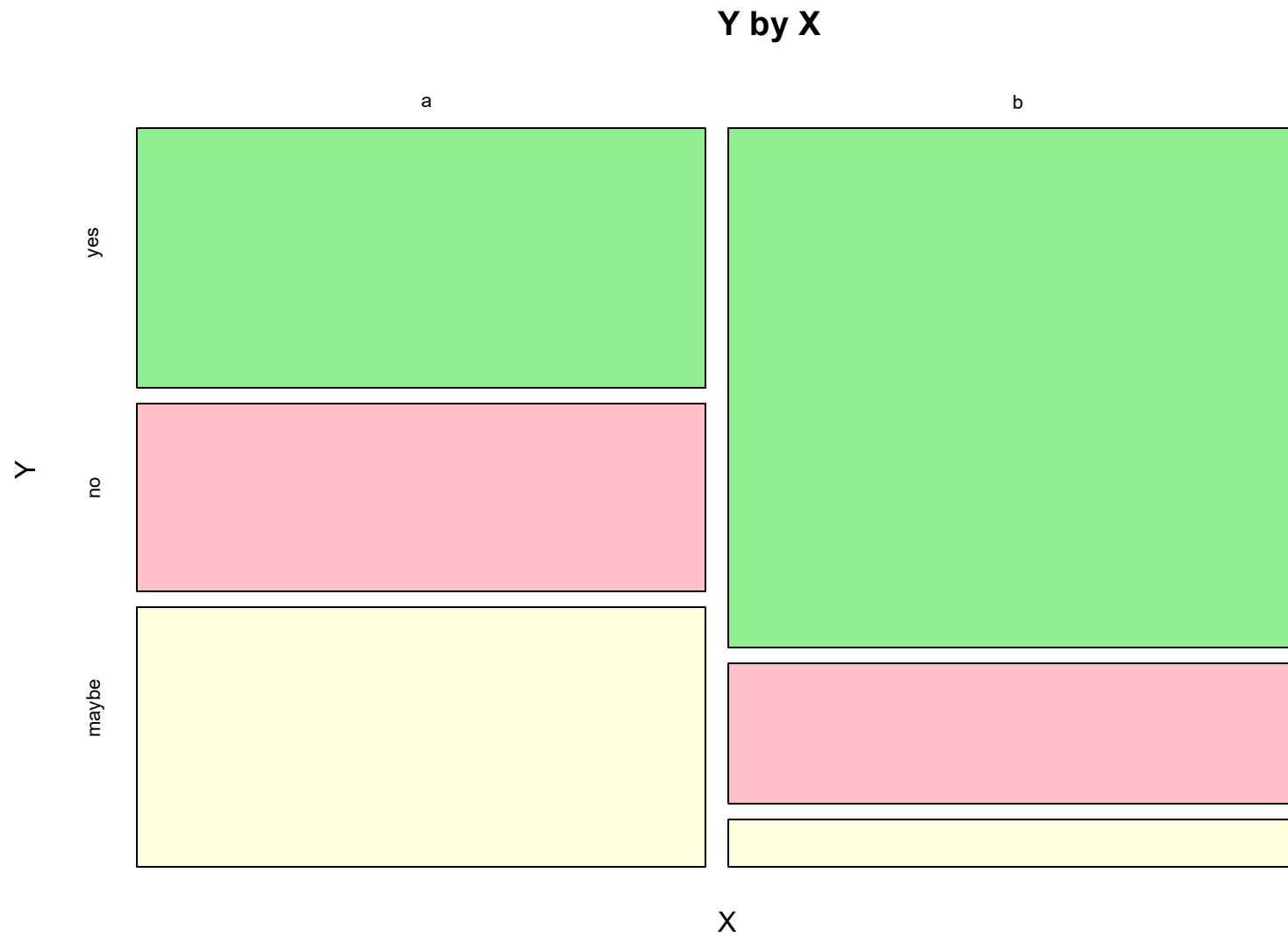
Samples	Response Categories	Test Name	Exact Test?	Report
2	$\geq 2$	Fisher's exact test	Yes, use with $N < 200$	"Table 1 shows the counts of 'yes', 'no', and 'maybe' responses (Y) for each of 'a' and 'b' (X). Figure 1 plots these proportions. Fisher's exact test indicated a statistically significant association between X and Y ( $p = .005$ )."
		G-test	No, use with $N < 200$	"Table 1 shows the counts of 'yes', 'no', and 'maybe' responses (Y) for each of 'a' and 'b' (X). Figure 1 plots these proportions. A G-test indicated a statistically significant association between X and Y ( $G(2) = 10.88, p = .004$ )."
		Two-sample chi-squared test	No, use with $N \geq 200$	"Table 1 shows the counts of 'yes', 'no', and 'maybe' responses (Y) for each of 'a' and 'b' (X). Figure 1 plots these proportions. A two-sample Pearson chi-squared test indicated a statistically significant association between X and Y ( $\chi^2(2, N=60) = 10.18, p = .006$ )."



**Table 1**

		<b>Y</b>		
		<b>yes</b>	<b>no</b>	<b>maybe</b>
<b>X</b>	<b>a</b>	11	8	11
	<b>b</b>	22	6	2

# Figure 1



# Association

## Dependent samples

Samples	Response Categories	Test Name	Exact Test?	R Code
2 <sup>†</sup>	≥2	Symmetry test	No, asymptotic	<pre># df is a long-format data table w/columns for participant (PIId), a within-Ss. factor (X), # and N-category outcome (Y) library(coin) # for symmetry_test df\$PIId = factor(df\$PIId) # participant is nominal df\$X = factor(df\$X)      # X is a within-Ss. factor of ≥2 levels df\$Y = factor(df\$Y)      # Y is an outcome of ≥2 categories symmetry_test(Y ~ X   PIId, data=df)</pre>

<sup>†</sup>Dependent samples

# Association

## Dependent samples

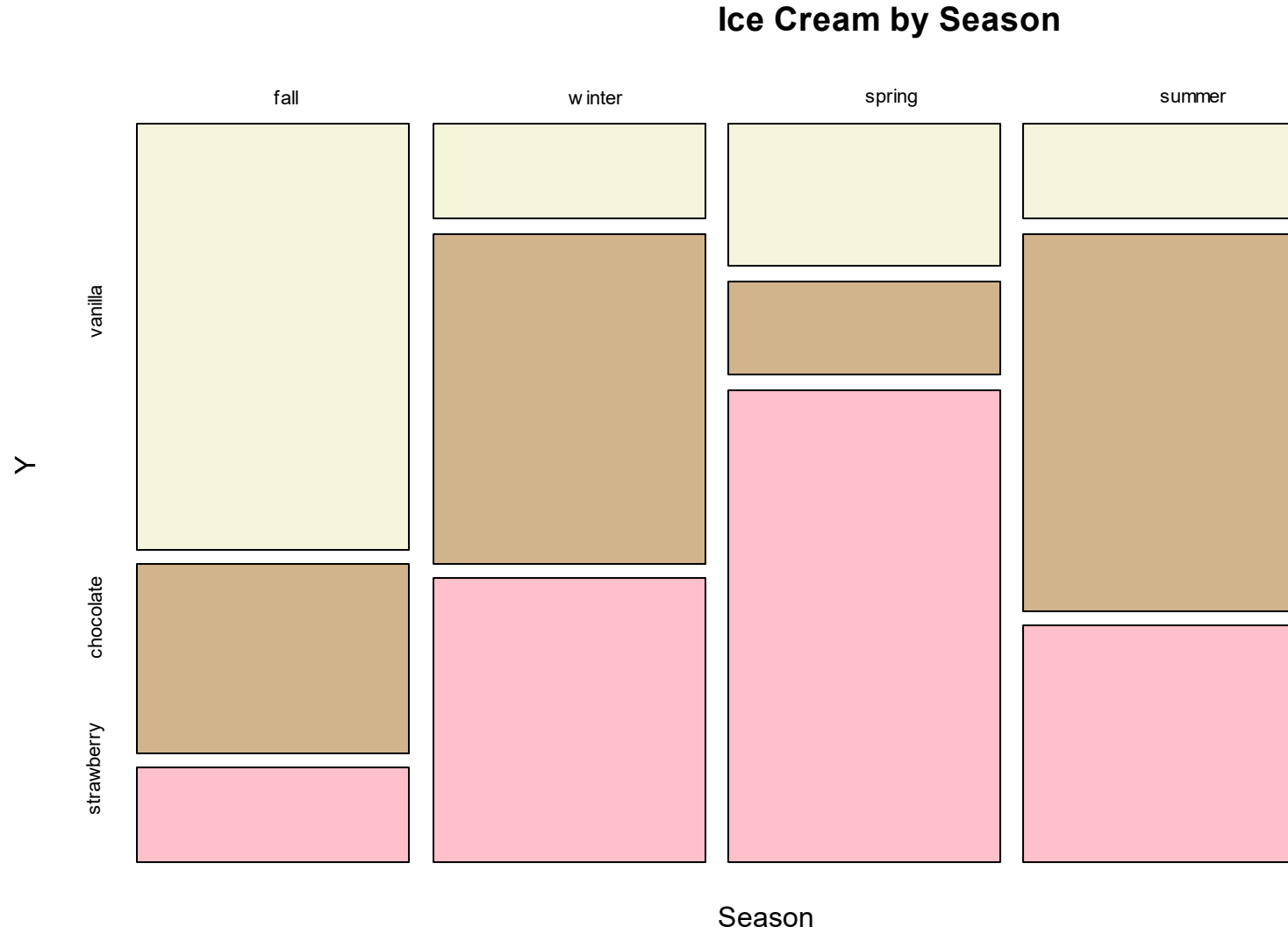
Samples	Response Categories	Test Name	Exact Test?	Report
2 <sup>†</sup>	≥2	Symmetry test	No, asymptotic	“Fifteen participants each provided four responses indicating their favorite ice cream flavor in each season (‘fall’, ‘winter’, ‘spring’, and ‘summer’). Table 2 shows the counts and Figure 2 plots the proportions. Out of the 60 responses, 16 were ‘vanilla’, 21 were ‘chocolate’, and 23 were ‘strawberry’. A symmetry test shows that the ice cream preferences across seasons were significantly different ( $p = .013$ ).”

<sup>†</sup>Dependent samples

**Table 2**

		<b>Y</b>		
		<b>vanilla</b>	<b>chocolate</b>	<b>strawberry</b>
<b>X</b>	<b>fall</b>	9	4	2
	<b>winter</b>	2	7	6
	<b>spring</b>	3	2	10
	<b>summer</b>	2	8	5

# Figure 2



# Proportions & Association

*Post hoc comparisons*

# Proportions

## Post hoc tests – One sample

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
1	≥2	Multinomial test	Pairwise binomial tests	<pre># xt holds the yes, no, and maybe counts created for the multinomial test yn = binom.test(c(xt[1], xt[2]), p=1/2) # yes vs. no ym = binom.test(c(xt[1], xt[3]), p=1/2) # yes vs. maybe nm = binom.test(c(xt[2], xt[3]), p=1/2) # no vs. maybe p.adjust(c(yn\$p.value, ym\$p.value, nm\$p.value), method="holm")  # or, equivalently library(RVAideMemoire) # for multinomial.multcomp multinomial.multcomp(xt, p.method="holm") # same results as above</pre>
1	≥2	One-sample chi-squared test	Pairwise chi-squared tests	<pre># xt holds the yes, no, and maybe counts created for the chi-squared test library(RVAideMemoire) # for chisq.multcomp chisq.multcomp(xt, p.method="holm") # xt shows levels  # to get the chi-squared statistics, use qchisq(1-p, df=1), # where p is the uncorrected (p.method="none") pairwise p-value: qchisq(1 - 0.0038, df=1) # 8.376996</pre>
1	≥2	Multinomial test, one-sample chi-squared test	Individual binomial tests against chance	<pre># For Y's response categories, test each proportion against chance. # xt holds the yes, no, and maybe counts y = binom.test(xt[1], nrow(df), p=1/length(xt)) # yes n = binom.test(xt[2], nrow(df), p=1/length(xt)) # no m = binom.test(xt[3], nrow(df), p=1/length(xt)) # maybe p.adjust(c(y\$p.value, n\$p.value, m\$p.value), method="holm")</pre>



# Proportions

## *Post hoc* tests – One sample

Samples	Response Categories	Omnibus Test	Contrast Test	Report
1	≥2	Multinomial test	Pairwise binomial tests	“Three <i>post hoc</i> pairwise comparisons using exact binomial tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that the proportions of ‘yes’ vs. ‘no’ and ‘yes’ vs. ‘maybe’ were not significantly different, but that the proportions of ‘no’ vs. ‘maybe’ were ( $p = .016$ ).”
1	≥2	One-sample chi-squared test	Pairwise chi-squared tests	“Three <i>post hoc</i> pairwise comparisons using Pearson chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that only the proportions of ‘no’ vs. ‘maybe’ were significantly different ( $\chi^2(1, N=43) = 8.38, p = .011$ ).”
1	≥2	Multinomial test, one-sample chi-squared test	Individual binomial tests against chance	“Three <i>post hoc</i> binomial tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that only the number of ‘maybe’ responses was significantly different from chance ( $p = .011$ ).”

# Association

## Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
2	≥2	Fisher's exact test	Pairwise Fisher's exact tests on 2×2 tables	<pre># xt is the m×n crosstabs created for Fisher's exact test yn = fisher.test(xt[,c(1,2)]) # yes vs. no ym = fisher.test(xt[,c(1,3)]) # yes vs. maybe nm = fisher.test(xt[,c(2,3)]) # no vs. maybe p.adjust(c(yn\$p.value, ym\$p.value, nm\$p.value), method="holm")  # or, equivalently library(RVAideMemoire) # for fisher.multcomp fisher.multcomp(xt, p.method="holm") # xt shows levels</pre>
			Binomial tests of each table column against chance	<pre># xt is the m×n crosstabs created for Fisher's exact test y = binom.test(xt[,1]) # yes n = binom.test(xt[,2]) # no m = binom.test(xt[,3]) # maybe p.adjust(c(y\$p.value, n\$p.value, m\$p.value), method="holm")</pre>
			Multinomial tests of each table row against chance	<pre># xt is the m×n crosstabs created for Fisher's exact test a = xmulti(xt[1,], rep(1/length(xt[1,]), length(xt[1,])), statName="Prob") # X=a b = xmulti(xt[2,], rep(1/length(xt[2,]), length(xt[2,])), statName="Prob") # X=b p.adjust(c(a\$pProb, b\$pProb), method="holm")</pre>

# Association

## *Post hoc* tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	$\geq 2$	Fisher's exact test	Pairwise Fisher's exact tests on 2×2 tables	“Three <i>post hoc</i> Fisher's exact tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), were conducted on each 2×2 subset of Table 1. Results indicated that there was a significant association between X and Y for the 'yes' and 'maybe' columns ( $p = .008$ ).”
			Binomial tests of each table column against chance	“Three <i>post hoc</i> binomial tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), were conducted on each column of Table 1. Results indicated that no column proportions were significantly different from chance.”
			Multinomial tests of each table row against chance	“Two <i>post hoc</i> multinomial tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), were conducted on each row of Table 1. Results indicated that the proportion of 'yes', 'no', and 'maybe' responses within 'b' were significantly different from chance ( $p < .0001$ ).”

# Association

## *Post hoc* tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
2	$\geq 2$	G-test	Pairwise G-tests on 2×2 tables	<pre># xt is the m×n crosstabs created for the G test yn = G.test(xt[,c(1,2)]) # yes vs. no ym = G.test(xt[,c(1,3)]) # yes vs. maybe nm = G.test(xt[,c(2,3)]) # no vs. maybe p.adjust(c(yn\$p.value, ym\$p.value, nm\$p.value), method="holm")</pre>
			Pairwise G-tests between table cells	<pre># xt is the m×n crosstabs created for the G test library(RVAideMemoire) # for G.multcomp G.multcomp(xt, p.method="holm") # xt shows levels</pre>

# Association

## *Post hoc* tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	$\geq 2$	G-test	Pairwise <i>G</i> -tests on 2×2 tables	“Three <i>post hoc G</i> -tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each 2×2 subset of Table 1. Results indicated that there was a significant association between X and Y for the ‘yes’ and ‘maybe’ columns ( $G(1) = 10.51, p = .004$ ).”
			Pairwise <i>G</i> -tests between table cells	“Fifteen <i>post hoc G</i> -tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each pair of cells in Table 1. Results indicated that there was a significant difference between the counts in cells {b, yes} vs. {b, maybe} ( $p < .001$ ) and {b, yes} vs. {b, no} ( $p = .026$ ).”

# Association

## Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
2	$\geq 2$	G-test	G-tests on each table column (or row) against chance	<pre># xt is the m×n crosstabs created for the G test # test column proportions: y = G.test(xt[,1]) # yes n = G.test(xt[,2]) # no m = G.test(xt[,3]) # maybe p.adjust(c(y\$p.value, n\$p.value, m\$p.value), method="holm")  # test row proportions: a = G.test(xt[1,]) # a b = G.test(xt[2,]) # b p.adjust(c(a\$p.value, b\$p.value), method="holm")</pre>
			G-tests on each table column (or row) against expected frequencies	<pre># xt is the m×n crosstabs created for the G test # test column proportions: ex = G.test(xt)\$expected[,1] # expected 'yes' y = G.test(xt[,1], p=ex/sum(ex)) ex = G.test(xt)\$expected[,2] # expected 'no' n = G.test(xt[,2], p=ex/sum(ex)) ex = G.test(xt)\$expected[,3] # expected 'maybe' m = G.test(xt[,3], p=ex/sum(ex)) p.adjust(c(y\$p.value, n\$p.value, m\$p.value), method="holm")  # test row proportions: ex = G.test(xt)\$expected[1,] # expected 'a' a = G.test(xt[1,], p=ex/sum(ex)) ex = G.test(xt)\$expected[2,] # expected 'b' b = G.test(xt[2,], p=ex/sum(ex)) p.adjust(c(a\$p.value, b\$p.value), method="holm")</pre>

# Association

## *Post hoc* tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	$\geq 2$	G-test	G-tests on each table column (or row) against chance	<p>“Three <i>post hoc</i> G-tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each column of Table 1. Results indicated that the proportion of ‘a’ and ‘b’ responses within ‘maybe’ significantly differed from chance (<math>G(1) = 6.86, p = .026</math>.)”</p> <p>“Two <i>post hoc</i> G-tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each row of Table 1. Results indicated that the proportion of ‘yes’, ‘no’, and ‘maybe’ responses within ‘b’ significantly differed from chance (<math>G(2) = 22.12, p &lt; .0001</math>.)”</p>
			G-tests on each table column (or row) against expected frequencies	<p>“Three <i>post hoc</i> G-tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each column of Table 1. Results indicated that the proportion of ‘a’ and ‘b’ responses within ‘maybe’ significantly differed from expected frequencies (<math>G(1) = 6.86, p = .026</math>.)”</p> <p>“Two <i>post hoc</i> G-tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each row of Table 1. Results indicated that the proportion of ‘yes’, ‘no’, and ‘maybe’ responses did not significantly differ from expected frequencies.”</p>

# Association

## *Post hoc* tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
2	≥2	chi-squared test	Pairwise chi-squared tests on 2×2 tables	<pre># xt is the m×n crosstabs created for the chi-squared test yn = chisq.test(xt[,c(1,2)]) # yes vs. no ym = chisq.test(xt[,c(1,3)]) # yes vs. maybe nm = chisq.test(xt[,c(2,3)]) # no vs. maybe p.adjust(c(yn\$p.value, ym\$p.value, nm\$p.value), method="holm")</pre>
			Pairwise chi-squared tests between table cells	<pre># xt is the m×n crosstabs created for the chi-squared test library(RVAideMemoire) # for chisq.multcomp chisq.multcomp(xt, p.method="holm") # xt shows levels  # to get the chi-squared statistics, use qchisq(1-p, df=1), # where p is the uncorrected (p.method="none") pairwise p-value: qchisq(1 - 4.5e-05, df=1) # 16.6479</pre>
			Chi-squared tests to compare each cell to its expected frequency	<pre># xt is the m×n crosstabs created for the chi-squared test library(chisq.posthoc.test) # for chisq.posthoc.test chisq.posthoc.test(xt, method="holm")  # to get the chi-squared statistics, use qchisq(1-p, df=1), # where p is the uncorrected (p.method="none") p-value: qchisq(1 - 0.004311, df=1) # 8.147944</pre>



# Association

## *Post hoc* tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	$\geq 2$	chi-squared test	Pairwise chi-squared tests on 2×2 tables	“Three <i>post hoc</i> chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each 2×2 subset of Table 1. Results indicated that there was a significant association between X and Y for the ‘yes’ and ‘maybe’ columns ( $\chi^2(1, N=46) = 7.88, p = .015$ ).”
			Pairwise chi-squared tests between table cells	“Fifteen <i>post hoc</i> chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each pair of cells in Table 1. Results indicated that there was a significant difference between the counts in cells {b, yes} vs. {b, maybe} ( $\chi^2(1, N=24) = 16.65, p = .001$ ) and {b, yes} vs. {b, no} ( $\chi^2(1, N=28) = 9.14, p = .035$ ).”
			Chi-squared tests to compare each cell to its expected frequency	“Six <i>post hoc</i> chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each cell in Table 1. Results indicated that {a, yes} ( $\chi^2(1, N=11) = 8.15, p = .026$ ), {b, yes} ( $\chi^2(1, N=22) = 8.15, p = .026$ ), {a, maybe} ( $\chi^2(1, N=11) = 7.95, p = .026$ ), and {b, maybe} ( $\chi^2(1, N=2) = 7.95, p = .026$ ) were significantly different from their expected frequencies.”

# Association

## Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
2	$\geq 2$	chi-squared test	chi-squared tests on each table column (or row) against chance	<pre># xt is the m×n crosstabs created for the chi-squared test # test column proportions: y = chisq.test(xt[,1]) # yes n = chisq.test(xt[,2]) # no m = chisq.test(xt[,3]) # maybe p.adjust(c(y\$p.value, n\$p.value, m\$p.value), method="holm")  # test row proportions: a = chisq.test(xt[1,]) # a b = chisq.test(xt[2,]) # b p.adjust(c(a\$p.value, b\$p.value), method="holm")</pre>
			chi-squared tests on each table column (or row) against expected frequencies	<pre># xt is the m×n crosstabs created for the chi-squared test # test column proportions: ex = chisq.test(xt)\$expected[,1] # expected 'yes' y = chisq.test(xt[,1], p=ex/sum(ex)) ex = chisq.test(xt)\$expected[,2] # expected 'no' n = chisq.test(xt[,2], p=ex/sum(ex)) ex = chisq.test(xt)\$expected[,3] # expected 'maybe' m = chisq.test(xt[,3], p=ex/sum(ex)) p.adjust(c(y\$p.value, n\$p.value, m\$p.value), method="holm")  # test row proportions: ex = chisq.test(xt)\$expected[1,] # expected 'a' a = chisq.test(xt[1,], p=ex/sum(ex)) ex = chisq.test(xt)\$expected[2,] # expected 'b' b = chisq.test(xt[2,], p=ex/sum(ex)) p.adjust(c(a\$p.value, b\$p.value), method="holm")</pre>

# Association

## *Post hoc* tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	$\geq 2$	chi-squared test	chi-squared tests on each table column (or row) against chance	<p>“Three <i>post hoc</i> chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each column of Table 1. Results indicated that the proportion of ‘a’ and ‘b’ responses within ‘maybe’ significantly differed from chance (<math>\chi^2(1, N=13) = 6.23, p = .038.</math>)”</p> <p>“Two <i>post hoc</i> chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each row of Table 1. Results indicated that the proportion of ‘yes’, ‘no’, and ‘maybe’ responses within ‘b’ were significantly different from chance (<math>\chi^2(2, N=30) = 22.40, p &lt; .0001.</math>)”</p>
			chi-squared tests on each table column (or row) against expected frequencies	<p>“Three <i>post hoc</i> chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each column of Table 1. Results indicated that the proportion of ‘a’ and ‘b’ responses within ‘maybe’ significantly differed from expected frequencies (<math>\chi^2(1, N=13) = 6.23, p = .038.</math>)”</p> <p>“Two <i>post hoc</i> chi-squared tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted on each row of Table 1. Results indicated that the proportion of ‘yes’, ‘no’, and ‘maybe’ responses were not significantly different from expected frequencies.”</p>

# Association

## Post hoc tests – Dependent samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
2	≥2	Symmetry test	Pairwise symmetry tests	<pre># df is a long-format data table w/columns for participant (PIId), a within-Ss. factor (X), # and N-category outcome (Y) library(coin) # for symmetry_test, pvalue pairwise.symmetry.test &lt;- function(s1, s2, data=df) { # compare seasons s1, s2   df2 &lt;- df[df\$X == s1   df\$X == s2,] # table subset   df2\$X = factor(df2\$X) # update factor levels   return (pvalue(symmetry_test(Y ~ X   PId, data=df2))) } fa.wi = pairwise.symmetry.test("fall", "winter", data=df) fa.sp = pairwise.symmetry.test("fall", "spring", data=df) fa.su = pairwise.symmetry.test("fall", "summer", data=df) wi.sp = pairwise.symmetry.test("winter", "spring", data=df) wi.su = pairwise.symmetry.test("winter", "summer", data=df) sp.su = pairwise.symmetry.test("spring", "summer", data=df) p.adjust(c(fa.wi, fa.sp, fa.su, wi.sp, wi.su, sp.su), method="holm")</pre>
2	≥2	Symmetry test	Pairwise sign tests	<pre># df is a long-format data table w/columns for participant (PIId), a within-Ss. factor (X), # and N-category outcome (Y) library(coin) # for sign_test, pvalue pairwise.sign.test &lt;- function(flavor, s1, s2, data=df) { # compare flavor in seasons s1, s2   df\$chose.flavor.in.s1 = ifelse(df\$Y == flavor &amp; df\$X == s1, 1, 0)   df\$chose.flavor.in.s2 = ifelse(df\$Y == flavor &amp; df\$X == s2, 1, 0)   return (pvalue(sign_test(chose.flavor.in.s1 ~ chose.flavor.in.s2, data=df))) } fa.wi = pairwise.sign.test("vanilla", "fall", "winter", data=df) fa.sp = pairwise.sign.test("vanilla", "fall", "spring", data=df) fa.su = pairwise.sign.test("vanilla", "fall", "summer", data=df) wi.sp = pairwise.sign.test("vanilla", "winter", "spring", data=df) wi.su = pairwise.sign.test("vanilla", "winter", "summer", data=df) sp.su = pairwise.sign.test("vanilla", "spring", "summer", data=df) p.adjust(c(fa.wi, fa.sp, fa.su, wi.sp, wi.su, sp.su), method="holm")</pre>

# Association

## *Post hoc* tests – Dependent samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
1	≥2	Symmetry test	Pairwise symmetry tests	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), were conducted between all four seasons using symmetry tests. Flavor preferences for no two seasons were significantly different.”
2	≥2	Symmetry test	Pairwise sign tests	“The pairwise preferences for vanilla ice cream were compared among the four seasons using six <i>post hoc</i> sign tests corrected with Holm’s sequential Bonferroni procedure (Holm 1979). The preferences for vanilla in fall, winter, spring, and summer did not significantly differ.”

# Bibliography (contingency tables, proportions, and association)

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# Assumptions

# ANOVA Assumptions

## Normality

Assumption	Test Name	Context of Use	R Code
Normality	Shapiro-Wilk test (on the response in each condition)	t-test, ANOVA	<pre># df has two factors (X1,X2) each w/two levels (a,b) and continuous response Y shapiro.test(df[df\$X1 == "a" &amp; df\$X2 == "a",]\$Y) # condition a,a shapiro.test(df[df\$X1 == "a" &amp; df\$X2 == "b",]\$Y) # condition a,b shapiro.test(df[df\$X1 == "b" &amp; df\$X2 == "a",]\$Y) # condition b,a shapiro.test(df[df\$X1 == "b" &amp; df\$X2 == "b",]\$Y) # condition b,b</pre>
Normality	Shapiro-Wilk test (on residuals)	t-test, ANOVA	<pre># df has two factors (X1,X2) each w/two levels (a,b) and continuous response (Y) library(afex) # for aov_ez library(EnvStats) # for gofTest library(performance) # for check_normality m = aov_ez(dv="Y", within="X1", between="X2", id="PIId", type=3, data=df) # build model r = residuals(m\$lm) # extract residuals  ## Common code - see below... ## mean(r); sum(r) # both should be ~0 plot(r[1:length(r)], main="Residuals"); abline(h=0) # should look random qqnorm(r); qqline(r) # Q-Q plot hist(r, main="Histogram of residuals", freq=FALSE) # should look normal f = gofTest(r, distribution="norm") # GOF test curve(dnorm(x, mean=f\$distribution.parameters[1], sd=f\$distribution.parameters[2]),       lty=1, lwd=3, col="blue", add=TRUE) print(f) # display fit shapiro.test(r) # Shapiro-Wilk test print(check_normality(m)) # same</pre>
Normality	Shapiro-Wilk test (on residuals)	Linear mixed model (LMM)	<pre># df has two factors (X1,X2) each w/two levels (a,b) and continuous response (Y) library(lme4) # for lmer library(lmerTest) m = lmer(Y ~ X1*X2 + (1 PIId), data=df) # make linear mixed model r = residuals(m) # extract residuals  ## Continue with "common code," above ... ##</pre>

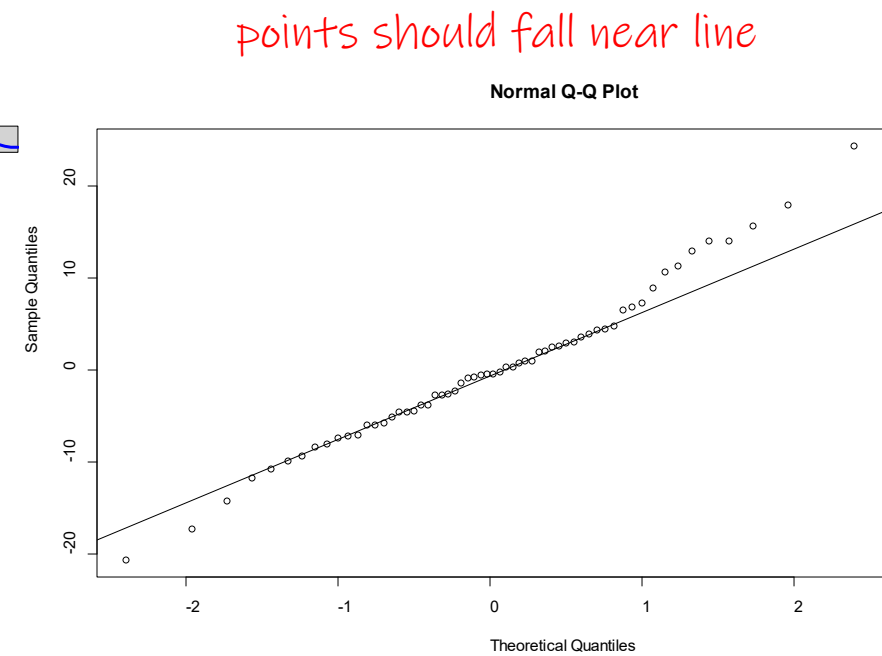
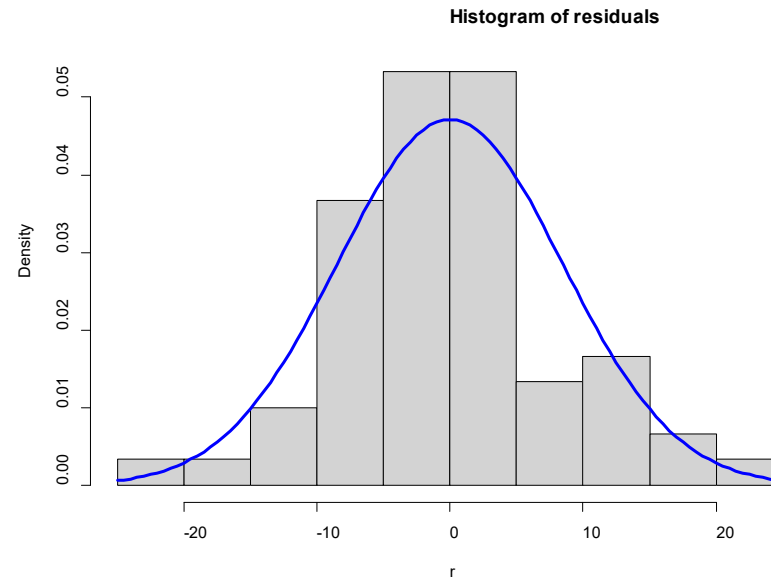
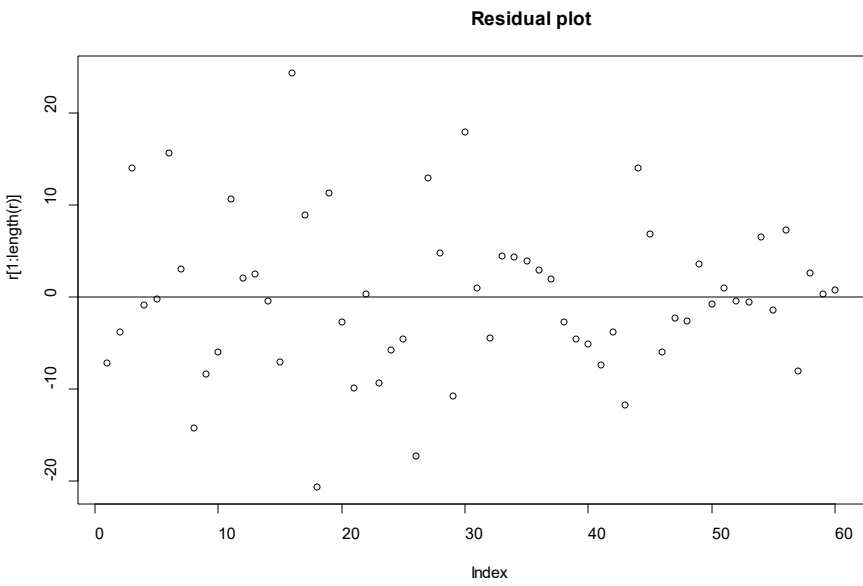


# ANOVA Assumptions

## Normality

Assumption	Test Name	Context of Use	Report
Normality	Shapiro-Wilk test (on the response in each condition)	<i>t</i> -test, ANOVA	“To test the normality assumption, a Shapiro-Wilk test was run on the response Y for each combination of levels of factors X1 and X2. All combinations were found to be statistically non-significant, indicating compliance with the normality assumption.”
Normality	Shapiro-Wilk test (on residuals)	<i>t</i> -test, ANOVA	“To test the normality assumption, a Shapiro-Wilk test was run on the residuals of a between-subjects full-factorial ANOVA model. The test was statistically non-significant ( $W = .984, p = .627$ ), indicating compliance with the normality assumption. A plot of residuals, histogram of residuals, and Q-Q plot all visually confirm the same (Figure 3).”
Normality	Shapiro-Wilk test (on residuals)	Linear mixed model (LMM)	“To test the normality assumption, a Shapiro-Wilk test was run on the residuals of a within-subjects linear mixed model (LMM). The test was statistically non-significant ( $W = .984, p = .627$ ), indicating compliance with the normality assumption. A plot of residuals, histogram of residuals, and Q-Q plot all visually confirm the same (Figure 3).”

# Figure 3



# ANOVA Assumptions

## Homoscedasticity & sphericity

Assumption	Test Name	Context of Use	R Code
Homogeneity of variance	Levene's test	Any ANOVA model with at least one between-subjects factor	<pre> # df has one between-Ss factor (X1), one within-Ss factor (X2), and continuous response (Y) library(afex) # for aov_ez library(performance) # for check_homogeneity library(lme4) # for lmer Library(lmerTest) library(car) # for Anova  m = aov_ez(dv="Y", between="X1", within="X2", id="PIId", type=3, data=df) print(check_homogeneity(m)) # Levene's test  # if a violation occurs (p&lt;.05), use a Welch t-test for one factor of 2 levels... t.test(Y ~ X1, data=df, var.equal=FALSE)  # ...or a Welch ANOVA for one factor of &gt;2 levels... oneway.test(Y ~ X1, data=df, var.equal=FALSE)  # ...or a White-adjusted ANOVA for &gt;1 factor (with within-Ss. factors, use an LMM) m = lmer(Y ~ X1*X2 + (1 PIId), data=df) Anova(m, type=3, test.statistic="F", white.adjust=TRUE) </pre>
Sphericity	Mauchly's test of sphericity	Any ANOVA model with at least one within-subjects factor	<pre> # df has one between-Ss factor (X1), one within-Ss factor (X2), and continuous response (Y) library(afex) # for aov_ez library(performance) # for check_sphericity  m = aov_ez(dv="Y", between="X1", within="X2", id="PIId", type=3, data=df)  summary(m)\$sphericity.tests # Mauchly's test of sphericity print(check_sphericity(m)) # same  anova(m, correction="none") # use if p≥.05, no violation of sphericity anova(m, correction="GG") # use if p&lt;.05, sphericity violation </pre>

# ANOVA Assumptions

## Homoscedasticity & sphericity

Assumption	Test Name	Context of Use	Report
Homogeneity of variance	Levene's test	Any ANOVA model with at least one between-subjects factor	"To test the homogeneity of variance assumption, Levene's test was run on a mixed factorial ANOVA with a between-subjects factor X1 and a within-subjects factor X2. The test was statistically non-significant ( $p = .753$ ), indicating no violation."
Sphericity	Mauchly's test of sphericity	Any ANOVA model with at least one within-subjects factor	"To test the sphericity assumption, Mauchly's test of sphericity was run on a mixed factorial ANOVA with a between-subjects factor X1 and a within-subjects factor X2. The test was statistically non-significant ( $p = .999$ ), indicating no sphericity violation."

# Bibliography (normality, homoscedasticity, and sphericity)

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# Distributions

# Distributions

Distribution	Parameterization	R Distribution Fns	R Code
Normal	mean ( $\mu$ ): mean standard deviation ( $\sigma$ ): sd	_norm: dnorm pnorm qnorm rnorm	<pre> # df has one factor (X) w/two levels (a,b) and continuous response Y library(EnvStats) # for gofTest hist(df[df\$X == "a",]\$Y, main="Histogram of Y for X=a", col="pink", freq=FALSE) # X=a fa = gofTest(df[df\$X == "a",]\$Y, distribution="norm") curve(dnorm(x, mean=fa\$distribution.parameters[1], sd=fa\$distribution.parameters[2]),       lty=1, lwd=3, col="red", add=TRUE) print(fa) # Shapiro-Wilk GOF  hist(df[df\$X == "b",]\$Y, main="Histogram of Y for X=b", col="lightblue", freq=FALSE) # X=b fb = gofTest(df[df\$X == "b",]\$Y, distribution="norm") curve(dnorm(x, mean=fb\$distribution.parameters[1], sd=fb\$distribution.parameters[2]),       lty=1, lwd=3, col="blue", add=TRUE) print(fb) # Shapiro-Wilk GOF </pre>
Lognormal	mean ( $\mu$ ): meanlog standard deviation ( $\sigma$ ): sdlog	_lnorm: dlnorm plnorm qlnorm rlnorm	<pre> # df has one factor (X) w/two levels (a,b) and positively skewed response Y library(EnvStats) # for gofTest hist(df[df\$X == "a",]\$Y, main="Histogram of Y for X=a", col="pink", freq=FALSE) # X=a fa = gofTest(df[df\$X == "a",]\$Y, distribution="lnorm") curve(dlnorm(x, meanlog=fa\$distribution.parameters[1], sdlog=fa\$distribution.parameters[2]),       lty=1, lwd=3, col="red", add=TRUE) print(fa) # Shapiro-Wilk GOF  hist(df[df\$X == "b",]\$Y, main="Histogram of Y for X=b", col="lightblue", freq=FALSE) # X=b fb = gofTest(df[df\$X == "b",]\$Y, distribution="lnorm") curve(dlnorm(x, meanlog=fb\$distribution.parameters[1], sdlog=fb\$distribution.parameters[2]),       lty=1, lwd=3, col="blue", add=TRUE) print(fb) # Shapiro-Wilk GOF </pre>

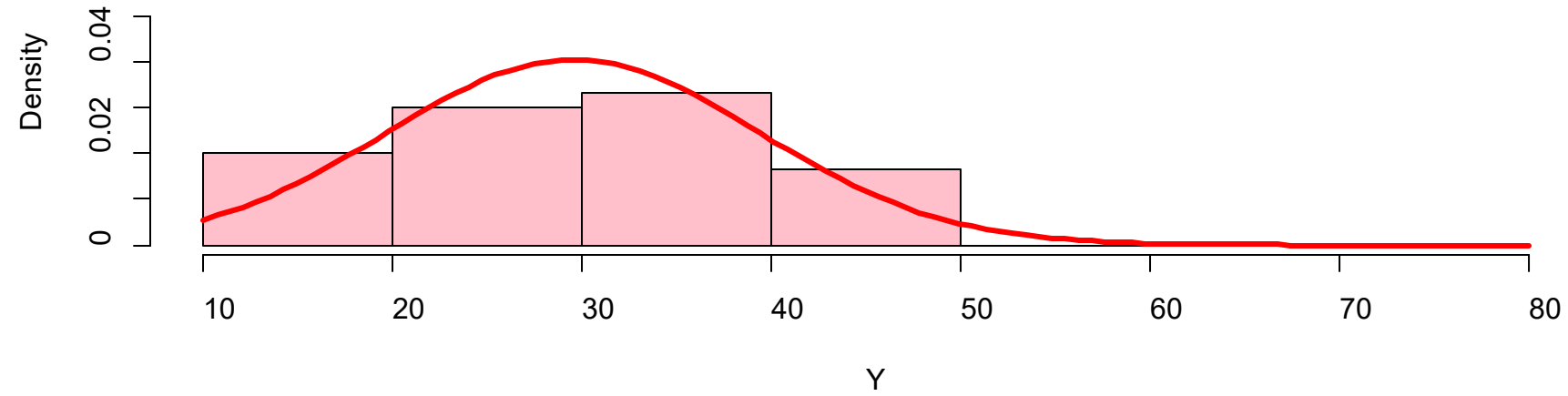
# Distributions

Distribution	Parameterization	R Distribution Fns	Report
Normal	mean ( $\mu$ ): <code>mean</code> standard deviation ( $\sigma$ ): <code>sd</code>	<code>_norm:</code> <code>dnorm</code> <code>pnorm</code> <code>qnorm</code> <code>rnorm</code>	“Figure 4 shows the distributions of response Y for both levels of factor X. To test whether these distributions were normally distributed, a Shapiro-Wilk goodness-of-fit test was run on Y for both levels of X. The test for level ‘a’ was statistically non-significant ( $W = .979, p = .796$ ), as was the test for level ‘b’ ( $W = .987, p = .961$ ), indicating no detectable departure from a normal distribution for either level of X.”
Lognormal	mean ( $\mu$ ): <code>meanlog</code> standard deviation ( $\sigma$ ): <code>sdlog</code>	<code>_lnorm:</code> <code>dlnorm</code> <code>plnorm</code> <code>qlnorm</code> <code>rlnorm</code>	“Figure 5 shows the distributions of response Y for both levels of factor X. To test whether these distributions were lognormally distributed, a Shapiro-Wilk goodness-of-fit test was run on Y for both levels of X. The test for level ‘a’ was statistically non-significant ( $W = .979, p = .796$ ), as was the test for level ‘b’ ( $W = .987, p = .961$ ), indicating no detectable departure from a lognormal distribution for either level of X.”

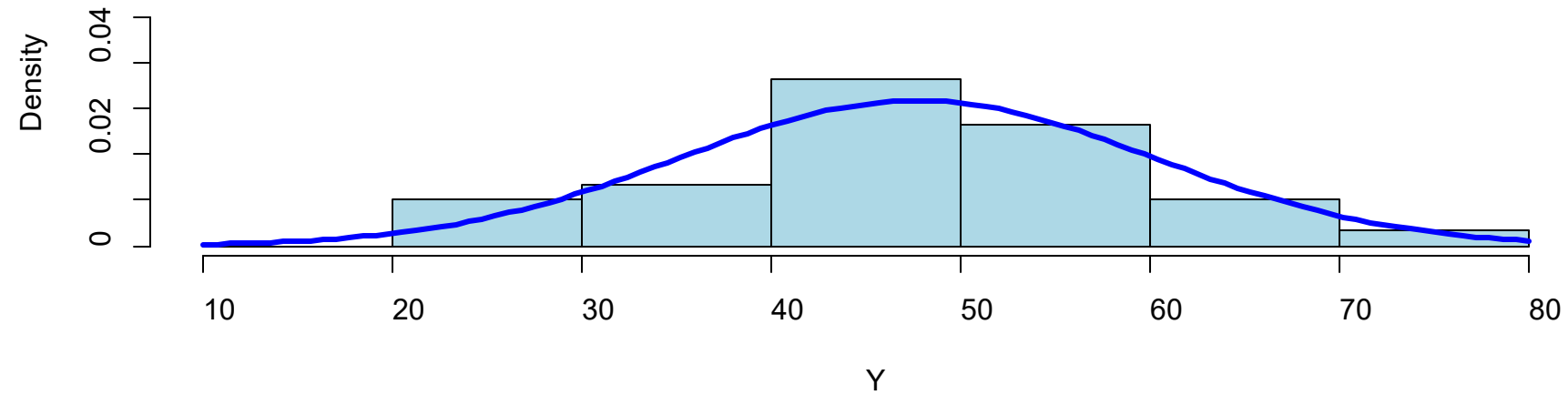


# Figure 4

Histogram of Y for X=a

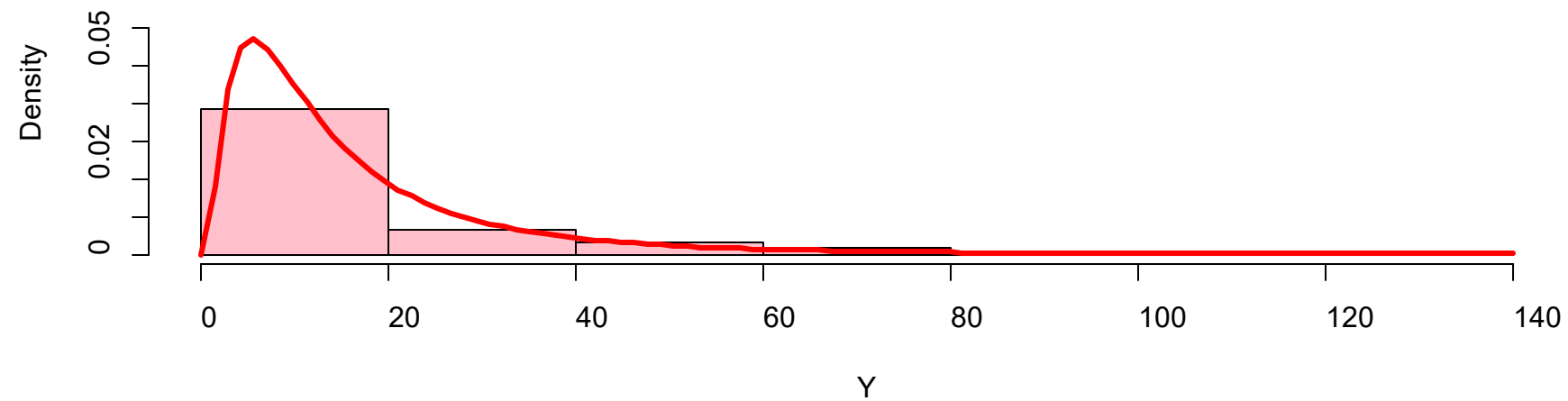


Histogram of Y for X=b

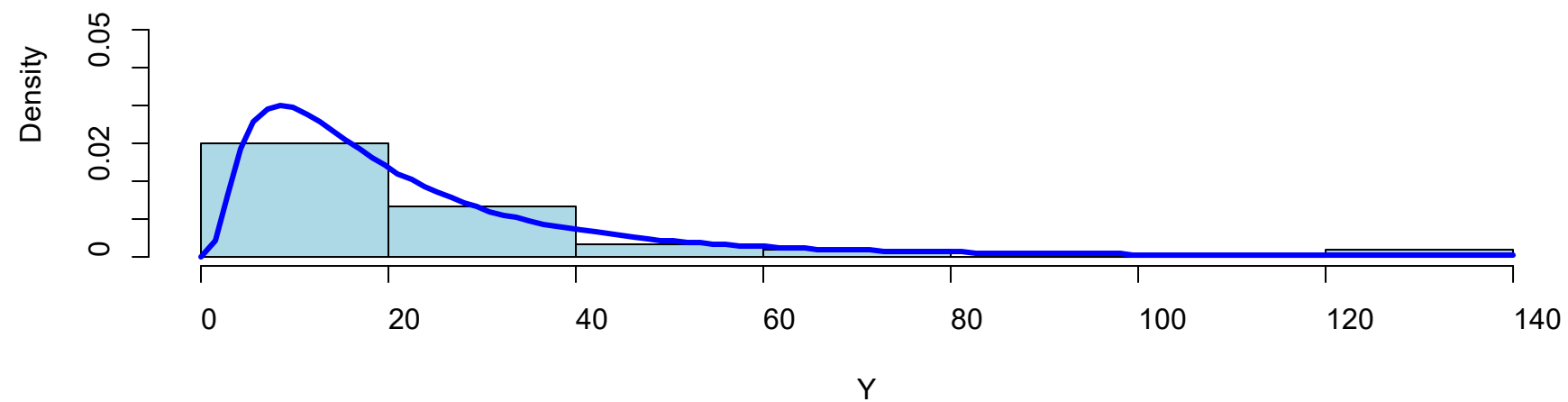


# Figure 5

Histogram of Y for X=a



Histogram of Y for X=b



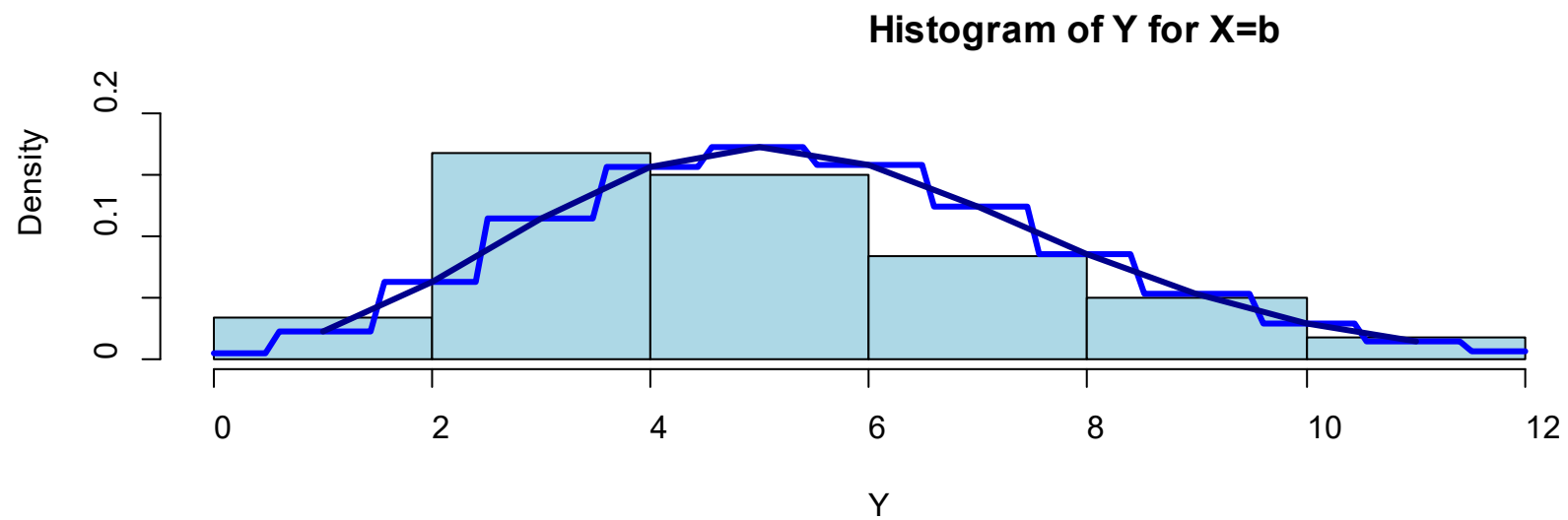
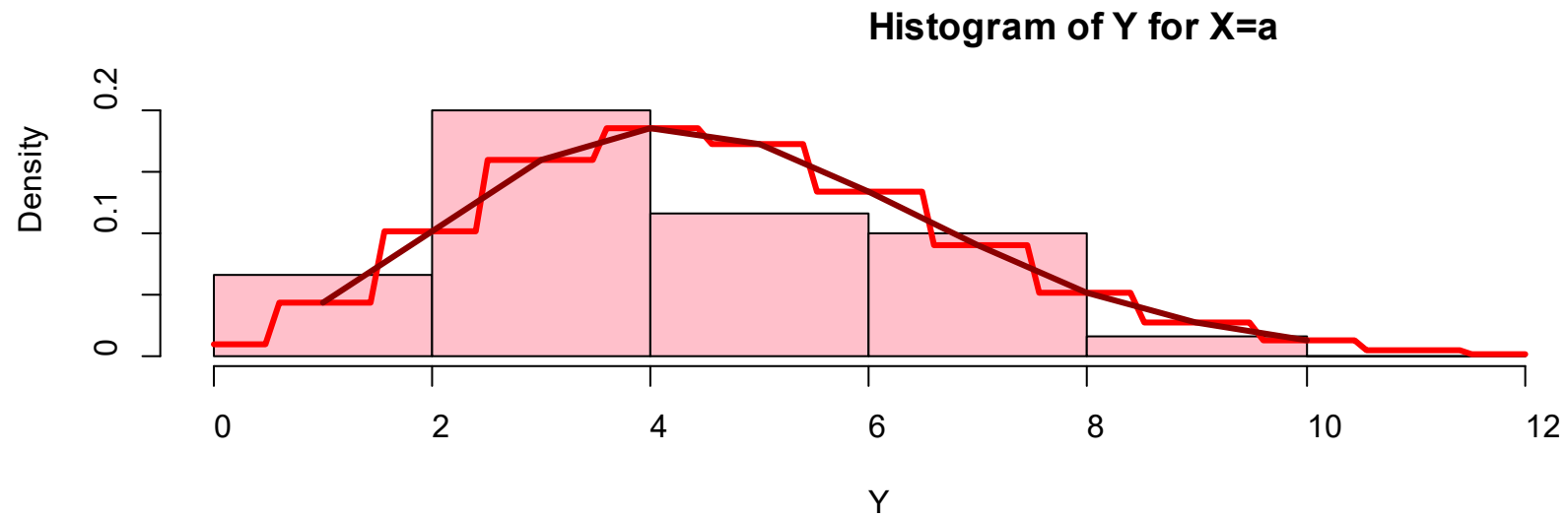
# Distributions

Distribution	Parameterization	R Distribution Fns	R Code
Poisson	mean, variance ( $\lambda$ ): lambda	<pre>_pois: dpois ppois qpois rpois</pre>	<pre># df has one factor (X) w/two levels (a,b) and integer count response Y library(fitdistrplus) # for fitdist, gofstat  hist(df[df\$X == "a",]\$Y, main="Histogram of Y for X=a", col="pink", freq=FALSE) # X=a fa = fitdist(df[df\$X == "a",]\$Y, distr="pois") curve(dpois(round(x,0), lambda=fa\$estimate[1]), lty=1, lwd=3, col="red", add=TRUE) xa = seq(floor(min(df[df\$X == "a",]\$Y)), ceiling(max(df[df\$X == "a",]\$Y)), by=1) lines(xa, dpois(xa, lambda=fa\$estimate[1]), lty=1, lwd=3, col="darkred") gofstat(fa) # chi-squared GOF  hist(df[df\$X == "b",]\$Y, main="Histogram of Y for X=b", col="lightblue", freq=FALSE) # X=b fb = fitdist(df[df\$X == "b",]\$Y, distr="pois") curve(dpois(round(x,0), lambda=fb\$estimate[1]), lty=1, lwd=3, col="blue", add=TRUE) xb = seq(floor(min(df[df\$X == "b",]\$Y)), ceiling(max(df[df\$X == "b",]\$Y)), by=1) lines(xb, dpois(xb, lambda=fb\$estimate[1]), lty=1, lwd=3, col="darkblue") gofstat(fb) # chi-squared GOF  # if var/ mean  &gt; 1.15, we have overdispersion; use quasipoisson or an nbinom GL(M)M var(df[df\$X == "a",]\$Y) / abs(mean(df[df\$X == "a",]\$Y)) &gt; 1.15 var(df[df\$X == "b",]\$Y) / abs(mean(df[df\$X == "b",]\$Y)) &gt; 1.15</pre>

# Distributions

Distribution	Parameterization	R Distribution Fns	Report
Poisson	mean, variance ( $\lambda$ ): lambda	<pre>_pois: dpois ppois qpois rpois</pre>	<p>“Figure 6 shows the distributions of response Y for both levels of factor X. To test whether these distributions were Poisson distributed, a chi-squared goodness-of-fit test was run on Y for both levels of X. The test for level ‘a’ was statistically non-significant (<math>\chi^2(4, N=30) = 0.56, p = .967</math>), as was the test for level ‘b’ (<math>\chi^2(4, N=30) = 3.89, p = .422</math>), indicating no detectable departure from a Poisson distribution for either level of X.”</p>

# Figure 6



# Distributions

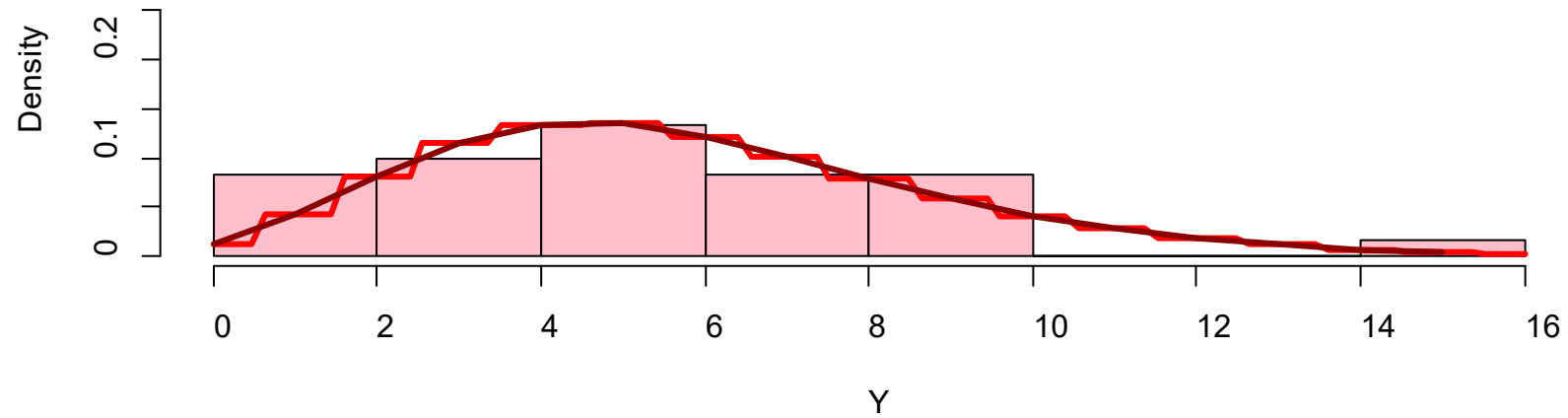
Distribution	Parameterization	R Distribution Fns	R Code
Negative Binomial	dispersion ( $\theta$ ): size mean ( $\mu$ ): $\mu$	_nbinom: dnbinom pnbinom qnbinom rnbinom	<pre> # df has one factor (X) w/two levels (a,b) and integer count response Y library(fitdistrplus) # for fitdist, gofstat hist(df[df\$X == "a",]\$Y, main="Histogram of Y for X=a", col="pink", freq=FALSE) # X=a fa = fitdist(df[df\$X == "a",]\$Y, distr="nbinom") curve(dnbinom(round(x,0), size=fa\$estimate[1], mu=fa\$estimate[2]),       lty=1, lwd=3, col="red", add=TRUE) xa = seq(floor(min(df[df\$X == "a",]\$Y)), ceiling(max(df[df\$X == "a",]\$Y)), by=1) lines(xa, dnbinom(xa, size=fa\$estimate[1], mu=fa\$estimate[2]), lty=1, lwd=3, col="darkred") gofstat(fa) # chi-squared GOF  hist(df[df\$X == "b",]\$Y, main="Histogram of Y for X=b", col="lightblue", freq=FALSE) # X=b fb = fitdist(df[df\$X == "b",]\$Y, distr="nbinom") curve(dnbinom(round(x,0), size=fb\$estimate[1], mu=fb\$estimate[2]),       lty=1, lwd=3, col="blue", add=TRUE) xb = seq(floor(min(df[df\$X == "b",]\$Y)), ceiling(max(df[df\$X == "b",]\$Y)), by=1) lines(xb, dnbinom(xb, size=fb\$estimate[1], mu=fb\$estimate[2]), lty=1, lwd=3, col="darkblue") gofstat(fb) # chi-squared GOF </pre>

# Distributions

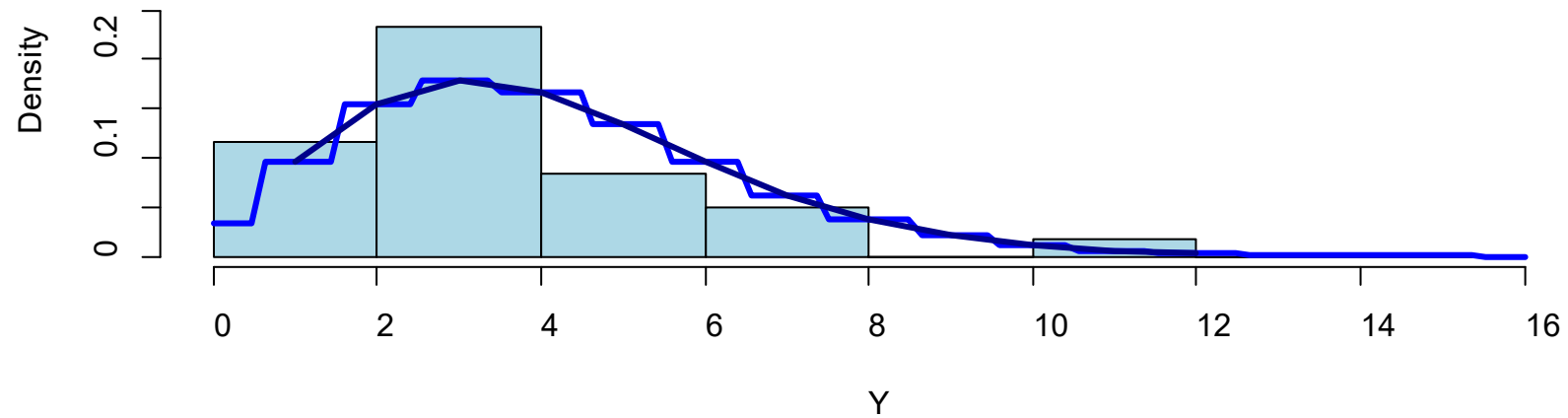
Distribution	Parameterization	R Distribution Fns	Report
Negative Binomial	dispersion ( $\theta$ ): size mean ( $\mu$ ): mu	<code>_nbinom:</code> <code>dnbinom</code> <code>pnbinom</code> <code>qnbinom</code> <code>rnbinom</code>	<p>“Figure 7 shows the distributions of response Y for both levels of factor X. To test whether these distributions were negative binomially distributed, a chi-squared goodness-of-fit test was run on Y for both levels of X. The test for level ‘a’ was statistically non-significant (<math>\chi^2(4, N=30) = 0.88, p = .927</math>), as was the test for level ‘b’ (<math>\chi^2(2, N=30) = 0.81, p = .666</math>), indicating no detectable departure from a negative binomial distribution for either level of X.”</p>

# Figure 7

Histogram of Y for X=a



Histogram of Y for X=b





# Distribution Tests

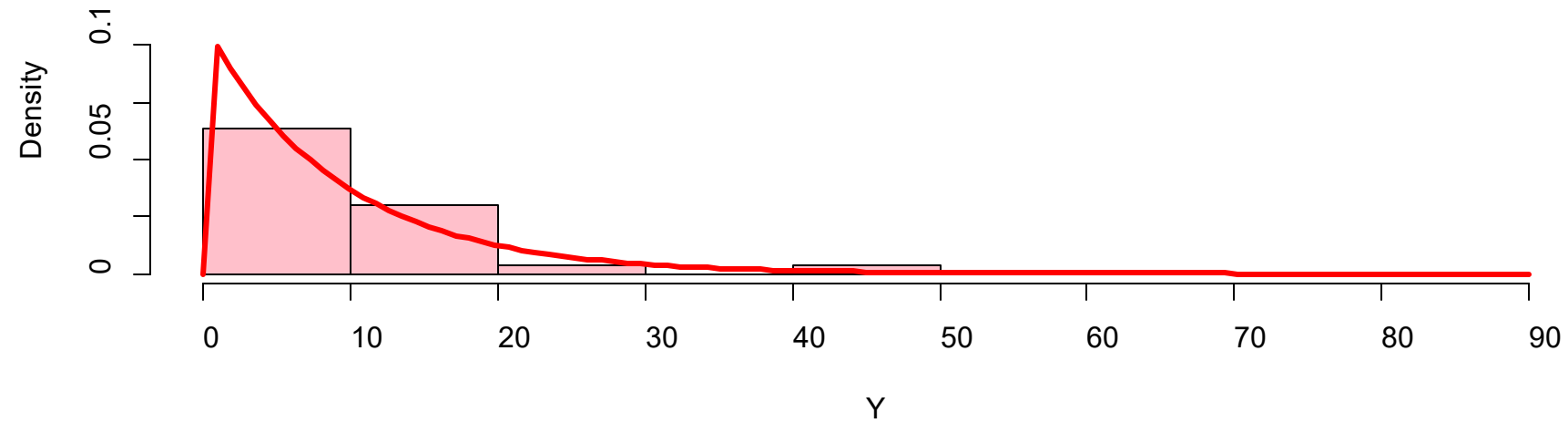
Distribution	Parameterization	R Distribution Fns	R Code
Exponential	rate ( $\lambda$ ): rate	_exp: dexp pexp qexp rexp	<pre> # df has one factor (X) w/two levels (a,b) and exponential response Y library(EnvStats) # for gofTest hist(df[df\$X == "a",]\$Y, main="Histogram of Y for X=a", col="pink", freq=FALSE) # X=a fa = gofTest(df[df\$X == "a",]\$Y, distribution="exp") curve(dexp(x, rate=fa\$distribution.parameters[1]), lty=1, lwd=3, col="red", add=TRUE) print(fa) # Shapiro-Wilk-Chen-Balakrishnan GOF  hist(df[df\$X == "b",]\$Y, main="Histogram of Y for X=b", col="lightblue", freq=FALSE) # X=b fb = gofTest(df[df\$X == "b",]\$Y, distribution="exp") curve(dexp(x, rate=fb\$distribution.parameters[1]), lty=1, lwd=3, col="blue", add=TRUE) print(fb) # Shapiro-Wilk-Chen-Balakrishnan GOF </pre>
Gamma	shape ( $\alpha$ ): shape scale ( $\beta$ ): scale	_gamma: dgamma pgamma qgamma rgamma	<pre> # df has one factor (X) w/two levels (a,b) and positively skewed response Y library(EnvStats) # for gofTest hist(df[df\$X == "a",]\$Y, main="Histogram of Y for X=a", col="pink", freq=FALSE) # X=a fa = gofTest(df[df\$X == "a",]\$Y, distribution="gamma") curve(dgamma(x, shape=fa\$distribution.parameters[1], scale=fa\$distribution.parameters[2]),       lty=1, lwd=3, col="red", add=TRUE) print(fa) # Shapiro-Wilk-Chen-Balakrishnan GOF  hist(df[df\$X == "b",]\$Y, main="Histogram of Y for X=b", col="lightblue", freq=FALSE) # X=b fb = gofTest(df[df\$X == "b",]\$Y, distribution="gamma") curve(dgamma(x, shape=fa\$distribution.parameters[1], scale=fa\$distribution.parameters[2]),       lty=1, lwd=3, col="blue", add=TRUE) print(fb) # Shapiro-Wilk-Chen-Balakrishnan GOF </pre>

# Distribution Tests

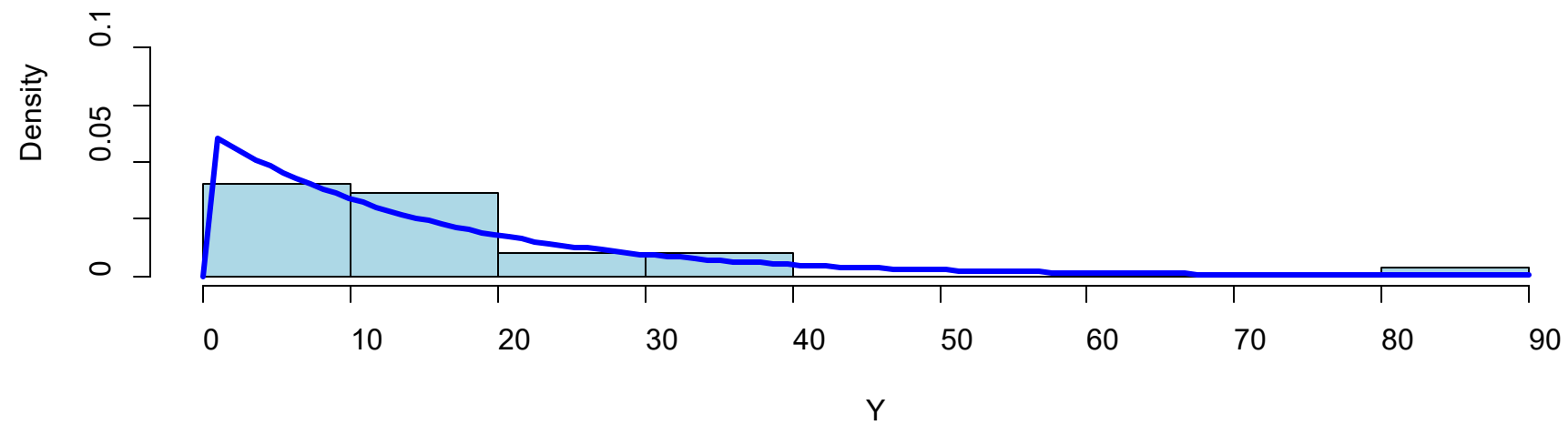
Distribution	Parameterization	R Distribution Fns	Report
Exponential	rate ( $\lambda$ ): <code>rate</code>	<code>_exp:</code> <code>dexp</code> <code>pexp</code> <code>qexp</code> <code>rexp</code>	“Figure 8 shows the distributions of response Y for both levels of factor X. To test whether these distributions were exponentially distributed, a Shapiro-Wilk goodness-of-fit test was run on Y for both levels of X. The test for level ‘a’ was statistically non-significant ( $W = .966, p = .428$ ), as was the test for level ‘b’ ( $W = .952, p = .190$ ), indicating no detectable departure from an exponential distribution for either level of X.”
Gamma	shape ( $\alpha$ ): <code>shape</code> scale ( $\beta$ ): <code>scale</code>	<code>_gamma:</code> <code>dgamma</code> <code>pgamma</code> <code>qgamma</code> <code>rgamma</code>	“Figure 9 shows the distributions of response Y for both levels of factor X. To test whether these distributions were gamma distributed, a Shapiro-Wilk goodness-of-fit test was run on Y for both levels of X. The test for level ‘a’ was statistically non-significant ( $W = .968, p = .483$ ), as was the test for level ‘b’ ( $W = .967, p = .459$ ), indicating no detectable departure from a gamma distribution for either level of X.”

# Figure 8

Histogram of Y for X=a

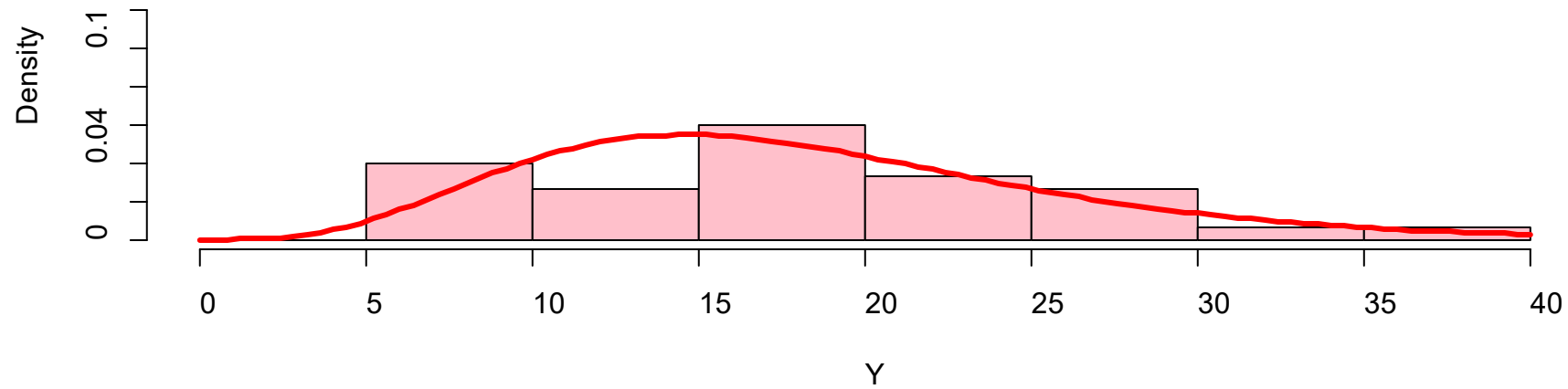


Histogram of Y for X=b

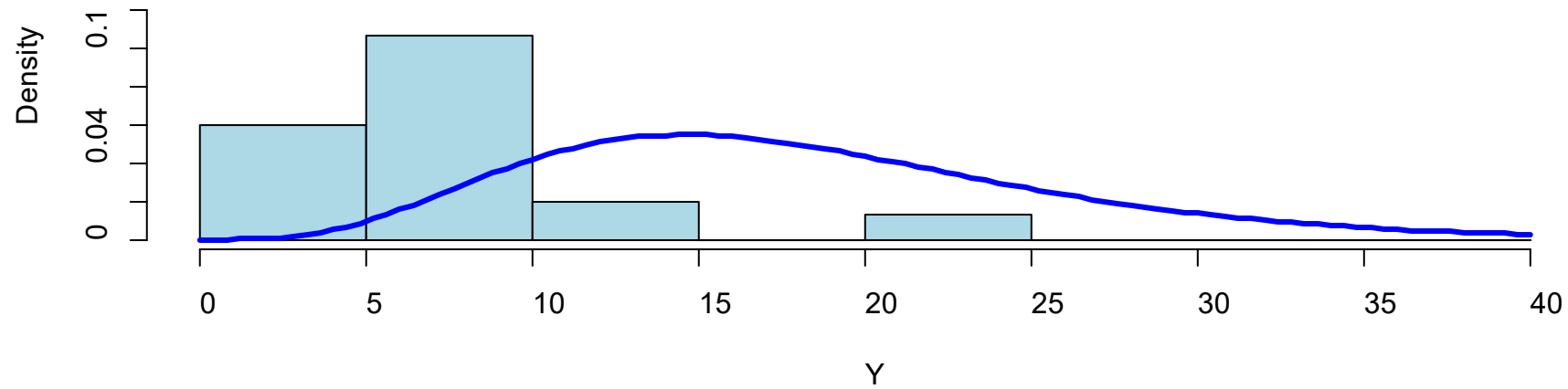


# Figure 9

Histogram of Y for X=a



Histogram of Y for X=b



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# Parametric Tests

# Parametric Tests

## One between-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	R Code
1	2	Between	Independent-samples <i>t</i> -test	<pre># df has one between-Ss. factor (X) w/levels (a,b) and continuous response (Y) library(car) # for leveneTest df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$X = factor(df\$X) # X is a 2-level factor contrasts(df\$X) &lt;- "contr.sum"  leveneTest(Y ~ X, data=df, center=mean) # check homogeneity of variance  t.test(Y ~ X, data=df, var.equal=TRUE) # if p≥.05, no violation of homogeneity t.test(Y ~ X, data=df, var.equal=FALSE) # if p&lt;.05, Welch t-test</pre>
1	≥2	Between	One-way ANOVA	<pre># df has one between-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(afex) # for aov_ez library(performance) # for check_homogeneity library(car) # for Anova df\$PIId = factor(df\$PIId) # participant is nominal df\$X = factor(df\$X) # X is a 3-level factor contrasts(df\$X) &lt;- "contr.sum"  m = aov_ez(dv="Y", between="X", id="PIId", type=3, data=df) # fit model leveneTest(Y ~ X, data=df, center=mean) # Levene's test print(check_homogeneity(m)) # same  anova(m) # use if p≥.05, no violation of homoscedasticity, else use... oneway.test(Y ~ X, data=df, var.equal=FALSE) # Welch ANOVA Anova(m\$lm, type=3, white.adjust=TRUE) # White-adjusted ANOVA</pre>

# Parametric Tests

## One between-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	Report
1	2	Between	Independent-samples <i>t</i> -test	“The mean of ‘a’ was 29.29 ( <i>SD</i> = 14.72) and of ‘b’ was 47.68 ( <i>SD</i> = 12.53). This difference was statistically significant according to an independent-samples <i>t</i> -test ( $t(58) = -5.21, p < .0001$ ).”
1	≥2	Between	One-way ANOVA	“The mean of ‘a’ was 32.12 ( <i>SD</i> = 14.59), of ‘b’ was 44.23 ( <i>SD</i> = 12.45), and of ‘c’ was 41.60 ( <i>SD</i> = 14.36). These differences were statistically significant according to a one-way ANOVA ( $F(2, 57) = 4.24, p = .019$ ).”

**NB.** “*SD*” stands for “standard deviation,” i.e., the spread of values around the mean.



# Parametric Tests

## One within-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	R Code
1	2	Within	Paired-samples t-test	<pre># df has one within-Ss. factor (X) w/levels (a,b) and continuous response (Y) library(reshape2) # for dcast df\$PIId = factor(df\$PIId) # participant is nominal df\$X = factor(df\$X) # X is a 2-level factor contrasts(df\$X) &lt;- "contr.sum"  df2 &lt;- dcast(df, PIId ~ X, value.var="Y") # make wide-format table t.test(df2\$a, df2\$b, paired=TRUE) # neither homoscedasticity nor sphericity applies to a paired t-test</pre>
1	≥2	Within	One-way repeated measures ANOVA	<pre># df has one within-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(afex) # for aov_ez library(performance) # for check_sphericity df\$PIId = factor(df\$PIId) # participant is nominal df\$X = factor(df\$X) # X is a 3-level factor contrasts(df\$X) &lt;- "contr.sum"  m = aov_ez(dv="Y", within="X", id="PIId", type=3, data=df) # fit model summary(m)\$sphericity.tests # Mauchly's test of sphericity print(check_sphericity(m)) # same  anova(m, correction="none") # if p≥.05, no violation of sphericity anova(m, correction="GG") # if p&lt;.05, violation of sphericity</pre>

# Parametric Tests

## One within-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	Report
1	2	Within	Paired-samples <i>t</i> -test	“The mean of ‘a’ was 29.29 ( <i>SD</i> = 14.72) and of ‘b’ was 47.68 ( <i>SD</i> = 12.53). This difference was statistically significant according to a paired-samples <i>t</i> -test ( $t(29) = -4.85, p < .0001$ ).”
1	≥2	Within	One-way repeated measures ANOVA	“The mean of ‘a’ was 32.12 ( <i>SD</i> = 14.59), of ‘b’ was 44.23 ( <i>SD</i> = 12.45), and of ‘c’ was 41.60 ( <i>SD</i> = 14.36). These differences were statistically significant ( $F(2, 38) = 4.06, p = .025$ ).”

**NB.** “*SD*” stands for “standard deviation,” i.e., the spread of values around the mean.

# Parametric Tests

## Multiple between-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	R Code
≥2	≥2	Between	Factorial ANOVA	<pre># df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(afex) # for aov_ez library(performance) # for check_homogeneity library(car) # for Anova df\$PIId = factor(df\$PIId) # participant is nominal df\$X1 = factor(df\$X1) # X1 is a 2-level factor df\$X2 = factor(df\$X2) # X2 is a 2-level factor contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum"  m = aov_ez(dv="Y", between=c("X1","X2"), id="PIId", type=3, data=df) # fit model leveneTest(Y ~ X1*X2, data=df, center=mean) # Levene's test print(check_homogeneity(m)) # same  anova(m) # use if p≥.05, no violation of homogeneity, else use... Anova(m\$lm, type=3, white.adjust=TRUE) # White-adjusted ANOVA</pre>
			Linear model (LM)	<pre># df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(performance) # for check_homogeneity library(car) # for Anova df\$PIId = factor(df\$PIId) # participant is nominal (unused) df\$X1 = factor(df\$X1) # X1 is a 2-level factor df\$X2 = factor(df\$X2) # X2 is a 2-level factor contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum"  m = lm(Y ~ X1*X2, data=df) # fit model leveneTest(Y ~ X1*X2, data=df, center=mean) # Levene's test print(check_homogeneity(m)) # same  anova(m) # use if p≥.05, no violation of homogeneity, else use... Anova(m, type=3, white.adjust=TRUE) # White-adjusted ANOVA</pre>

# Parametric Tests

## Multiple between-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	Report
≥2	≥2	Between	Factorial ANOVA	“Figure 10 shows an interaction plot with $\pm 1$ standard deviation error bars for X1 and X2. Levene’s test indicated a violation of the assumption of homogeneity of variance ( $F(3, 56) = 6.86, p = .001$ ). Therefore, a White-adjusted factorial ANOVA was used. It indicated a significant effect on Y of X1 ( $F(1, 56) = 20.51, p < .0001$ ), no significant effect of X2 ( $F(1, 56) = 0.09, p = .766$ ), and a significant X1×X2 interaction ( $F(1, 56) = 7.15, p = .010$ ).”
			Linear model (LM)	“Figure 10 shows an interaction plot with $\pm 1$ standard deviation error bars for X1 and X2. Levene’s test indicated a violation of the assumption of homogeneity of variance ( $F(3, 56) = 6.86, p = .001$ ). Therefore, a White-adjusted factorial ANOVA was used. It indicated a significant effect on Y of X1 ( $F(1, 56) = 20.51, p < .0001$ ), no significant effect of X2 ( $F(1, 56) = 0.09, p = .766$ ), and a significant X1×X2 interaction ( $F(1, 56) = 7.15, p = .010$ ).”

# Parametric Tests

## Multiple within-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	R Code
≥2	≥2	Within	Factorial repeated measures ANOVA	<pre># df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(afex) # for aov_ez library(performance) # for check_sphericity df\$PIId = factor(df\$PIId) # participant is nominal df\$X1 = factor(df\$X1) # X1 is a 2-level factor df\$X2 = factor(df\$X2) # X2 is a 2-level factor contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum"  m = aov_ez(dv="Y", within=c("X1","X2"), id="PIId", type=3, data=df) # fit model summary(m)\$sphericity.tests # Mauchly's test of sphericity print(check_sphericity(m)) # same anova(m, correction="none") # use if p≥.05, no violation of sphericity anova(m, correction="GG") # Greenhouse-Geisser correction</pre>
≥2	≥2	Within	Linear mixed model (LMM)*	<pre># df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(lme4) # for lmer library(lmerTest) library(car) # for Anova df\$PIId = factor(df\$PIId) # participant is nominal df\$X1 = factor(df\$X1) # X1 is a 2-level factor df\$X2 = factor(df\$X2) # X2 is a 2-level factor contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum"  m = lmer(Y ~ X1*X2 + (1 PIId), data=df) # sphericity is N/A for LMMs Anova(m, type=3, test.statistic="F")</pre>

**\*NB.** The LMM sample code uses a random intercept for participant (*PIId*). There are also random slope models, which are used when the response changes at different rates for each *PIId* over a repeated factor. A 2-minute random slope example of county population growth over time can be seen here (<https://www.youtube.com/watch?v=YDe6F7CXjWw>). A free webinar on the topic of random intercept and random slope models is available here (<https://craft.theanalysisfactor.com/webinar-recording-signup/?cosid=502>).

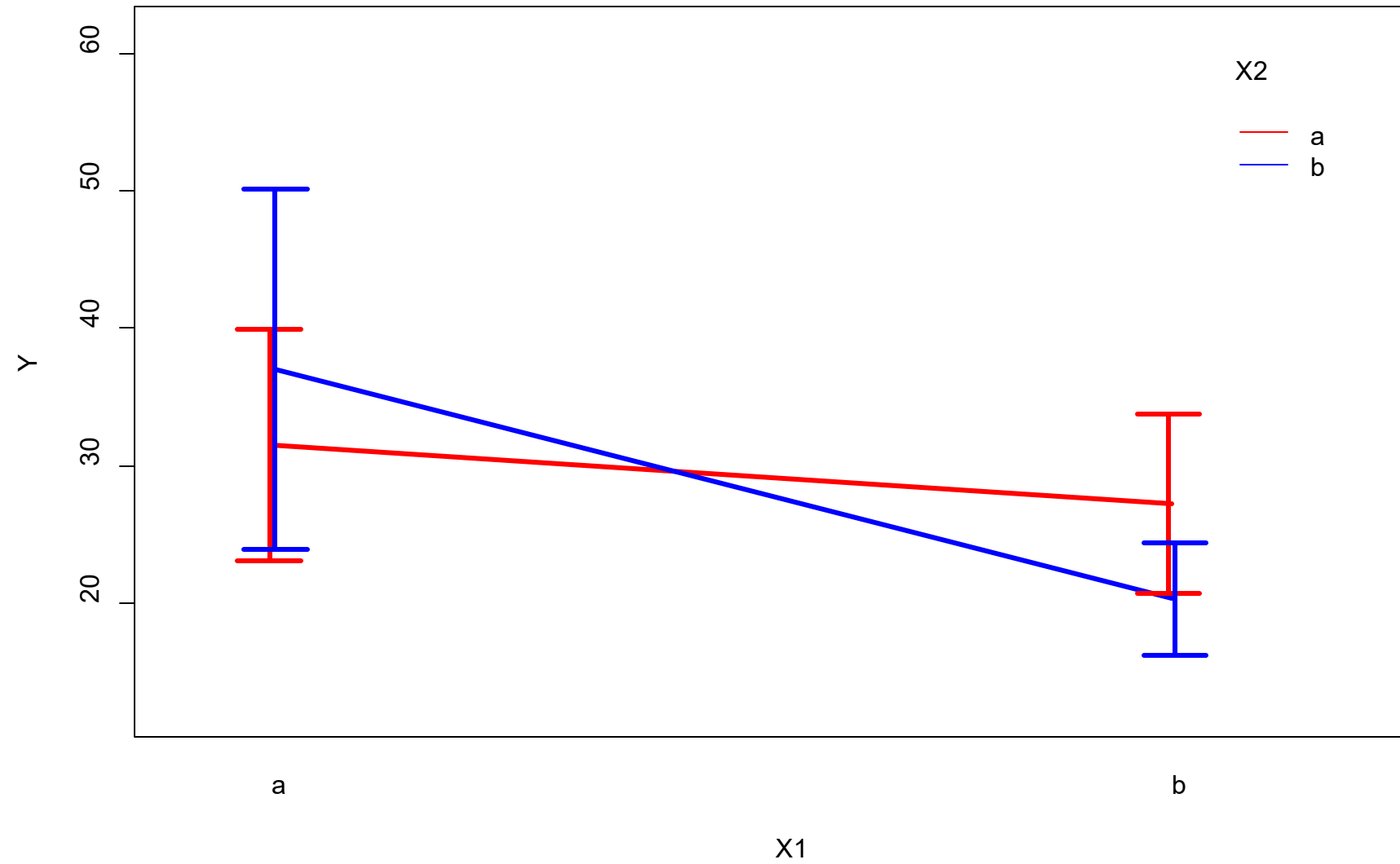
# Parametric Tests

## Multiple within-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	Report
≥2	≥2	Within	Factorial repeated measures ANOVA	“Figure 10 shows an interaction plot with $\pm 1$ standard deviation error bars for X1 and X2. A factorial repeated measures ANOVA indicated a significant effect on Y of X1 ( $F(1, 14) = 29.58, p < .0001$ ), no significant effect of X2 ( $F(1, 14) = 0.08, p = .785$ ), and a significant X1×X2 interaction ( $F(1, 14) = 5.11, p = .040$ ).”
≥2	≥2	Within	Linear mixed model (LMM)	“Figure 10 shows an interaction plot with $\pm 1$ standard deviation error bars for X1 and X2. An analysis of variance based on a linear mixed model (LMM) indicated a significant effect on Y of X1 ( $F(1, 42) = 21.98, p < .0001$ ), no significant effect of X2 ( $F(1, 42) = 0.10, p = .758$ ), and a significant X1×X2 interaction ( $F(1, 42) = 7.66, p = .008$ ).”

# Figure 10

Y by X1, X2



# Parametric Tests

*Post hoc pairwise comparisons*



# Parametric Tests

## *Post hoc* pairwise comparisons – One factor

Factors	Levels	Omnibus Test	Test Name	B/W	R Code
1	>2	One-way ANOVA	Independent samples <i>t</i> -test	Btwn	<pre># df has one between-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from afex::aov_ez</pre>
1	>2	One-way repeated measures ANOVA	Paired samples <i>t</i> -test	Within	<pre># df has one within-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from afex::aov_ez</pre>

# Parametric Tests

## *Post hoc* pairwise comparisons – One factor

Factors	Levels	Omnibus Test	Test Name	B/W	Report
1	$\geq 2$	One-way ANOVA	Independent samples <i>t</i> -test	Btwn	“Three <i>post hoc</i> pairwise comparisons using independent-samples <i>t</i> -tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ was significantly different ( $t(57) = -2.77, p = .023$ ), but ‘a’ vs. ‘c’ and ‘b’ vs. ‘c’ were not.”
1	$\geq 2$	One-way repeated measures ANOVA	Paired samples <i>t</i> -test	Within	“Three <i>post hoc</i> pairwise comparisons using paired-samples <i>t</i> -tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ was significantly different ( $t(19) = -2.70, p = .042$ ), but ‘a’ vs. ‘c’ and ‘b’ vs. ‘c’ were not.”

# Parametric Tests

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Test	Test Name	B/W	R Code
≥2	≥2	Factorial ANOVA, linear model (LM)	Independent samples <i>t</i> -test	Btwn	<pre># df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from lm, aov, or afex::aov_ez</pre>
≥2	≥2	Factorial repeated measures ANOVA, linear mixed model (LMM)	Paired samples <i>t</i> -test	Within	<pre># df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from afex::aov_ez or lme4::lmer</pre>

# Parametric Tests

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Test	Test Name	B/W	Report
≥2	≥2	Factorial ANOVA, Linear model (LM)	Independent samples <i>t</i> -test	Btwn	“Six <i>post hoc</i> pairwise comparisons using independent-samples <i>t</i> -tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,b} ( $t(56) = 3.53, p = .004$ ), {b,a} vs. {a,b} ( $t(56) = -3.10, p = .012$ ), and {a,b} vs. {b,b} ( $t(56) = 5.27, p < .0001$ ) were significantly different. The other three pairwise comparisons were not detectably different.”
≥2	≥2	Factorial repeated measures ANOVA	Paired samples <i>t</i> -test	Within	“Six <i>post hoc</i> pairwise comparisons using paired-samples <i>t</i> -tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,b} ( $t(14) = 4.82, p = .002$ ), {b,a} vs. {b,b} ( $t(14) = 3.27, p = .023$ ), {a,b} vs. {b,b} ( $t(14) = 4.25, p = .004$ ) were significantly different. The other three pairwise comparisons were not detectably different.”
≥2	≥2	Linear mixed model (LMM)	Paired samples <i>t</i> -test	Within	“Six <i>post hoc</i> pairwise comparisons using paired-samples <i>t</i> -tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,b} ( $t(42) = 3.53, p = .005$ ), {b,a} vs. {a,b} ( $t(42) = -3.10, p = .014$ ), and {a,b} vs. {b,b} ( $t(42) = 5.27, p < .0001$ ) were significantly different. The other three pairwise comparisons were not detectably different.”

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# Variance-Covariance Structures

(for use with `nlme::lme` instead of `lme4::lmer`)

# Covariance Structures

Optional when fitting linear mixed models (LMMs)

Abbreviation	Name	Description	R Code
ID	Scaled identity	All variances are equal, and all covariances are zero.	<pre># df has one within-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(nlme)           # for lme library(car)            # for Anova library(emmeans)        # for emmeans df\$PIid = factor(df\$PIid) # participant is nominal df\$X = factor(df\$X)      # X is a 3-level factor contrasts(df\$X) &lt;- "contr.sum" m = lme(Y ~ X, random=~1 PIid, data=df) # ID getVarCov(m, type="marginal")          # get VCV matrix anova(m, type="marginal")               # for F-test Anova(m, type=3, test.statistic="Chisq") # for chisq test emmeans(m, pairwise ~ X, adjust="holm", mode="containment") # post hoc tests</pre>
DIAG	Diagonal	All variances can differ; otherwise, like ID.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIid, data=df, weights=varIdent(form=~1 X)) # DIAG</pre>
CS	Compound symmetry	All variances are equal, and all covariances are equal.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIid, data=df, correlation=corCompSymm(form=~1 PIid)) # CS</pre>
CSH	Heterogeneous compound symmetry	All variances can differ; otherwise, like CS.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIid, data=df, correlation=corCompSymm(form=~1 PIid),         weights=varIdent(form=~1 X)) # CSH</pre>

**NB.** The `lme4::lmer` function does not allow specifying common variance-covariance (VCV) structures for repeated factors or residuals. Therefore, we must use `nlme::lme` for this. For a list of common VCV structures, see <https://www.ibm.com/docs/en/spss-statistics/30.0.0?topic=mixed-covariance-structure-list-command>. For their matrix formulations, see <https://www.ibm.com/docs/en/spss-statistics/30.0.0?topic=statistics-covariance-structures>. For a treatment in R, see <https://rpubs.com/samuelkn/CovarianceStructuresInR>.

**NB.** The `correlation` parameter sets covariances (matrix off-diagonal) and the `weights` parameter sets variances (matrix on-diagonal). When `correlation=NULL` or is unspecified, the off-diagonal values are zero. When `weights=NULL` or is unspecified, the on-diagonal variances are equal. The R help pages called up with `?corClasses` and `?varClasses` explain these parameters.



# Covariance Structures

Optional when fitting linear mixed models (LMMs)

Abbreviation	Name	Description	R Code
AR1	First-order autoregressive	All variances are equal, and all covariances decrease with distance.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIId, data=df, correlation=corAR1(form=~1 PIId)) # AR1</pre>
ARH1	Heterogeneous first-order autoregressive	All variances can differ; otherwise, like AR1.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIId, data=df, correlation=corAR1(form=~1 PIId),         weights=varIdent(form=~1 X)) # ARH1</pre>
ARMA11	Autoregressive moving average	All variances are equal, and all covariances decrease with distance, influenced by a moving average.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIId, data=df, correlation=corARMA(form=~1 PIId, p=1, q=1)) # ARMA11 # Note that (p,q)=(1,0) is AR1. The 'q' parameter determines the moving average.</pre>
TP	Toeplitz	All variances are equal, and covariances are equal across adjacent pairs, equal again across skip-adjacent pairs, and so on.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIId, data=df, correlation=corARMA(form=~1 PIId, p=2, q=0)) # TP</pre>
TPH	Heterogeneous Toeplitz	All variances can differ; otherwise, like TP.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIId, data=df, correlation=corARMA(form=~1 PIId, p=2, q=0),         weights=varIdent(form=~1 X)) # TPH</pre>
UN	Unstructured	All variances and covariances can differ.	<pre># See R Code for ID. Only the blue model-building line changes to: m = lme(Y ~ X, random=~1 PIId, data=df, correlation=corSymm(form=~1 PIId),         weights=varIdent(form=~1 X)) # UN</pre>

**NB.** See `?corClasses` and `?varClasses` for additional variance-covariance structures. Or see <https://rdrr.io/cran/nlme/man/corClasses.html> and <https://rdrr.io/cran/nlme/man/varClasses.html>.

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# Nonparametric Tests

# Nonparametric Tests

## One factor with 2 levels

Factors	Levels	Between or Within Subjects	Test Name	R Code
1	2	Between	Median test	<pre># df has one between-Ss. factor (X) w/levels (a,b) and a (1,0) response library(coin) # for median_test df\$PId = factor(df\$PId) # participant is nominal (unused) df\$X = factor(df\$X) # X is a 2-level factor contrasts(df\$X) &lt;- "contr.sum" median_test(Y ~ X, data=df)</pre>
1	2	Between	Mann-Whitney <i>U</i> test	<pre># df has one between-Ss. factor (X) w/levels (a,b) and continuous response (Y) library(coin) # for wilcox_test df\$PId = factor(df\$PId) # participant is nominal (unused) df\$X = factor(df\$X) # X is a 2-level factor contrasts(df\$X) &lt;- "contr.sum" wilcox_test(Y ~ X, data=df, distribution="exact")</pre>
1	2	Within	Sign test	<pre># df has one within-Ss. factor (X) w/levels (a,b) and a (1,0) response library(coin) # for sign_test df\$PId = factor(df\$PId) # participant is nominal df\$X = factor(df\$X) # X is a 2-level factor contrasts(df\$X) &lt;- "contr.sum" sign_test(Y ~ X   PId, data=df)</pre>
1	2	Within	Wilcoxon signed-rank test	<pre># df has one within-Ss. factor (X) w/levels (a,b) and continuous response (Y) library(coin) # for wilcoxsign_test df\$PId = factor(df\$PId) # participant is nominal df\$X = factor(df\$X) # X is a 2-level factor contrasts(df\$X) &lt;- "contr.sum" wilcoxsign_test(Y ~ X   PId, data=df, distribution="exact")</pre>

**NB.** The Mann-Whitney *U* test is also known as the Wilcoxon-Mann-Whitney test and the Wilcoxon rank-sum test, neither to be confused with the Wilcoxon signed-rank test.

# Nonparametric Tests

One factor with 2 levels

Factors	Levels	Between or Within Subjects	Test Name	Report
1	2	Between	Median test	“The sum of ‘a’ was 20 and of ‘b’ was 8. This difference was statistically significant according to a median test ( $Z = 3.08, p = .002$ ).”
1	2	Between	Mann-Whitney $U$ test	“The median of ‘a’ was 29.12 ( $IQR = 13.92$ ) and of ‘b’ was 45.72 ( $IQR = 15.91$ ). This difference was statistically significant according to a Mann-Whitney $U$ test ( $Z = -4.70, p < .0001$ ).”
1	2	Within	Sign test	“The sum of ‘a’ was 20 and of ‘b’ was 8. This difference was statistically significant according to a sign test ( $Z = 2.83, p = .005$ ).”
1	2	Within	Wilcoxon signed-rank test	“The median of ‘a’ was 29.12 ( $IQR = 13.92$ ) and of ‘b’ was 45.72 ( $IQR = 15.91$ ). This difference was statistically significant according to a Wilcoxon signed-rank test ( $Z = -3.92, p < .0001$ ).”

**NB.** “ $IQR$ ” stands for “interquartile range,” i.e., the distance between the top and bottom of the box in a boxplot (25% - 75% quartile range).

# Nonparametric Tests

One factor with  $\geq 2$  levels

Factors	Levels	Between or Within Subjects	Test Name	R Code
1	$\geq 2$	Between	Kruskal-Wallis test	<pre># df has one between-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(coin) # for kruskal_test df\$PId = factor(df\$PId) # participant is nominal (unused) df\$X = factor(df\$X) # X is a 3-level factor contrasts(df\$X) &lt;- "contr.sum" kruskal_test(Y ~ X, data=df, distribution="asymptotic")</pre>
1	$\geq 2$	Within	Friedman test	<pre># df has one within-Ss. factor (X) w/levels (a,b,c), and continuous response (Y) library(coin) df\$PId = factor(df\$PId) # participant is nominal df\$X = factor(df\$X) # X is a 3-level factor friedman_test(Y ~ X   PId, data=df, distribution="asymptotic")</pre>

# Nonparametric Tests

One factor with  $\geq 2$  levels

Factors	Levels	Between or Within Subjects	Test Name	Report
1	$\geq 2$	Between	Kruskal-Wallis test	“The median of ‘a’ was 31.44 ( $IQR = 12.50$ ), of ‘b’ was 42.90 ( $IQR = 20.60$ ), and of ‘c’ was 39.50 ( $IQR = 14.73$ ). These differences were statistically significant according to a Kruskal-Wallis test ( $\chi^2(2, N=60) = 9.36, p = .009$ ).”
1	$\geq 2$	Within	Friedman test	“The median of ‘a’ was 31.44 ( $IQR = 12.50$ ), of ‘b’ was 42.90 ( $IQR = 20.60$ ), and of ‘c’ was 39.50 ( $IQR = 14.73$ ). These differences were statistically significant according to a Friedman test ( $\chi^2(2, N=60) = 12.90, p = .002$ ).”

**NB.** “*IQR*” stands for “interquartile range,” i.e., the distance between the top and bottom of the box in a boxplot (25% - 75% quartile range).

# Nonparametric Tests

## Multiple factors

Factors	Levels	Between or Within Subjects	Test Name	R Code
≥2	≥2	Between	Aligned Rank Transform (ART)	<pre># df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(ARTool) df\$PId = factor(df\$PId) # participant is nominal (unused) df\$X1 = factor(df\$X1)   # X1 is a 2-level factor df\$X2 = factor(df\$X2)   # X2 is a 2-level factor contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = art(Y ~ X1*X2, data=df) anova(m)</pre>
≥2	≥2	Within	Aligned Rank Transform (ART)*	<pre># df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(ARTool) df\$PId = factor(df\$PId) # participant is nominal df\$X1 = factor(df\$X1)   # X1 is a 2-level factor df\$X2 = factor(df\$X2)   # X2 is a 2-level factor contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = art(Y ~ X1*X2 + (1 PId), data=df) # PId is a random factor anova(m)</pre>

**\*NB.** The within-subjects ART sample code uses a random intercept for participant (*PId*). There are also random slope models, which are used when the response changes at different rates for each participant over a repeated factor. A 2-minute random slope example of county population growth over time can be seen here (<https://www.youtube.com/watch?v=YDe6F7CXjWw>). A free webinar on the topic of random intercept and random slope models is available here (<https://craft.theanalysisfactor.com/webinar-recording-signup/?cosid=502>).

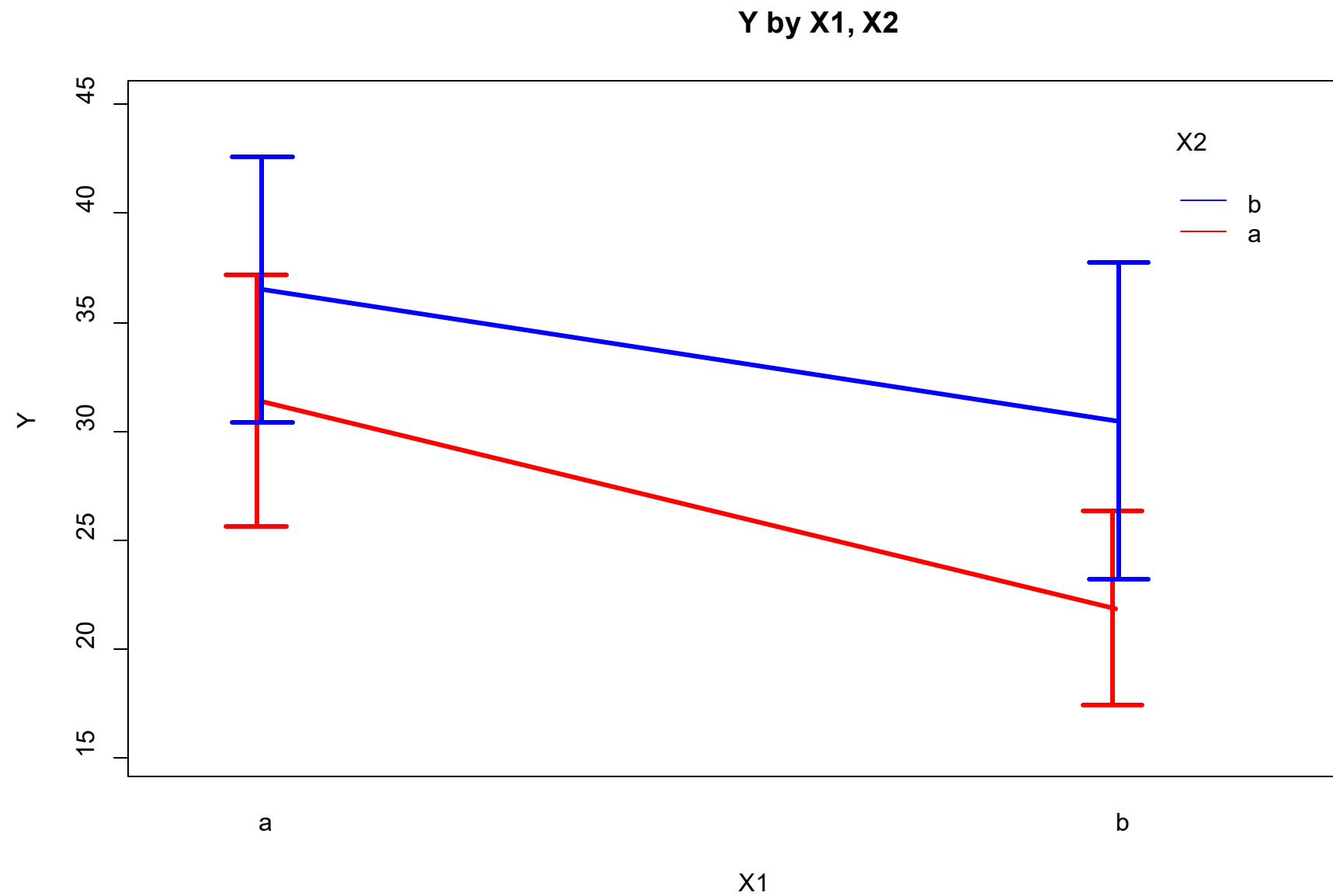


# Nonparametric Tests

## Multiple factors

Factors	Levels	Between or Within Subjects	Test Name	Report
≥2	≥2	Between	Aligned Rank Transform (ART)	“Figure 11 shows an interaction plot for Y by X1, X2 with $\pm 1$ <i>SD</i> error bars. A nonparametric analysis of variance based on the Aligned Rank Transform indicated a significant effect on Y of X1 ( $F(1, 56) = 24.85, p < .0001$ ) and of X2 ( $F(1, 56) = 19.54, p < .0001$ ), but no significant X1×X2 interaction ( $F(1, 56) = 0.98, p = .327$ ).”
≥2	≥2	Within	Aligned Rank Transform (ART)	“Figure 11 shows an interaction plot for Y by X1, X2 with $\pm 1$ <i>SD</i> error bars. A nonparametric analysis of variance based on the Aligned Rank Transform indicated a significant effect on Y of X1 ( $F(1, 42) = 24.85, p < .0001$ ) and of X2 ( $F(1, 42) = 19.54, p < .0001$ ), but no significant X1×X2 interaction ( $F(1, 42) = 0.98, p = .328$ ).”

# Figure 11



# Nonparametric Tests

*Post hoc pairwise comparisons*

# Nonparametric Tests

## *Post hoc* pairwise comparisons – One factor

Factors	Levels	Omnibus Test	Test Name	B/W	R Code
1	$\geq 2$	Kruskal-Wallis test	Mann-Whitney <i>U</i> test	Btwn	<pre># df has one between-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(rcompanion) # for wilcoxonZ ab = wilcox.test(df[df\$X == "a",]\$Y, df[df\$X == "b",]\$Y, exact=FALSE) # a vs. b ac = wilcox.test(df[df\$X == "a",]\$Y, df[df\$X == "c",]\$Y, exact=FALSE) # a vs. c bc = wilcox.test(df[df\$X == "b",]\$Y, df[df\$X == "c",]\$Y, exact=FALSE) # b vs. c p.adjust(c(ab\$p.value, ac\$p.value, bc\$p.value), method="holm") # p-values  wilcoxonZ(df[df\$X == "a",]\$Y, df[df\$X == "b",]\$Y) # Z-scores wilcoxonZ(df[df\$X == "a",]\$Y, df[df\$X == "c",]\$Y) wilcoxonZ(df[df\$X == "b",]\$Y, df[df\$X == "c",]\$Y)</pre>
1	$\geq 2$	Friedman test	Wilcoxon signed-rank test	Within	<pre># df has one within-Ss. factor (X) w/levels (a,b,c) and continuous response (Y) library(reshape2) # for dcast library(rcompanion) # for wilcoxonZ df2 &lt;- dcast(df, PId ~ X, value.var="Y") # make wide-format table ab = wilcox.test(df2\$a, df2\$b, paired=TRUE, exact=FALSE) # a vs. b ac = wilcox.test(df2\$a, df2\$c, paired=TRUE, exact=FALSE) # a vs. c bc = wilcox.test(df2\$b, df2\$c, paired=TRUE, exact=FALSE) # b vs. c p.adjust(c(ab\$p.value, ac\$p.value, bc\$p.value), method="holm") # p-values  wilcoxonZ(df2\$a, df2\$b, paired=TRUE) # Z-scores wilcoxonZ(df2\$a, df2\$c, paired=TRUE) wilcoxonZ(df2\$b, df2\$c, paired=TRUE)</pre>

# Nonparametric Tests

## *Post hoc* pairwise comparisons – One factor

Factors	Levels	Omnibus Test	Test Name	B/W	Report
1	$\geq 2$	Kruskal-Wallis test	Mann-Whitney <i>U</i> test	Btwn	“Three <i>post hoc</i> Mann-Whitney <i>U</i> tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -2.89, p = .012$ ) was significantly different, but that ‘a’ vs. ‘c’ and ‘b’ vs. ‘c’ were not.”
1	$\geq 2$	Friedman test	Wilcoxon signed-rank test	Within	“Three <i>post hoc</i> Wilcoxon signed-rank tests, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -2.87, p = .013$ ) was significantly different, but that ‘a’ vs. ‘c’ and ‘b’ vs. ‘c’ were not.”

# Nonparametric Tests

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Test	Test Name	B/W	R Code
≥2	≥2	Aligned Rank Transform (ART)	Aligned Rank Transform Contrasts (ART-C)	Btwn, Within	<pre># df has two factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(plyr) # for mutate library(dplyr) # for %&gt;% art.con(m, ~ X1*X2, adjust="holm") %&gt;% # run ART-C for X1×X2   summary() %&gt;% # (optional) add significance stars to the output   plyr::mutate(sig. = symnum(p.value, corr=FALSE, na=FALSE,                              cutpoints = c(0, .001, .01, .05, .10, 1),                              symbols = c("****", "***", "**", ".", " ")))</pre>

# Nonparametric Tests

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Test	Test Name	B/W	Report
≥2	≥2	Aligned Rank Transform (ART)	Aligned Rank Transform Contrasts (ART-C)	Btwn	“Six <i>post hoc</i> pairwise comparisons conducted with the ART-C procedure (Elkin <i>et al.</i> 2021), and corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,a} ( $t(56) = 4.37, p < .001$ ), {a,b} vs. {b,a} ( $t(56) = 6.67, p < .0001$ ), {a,b} vs. {b,b} ( $t(56) = 2.67, p = .030$ ), and {b,a} vs. {b,b} ( $t(56) = -4.00, p = .001$ ) were significantly different. The two other pairwise comparisons were not detectably different.”
				Within	“Six <i>post hoc</i> pairwise comparisons conducted with the ART-C procedure (Elkin <i>et al.</i> 2021), and corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,a} ( $t(42) = 4.37, p < .001$ ), {a,b} vs. {b,a} ( $t(42) = 6.67, p < .0001$ ), {a,b} vs. {b,b} ( $t(42) = 2.67, p = .032$ ), and {b,a} vs. {b,b} ( $t(42) = -4.00, p = .001$ ). The two other pairwise comparisons were not detectably different.”

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# Generalized Linear (Mixed) Models

# Terminology

		Generalize to Responses Unsuitable to ANOVA?			
		No	Yes		
Contain Random Factors?*	No	<p><b>(General) Linear Model (LM)</b></p> <p>(Sometimes abbreviated GLM)</p> <p><code>lm</code> in R</p> <p>(see also <code>anova</code>)</p>	<p><b>General<u>ized</u> Linear Model (GLM)</b></p> <p>(Sometimes abbreviated GZLM or GLIM)</p> <p><code>glm</code> in R</p>	Between-Ss.	
	Yes	<p><b>(General) Linear Mixed Model (LMM)</b></p> <p><code>lme4::lmer</code> in R</p> <p>(see also <code>nlme::lme</code>)</p>	<p><b>General<u>ized</u> Linear Mixed Model (GLMM)</b></p> <p><code>lme4::glmer</code> in R</p>	Within-Ss.	
		Normal and lognormal	Normal, lognormal, binomial, multinomial, ordinal, Poisson, negative binomial, zero-inflated models, exponential, gamma		

\*NB. Random factors enable the modeling of correlated responses, i.e., within-subjects data, repeated measures data, longitudinal data, panel data, etc.

Distribution	GLM	GLMM
<b>Gaussian</b>	<code>lm()</code> <sup>[1]</sup> <code>glm()</code> <code>family=gaussian</code>	<code>lme4::lmer()</code> <sup>[2]</sup> <code>lme4::glmer()</code> <code>family=gaussian</code>
<b>Binomial</b>	<code>glm()</code> <code>family=binomial</code>	<code>lme4::glmer()</code> <code>family=binomial</code>
<b>Multinomial</b> <sup>[3]</sup>	<code>nnet::multinom()</code> <b>or</b> <code>multpois::glm.mp()</code> <code>multpois::Anova.mp()</code>	<code>multpois::glmer.mp()</code> <code>multpois::Anova.mp()</code>
<b>Ordinal</b>	<code>MASS::polr()</code>	<code>ordinal::clmm()</code> <code>RVAideMemoire::Anova.clmm()</code>
<b>Poisson</b>	<code>glm()</code> <code>family=poisson</code>	<code>lme4::glmer()</code> <code>family=poisson</code>
<b>Quasi-Poisson</b> <sup>[4]</sup>	<code>glm()</code> <code>family=quasipoisson</code>	N/A
<b>Zero-inflated Poisson (ZIP)</b> <sup>[5]</sup>	<code>glmmTMB::glmmTMB()</code> <code>family=poisson</code> <code>ziformula=~1</code>	<code>glmmTMB::glmmTMB()</code> <code>family=poisson</code> <code>ziformula=~1 REML=TRUE</code>
<b>Negative binomial</b>	<code>MASS::glm.nb()</code>	<code>lme4::glmer.nb()</code>
<b>Zero-inflated negative binomial (ZINB)</b> <sup>[5]</sup>	<code>glmmTMB::glmmTMB()</code> <code>family=nbinom2</code> <code>ziformula=~1</code>	<code>glmmTMB::glmmTMB()</code> <code>family=nbinom2</code> <code>ziformula=~1 REML=TRUE</code>
<b>Exponential</b>	<code>glm()</code> <code>family=Gamma(link="log")</code>	<code>lme4::glmer()</code> <code>family=Gamma(link="log")</code>
<b>Gamma</b> <sup>[6]</sup>	<code>glm()</code> <code>family=Gamma</code>	<code>lme4::glmer()</code> <code>family=Gamma</code>

# Footnotes

- [1] `lm` and `glm` are from the base `stats` package in R.
- [2] `lmer` and `glmer` are both from the `lme4` package. A `glmer` call with `family=gaussian` will fail to run with a message that one should just call `lmer`, which is equivalent.
- [3] Multinomial logistic regression can be achieved via the multinomial-Poisson transformation (Baker 1994), which converts a multinomial regression into a Poisson model. See **NB** below.
- [4] Use `family=quasipoisson` with mild overdispersion. With more overdispersion, use negative binomial regression. Unfortunately, `family=quasipoisson` is not available for `glmer`.
- [5] Use zero-inflated Poisson (ZIP) or zero-inflated negative binomial (ZINB) regression models when distributions show excessive zeroes. To test for zero-inflation, use `performance::check_zeroinflation(m)`, where `m` is a `glm` or `glmer` model with `family=poisson`, or a `glm.nb` or `glmer.nb` model.
- [6] The canonical link function for Gamma regression is the inverse function. If this fails, using `family=Gamma(link="log")` is a common alternative.

**NB.** There is no `family=multinomial` option in `lme4::glmer`. There is also no GLMM equivalent to the `nnet::multinom` function for GLMs. There *are* a handful of options for polytomous responses with repeated measures, *e.g.*, based on Markov Chain Monte-Carlo (MCMC) simulations, but these deviate considerably from the consistent GLMM approaches herein. Fortunately, Baker (1994) showed the equivalence of multinomial logistic regression and Poisson regression via the multinomial-Poisson transformation (Baker 1994). The `multpois` package implements functions to carry out multinomial logistic regression using this “trick.”

# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)
Normal	identity	<i>Linear regression:</i> Normally distributed responses; equivalent to the linear model (LM) or linear mixed model (LMM)	<pre>library(car) # for Anova library(performance) # for check_* df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = lm(Y ~ X1*X2, data=df) print(check_normality(m)) print(check_homogeneity(m)) Anova(m, type=3, test.statistic="F")</pre>	<pre>library(lme4) # for lmer library(lmerTest) library(car) # for Anova library(performance) # for check_* df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = lmer(Y ~ X1*X2 + (1 PId), data=df) print(check_normality(m)) print(check_homogeneity(m)) Anova(m, type=3, test.statistic="F")</pre>
Lognormal	identity	<i>Linear regression:</i> Lognormally distributed responses (e.g., time measurements)	<pre>library(car) # for Anova library(performance) # for check_* df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = lm(log(Y) ~ X1*X2, data=df) print(check_normality(m)) print(check_homogeneity(m)) Anova(m, type=3, test.statistic="F")</pre>	<pre>library(lme4) # for lmer library(lmerTest) library(car) # for Anova library(performance) # for check_* df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = lmer(log(Y) ~ X1*X2 + (1 PId), data=df) print(check_normality(m)) print(check_homogeneity(m)) Anova(m, type=3, test.statistic="F")</pre>

**NB.** A normal distribution is also known as a Gaussian distribution. The GLMM sample code uses a random intercept for *participant* (*PId*). There are also random slope models, which are used when the response changes at different rates for each subject over the repeated factor(s). A random slope example of county population growth over time can be seen here (<https://www.youtube.com/watch?v=YDe6F7CXjWw>). A free webinar on the topic of random intercept and random slope models is available here (<https://craft.theanalysisfactor.com/webinar-recording-signup/?cosid=502>).

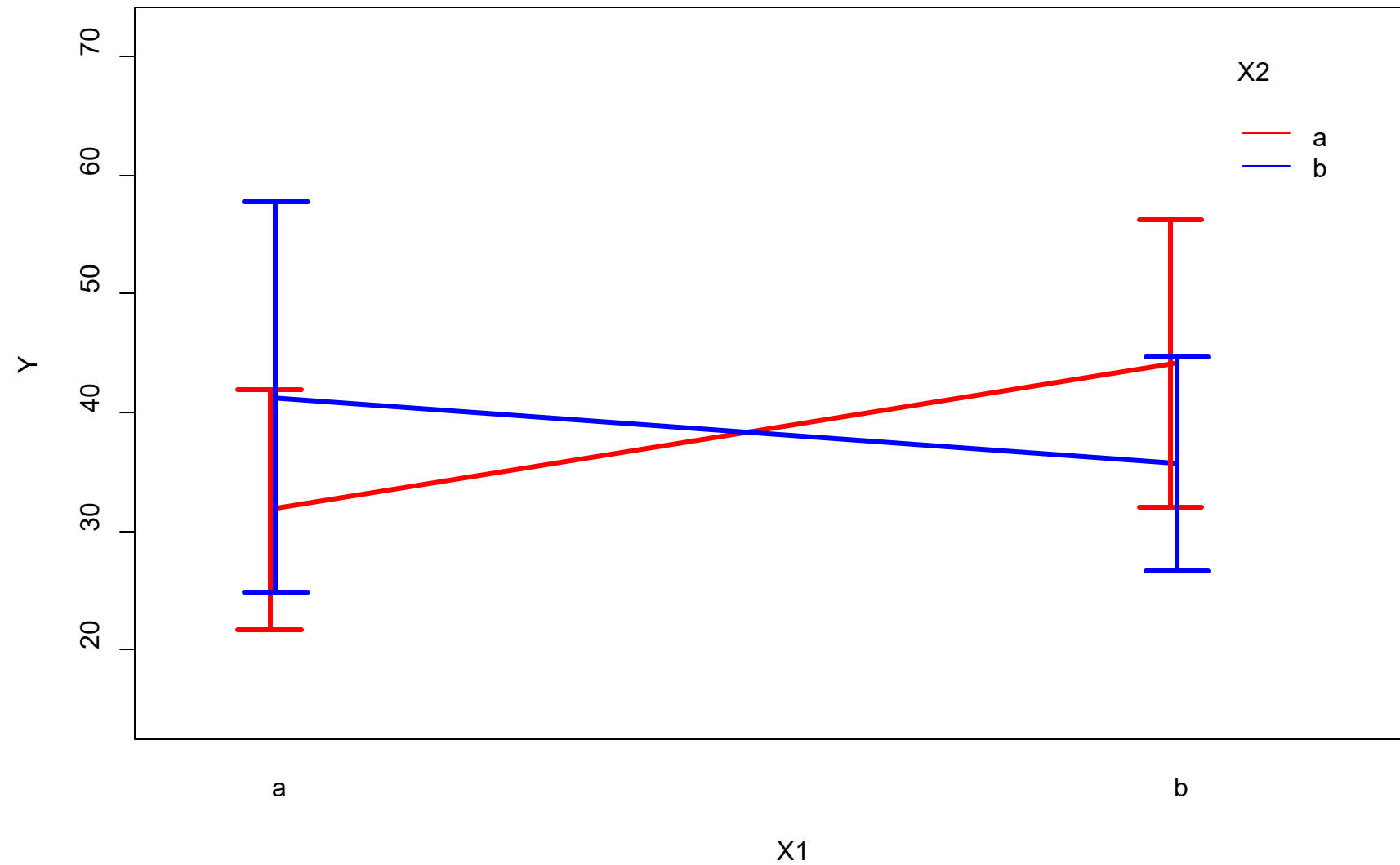
# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Normal	identity	<i>Linear regression:</i> Normally distributed responses; equivalent to the linear model (LM) or linear mixed model (LMM)	“Figure 12 shows an interaction plot with $\pm 1$ standard deviation error bars for X1 and X2. An analysis of variance based on a linear model indicated a statistically significant X1×X2 interaction ( $F(1, 56) = 8.05, p = .006$ ).”	“Figure 12 shows an interaction plot with $\pm 1$ standard deviation error bars for X1 and X2. An analysis of variance based on a linear <b>mixed</b> model indicated a statistically significant X1×X2 interaction ( $F(1, 42) = 8.05, p = .007$ ).”
Lognormal	identity	<i>Linear regression:</i> Lognormally distributed responses (e.g., time measurements)	“Figure 13 shows four lognormal histograms for each X1×X2 condition. An analysis of variance based on a linear model indicated no statistically significant effects on $\log(Y)$ of X1, X2, or the X1×X2 interaction.”	“Figure 13 shows four lognormal histograms for each X1×X2 condition. An analysis of variance based on a linear <b>mixed</b> model indicated no statistically significant effects on $\log(Y)$ of X1, X2, or the X1×X2 interaction.”

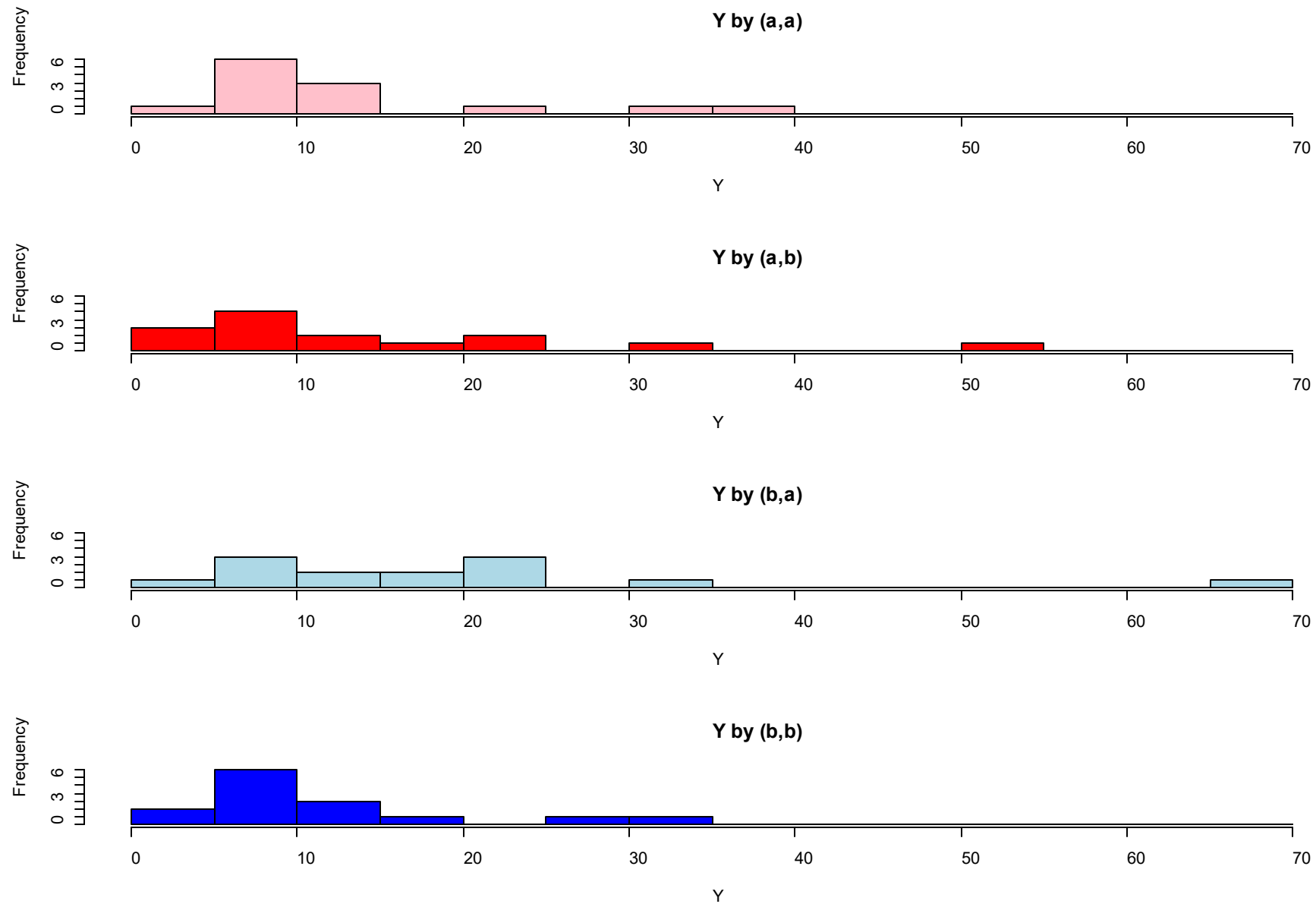
# Figure 12

Y by X1, X2





# Figure 13



# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)
Binomial	logit	<i>Logistic regression:</i> Dichotomous responses (i.e., nominal responses with two categories)	<pre>library(car) # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) df\$Y = factor(df\$Y) # dichotomous response contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glm(Y ~ X1*X2, data=df, family=binomial) Anova(m, type=3)</pre>	<pre>library(lme4) # for glmer library(lmerTest) library(car) # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) df\$Y = factor(df\$Y) # dichotomous response contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glmer(Y ~ X1*X2 + (1 PId), data=df, family=binomial) Anova(m, type=3)</pre>
Multinomial	logit	<i>Multinomial logistic regression:</i> Polytomous responses (i.e., nominal responses with more than two categories)	<pre>library(multpois) # for glm.mp, Anova.mp df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) df\$Y = factor(df\$Y) # polytomous response contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glm.mp(Y ~ X1*X2, data=df) # * Anova.mp(m, type=3)          # *  # This also can be used in place of '*' above: library(nnet) # for multinom library(car) # for Anova m = multinom(Y ~ X1*X2, data=df, trace=FALSE) Anova(m, type=3)</pre>	<pre>library(multpois) # for glmer.mp, Anova.mp df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) df\$Y = factor(df\$Y) # polytomous response contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glmer.mp(Y ~ X1*X2 + (1 PId), data=df) Anova.mp(m, type=3)</pre>

**NB.** Logistic regression is also known as binomial regression. Multinomial logistic regression is also known as nominal logistic regression. It is carried out here using the multinomial-Poisson transformation (Baker 1994). An alternative from the `nnet` package is also shown, but *post hoc* pairwise comparisons will be more conservative.

# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Binomial	logit	<i>Logistic regression:</i> Dichotomous responses (i.e., nominal responses with two categories)	“Figure 14 shows the number of ‘yes’ and ‘no’ responses for each $X1 \times X2$ condition. An analysis of variance based on logistic regression indicated a statistically significant effect of X2 on Y ( $\chi^2(1, N=60) = 11.69, p = .001$ ).”	“Figure 14 shows the number of ‘yes’ and ‘no’ responses for each $X1 \times X2$ condition. An analysis of variance based on <b>mixed</b> logistic regression indicated a statistically significant effect of X2 on Y ( $\chi^2(1, N=60) = 9.13, p = .003$ ).”
Multinomial	logit	<i>Multinomial logistic regression:</i> Polytomous responses (i.e., nominal responses with more than two categories)	“Figure 15 shows the number of ‘yes’, ‘no’, and ‘maybe’ responses for each $X1 \times X2$ condition. An analysis of variance based on multinomial logistic regression, implemented using the multinomial-Poisson transformation (Baker 1994), indicated a statistically significant effect of X1 on Y ( $\chi^2(2, N=60) = 10.33, p = .006$ ).”	“Figure 15 shows the number of ‘yes’, ‘no’, and ‘maybe’ responses for each $X1 \times X2$ condition. An analysis of variance based on <b>mixed</b> multinomial logistic regression, implemented using the multinomial-Poisson transformation (Baker 1994), indicated a statistically significant effect of X1 on Y ( $\chi^2(2, N=60) = 9.28, p = .010$ ).”

# Figure 14

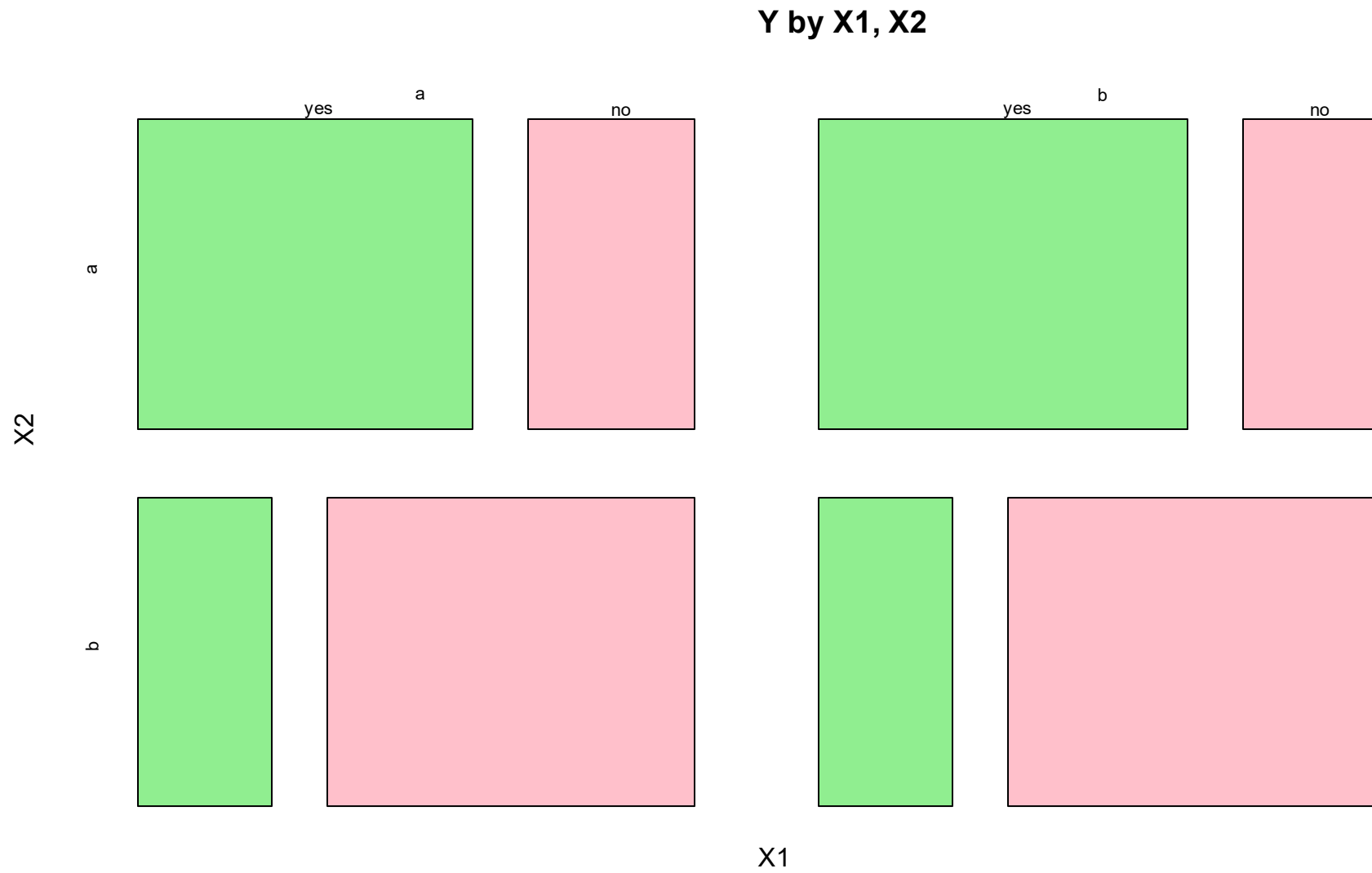
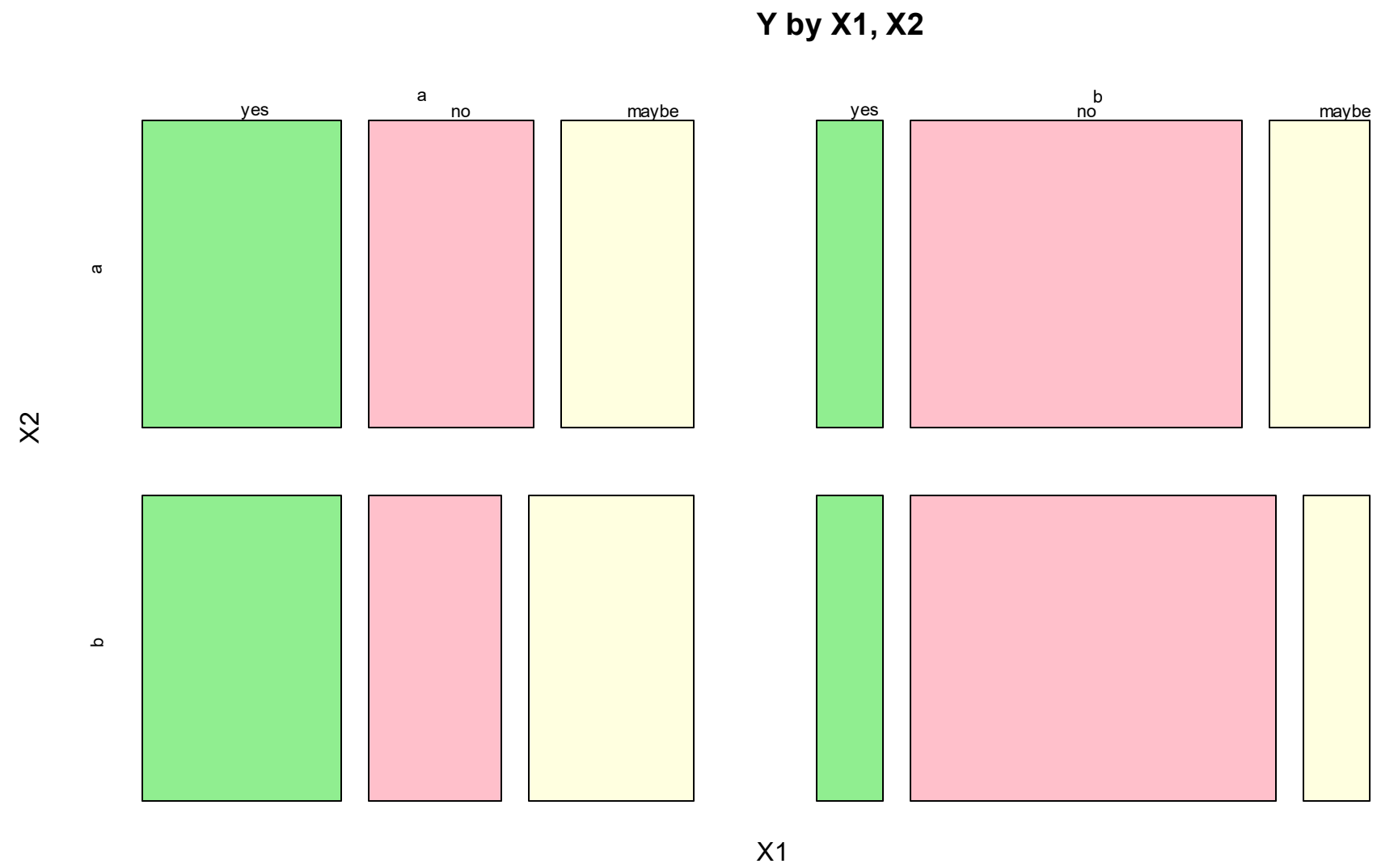


Figure 15



# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)
Ordinal	cumulative logit	<i>Ordinal logistic regression:</i> Ordinal responses (e.g., Likert-type scales)	<pre>library(MASS) # for polr library(car)  # for Anova df\$PIId = factor(df\$PIId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) df\$Y = ordered(df\$Y) # ordinal response contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = polr(Y ~ X1*X2, data=df, Hess=TRUE) Anova(m, type=3)</pre>	<pre>library(ordinal) # for clmm library(RVAideMemoire) # for Anova.clmm dt\$PIId = factor(dt\$PIId) dt\$X1 = factor(dt\$X1) dt\$X2 = factor(dt\$X2) dt\$Y = ordered(dt\$Y) # ordinal response contrasts(dt\$X1) &lt;- "contr.sum" contrasts(dt\$X2) &lt;- "contr.sum" # Anova.clmm fails if 'data' is 'df'; use 'dt' instead m = clmm(Y ~ X1*X2 + (1 PIId), data=dt, Hess=TRUE, link="logit") # logit, probit, cloglog, loglog, and cauchit links are options Anova.clmm(m)</pre>

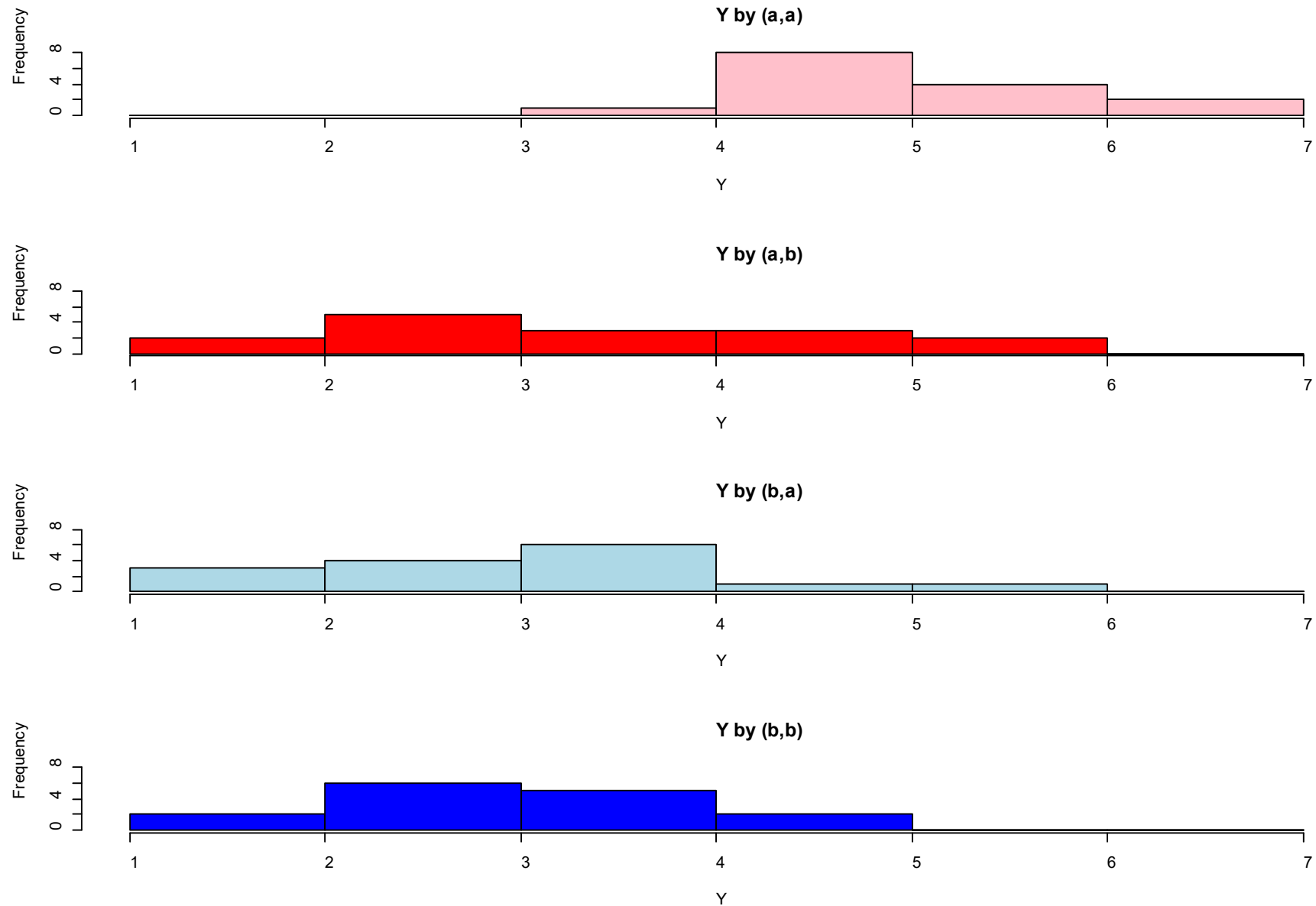
**NB.** Ordinal logistic regression is also known as cumulative logistic regression.

# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss)	Report for GLMM (within-Ss)
Ordinal	cumulative logit	<i>Ordinal logistic regression:</i> Ordinal responses (e.g., Likert-type scales)	“Figure 16 shows the distribution of Likert responses (1-7) for each X1×X2 condition. An analysis of variance based on ordinal logistic regression indicated a statistically significant effect on Y of X1 ( $\chi^2(1, N=60) = 15.28, p < .0001$ ), X2( $\chi^2(1, N=60) = 8.39, p = .004$ ), and an X1×X2 interaction ( $\chi^2(1, N=60) = 7.60, p = .006$ ).”	“Figure 16 shows the distribution of Likert responses (1-7) for each X1×X2 condition. An analysis of variance based on <b>mixed</b> ordinal logistic regression indicated a statistically significant effect on Y of X1 ( $\chi^2(1, N=60) = 13.75, p < .001$ ), X2( $\chi^2(1, N=60) = 6.86, p = .009$ ), and an X1×X2 interaction ( $\chi^2(1, N=60) = 7.60, p = .006$ ).”

# Figure 16





# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)
Poisson	log	<i>Poisson regression:</i> Count responses	<pre>library(car) # for Anova library(performance) # for check_overdispersion df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glm(Y ~ X1*X2, data=df, family=poisson) print(check_overdispersion(m)) # use family=quasipoisson or negative binomial # regression if overdispersed Anova(m, type=3)</pre>	<pre>library(lme4) # for glmer library(lmerTest) library(car) # for Anova library(performance) # for check_overdispersion df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glmer(Y ~ X1*X2 + (1 PId), data=df, family=poisson) print(check_overdispersion(m)) # use mixed negative binomial regression if overdispersed Anova(m, type=3)</pre>
Zero-Inflated Poisson	log	<i>Zero-inflated Poisson regression:</i> Zero-inflated count responses	<pre>library(glmmTMB) # for glmmTMB library(car) # for Anova library(performance) # for check_zeroinflation df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m0 = glm(Y ~ X1*X2, data=df, family=poisson) print(check_zeroinflation(m0)) m = glmmTMB(Y ~ X1*X2, data=df, family=poisson,             ziformula=~1) Anova(m, type=3)</pre>	<pre>library(lme4) # for glmer library(lmerTest) library(glmmTMB) # for glmmTMB library(car) # for Anova library(performance) # for check_zeroinflation df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m0 = glmer(Y ~ X1*X2 + (1 PId), data=df, family=poisson) print(check_zeroinflation(m0)) m = glmmTMB(Y ~ X1*X2 + (1 PId), data=df, family=poisson,             ziformula=~1, REML=TRUE) Anova(m, type=3)</pre>

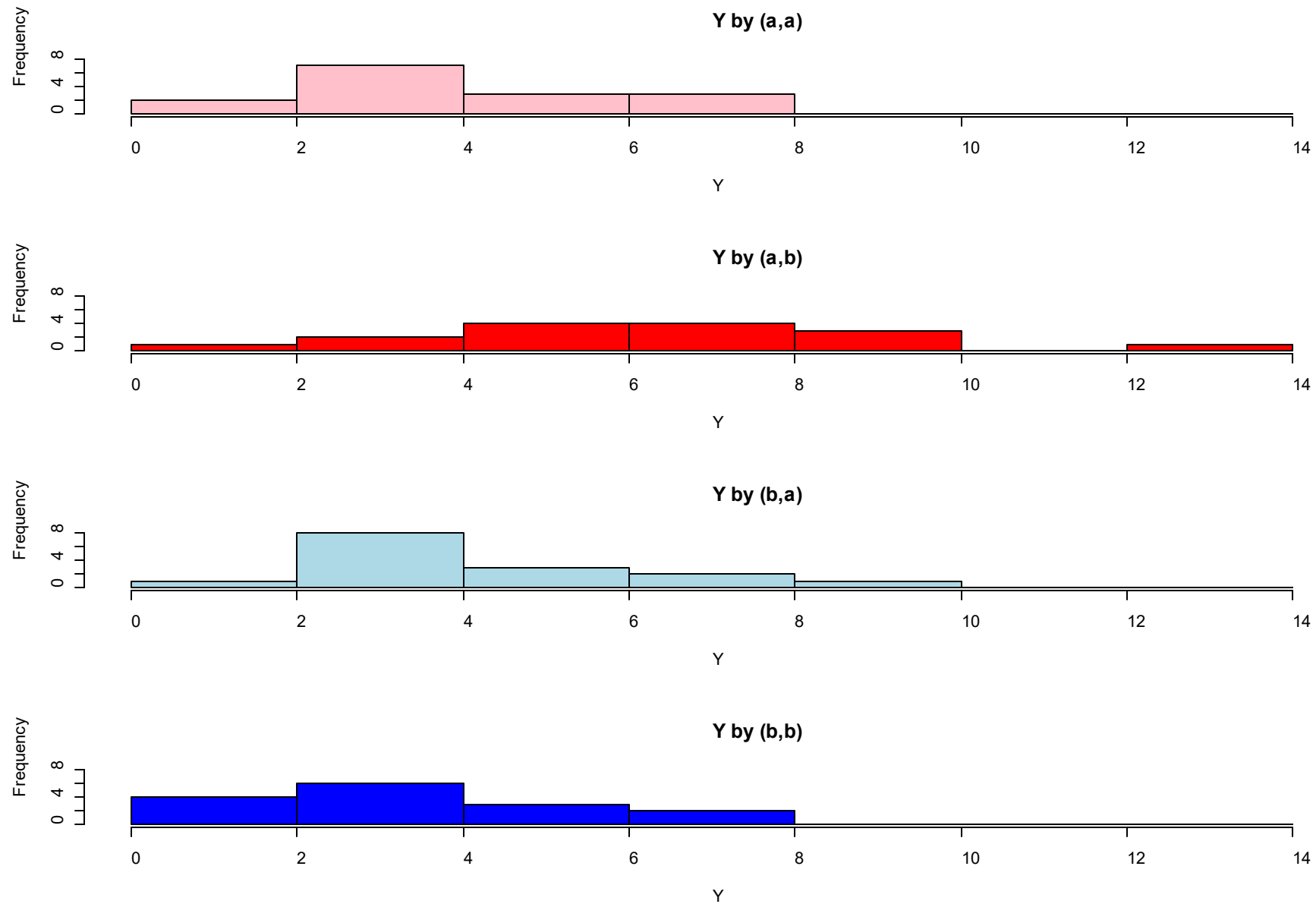
**NB.** When count data is overdispersed, it means the variance of the response in each condition is greater than its mean. To test for overdispersion, one can use `performance::check_overdispersion(m)`, where “m” is a fitted model with `family=poisson`. One can also use `var(Y)/abs(mean(Y)) > 1.15`, where “Y” is the response in each condition. For mildly overdispersed count data, `family=quasipoisson` can be used with `glm` but not with `lme4::glmer`. With high overdispersion, use negative binomial regression.

# GLM / GLMM

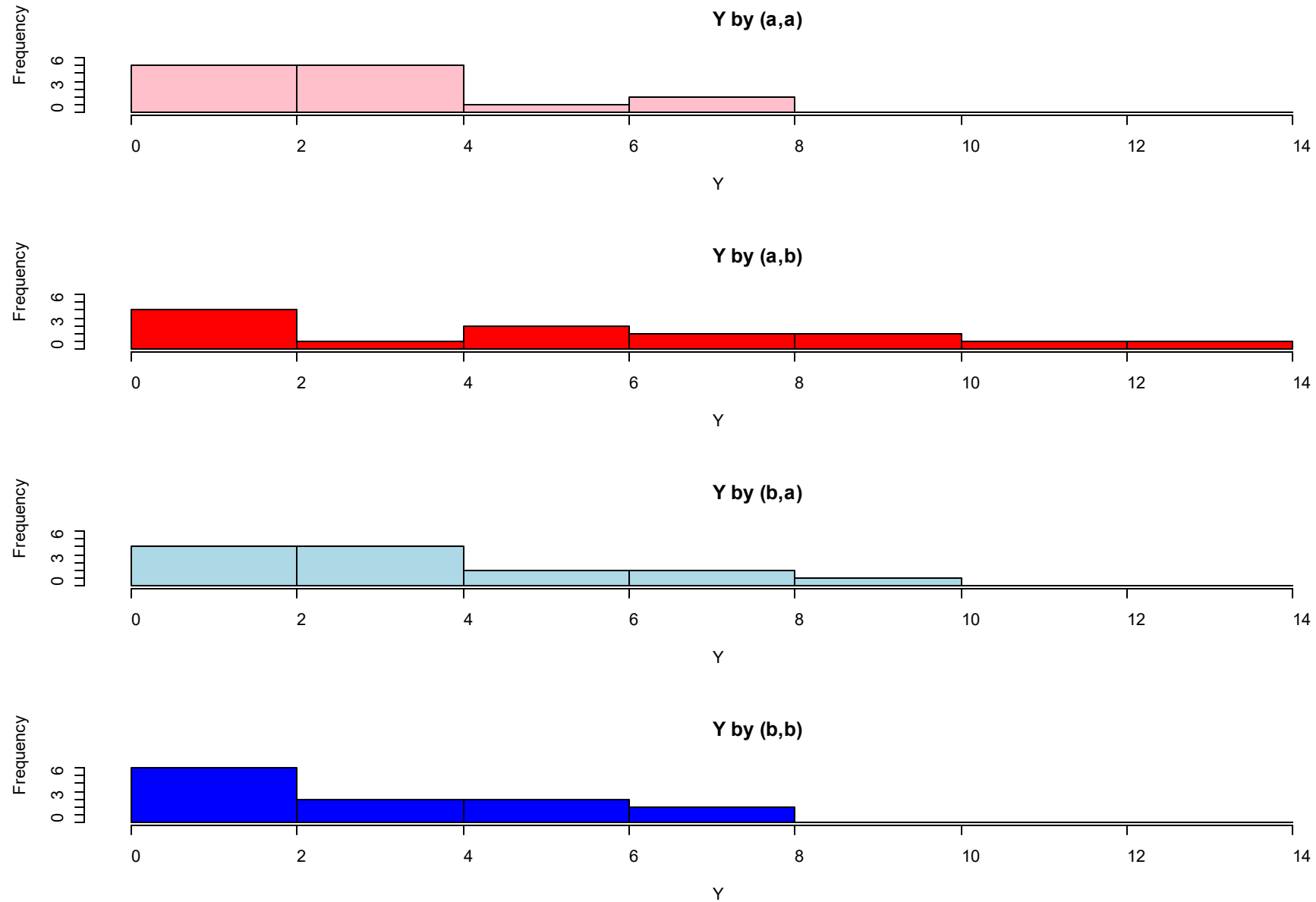
## Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Poisson	log	<i>Poisson regression:</i> Count responses	“Figure 17 shows histograms of count responses in each $X1 \times X2$ condition. An analysis of variance based on Poisson regression indicated a statistically significant effect of $X1$ on $Y$ ( $\chi^2(1, N=60) = 4.47, p = .034$ ) and a significant $X1 \times X2$ interaction ( $\chi^2(1, N=60) = 5.59, p = .018$ ).”	“Figure 17 shows histograms of count responses in each $X1 \times X2$ condition. An analysis of variance based on <b>mixed</b> Poisson regression indicated a statistically significant effect of $X1$ on $Y$ ( $\chi^2(1, N=60) = 4.44, p = .035$ ) and a significant $X1 \times X2$ interaction ( $\chi^2(1, N=60) = 5.54, p = .019$ ).”
Zero-Inflated Poisson	log	<i>Zero-inflated Poisson regression:</i> Zero-inflated count responses	“Figure 18 shows histograms of zero-inflated count responses in each $X1 \times X2$ condition. An analysis of variance based on zero-inflated Poisson regression indicated a statistically significant $X1 \times X2$ interaction ( $\chi^2(1, N=60) = 7.34, p = .007$ ).”	“Figure 18 shows histograms of zero-inflated count responses in each $X1 \times X2$ condition. An analysis of variance based on <b>mixed</b> zero-inflated Poisson regression indicated a statistically significant $X1 \times X2$ interaction ( $\chi^2(1, N=60) = 7.34, p = .007$ ).”

# Figure 17



# Figure 18



# GLM / GLMM

## Distributions and canonical links

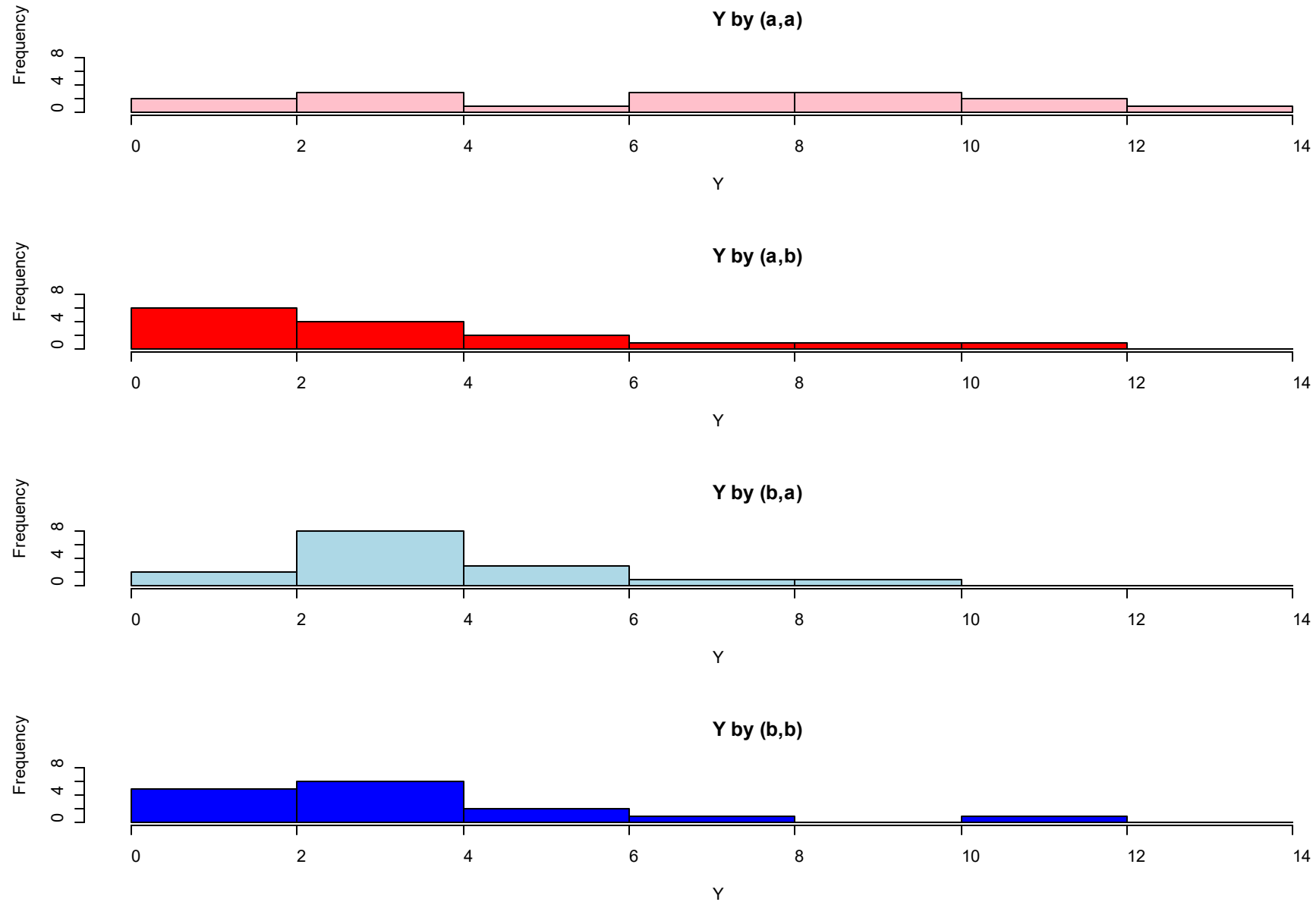
Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)
Negative Binomial	log	<i>Negative binomial regression:</i> Overdispersed count responses	<pre>library(MASS) # for glm.nb library(car)  # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glm.nb(Y ~ X1*X2, data=df) Anova(m, type=3)</pre>	<pre>library(lme4) # for glmer.nb library(lmerTest) library(car)  # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glmer.nb(Y ~ X1*X2 + (1 PId), data=df) Anova(m, type=3)</pre>
Zero-Inflated Negative Binomial	log	<i>Zero-inflated negative binomial regression:</i> Overdispersed zero-inflated count responses	<pre>library(MASS) # for glm.nb library(glmmTMB) # for glmmTMB library(car) # for Anova library(performance) # for check_zeroinflation df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m0 = glm.nb(Y ~ X1*X2, data=df) print(check_zeroinflation(m0)) m = glmmTMB(Y ~ X1*X2, data=df, family=nbinom2,             ziformula=~1) Anova(m, type=3)</pre>	<pre>library(lme4) # for glmer.nb library(lmerTest) library(glmmTMB) # for glmmTMB library(car) # for Anova library(performance) # for check_zeroinflation df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m0 = glmer.nb(Y ~ X1*X2 + (1 PId), data=df) print(check_zeroinflation(m0)) m = glmmTMB(Y ~ X1*X2 + (1 PId), data=df, family=nbinom2,             ziformula=~1, REML=TRUE) Anova(m, type=3)</pre>

# GLM / GLMM

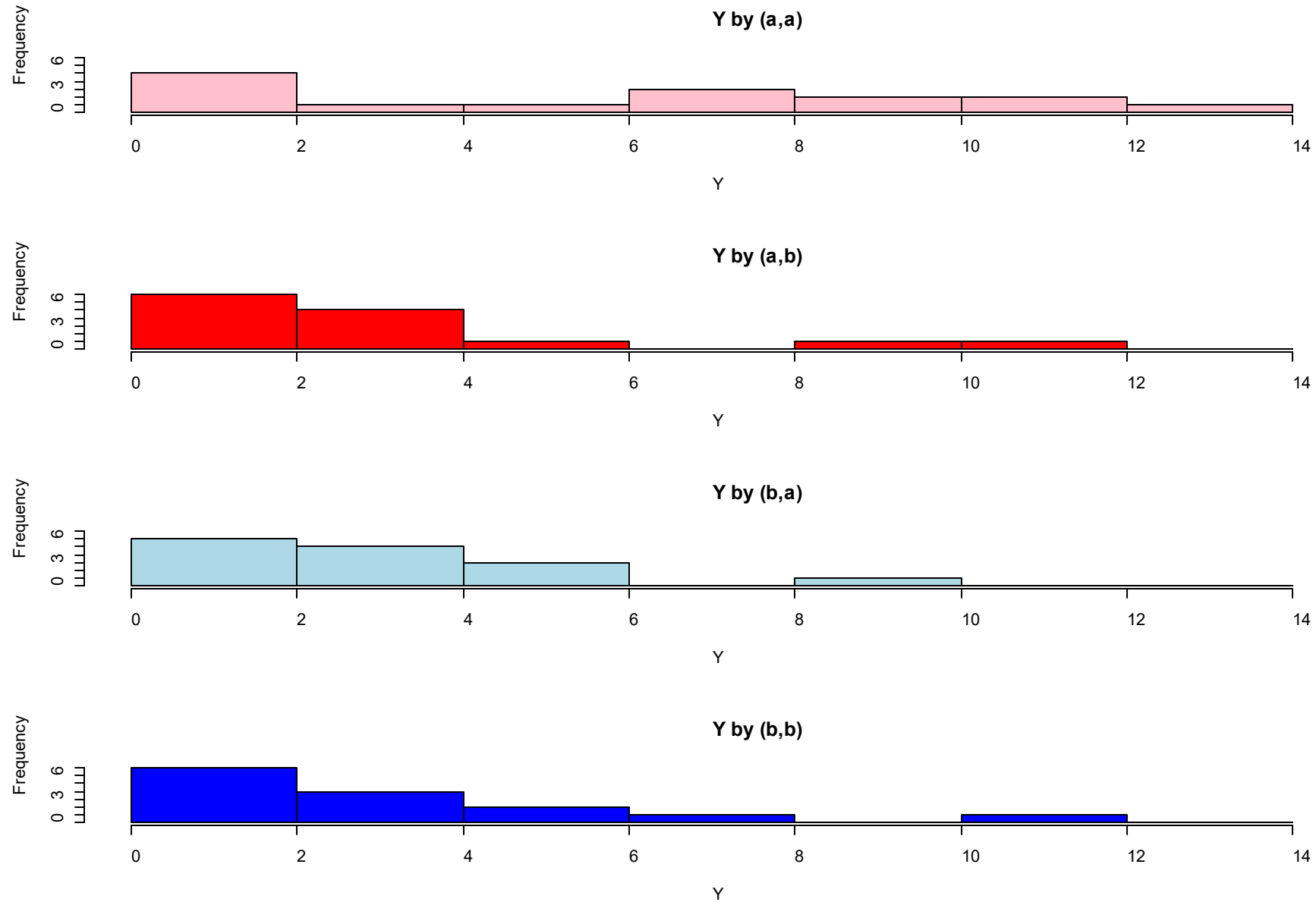
## Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Negative Binomial	log	<i>Negative binomial regression:</i> Overdispersed count responses	“Figure 19 shows histograms of count responses in each X1×X2 condition. An analysis of variance based on negative binomial regression indicated a statistically significant effect of X1 on Y ( $\chi^2(1, N=60) = 4.20, p = .040$ ).”	“Figure 19 shows histograms of count responses in each X1×X2 condition. An analysis of variance based on <b>mixed</b> negative binomial regression indicated a statistically significant effect of X1 on Y ( $\chi^2(1, N=60) = 4.21, p = .040$ ).”
Zero-Inflated Negative Binomial	log	<i>Zero-inflated negative binomial regression:</i> Overdispersed zero-inflated count responses	“Figure 20 shows histograms of zero-inflated count responses in each X1×X2 condition. An analysis of variance based on zero-inflated negative binomial regression indicated a statistically significant effect of X1 on Y ( $\chi^2(1, N=60) = 6.25, p = .012$ ).”	“Figure 20 shows histograms of zero-inflated count responses in each X1×X2 condition. An analysis of variance based on <b>mixed</b> zero-inflated negative binomial regression indicated a statistically significant effect of X1 on Y ( $\chi^2(1, N=60) = 5.52, p = .019$ ).”

# Figure 19



# Figure 20





# GLM / GLMM

## Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)
Exponential	log	<i>Exponential regression:</i> Exponentially distributed responses (e.g., income)	<pre>library(car) # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glm(Y ~ X1*X2, data=df,         family=Gamma(link="log")) Anova(m, type=3)</pre>	<pre>library(lme4) # for glmer library(lmerTest) library(car) # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glmer(Y ~ X1*X2 + (1 PId), data=df,           family=Gamma(link="log")) Anova(m, type=3)</pre>
Gamma	inverse	<i>Gamma regression:</i> Skewed continuous responses (e.g., time measurements)	<pre>library(car) # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glm(Y ~ X1*X2, data=df, family=Gamma) Anova(m, type=3)</pre>	<pre>library(lme4) # for glmer library(lmerTest) library(car) # for Anova df\$PId = factor(df\$PId) df\$X1 = factor(df\$X1) df\$X2 = factor(df\$X2) contrasts(df\$X1) &lt;- "contr.sum" contrasts(df\$X2) &lt;- "contr.sum" m = glmer(Y ~ X1*X2 + (1 PId), data=df, family=Gamma) Anova(m, type=3)</pre>

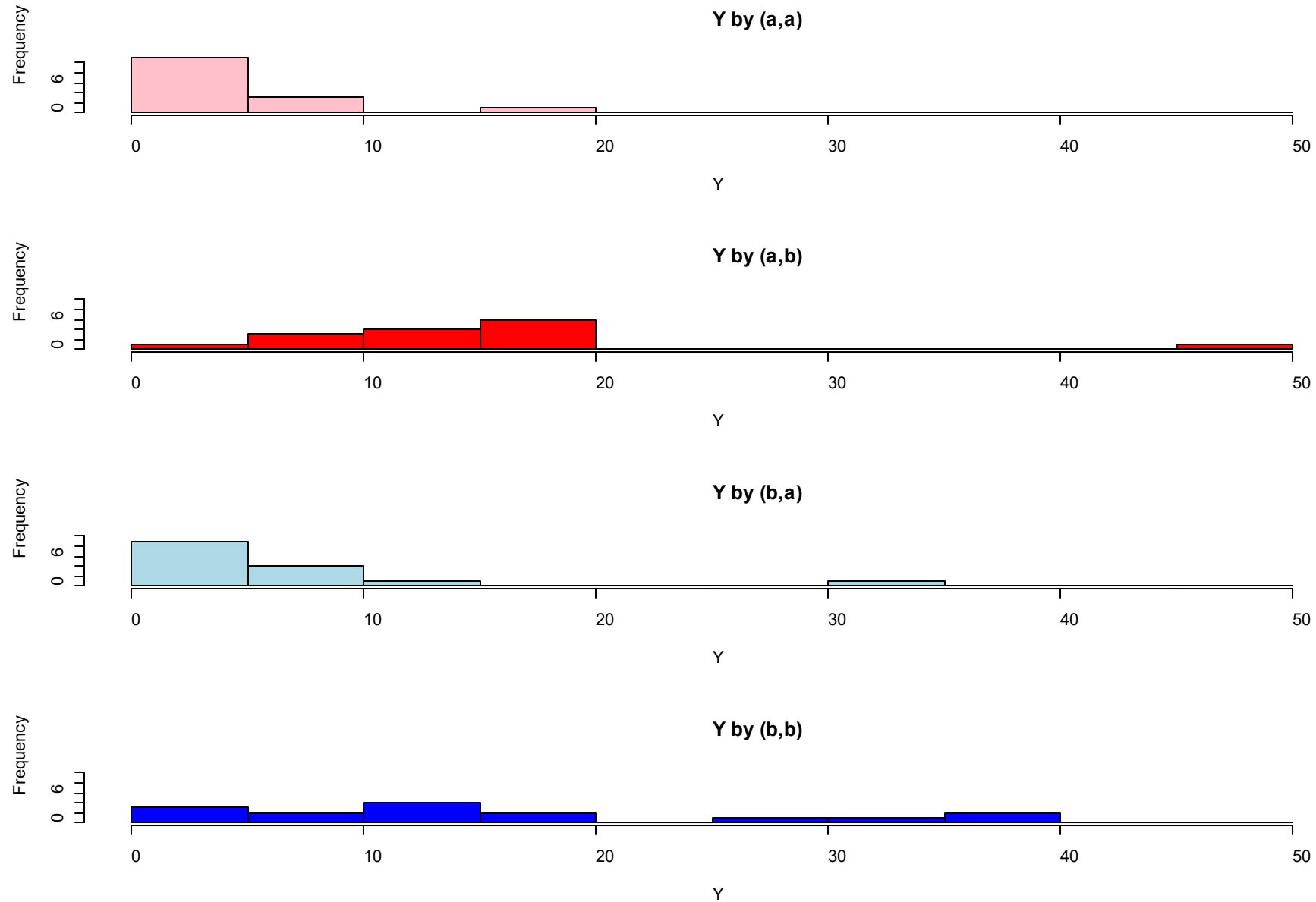
**NB.** Gamma distributions are parameterized by *shape* and *scale* (or sometimes *rate*, which is  $1/\text{scale}$ ). Exponential distributions are special cases of gamma distributions where *shape* always equals 1. The log link function is used with the exponential distribution to fix the dispersion parameter at 1.0.

# GLM / GLMM

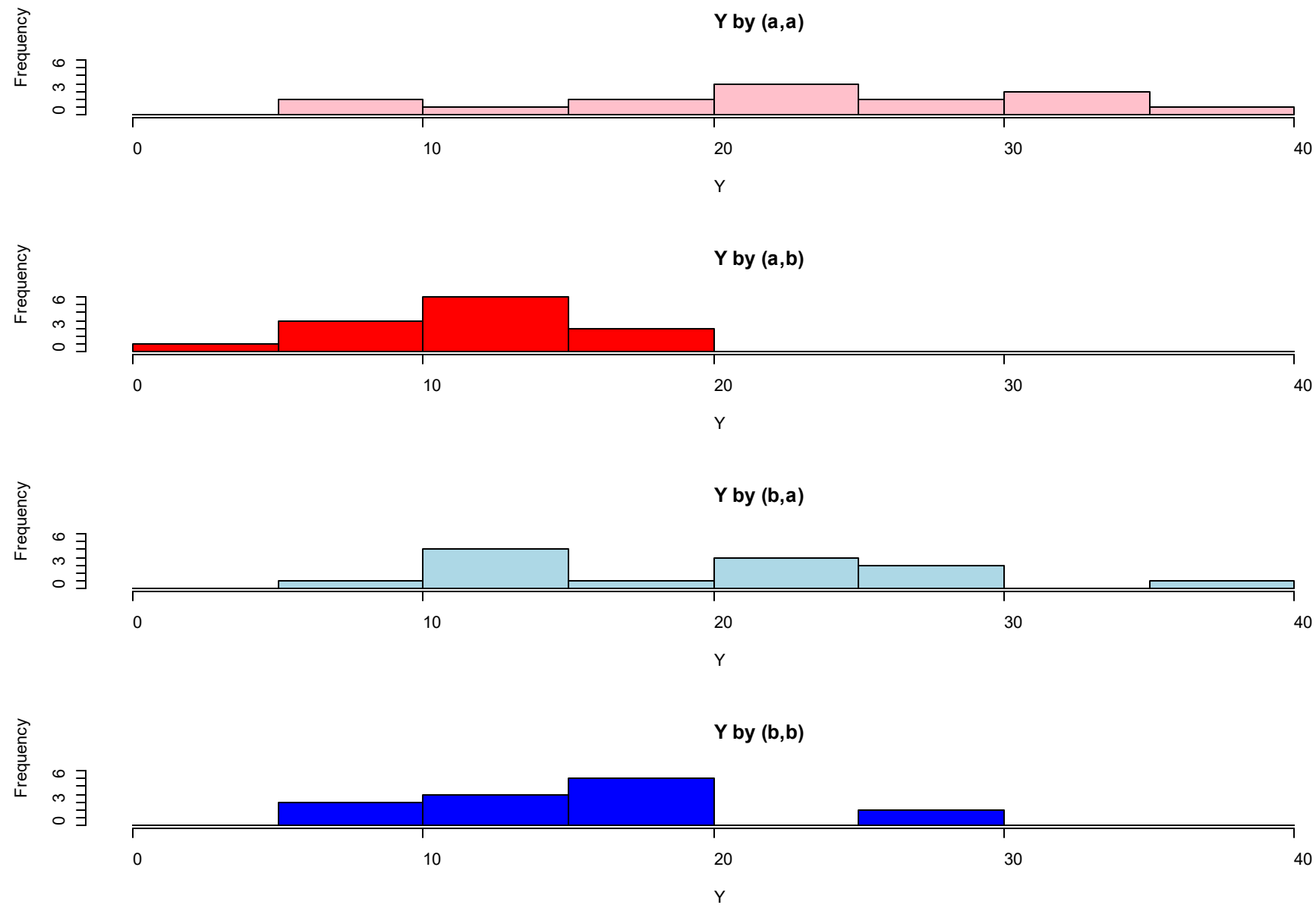
## Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Exponential	log	<i>Exponential regression:</i> Exponentially distributed responses (e.g., income)	“Figure 21 shows exponential histograms for each $X1 \times X2$ condition. An analysis of variance based on exponential regression indicated a statistically significant effect of $X2$ on $Y$ ( $\chi^2(1, N=60) = 20.96, p < .0001$ ).”	“Figure 21 shows exponential histograms for each $X1 \times X2$ condition. An analysis of variance based on <b>mixed</b> exponential regression indicated a statistically significant effect of $X2$ on $Y$ ( $\chi^2(1, N=60) = 31.00, p < .0001$ ).”
Gamma	inverse	<i>Gamma regression:</i> Skewed continuous responses (e.g., time measurements)	“Figure 22 shows gamma histograms for each $X1 \times X2$ condition. An analysis of variance based on gamma regression indicated a statistically significant effect of $X2$ on $Y$ ( $\chi^2(1, N=60) = 24.22, p < .0001$ ) and an $X1 \times X2$ interaction ( $\chi^2(1, N=60) = 7.97, p = .005$ ).”	“Figure 22 shows gamma histograms for each $X1 \times X2$ condition. An analysis of variance based on <b>mixed</b> gamma regression indicated a statistically significant effect of $X2$ on $Y$ ( $\chi^2(1, N=60) = 25.36, p < .0001$ ) and an $X1 \times X2$ interaction ( $\chi^2(1, N=60) = 8.86, p = .003$ ).”

# Figure 21



# Figure 22



# Generalized Linear (Mixed) Models

*Post hoc pairwise comparisons*

# GLM / GLMM

## Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	R Code
1	≥2	Linear regression	t-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from lm or lme4::lmer</pre>
1	≥2	Logistic regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and dichotomous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from glm or lme4::glmer with family=binomial</pre>
1	≥2	Multinomial logistic regression	Chi-squared test	Btwn	<pre># df has one between-Ss. factor (X) w/levels (a,b,c) and polytomous response (Y) library(multpois) # for glm.mp.con glm.mp.con(m, pairwise ~ X, adjust="holm") # m is from multpois::glm.mp  # if m is built using nnet::multinom, emmeans can be used this way: library(emmeans) # for emmeans, test emmeans::test(   contrast(emmeans(m, ~ X   Y, mode="latent"), method="pairwise", ref=1),   joint=TRUE, by="contrast" )</pre>
				Within	<pre># df has one within-Ss. factor (X) w/levels (a,b,c) and polytomous response (Y) library(multpois) # for glmer.mp.con glmer.mp.con(m, pairwise ~ X, adjust="holm") # m is from multpois::glmer.mp</pre>
1	≥2	Ordinal logistic regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and ordinal response (1-7) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from MASS::polr or ordinal::clmm</pre>

**NB.** Between-subjects models are from GLMs, within-subjects models are from GLMMs. Multinomial logistic regression is implemented via the multinomial-Poisson transformation (Baker 1994).

# GLM / GLMM

## Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	Report
1	≥2	Linear regression	t-test	Btwn	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $t(57) = -3.16, p = .008$ ) and ‘a’ vs. ‘c’ ( $t(57) = -2.47, p = .033$ ) were significantly different, but not ‘b’ vs. ‘c’.”
				Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $t(38) = -3.16, p = .009$ ) and ‘a’ vs. ‘c’ ( $t(38) = -2.47, p = .036$ ) were significantly different, but not ‘b’ vs. ‘c’.”
1	≥2	Logistic regression	Z-test	Btwn	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘c’ was significantly different ( $Z = -2.46, p = .041$ ), but not ‘a’ vs. ‘b’ or ‘b’ vs. ‘c’.”
				Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that no two levels were significantly different.”
1	≥2	Multinomial logistic regression	Chi-squared test	Btwn	“Three <i>post hoc</i> pairwise comparisons, conducted using the multinomial-Poisson transformation (Baker 1994), and corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘c’ ( $\chi^2(2, N=40) = 14.71, p = .001$ ) and ‘b’ vs. ‘c’ ( $\chi^2(2, N=40) = 17.65, p < .001$ ) were significantly different, but not ‘a’ vs. ‘b’.”
				Within	“Three <i>post hoc</i> pairwise comparisons, conducted using the multinomial-Poisson transformation (Baker 1994), and corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘c’ ( $\chi^2(2, N=40) = 12.22, p = .007$ ) and ‘b’ vs. ‘c’ ( $\chi^2(2, N=40) = 10.73, p = .009$ ) were significantly different, but not ‘a’ vs. ‘b’.”
1	≥2	Ordinal logistic regression	Z-test	Btwn, Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘b’ vs. ‘c’ was significantly different ( $Z = 2.40, p = .049$ ), but not ‘a’ vs. ‘b’ or ‘a’ vs. ‘c’.”

# GLM / GLMM

## *Post hoc* pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	R Code
1	≥2	Poisson regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from glm or lme4::glmer with family=poisson</pre>
1	≥2	Zero-inflated Poisson regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and zero-inflated count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from glmmTMB::glmmTMB with family=poisson</pre>
1	≥2	Negative binomial regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and overdispersed count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from MASS::glm.nb or lme4::glmer.nb</pre>
1	≥2	Zero-inflated negative binomial regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and zero-inflated overdispersed count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from glmmTMB::glmmTMB with family=nbinom2</pre>

**NB.** Between-subjects models are from GLMs, within-subjects models are from GLMMs.



# GLM / GLMM

## Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	Report
1	≥2	Poisson regression	Z-test	Btwn, Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -2.92, p = .007$ ) and ‘b’ vs. ‘c’ ( $Z = 3.28, p = .003$ ) were significantly different, but not ‘a’ vs. ‘c’.”
1	≥2	Zero-inflated Poisson regression	Z-test	Btwn	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -2.81, p = .010$ ) and ‘b’ vs. ‘c’ ( $Z = 2.98, p = .009$ ) were significantly different, but not ‘a’ vs. ‘c’.”
				Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -2.81, p = .010$ ) and ‘b’ vs. ‘c’ ( $Z = 2.99, p = .009$ ) were significantly different, but not ‘a’ vs. ‘c’.”
1	≥2	Negative binomial regression	Z-test	Btwn, Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ was significantly different ( $Z = -2.50, p = .038$ ), but not ‘a’ vs. ‘c’ or ‘b’ vs. ‘c’.”
1	≥2	Zero-inflated negative binomial regression	Z-test	Btwn	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -4.37, p < .0001$ ) and ‘b’ vs. ‘c’ ( $Z = 4.47, p < .0001$ ) were significantly different, but not ‘a’ vs. ‘c’.”
				Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -4.24, p < .0001$ ) and ‘b’ vs. ‘c’ ( $Z = 4.32, p < .0001$ ) were significantly different, but not ‘a’ vs. ‘c’.”

# GLM / GLMM

## *Post hoc* pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	R Code
1	≥2	Exponential regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and exponential response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from glm or lme4::glmer with  # family=Gamma(link="log")</pre>
1	≥2	Gamma regression	Z-test	Btwn, Within	<pre># df has one factor (X) w/levels (a,b,c) and skewed continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X, adjust="holm") # m is from glm or lme4::glmer with family=Gamma</pre>

**NB.** Between-subjects models are from GLMs, within-subjects models are from GLMMs.

# GLM / GLMM

## *Post hoc* pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	Report
1	≥2	Exponential regression	Z-test	Btwn	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -3.15, p = .008$ ) and ‘b’ vs. ‘c’ ( $Z = 2.36, p = .044$ ) were significantly different, but not ‘a’ vs. ‘c’.”
				Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -3.64, p = .001$ ) and ‘b’ vs. ‘c’ ( $Z = 2.86, p = .008$ ) were significantly different, but not ‘a’ vs. ‘c’.”
1	≥2	Gamma regression	Z-test	Btwn	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -5.44, p < .0001$ ), ‘a’ vs. ‘c’ ( $Z = -3.20, p = .005$ ), and ‘b’ vs. ‘c’ ( $Z = 3.00, p = .005$ ) were all significantly different.”
				Within	“Three <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that ‘a’ vs. ‘b’ ( $Z = -6.15, p < .0001$ ), ‘a’ vs. ‘c’ ( $Z = -3.58, p = .001$ ), and ‘b’ vs. ‘c’ ( $Z = 3.48, p = .001$ ) were all significantly different.”

# GLM / GLMM

## Post hoc pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	R Code
≥2	≥2	Linear regression	t-test	Btwn, Within	<pre># df has two factors (X1,X2) each w/levels (a,b) and continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from lm or lme4::lmer</pre>
≥2	≥2	Logistic regression	Z-test	Btwn, Within	<pre># df has two factors (X1,X2) each w/levels (a,b) and dichotomous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glm or lme4::glmer with family=binomial</pre>
≥2	≥2	Multinomial logistic regression	Chi-squared test	Btwn	<pre># df has two between-Ss. factors (X1,X2) each w/levels (a,b) and polytomous response (Y) library(multpois) # for glm.mp.con glm.mp.con(m, pairwise ~ X1*X2, adjust="holm") # m is from multpois::glm.mp  # if m is built using nnet::multinom, emmeans can be used this way: library(emmeans) # for emmeans, test emmeans::test(   contrast(emmeans(m, ~ X1*X2   Y, mode="latent"), method="pairwise", ref=1),   joint=TRUE, by="contrast" )</pre>
				Within	<pre># df has two within-Ss. factors (X1,X2) each w/levels (a,b) and polytomous response (Y) library(multpois) # for glmer.mp.con glmer.mp.con(m, pairwise ~ X1*X2, adjust="holm") # m is from multpois::glmer.mp</pre>
≥2	≥2	Ordinal logistic regression	Z-test	Btwn, Within	<pre># df has two factors (X1,X2) each w/levels (a,b) and ordinal response (1-7) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from MASS::polr or ordinal::clmm</pre>

**NB.** Between-subjects models are from GLMs, within-subjects models are from GLMMs. Multinomial logistic regression is implemented via the multinomial-Poisson transformation (Baker 1994).

# GLM / GLMM

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	Report
≥2	≥2	Linear regression	t-test	Btwn	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,a} was significantly different ( $t(56) = -2.75, p = .048$ ). All other pairwise comparisons were not detectably different.”
				Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that no pairwise comparison was detectably different.”
≥2	≥2	Logistic regression	Z-test	Btwn, Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that no pairwise comparisons were detectably different.”
≥2	≥2	Multinomial logistic regression	Chi-squared test	Btwn, Within	“Six <i>post hoc</i> pairwise comparisons, conducted using the multinomial-Poisson transformation (Baker 1994), and corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that no pairwise comparisons were detectably different.”
≥2	≥2	Ordinal logistic regression	Z-test	Btwn, Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,a} ( $Z = 4.17, p < .001$ ), {a,a} vs. {a,b} ( $Z = 3.53, p = .002$ ), and {a,a} vs. {b,b} ( $Z = 4.29, p < .001$ ) were significantly different. No other pairwise comparisons were detectably different.”

# GLM / GLMM

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	R Code
≥2	≥2	Poisson regression	Z-test	Btwn, Within	# df has two factors (X1,X2) each w/levels (a,b) and count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glm or lme4::glmer with family=poisson
≥2	≥2	Zero-inflated Poisson regression	Z-test	Btwn, Within	# df has two factors (X1,X2) each w/levels (a,b) and zero-inflated count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glmmTMB::glmmTMB with family=poisson
≥2	≥2	Negative binomial regression	Z-test	Btwn, Within	# df has two factors (X1,X2) each w/levels (a,b) and overdispersed count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from MASS::glm.nb or lme4::glmer.nb
≥2	≥2	Zero-inflated negative binomial regression	Z-test	Btwn, Within	# df has two factors (X1,X2) each w/levels (a,b) and zero-inflated overdispersed count response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glmmTMB::glmmTMB with family=nbinom2

**NB.** Between-subjects models are from GLMs, within-subjects models are from GLMMs.

# GLM / GLMM

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	Report
≥2	≥2	Poisson regression	Z-test	Btwn, Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,b} vs. {b,b} was significantly different ( $Z = 3.21, p = .008$ ). All other pairwise comparisons were not detectably different.”
≥2	≥2	Zero-inflated Poisson regression	Z-test	Btwn	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {a,b} ( $Z = -3.10, p = .012$ ) and {a,b} vs. {b,b} ( $Z = 3.01, p = .013$ ) were significantly different. Other pairwise comparisons were not detectably different.”
				Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {a,b} ( $Z = -3.10, p = .011$ ) and {a,b} vs. {b,b} ( $Z = 3.01, p = .013$ ) were significantly different. Other pairwise comparisons were not detectably different.”
≥2	≥2	Negative binomial regression	Z-test	Btwn	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,b} was significantly different ( $Z = 2.82, p = .029$ ). All other pairwise comparisons were not detectably different.”
				Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,b} was significantly different ( $Z = 2.83, p = .028$ ). All other pairwise comparisons were not detectably different.”
≥2	≥2	Zero-inflated negative binomial regression	Z-test	Btwn	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,a} ( $Z = 2.99, p = .017$ ) and {a,a} vs. {b,b} ( $Z = 2.66, p = .040$ ) were significantly different. Other pairwise comparisons were not detectably different.”
				Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {b,a} was significantly different ( $Z = 2.82, p = .029$ ). All other pairwise comparisons were not detectably different.”

# GLM / GLMM

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	R Code
≥2	≥2	Exponential regression	Z-test	Btwn, Within	<pre># df has two factors (X1,X2) each w/levels (a,b) and exponential response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glm or lme4::glmer with # family=Gamma(link="log")</pre>
≥2	≥2	Gamma regression	Z-test	Btwn, Within	<pre># df has two factors (X1,X2) each w/levels (a,b) and skewed continuous response (Y) library(emmeans) # for emmeans emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glm or lme4::glmer with family=Gamma</pre>

**NB.** Between-subjects models are from GLMs, within-subjects models are from GLMMs.



# GLM / GLMM

## *Post hoc* pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	Report
≥2	≥2	Exponential regression	Z-test	Btwn	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {a,b} ( $Z = -3.97, p = .001$ ), {a,a} vs. {b,b} ( $Z = -4.31, p < .001$ ), and {b,a} vs. {b,b} ( $Z = -2.70, p = .037$ ) were significantly different. Other pairwise comparisons were not detectably different.”
				Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {a,b} ( $Z = -4.66, p < .0001$ ), {a,a} vs. {b,b} ( $Z = -5.06, p < .0001$ ), {b,a} vs. {a,b} ( $Z = -2.86, p = .013$ ), and {b,a} vs. {b,b} ( $Z = -3.27, p = .004$ ) were significantly different. The other two pairwise comparisons were not detectably different.”
≥2	≥2	Gamma regression	Z-test	Btwn	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {a,b} ( $Z = -4.77, p < .001$ ), {a,a} vs. {b,b} ( $Z = -2.65, p = .042$ ), {b,a} vs. {a,b} ( $Z = -3.87, p = .001$ ), and {a,b} vs. {b,b} ( $Z = 2.52, p = .044$ ) were significantly different. The other two pairwise comparisons were not detectably different.”
				Within	“Six <i>post hoc</i> pairwise comparisons, corrected with Holm’s sequential Bonferroni procedure (Holm 1979), indicated that {a,a} vs. {a,b} ( $Z = -5.13, p < .0001$ ), {a,a} vs. {b,b} ( $Z = -2.85, p = .018$ ), {b,a} vs. {a,b} ( $Z = -4.16, p < .001$ ), and {a,b} vs. {b,b} ( $Z = 2.71, p = .020$ ) were significantly different. The other two pairwise comparisons were not detectably different.”

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