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#Rstats

Statistical Inference in R

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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, *G*-test, Fisher's exact test
2[†]	≥2	Symmetry test

[†]*Dependent samples*

Assumptions

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

Distributions

Shapiro-Wilk test
Chi-squared GOF test

Analyses of Variance

Factors	Levels	Between or Within	Parametric Tests	Nonparametric Tests	
			Linear Models	Generalized Models	
1	2	B	Independent-samples *t*-test	Median test	Mann-Whitney *U* test
1	2	W	Paired-samples *t*-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 Linear Model (LM)	Aligned Rank Transform (ART) Generalized Linear Model (GLM)	
≥2	≥2	W	Factorial repeated measures ANOVA Linear Mixed Model (LMM)	Aligned Rank Transform (ART) Generalized Linear Mixed Model (GLMM)	

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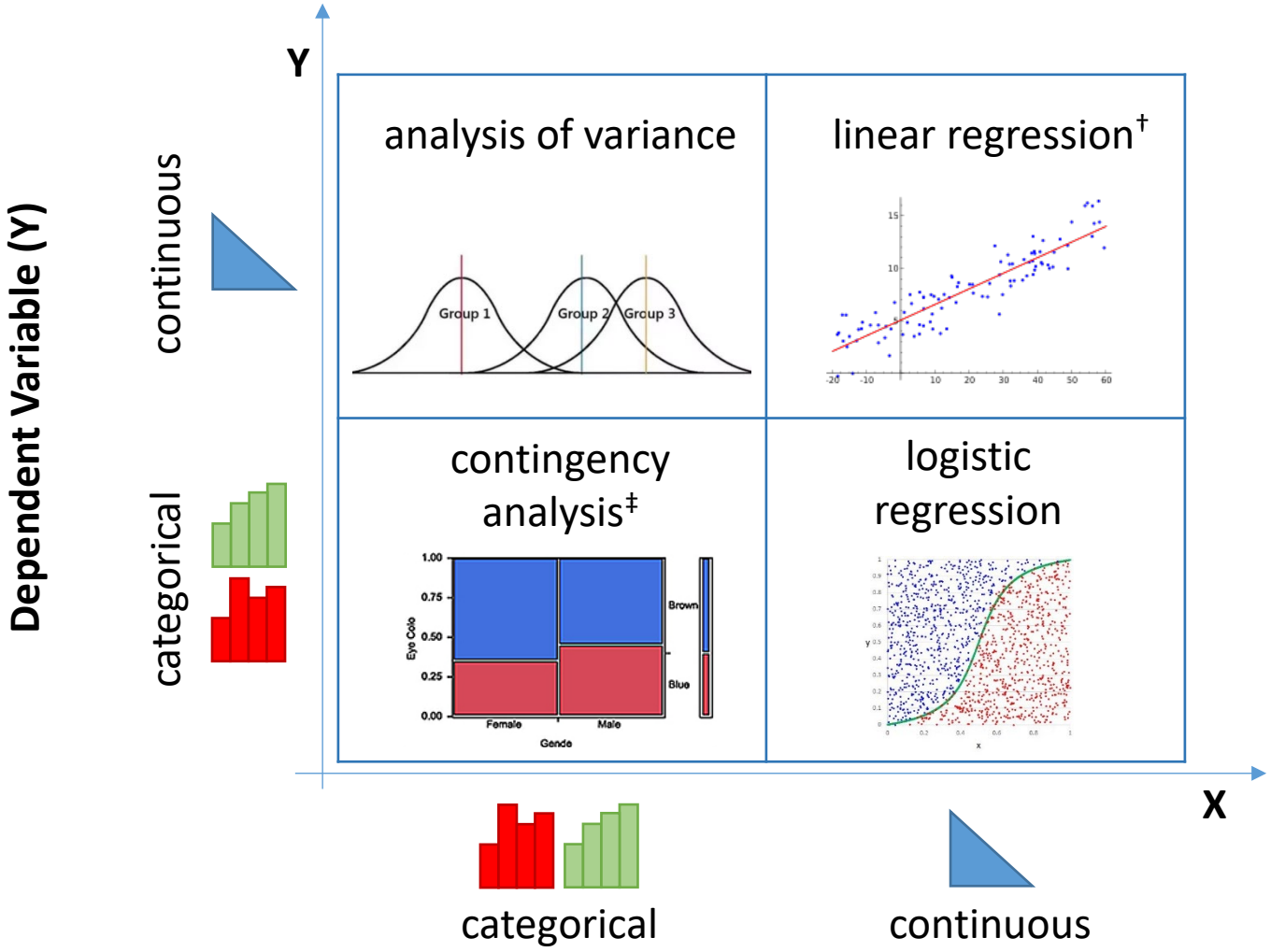
Analysis Categories



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

†All of the parametric tests in the previous table are forms of linear regression.

‡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	`# df is a long-format data table w/columns for participant (PId) and 2-category outcome (Y)`
				`df$PId = factor(df$PId) # 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")`

1	≥2	Multinomial test	Yes, use with *N*<200	`# df is a long-format data table w/columns for participant (PId) and N-category outcome (Y)`
				`library(XNomial) # for xmulti`
				`df$PId = factor(df$PId) # 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)`

		One-sample chi-squared test	No, use with *N*≥200	`# df is a long-format data table w/columns for participant (PId) and N-category outcome (Y)`
				`df$PId = factor(df$PId) # 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)`

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	≥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*≥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	≥2	Fisher's exact test	Yes, use with *N*<200	`# df is a long-format data table w/participant (PId), factor (X), and N-category outcome (Y)`
				`df$PId = factor(df$PId) # 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)`

		G-test	No, use with *N*<200	`# df is a long-format data table w/participant (PId), factor (X), and N-category outcome (Y)`
				`library(RVAideMemoire) # for G.test`
				`df$PId = factor(df$PId) # 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)`

		Two-sample chi-squared test	No, use with *N*≥200	`# df is a long-format data table w/participant (PId), factor (X), and N-category outcome (Y)`
				`df$PId = factor(df$PId) # 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)`

Association

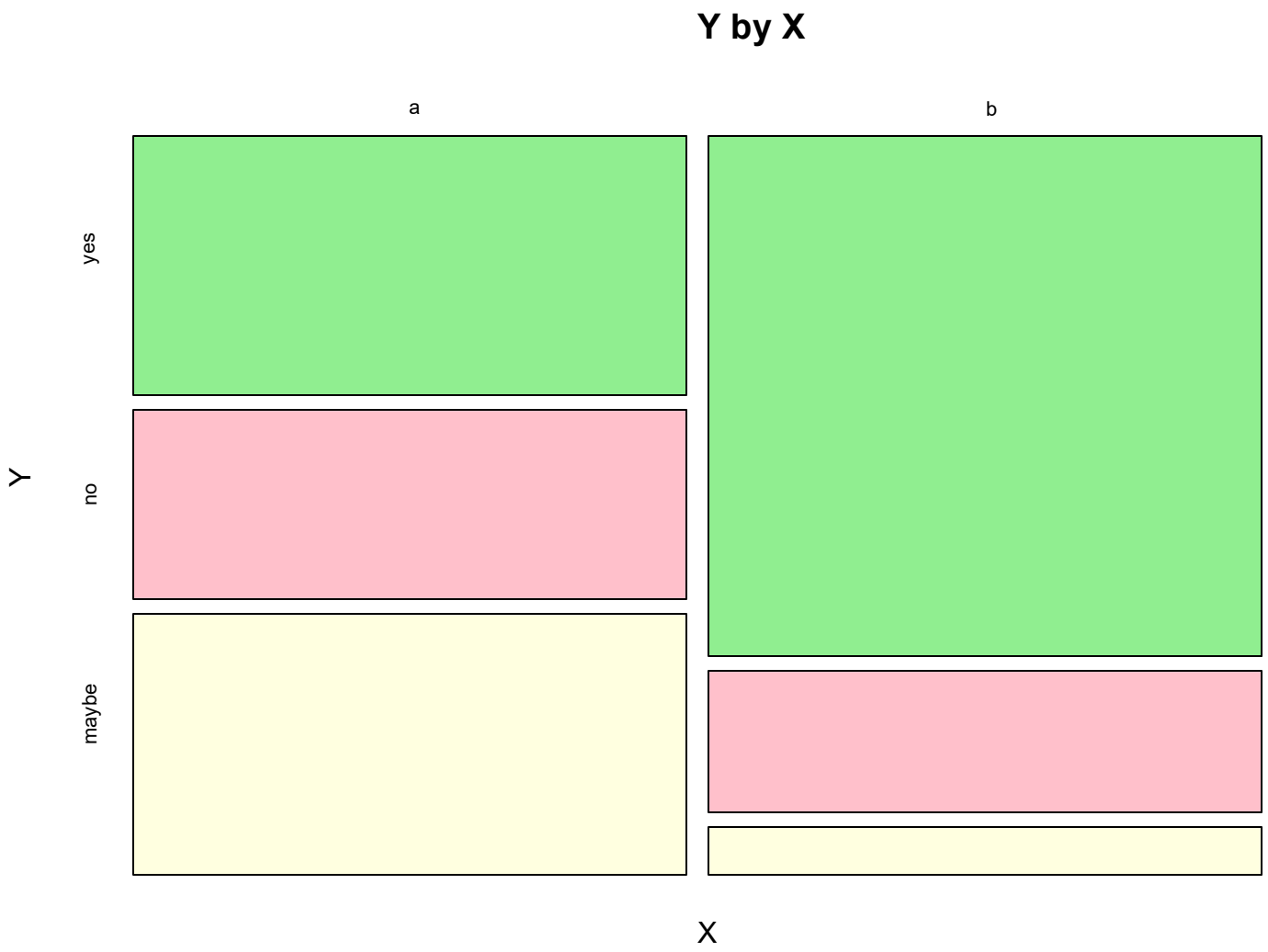
Two samples

Samples	Response Categories	Test Name	Exact Test?	Report
2	≥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 $N\geq200$	"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

		Y		
		yes	**no**	**maybe**
X	**a**	11	8	11
	b	22	6	2

Figure 1



Association

Dependent samples

Samples	Response Categories	Test Name	Exact Test?	R Code

2†	≥2	Symmetry test	No, asymptotic	`# df is a long-format data table w/columns for participant (PId), a within-Ss. factor (X),`
				`# and N-category outcome (Y)`
				`library(coin) # for symmetry_test`
				`df$PId = factor(df$PId) # 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 | PId, data=df)`

†*Dependent samples*

Association

Dependent samples

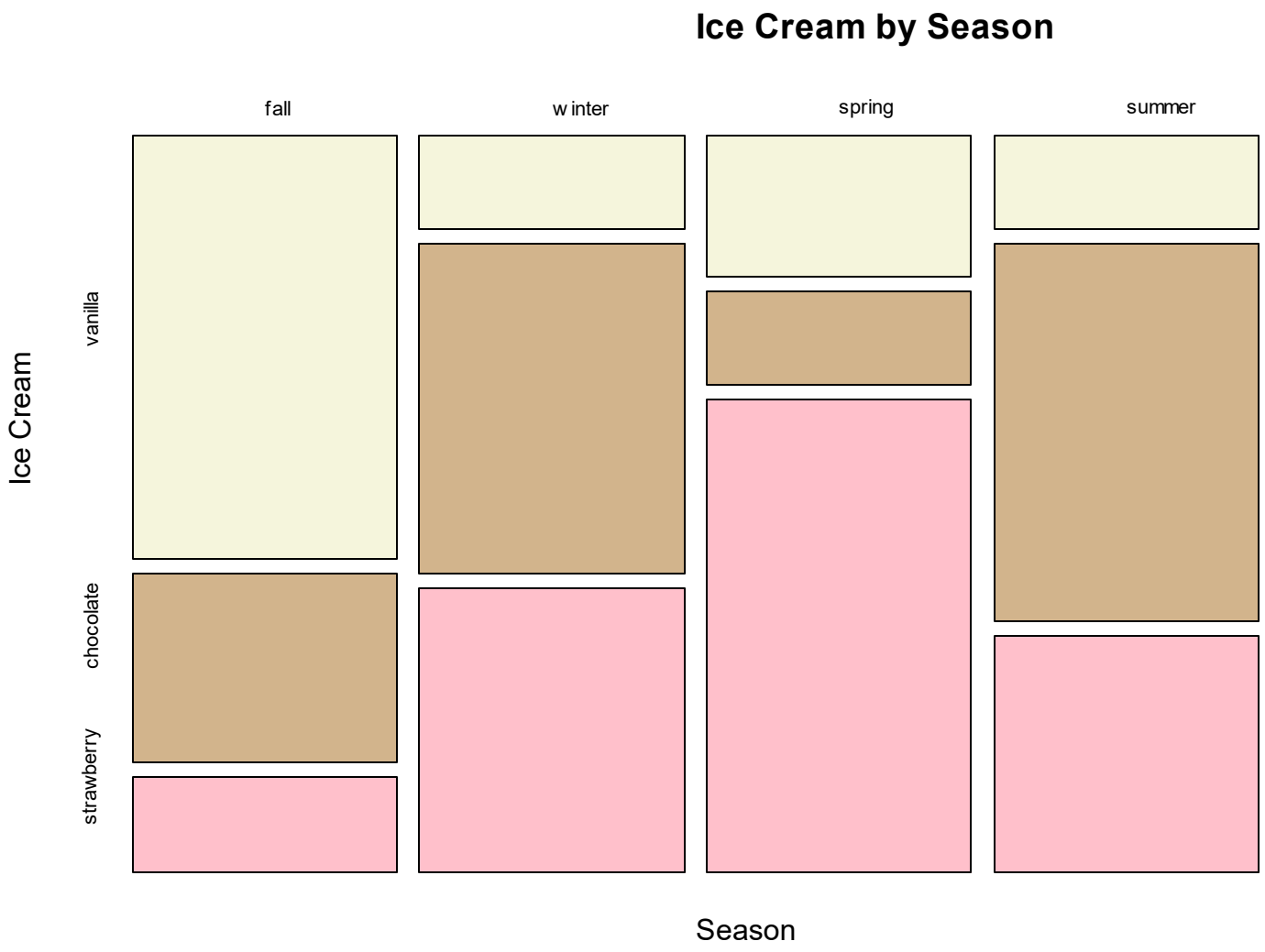
Samples	Response Categories	Test Name	Exact Test?	Report
2†	≥2	Symmetry test	No, asymptotic	"Fifteen participants each provided four responses indicating their favorite ice cream flavor in each season ('fall', 'winter', 'spring', and 'summer'). Table 2 shows the counts and Figure 2 plots the proportions. 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)."

†*Dependent samples*

Table 2

		Y		
		vanilla	**chocolate**	**strawberry**
X	**fall**	9	4	2
	winter	2	7	6
	spring	3	2	10
	summer	2	8	5

Figure 2


Ice Cream by Season
fall
winter
spring
summer
vanilla
chocolate
strawberry
Ice Cream
Season

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	`# 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`

1	≥2	One-sample chi-squared test	Pairwise chi-squared tests	`# 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:`
				`chisq.multcomp(xt, p.method="none")`
				`qchisq(1 - 0.0038, df=1) # 8.376996`

1	≥2	Multinomial test, one-sample chi-squared test	Individual binomial tests against chance	`# 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")`

Proportions

Post hoc tests – One sample

Samples	Response Categories	Omnibus Test	Contrast Test	Report
1	≥2	Multinomial test	Pairwise binomial tests	"Three *post hoc* 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 *post hoc* 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 *post hoc* 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	`# 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`

			Binomial tests of each table column against chance	`# 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")`

			Multinomial tests of each table row against chance	`# 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")`

Association

Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	≥2	Fisher's exact test	Pairwise Fisher's exact tests on 2×2 tables	"Three *post hoc* 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 *post hoc* 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 *post hoc* 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	≥2	*G*-test	Pairwise *G*-tests on 2×2 tables	`# 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")`

			Pairwise *G*-tests between table cells	`# 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`

Association

Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	≥2	*G*-test	Pairwise *G*-tests on 2×2 tables	"Three *post hoc* *G*-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 *G*-tests between table cells	"Fifteen *post hoc* *G*-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	≥2	*G*-test	*G*-tests on each table column (or row) against chance	`# 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")`

			G-tests on each table column (or row) against expected frequencies	`# 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")`

Association

Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	≥2	*G*-test	*G*-tests on each table column (or row) against chance	"Three *post hoc 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 ($G(1) = 6.86$, $p = .026$.)" "Two *post hoc 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 ($G(2) = 22.12$, $p < .0001$.)"
			G-tests on each table column (or row) against expected frequencies	"Three *post hoc 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 ($G(1) = 6.86$, $p = .026$.)" "Two *post hoc 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."

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	`# 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")`

			Pairwise chi-squared tests between table cells	`# 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:`
				`chisq.multcomp(xt, p.method="none")`
				`qchisq(1 - 4.5e-05, df=1) # 16.6479`

			Chi-squared tests to compare each cell to its expected frequency	`# 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:`
				`chisq.multcomp(xt, p.method="none")`
				`qchisq(1 - 0.004311, df=1) # 8.147944`

Association

Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	≥2	Chi-squared test	Pairwise chi-squared tests on 2×2 tables	"Three *post hoc* 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 *post hoc* 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 *post hoc* 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} ($\chi^2(1, N=11) = 8.15, p = .206$), {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	≥2	Chi-squared test	Chi-squared tests on each table column (or row) against chance	`# 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")`

			Chi-squared tests on each table column (or row) against expected frequencies	`# 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")`

Association

Post hoc tests – Two samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	≥2	Chi-squared test	chi-squared tests on each table column (or row) against chance	"Three *post hoc* 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 ($\chi^2(1, N=13) = 6.23, p = .038.$)" "Two *post hoc* 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 ($\chi^2(2, N=30) = 22.40, p < .0001$)."
			chi-squared tests on each table column (or row) against expected frequencies	"Three *post hoc* 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 ($\chi^2(1, N=13) = 6.23, p = .038.$)" "Two *post hoc* 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."

Association

Post hoc tests – Dependent samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code

2	≥2	Symmetry test	Pairwise symmetry tests	`# df is a long-format data table w/columns for participant (PId), a within-Ss. factor (X),`
				`# and N-category outcome (Y)`
				`library(coin) # for symmetry_test, pvalue`
				`pairwise.symmetry.test <- function(s1, s2, data=df) { # compare seasons s1, s2`
				`  df2 <- 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")`

2	≥2	Symmetry test	Pairwise sign tests	`# df is a long-format data table w/columns for participant (PId), a within-Ss. factor (X),`
				`# and N-category outcome (Y)`
				`library(coin) # for sign_test, pvalue`
				`pairwise.sign.test <- function(flavor, s1, s2, data=df) { # compare flavor in seasons s1, s2`
				`  df$chose.flavor.in.s1 = ifelse(df$Y == flavor & df$X == s1, 1, 0)`
				`  df$chose.flavor.in.s2 = ifelse(df$Y == flavor & df$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")`

Association

Post hoc tests – Dependent samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
1	≥2	Symmetry test	Pairwise symmetry tests	"Six *post hoc* 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 *post hoc* 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."

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Assumptions

ANOVA Assumptions

Normality

Assumption	Test Name	Context of Use	R Code

Normality	Shapiro-Wilk test (on the conditional response)	*t*-test, ANOVA, LMM	`# df has two factors (X1,X2) each w/two levels (a,b) and continuous response Y`
			`shapiro.test(df[df$X1 == "a" & df$X2 == "a",]$Y) # condition a,a`
			`shapiro.test(df[df$X1 == "a" & df$X2 == "b",]$Y) # condition a,b`
			`shapiro.test(df[df$X1 == "b" & df$X2 == "a",]$Y) # condition b,a`
			`shapiro.test(df[df$X1 == "b" & df$X2 == "b",]$Y) # condition b,b`

Normality	Shapiro-Wilk test (on residuals)	*t*-test, ANOVA	`# df has two factors (X1,X2) each w/two levels (a,b) and continuous response (Y)`
			`library(afex) # for aov_ez`
			`m = aov_ez(dv="Y", within="X1", between="X2", id="PId", type=3, data=df) # build model`
			`r = residuals(m$lm) # extract residuals`
			
			`## Common Code ##`
			`library(EnvStats) # for gofTest`
			`mean(r); sum(r) # both should be ~0`
			`plot(r[1:length(r)], main="Residuals"); abline(h=0) # should be balanced and random`
			`qqnorm(r); qqline(r) # Q-Q plot`
			`xax = ceiling(max(abs(min(r)), abs(max(r)))) # balanced histogram`
			`hist(r, main="Histogram of residuals", xlim=c(-xax,+xax), freq=FALSE)`
			`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.gof(f) # display fit`
			`shapiro.test(r) # Shapiro-Wilk test`
			`check_normality(m)[1] # same p-value`

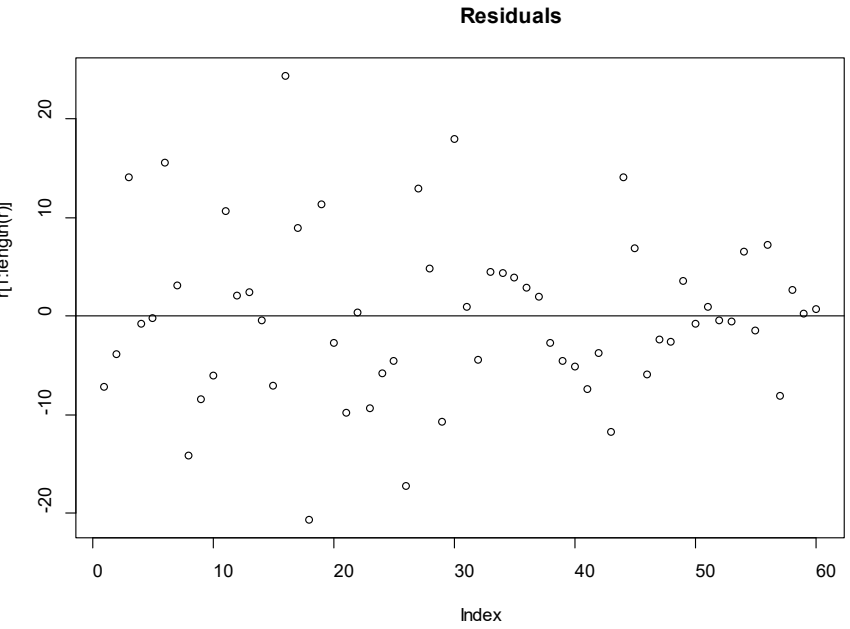
Normality	Shapiro-Wilk test (on residuals)	Linear mixed model (LMM)	`# df has two factors (X1,X2) each w/two levels (a,b) and continuous response (Y)`
			`library(lme4) # for lmer`
			`library(lmerTest)`
			`m = lmer(Y ~ X1*X2 + (1|PId), data=df) # make linear mixed model`
			`r = residuals(m) # extract residuals`
			
			`## Continue with "Common Code", above ... ##`

ANOVA Assumptions

Normality

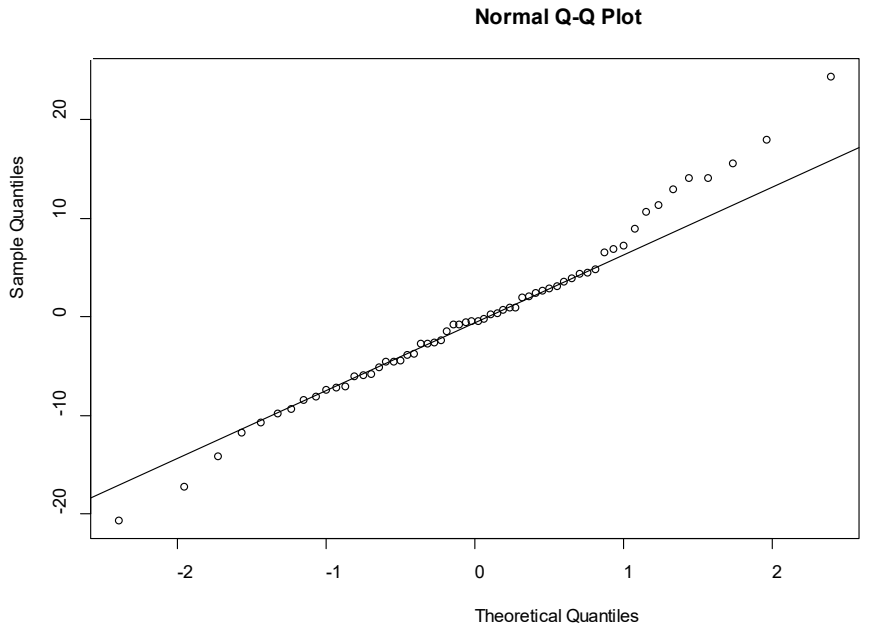
Assumption	Test Name	Context of Use	Report
Normality	Shapiro-Wilk test (on the conditional response)	*t*-test, ANOVA, LMM	"To test the normality assumption, a Shapiro-Wilk test was run on the response Y for each combination of levels of factors X1 and X2. All combinations were found to be statistically non-significant, indicating compliance with the normality assumption."
Normality	Shapiro-Wilk test (on residuals)	*t*-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, a Q-Q plot, and a residual histogram 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, a Q-Q plot, and a residual histogram all visually confirm the same (Figure 3)."

Figure 3

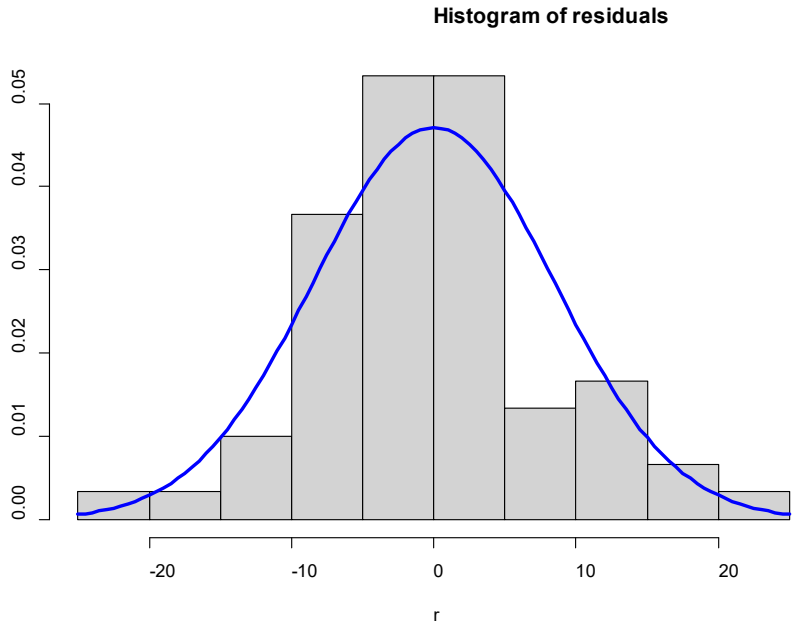


should look balanced and random

should fall near line



should look normal



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	`# 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`
			`library(effectsize)  # for cohens_d, eta_squared`
			
			`m = aov_ez(dv="Y", between="X1", within="X2", id="PId", type=3, data=df)`
			`check_homogeneity(m) # Levene's test`
			
			`# if a violation occurs (p<.05), use a Welch t-test for one factor of 2 levels...`
			`t.test(Y ~ X1, data=df, var.equal=FALSE)`
			`cohens_d(Y ~ X1, data=df, pooled_sd=FALSE)`
			
			`# ...or a Welch ANOVA for one factor of >2 levels...`
			`oneway.test(Y ~ X1, data=df, var.equal=FALSE)`
			
			`# ...or a White-adjusted ANOVA for >1 factor (with within-Ss. factors, use an LMM)`
			`m = lmer(Y ~ X1*X2 + (1|PId), data=df)`
			`Anova(m, type=3, test.statistic="F", white.adjust=TRUE)`
			`eta_squared(m, partial=TRUE)`

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."

ANOVA Assumptions

Homoscedasticity & sphericity

Assumption	Test Name	Context of Use	R Code

Sphericity	Mauchly's test of sphericity	Any ANOVA model with at least one within-subjects factor	`# 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`
			
			`m = aov_ez(dv="Y", between="X1", within="X2", id="PId", type=3, data=df)`
			
			`summary(m)$sphericity.tests # Mauchly's test of sphericity`
			`check_sphericity(m) # same`
			
			`anova(m, correction="none") # use if p≥.05, no violation of sphericity`
			`anova(m, correction="GG") # use if p<.05, sphericity violation`

ANOVA Assumptions

Homoscedasticity & sphericity

Assumption	Test Name	Context of Use	Report
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 repeated measures ANOVA with a within-subjects factor X. The test was statistically significant *(W* = 0.63, *p* = .016), indicating a sphericity violation. As a result, the Greenhouse-Geisser correction was applied to the degrees-of-freedom in the repeated measures ANOVA, which found that X had a significant effect on Y (F(1.46, 27.81) = 4.21, *p* = .036, η_G^2 = 0.13)."

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Distributions

Distributions

Distribution	Parameterization	R Distribution Fns	R Code

Normal	mean (μ): `mean`
	standard deviation (σ): `sd`
		`_norm:`
		`dnorm`
		`pnorm`
		`qnorm`
		`rnorm`
			`# 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.gof(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.gof(fb) # Shapiro-Wilk GOF`

Lognormal	mean (μ): `meanlog`
	standard deviation (σ): `sdlog`
		`_lnorm:`
		`dlnorm`
		`plnorm`
		`qlnorm`
		`rlnorm`
			`# 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.gof(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.gof(fb) # Shapiro-Wilk GOF`

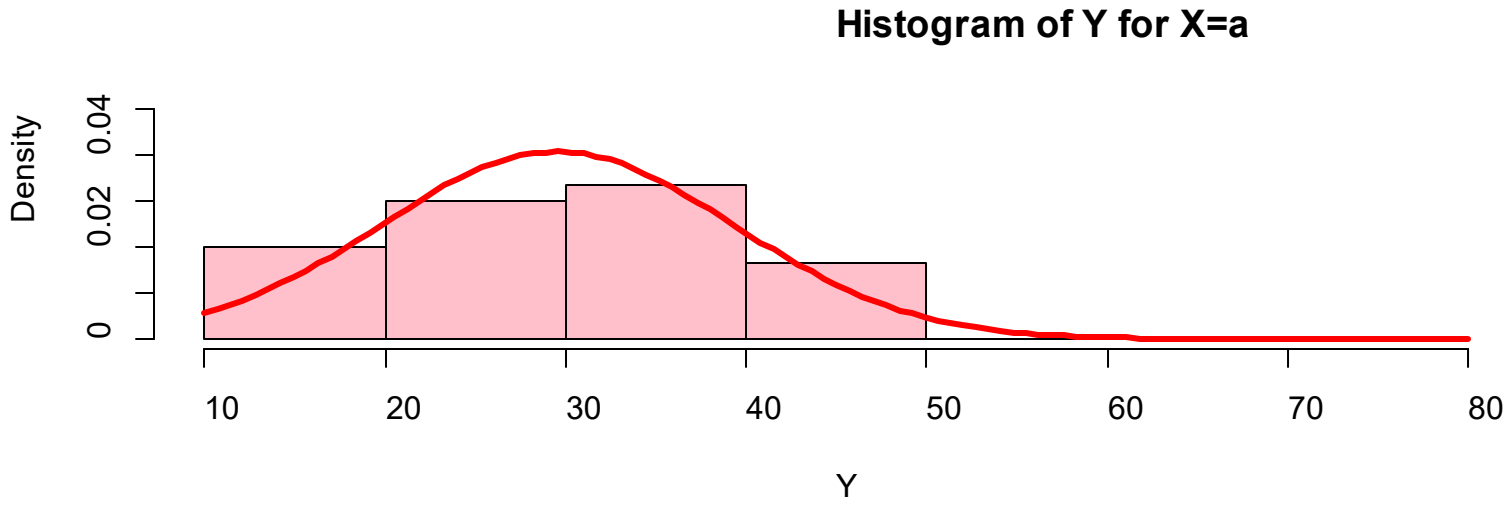
Distributions

Distribution	Parameterization	R Distribution Fns	Report

Normal	mean (μ): `mean`
	standard deviation (σ): `sd`
		`_norm:`
		`dnorm`
		`pnorm`
		`qnorm`
		`rnorm`
			"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 (μ): `meanlog`
	standard deviation (σ): `sdlog`
		`_lnorm:`
		`dlnorm`
		`plnorm`
		`qlnorm`
		`rlnorm`
			"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
Density
0
0.02
0.04
10
20
30
40
50
60
70
80
Y

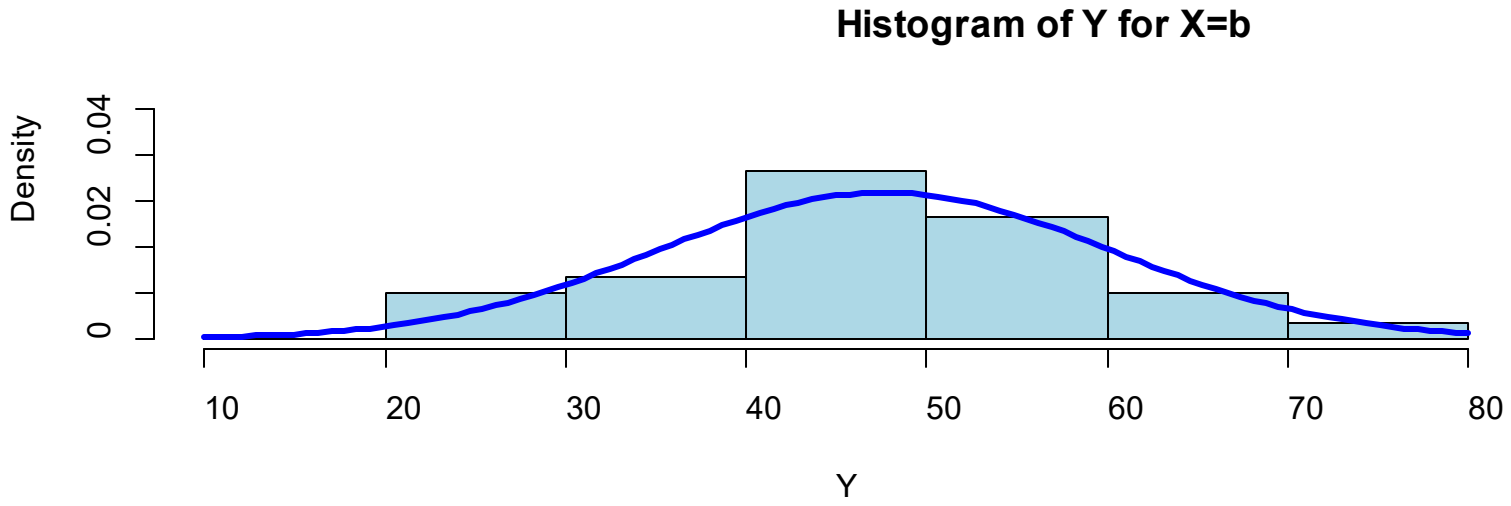
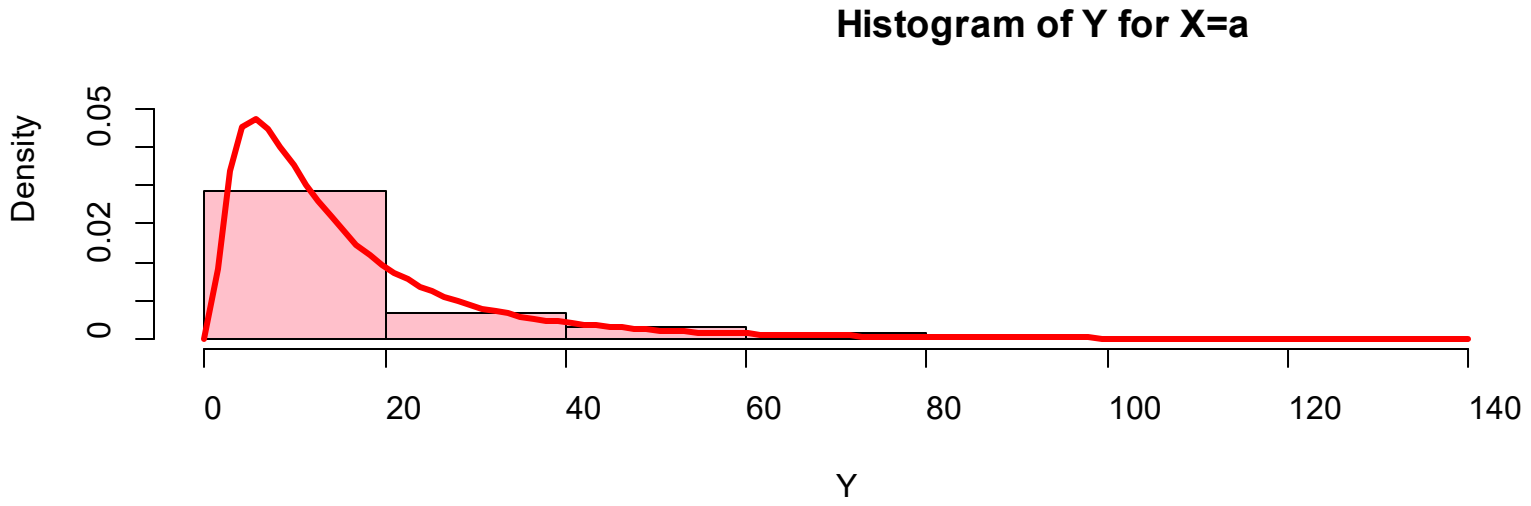
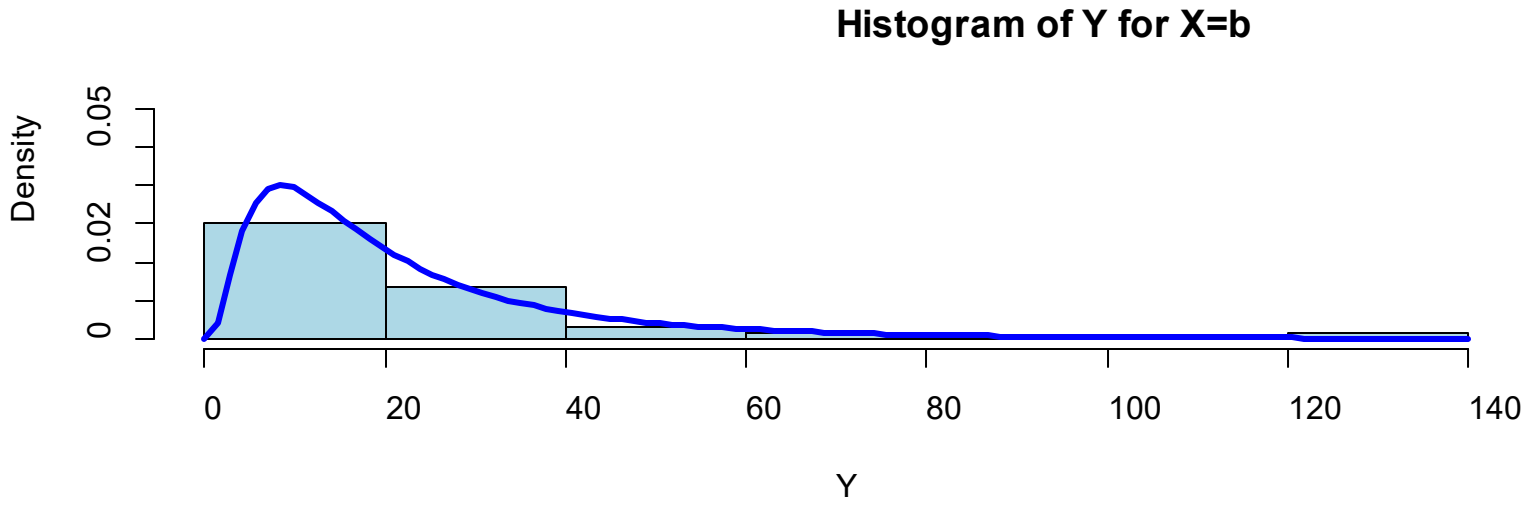

Histogram of Y for X=b
Density
0
0.02
0.04
10
20
30
40
50
60
70
80
Y

Figure 5


Histogram of Y for X=a
Density
0
0.02
0.05
0
20
40
60
80
100
120
140
Y


Histogram of Y for X=b
Density
0
0.02
0.05
0
20
40
60
80
100
120
140
Y

Distributions

Distribution	Parameterization	R Distribution Fns	R Code

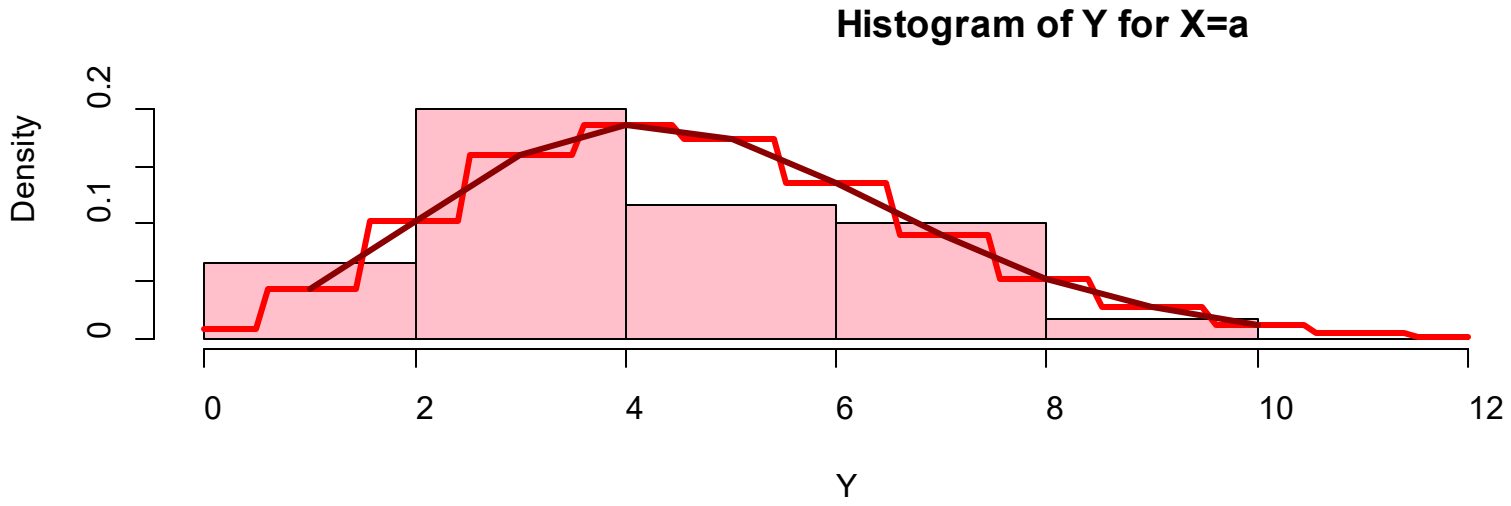
Poisson	mean, variance (λ): `lambda`	`_pois:`
		`dpois`
		`ppois`
		`qpois`
		`rpois`
			`# df has one factor (X) w/two levels (a,b) and integer count response Y`
			`library(fitdistrplus) # for fitdist, gofstat`
			
			`hist(df[df$X == "a",]$Y, main="Histogram of Y for X=a", col="pink", freq=FALSE) # 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| > 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)) > 1.15`
			`var(df[df$X == "b",]$Y) / abs(mean(df[df$X == "b",]$Y)) > 1.15`

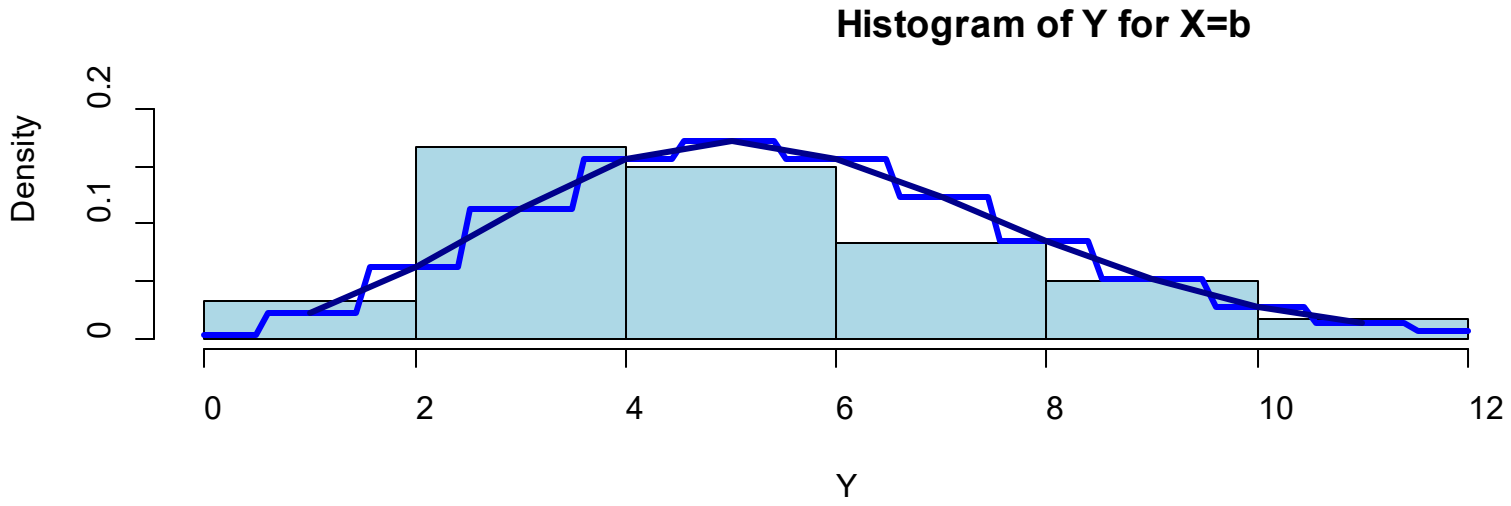
Distributions

Distribution	Parameterization	R Distribution Fns	Report

Poisson	mean, variance (λ): `lambda`	`_pois:`
		`dpois`
		`ppois`
		`qpois`
		`rpois`
			"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 ($\chi^2(4, N=30) = 0.56$, $p = .967$), as was the test for level 'b' ($\chi^2(4, N=30) = 3.89$, $p = .422$), indicating no detectable departure from a Poisson distribution for either level of X."

Figure 6


Histogram of Y for X=a
Density
0
0.1
0.2
0
2
4
6
8
10
12
Y


Histogram of Y for X=b
Density
0
0.1
0.2
0
2
4
6
8
10
12
Y

Distributions

Distribution	Parameterization	R Distribution Fns	R Code

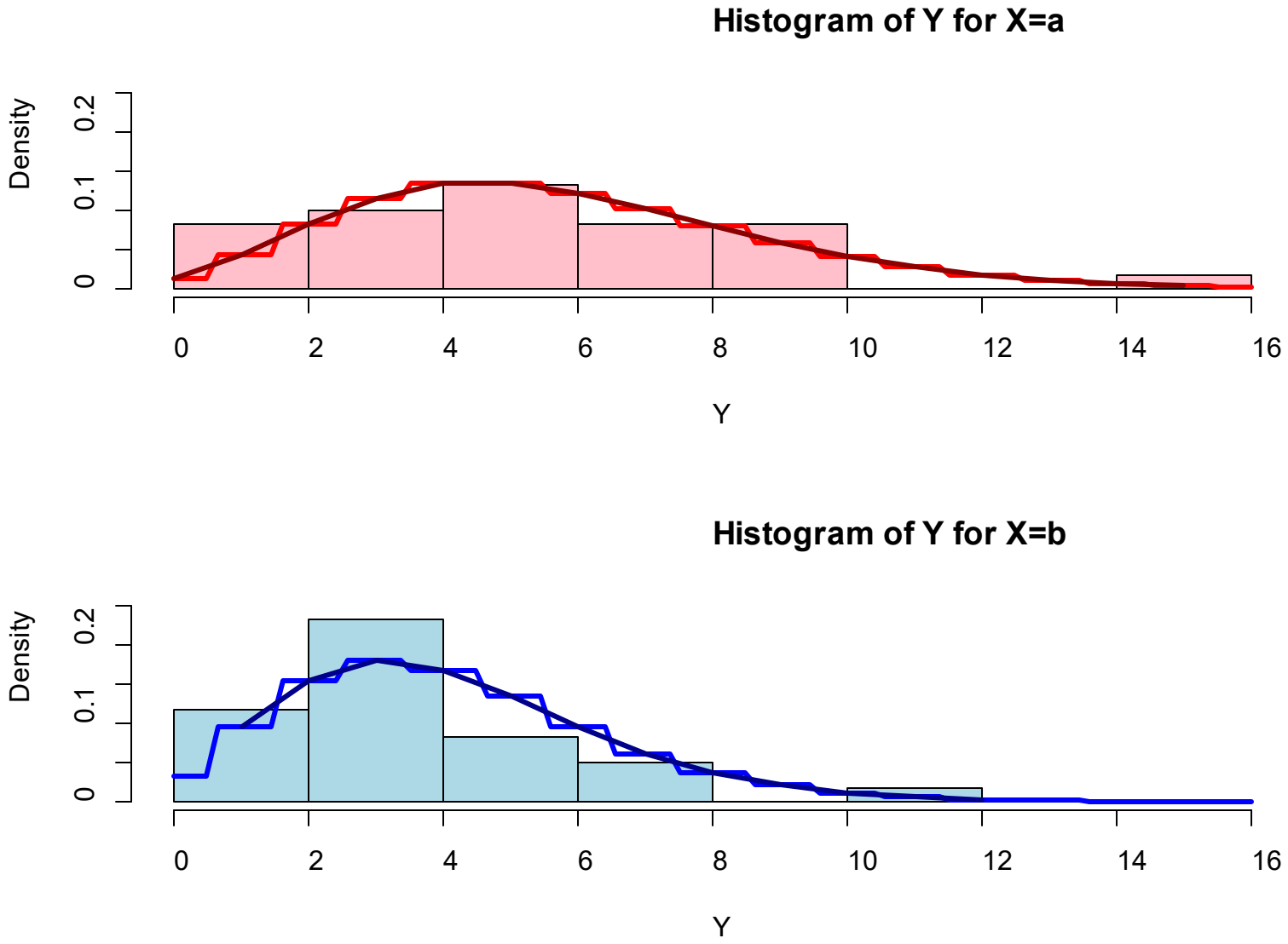
Negative Binomial	dispersion (θ): `size`
	mean (μ): `mu`
		`_nbinom:`
		`dnbinom`
		`pnbinom`
		`qnbinom`
		`rnbinom`
			`# df has one factor (X) w/two levels (a,b) and integer count response Y`
			`library(fitdistrplus) # for fitdist, gofstat`
			`hist(df[df$X == "a",]$Y, main="Histogram of Y for X=a", 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`

Distributions

Distribution	Parameterization	R Distribution Fns	Report

Negative Binomial	dispersion (θ): `size`
	mean (μ): `mu`
		`_nbinom:`
		`dnbinom`
		`pnbinom`
		`qnbinom`
		`rnbinom`
			"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 ($\chi^2(4, N=30) = 0.88, p = .927$), as was the test for level 'b' ($\chi^2(2, N=30) = 0.81, p = .666$), indicating no detectable departure from a negative binomial distribution for either level of X."

Figure 7


Histogram of Y for X=a
Density
0
0.1
0.2
0
2
4
6
8
10
12
14
16
Y
Histogram of Y for X=b
Density
0
0.1
0.2
0
2
4
6
8
10
12
14
16
Y

Distribution Tests

Distribution	Parameterization	R Distribution Fns	R Code

Exponential	rate (λ): `rate`	`_exp:`
		`dexp`
		`pexp`
		`qexp`
		`rexp`
			`# 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.gof(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.gof(fb) # Shapiro-Wilk-Chen-Balakrishnan GOF`

Gamma	shape (α): `shape`
	scale (β): `scale`
		`_gamma:`
		`dgamma`
		`pgamma`
		`qgamma`
		`rgamma`
			`# 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.gof(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.gof(fb) # Shapiro-Wilk-Chen-Balakrishnan GOF`

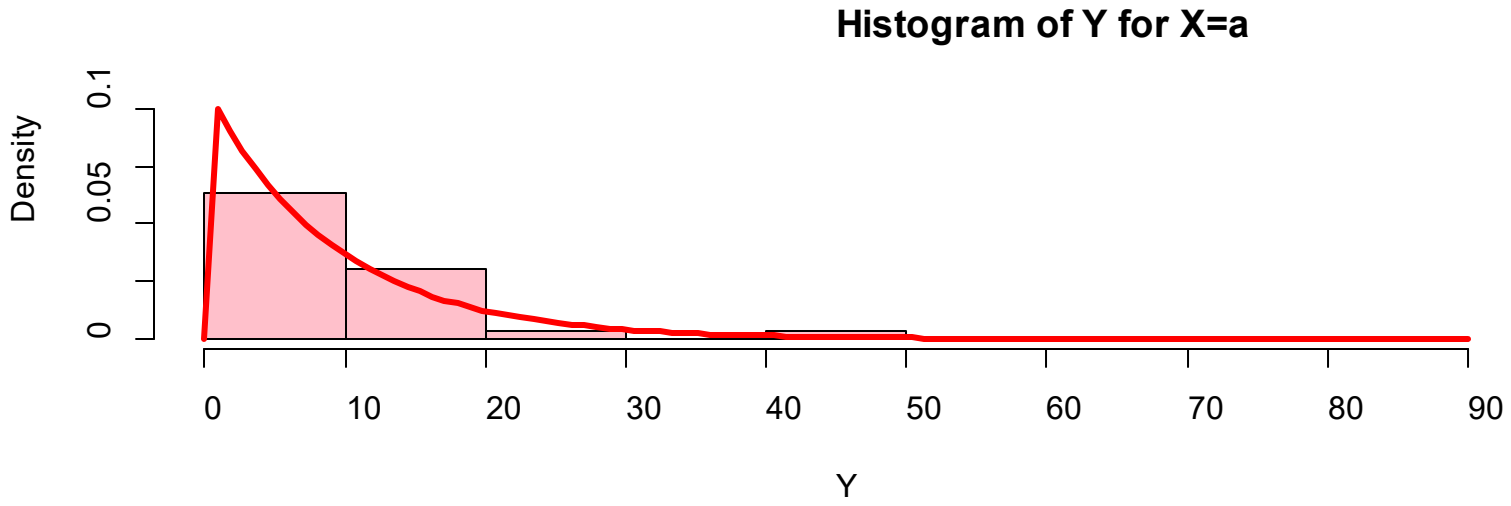
Distribution Tests

Distribution	Parameterization	R Distribution Fns	Report

Exponential	rate (λ): `rate`	`_exp:`
		`dexp`
		`pexp`
		`qexp`
		`rexp`
			"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 (α): `shape`
	scale (β): `scale`
		`_gamma:`
		`dgamma`
		`pgamma`
		`qgamma`
		`rgamma`
			"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
Density
0
0.05
0.1
0
10
20
30
40
50
60
70
80
90
Y

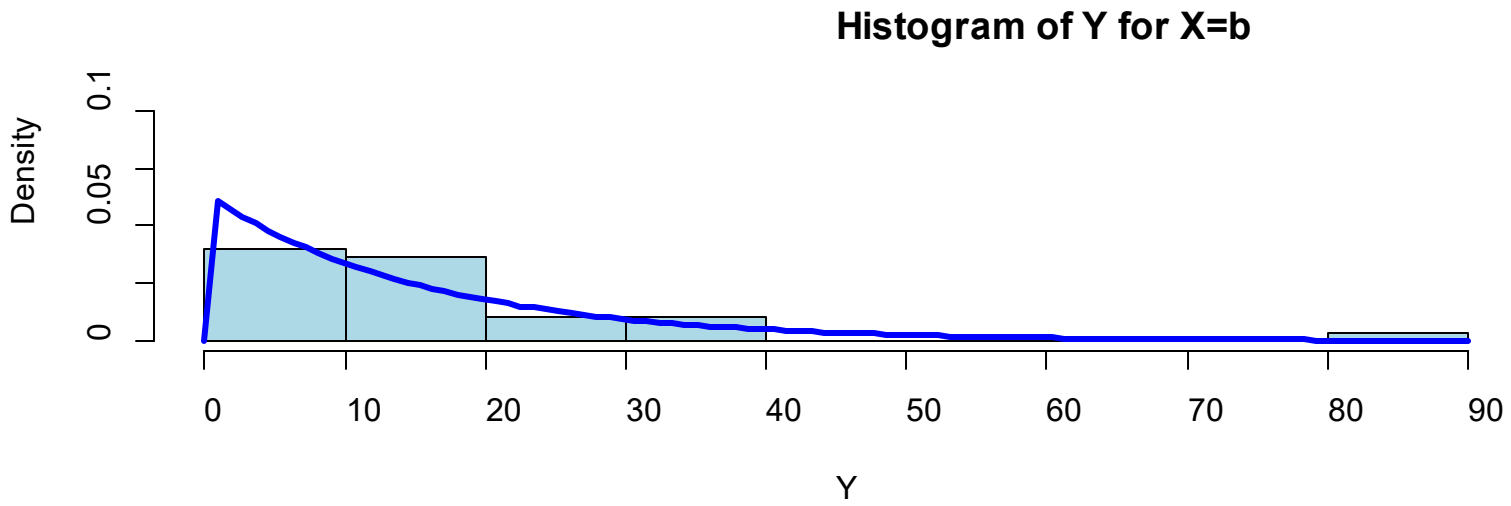
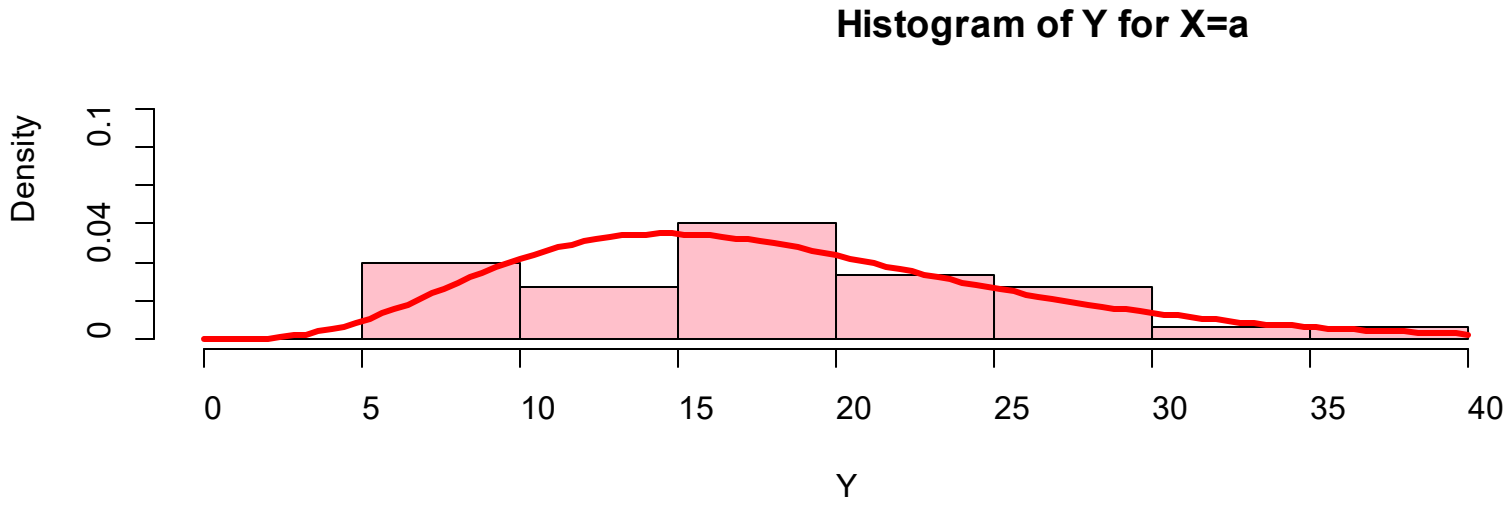
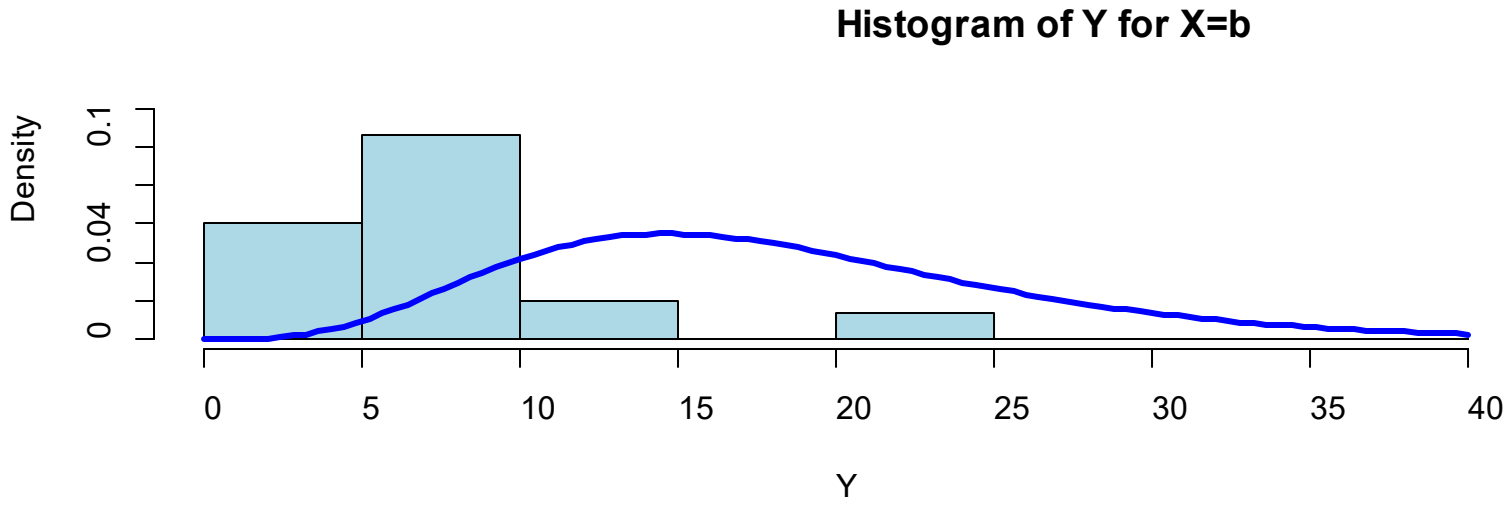

Histogram of Y for X=b
Density
0
0.05
0.1
0
10
20
30
40
50
60
70
80
90
Y

Figure 9


Histogram of Y for X=a
Density
0
0.04
0.1
0
5
10
15
20
25
30
35
40
Y


Histogram of Y for X=b
Density
0
0.04
0.1
0
5
10
15
20
25
30
35
40
Y

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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 *t*-test	`# df has one between-Ss. factor (X) w/levels (a,b) and continuous response (Y)`
				`library(car) # for leveneTest`
				`library(effectsize) # for cohens_d`
				`df$PId = factor(df$PId) # participant is nominal (unused)`
				`df$X = factor(df$X) # X is a 2-level factor`
				`contrasts(df$X) <- "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`
				`cohens_d(Y ~ X, data=df, pooled_sd=TRUE)`
				
				`t.test(Y ~ X, data=df, var.equal=FALSE) # if p<.05, Welch t-test`
				`cohens_d(Y ~ X, data=df, pooled_sd=FALSE)`

Parametric Tests

One between-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	Report
1	2	Between	Independent-samples *t*-test	"The mean of 'a' was 29.29 (*SD* = 14.72) and of 'b' was 47.68 (*SD* = 12.53). This difference was statistically significant according to an independent-samples *t*-test ($t(58) = -5.21$, $p < .0001$, $d = -1.35$)."

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

Parametric Tests

One between-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	R Code

1	≥2	Between	One-way ANOVA	`# 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`
				`library(effectsize) # for eta_squared`
				`df$PId = factor(df$PId) # participant is nominal`
				`df$X = factor(df$X)  # X is a 3-level factor`
				`contrasts(df$X) <- "contr.sum"`
				
				`m = aov_ez(dv="Y", between="X", id="PId", type=3, data=df) # fit model`
				`leveneTest(Y ~ X, data=df, center=mean) # Levene's test`
				`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$lm, type=3, white.adjust=TRUE)  # White-adjusted ANOVA`
				`eta_squared(m$lm, generalized=TRUE)`

Parametric Tests

One between-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	Report
1	≥2	Between	One-way ANOVA	"The mean of 'a' was 32.12 (*SD* = 14.59), of 'b' was 44.23 (*SD* = 12.45), and of 'c' was 41.60 (*SD* = 14.36). These differences were statistically significant according to a one-way ANOVA (F(2, 57) = 4.24, p = .019, η_G^2 = 0.13)."

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	`# df has one within-Ss. factor (X) w/levels (a,b) and continuous response (Y)`
				`library(reshape2)   # for dcast`
				`library(effectsize) # for cohens_d`
				`df$PId = factor(df$PId) # participant is nominal`
				`df$X = factor(df$X) # X is a 2-level factor`
				`contrasts(df$X) <- "contr.sum"`
				
				`df2 <- dcast(df, PId ~ 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`
				`cohens_d(df2$a, df2$b, paired=TRUE)`

1	≥2	Within	One-way repeated measures ANOVA	`# 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$PId = factor(df$PId) # participant is nominal`
				`df$X = factor(df$X) # X is a 3-level factor`
				`contrasts(df$X) <- "contr.sum"`
				
				`m = aov_ez(dv="Y", within="X", id="PId", type=3, data=df) # fit model`
				`summary(m)$sphericity.tests # Mauchly's test of sphericity`
				`check_sphericity(m)         # same`
				
				`anova(m, correction="none") # if p≥.05, no violation of sphericity`
				`anova(m, correction="GG")   # if p<.05, violation of sphericity`

Parametric Tests

One within-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	Report
1	2	Within	Paired-samples *t*-test	"The mean of 'a' was 29.29 (*SD* = 14.72) and of 'b' was 47.68 (*SD* = 12.53). This difference was statistically significant according to a paired-samples *t*-test ($t(29) = -4.85$, $p < .0001$, $d = -0.88$)."
1	≥2	Within	One-way repeated measures ANOVA	"The mean of 'a' was 32.12 (*SD* = 14.59), of 'b' was 44.23 (*SD* = 12.45), and of 'c' was 41.60 (*SD* = 14.36). These differences were statistically significant ($F(2, 38) = 4.06$, $p = .025$, $\eta_G^2 = 0.13$)."

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	`# 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`
				`library(effectsize) # for eta_squared`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = aov_ez(dv="Y", between=c("X1","X2"), id="PId", type=3, data=df) # fit model`
				`leveneTest(Y ~ X1*X2, data=df, center=mean) # Levene's test`
				`check_homogeneity(m) # same`
				
				`anova(m) # use if p≥.05, no violation of homogeneity, else use...`
				
				`Anova(m$lm, type=3, white.adjust=TRUE) # White-adjusted ANOVA`
				`eta_squared(m$lm, generalized=TRUE)`

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 ±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 ($F(1, 56) = 20.51$, $p < .0001$, $\eta_G^2 = 0.28$), no significant effect of X2 ($F(1, 56) = 0.09$, $p = .766$, $\eta_G^2 < 0.01$), and a significant X1×X2 interaction ($F(1, 56) = 7.15$, $p = .010$, $\eta_G^2 = 0.12$)."

Parametric Tests

Multiple between-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	R Code

≥2	≥2	Between	Linear model (LM)	`# 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`
				`library(effectsize)  # for eta_squared`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = lm(Y ~ X1*X2, data=df)  # fit model`
				`m = aov(Y ~ X1*X2, data=df) # equivalent`
				`leveneTest(Y ~ X1*X2, data=df, center=mean) # Levene's test`
				`check_homogeneity(m) # similar`
				
				`anova(m) # use if p≥.05, no violation of homogeneity, else use...`
				`eta_squared(m, generalized=TRUE)`
				
				`Anova(m, type=3, white.adjust=TRUE) # White-adjusted ANOVA`
				`eta_squared(m, generalized=TRUE)`

Parametric Tests

Multiple between-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	Report
≥2	≥2	Between	Linear model (LM)	"Figure 10 shows an interaction plot with ±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 ($F(1, 56) = 20.51$, $p < .0001$, $\eta_G^2 = 0.28$), no significant effect of X2 ($F(1, 56) = 0.09$, $p = .766$, $\eta_G^2 < 0.01$), and a significant X1×X2 interaction ($F(1, 56) = 7.15$, $p = .010$, $\eta_G^2 = 0.12$)."

Parametric Tests

Multiple within-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	R Code

≥2	≥2	Within	Factorial repeated measures ANOVA	`# 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$PId = factor(df$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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = aov_ez(dv="Y", within=c("X1","X2"), id="PId", type=3, data=df) # fit model`
				`summary(m)$sphericity.tests # Mauchly's test of sphericity`
				`check_sphericity(m) # same`
				
				`anova(m, correction="none") # use if p≥.05, no violation of sphericity`
				`anova(m, correction="GG") # Greenhouse-Geisser correction`

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 ±1 standard deviation error bars for X1 and X2. A factorial repeated measures ANOVA indicated a significant effect on Y of X1 ($F(1, 14) = 29.58$, $p < .0001$, $\eta_G^2 = 0.28$), no significant effect of X2 ($F(1, 14) = 0.08$, $p = .785$, $\eta_G^2 < 0.01$), and a significant X1×X2 interaction ($F(1, 14) = 5.11$, $p = .040$, $\eta_G^2 = 0.12$)."

Parametric Tests

Multiple within-Ss. factors

Factors	Levels	Between or Within Subjects	Test Name	R Code

≥2	≥2	Within	Linear mixed model (LMM)*	`# 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`
				`library(effectsize) # for eta_squared`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = lmer(Y ~ X1*X2 + (1|PId), data=df) # sphericity is N/A for LMMs`
				`Anova(m, type=3, test.statistic="F")`
				`eta_squared(m, partial=TRUE)`

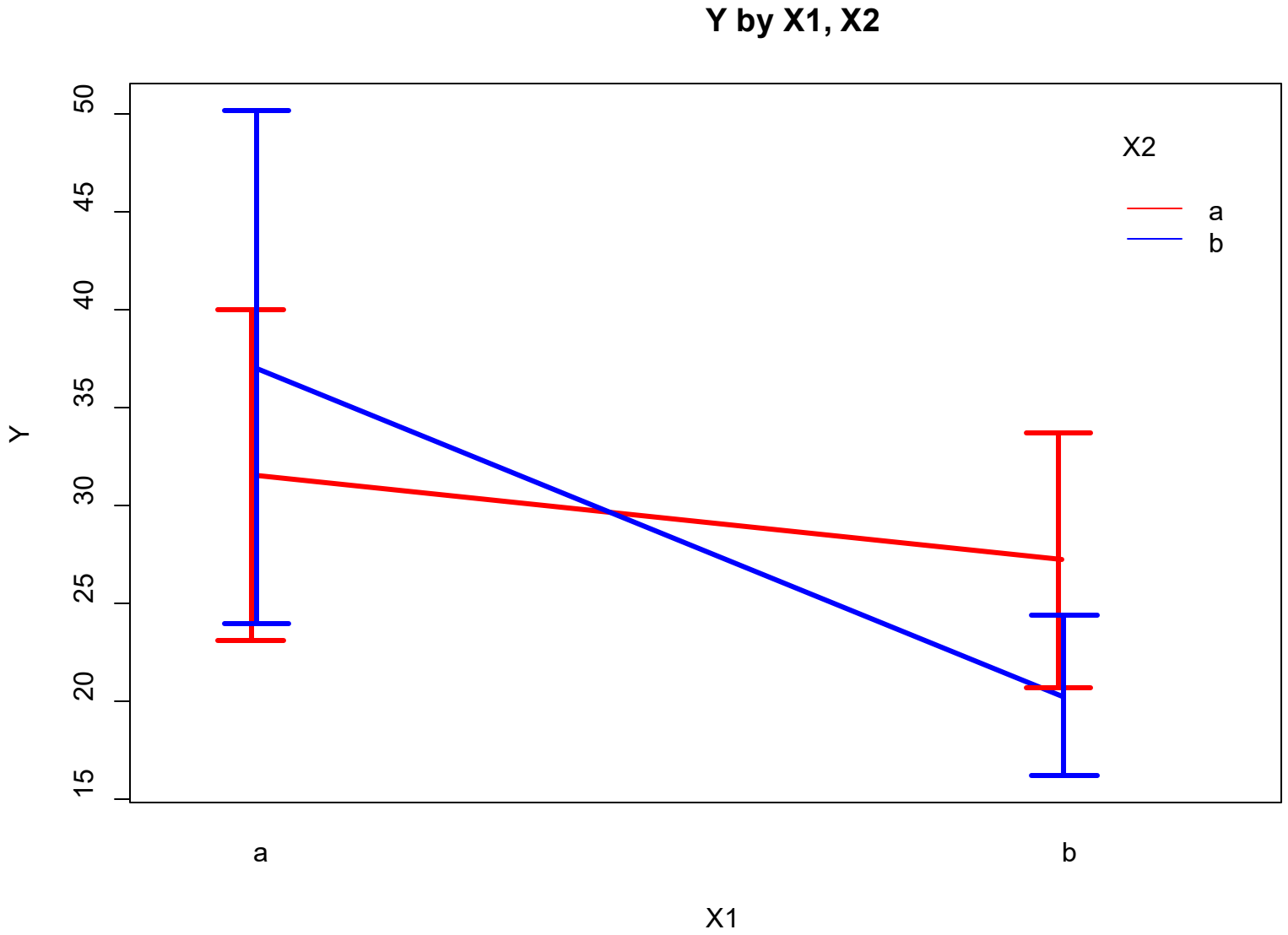
***NB.** The LMM sample code uses a random intercept for participant (*PId*). There are also random slope models, which are used when the response changes at different rates for each *PId* over a repeated factor. A 2-minute random slope example of county population growth over time can be seen here (https://www.youtube.com/watch?v=YDe6F7CXjWw). 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	Linear mixed model (LMM)	"Figure 10 shows an interaction plot with ±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 ($F(1, 42) = 21.98$, $p < .0001$, $\eta_p^2 = 0.28$), no significant effect of X2 ($F(1, 42) = 0.10$, $p = .758$, $\eta_p^2 < 0.01$), and a significant X1×X2 interaction ($F(1, 42) = 7.66$, $p = .008$, $\eta_p^2 = 0.28$)."

Figure 10



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 *t*-test	Btwn	`# df has one between-Ss. factor (X) w/levels (a,b,c) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X, adjust="holm") # m is from afex::aov_ez`
					`emm$contrasts`
					`eff_size(emm$emmeans, sigma=sigma(m$lm), edf=df.residual(m$lm))`

1	>2	One-way repeated measures ANOVA	Paired samples *t*-test	Within	`# df has one within-Ss. factor (X) w/levels (a,b,c) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X, adjust="holm") # m is from afex::aov_ez`
					`emm$contrasts`
					`sig = sqrt(anova(m, correction="none")["X","MSE"]) # pooled residual SD`
					`eff_size(emm$emmeans, sigma=sig, edf=df.residual(m$lm))`

Parametric Tests

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Test	Test Name	B/W	Report
1	≥2	One-way ANOVA	Independent samples *t*-test	Btwn	"Three *post hoc* pairwise comparisons using independent-samples *t*-tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' was significantly different ($t(57) = -2.77$, $p = .023$, $d = -0.88$), but 'a' *vs.* 'c' and 'b' *vs.* 'c' were not."
1	≥2	One-way repeated measures ANOVA	Paired samples *t*-test	Within	"Three *post hoc* pairwise comparisons using paired-samples *t*-tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' was significantly different ($t(19) = -2.70$, $p = .042$, $d = -0.86$), 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	Independent samples *t*-test	Btwn	`# df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from afex::aov_ez`
					`emm$contrasts`
					`eff_size(emm$emmeans, sigma=sigma(m$lm), edf=df.residual(m$lm))`

≥2	≥2	Linear model (LM)	Independent samples *t*-test	Btwn	`# df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from lm or aov`
					`emm$contrasts`
					`eff_size(emm$emmeans, sigma=sigma(m), edf=df.residual(m))`

≥2	≥2	Factorial repeated measures ANOVA	Paired samples *t*-test	Within	`# df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from afex::aov_ez`
					`emm$contrasts`
					`sig = sqrt(anova(m, correction="none")["X1:X2","MSE"]) # pooled residual SD`
					`eff_size(emm$emmeans, sigma=sig, edf=df.residual(m$lm))`

≥2	≥2	Linear mixed model (LMM)	Paired samples *t*-test	Within	`# df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from lme4::lmer`
					`emm$contrasts`
					`eff_size(emm$emmeans, sigma=sigma(m), edf=df.residual(m))`

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 *t*-test	Btwn	"Six *post hoc* pairwise comparisons using independent-samples *t*-tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {b,b} ($t(56) = 3.53$, $p = .004$, $d = 1.29$), {b,a} *vs.* {a,b} ($t(56) = -3.10$, $p = .012$, $d = -1.13$), and {a,b} *vs.* {b,b} ($t(56) = 5.27$, $p < .0001$, $d = 1.93$) were significantly different. The other three pairwise comparisons were not detectably different."
≥2	≥2	Factorial repeated measures ANOVA	Paired samples *t*-test	Within	"Six *post hoc* pairwise comparisons using paired-samples *t*-tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {b,b} ($t(14) = 4.82$, $p = .002$, $d = 1.05$), {b,a} *vs.* {b,b} ($t(14) = 3.27$, $p = .023$, $d = 0.65$), {a,b} *vs.* {b,b} ($t(14) = 4.25$, $p = .004$, $d = 1.57$) were significantly different. The other three pairwise comparisons were not detectably different."
≥2	≥2	Linear mixed model (LMM)	Paired samples *t*-test	Within	"Six *post hoc* pairwise comparisons using paired-samples *t*-tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {b,b} ($t(42) = 3.53$, $p = .005$, $d = 1.29$), {b,a} *vs.* {a,b} ($t(42) = -3.10$, $p = .014$, $d = -1.13$), and {a,b} *vs.* {b,b} ($t(42) = 5.27$, $p < .0001$, $d = 1.93$) 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.	`# 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, eff_size`
			`df$PId = factor(df$PId)  # participant is nominal`
			`df$X = factor(df$X)  # X is a 3-level factor`
			`contrasts(df$X) <- "contr.sum"`
			`m = lme(Y ~ X, random=~1|PId, data=df)  # ID`
			`getVarCov(m, type="marginal")  # get VCV matrix`
			`anova(m, type="marginal")  # for F-test`
			`eta_squared(m, partial=TRUE)`
			`emm = emmeans(m, pairwise ~ X, adjust="holm", mode="containment")  # post hoc tests`
			`emm$contrasts`
			`eff_size(emm$emmeans, sigma=sigma(m), edf=m$fixDF$terms[["X"]])  # Cohen's d effect sizes`

DIAG	Diagonal	All variances can differ; otherwise, like ID.	`# See R Code for ID. Only the blue model-building line changes to:` `m = lme(Y ~ X, random=~1|PId, data=df, weights=varIdent(form=~1|X))  # DIAG`
CS	Compound symmetry	All variances are equal, and all covariances are equal.	`# See R Code for ID. Only the blue model-building line changes to:` `m = lme(Y ~ X, random=~1|PId, data=df, correlation=corCompSymm(form=~1|PId))  # CS`

CSH	Heterogeneous compound symmetry	All variances can differ; otherwise, like CS.	`# See R Code for ID. Only the blue model-building line changes to:`
			`m = lme(Y ~ X, random=~1|PId, data=df, correlation=corCompSymm(form=~1|PId),`
			`  weights=varIdent(form=~1|X))  # CSH`

NB. The `lme4::lmer` function does not allow directly specifying 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/31.0.0?topic=mixed-covariance-structure-list-command. For their matrix formulations, see https://www.ibm.com/docs/en/spss-statistics/31.0.0?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.	`# See R Code for ID. Only the blue model-building line changes to:` `m = lme(Y ~ X, random=~1|PId, data=df, correlation=corAR1(form=~1|PId)) # AR1`

ARH1	Heterogeneous first-order autoregressive	All variances can differ; otherwise, like AR1.	`# See R Code for ID. Only the blue model-building line changes to:`
			`m = lme(Y ~ X, random=~1|PId, data=df, correlation=corAR1(form=~1|PId),`
			`weights=varIdent(form=~1|X)) # ARH1`

ARMA11	Autoregressive moving average	All variances are equal, and all covariances decrease with distance, influenced by a moving average.	`# See R Code for ID. Only the blue model-building line changes to:`
			`m = lme(Y ~ X, random=~1|PId, data=df, correlation=corARMA(form=~1|PId, p=1, q=1)) # ARMA11`
			`# Note that (p,q)=(1,0) is AR1. The 'q' parameter determines the moving average.`

TP	Toeplitz	All variances are equal, and covariances are equal across adjacent pairs, equal again across skip-adjacent pairs, and so on.	`# See R Code for ID. Only the blue model-building line changes to:` `m = lme(Y ~ X, random=~1|PId, data=df, correlation=corARMA(form=~1|PId, p=2, q=0)) # TP`

TPH	Heterogeneous Toeplitz	All variances can differ; otherwise, like TP.	`# See R Code for ID. Only the blue model-building line changes to:`
			`m = lme(Y ~ X, random=~1|PId, data=df, correlation=corARMA(form=~1|PId, p=2, q=0),`
			`weights=varIdent(form=~1|X)) # TPH`

UN	Unstructured	All variances and covariances can differ.	`# See R Code for ID. Only the blue model-building line changes to:`
			`m = lme(Y ~ X, random=~1|PId, data=df, correlation=corSymm(form=~1|PId),`
			`weights=varIdent(form=~1|X)) # UN`

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	`# 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) <- "contr.sum"`
				`median_test(Y ~ X, data=df)`

1	2	Between	Mann-Whitney *U* test	`# 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) <- "contr.sum"`
				`wilcox_test(Y ~ X, data=df, distribution="exact")`

1	2	Within	Sign test	`# 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) <- "contr.sum"`
				`sign_test(Y ~ X | PId, data=df)`

1	2	Within	Wilcoxon signed-rank test	`# 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) <- "contr.sum"`
				`wilcoxsign_test(Y ~ X | PId, data=df, distribution="exact")`

NB. The Mann-Whitney *U* test is also known as the Wilcoxon-Mann-Whitney test and the Wilcoxon rank-sum test, not 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 ≥2 levels

Factors	Levels	Between or Within Subjects	Test Name	R Code

1	≥2	Between	Kruskal-Wallis test	`# 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) <- "contr.sum"`
				`kruskal_test(Y ~ X, data=df, distribution="asymptotic")`

1	≥2	Within	Friedman test	`# 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")`

Nonparametric Tests

One factor with ≥2 levels

Factors	Levels	Between or Within Subjects	Test Name	Report
1	≥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	≥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)	`# 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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				`m = art(Y ~ X1*X2, data=df)`
				`anova(m)`

≥2	≥2	Within	Aligned Rank Transform (ART)*	`# 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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				`m = art(Y ~ X1*X2 + (1|PId), data=df) # PId is a random factor`
				`anova(m)`

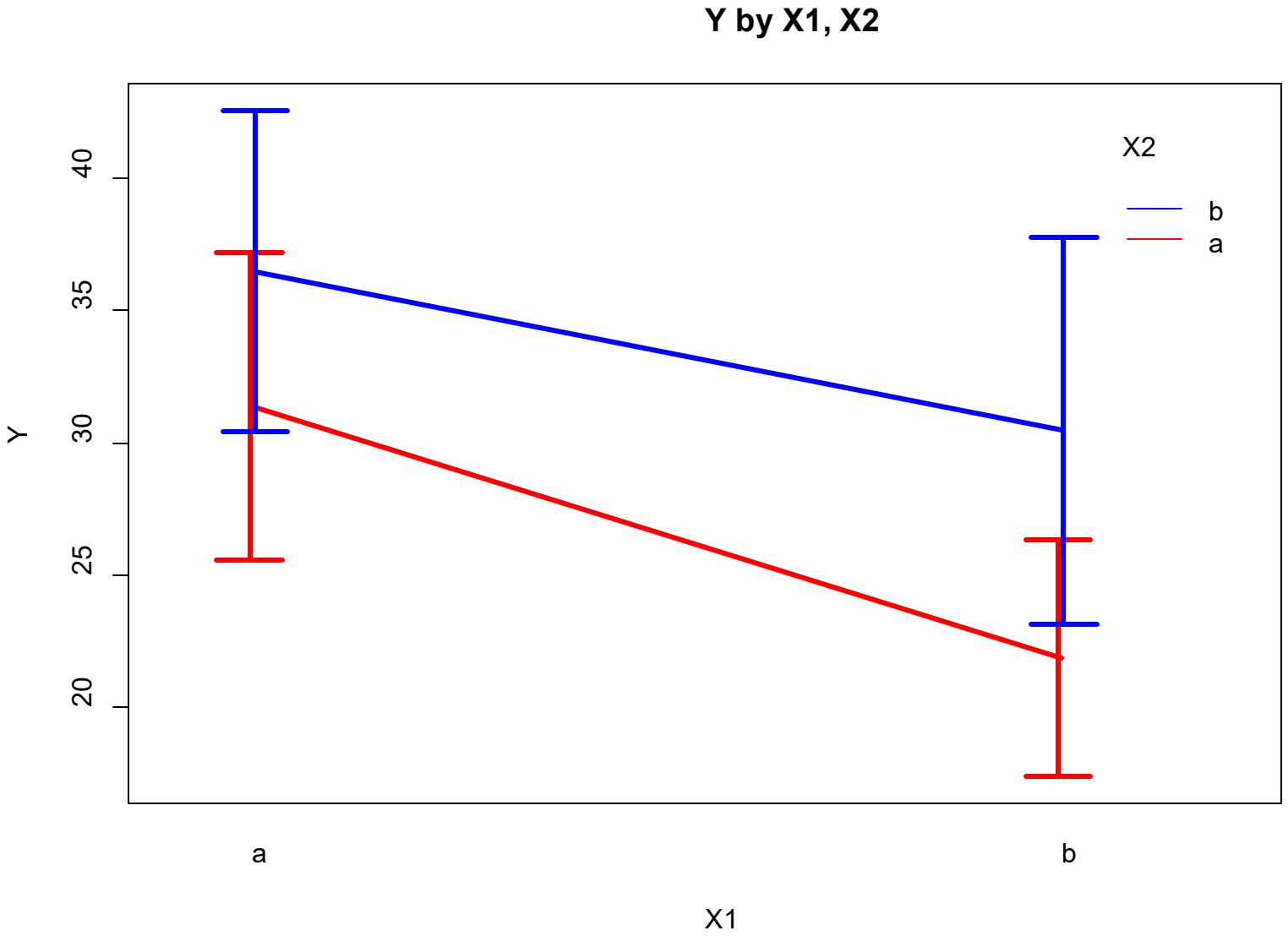
***NB.** The within-subjects ART sample code uses a random intercept for participant *(PId)*. There are also random slope models, which are used when the response changes at different rates for each participant over a repeated factor. A 2-minute random slope example of county population growth over time 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 ±1 *SD* 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 ±1 *SD* 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	≥2	Kruskal-Wallis test	Mann-Whitney *U* test	Btwn	`# 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-score`
					`wilcoxonZ(df[df$X == "a",]$Y, df[df$X == "c",]$Y) # Z-score`
					`wilcoxonZ(df[df$X == "b",]$Y, df[df$X == "c",]$Y) # Z-score`

1	≥2	Friedman test	Wilcoxon signed-rank test	Within	`# 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 <- 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-score`
					`wilcoxonZ(df2$a, df2$c, paired=TRUE) # Z-score`
					`wilcoxonZ(df2$b, df2$c, paired=TRUE) # Z-score`

Nonparametric Tests

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Test	Test Name	B/W	Report
1	≥2	Kruskal-Wallis test	Mann-Whitney *U* test	Btwn	"Three *post hoc* Mann-Whitney *U* 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	≥2	Friedman test	Wilcoxon signed-rank test	Within	"Three *post hoc* 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	`# df has two factors (X1,X2) each w/levels (a,b) and continuous response (Y)`
					`library(plyr)  # for mutate`
					`library(dplyr) # for %>%`
					`art.con(m, ~ X1*X2, adjust="holm") %>%  # run ART-C for X1×X2`
					`  summary() %>%  # (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("***", "**", "*", ".", " ")))`

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 *post hoc* pairwise comparisons conducted with the ART-C procedure (Elkin *et al*. 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 *post hoc* pairwise comparisons conducted with the ART-C procedure (Elkin *et al*. 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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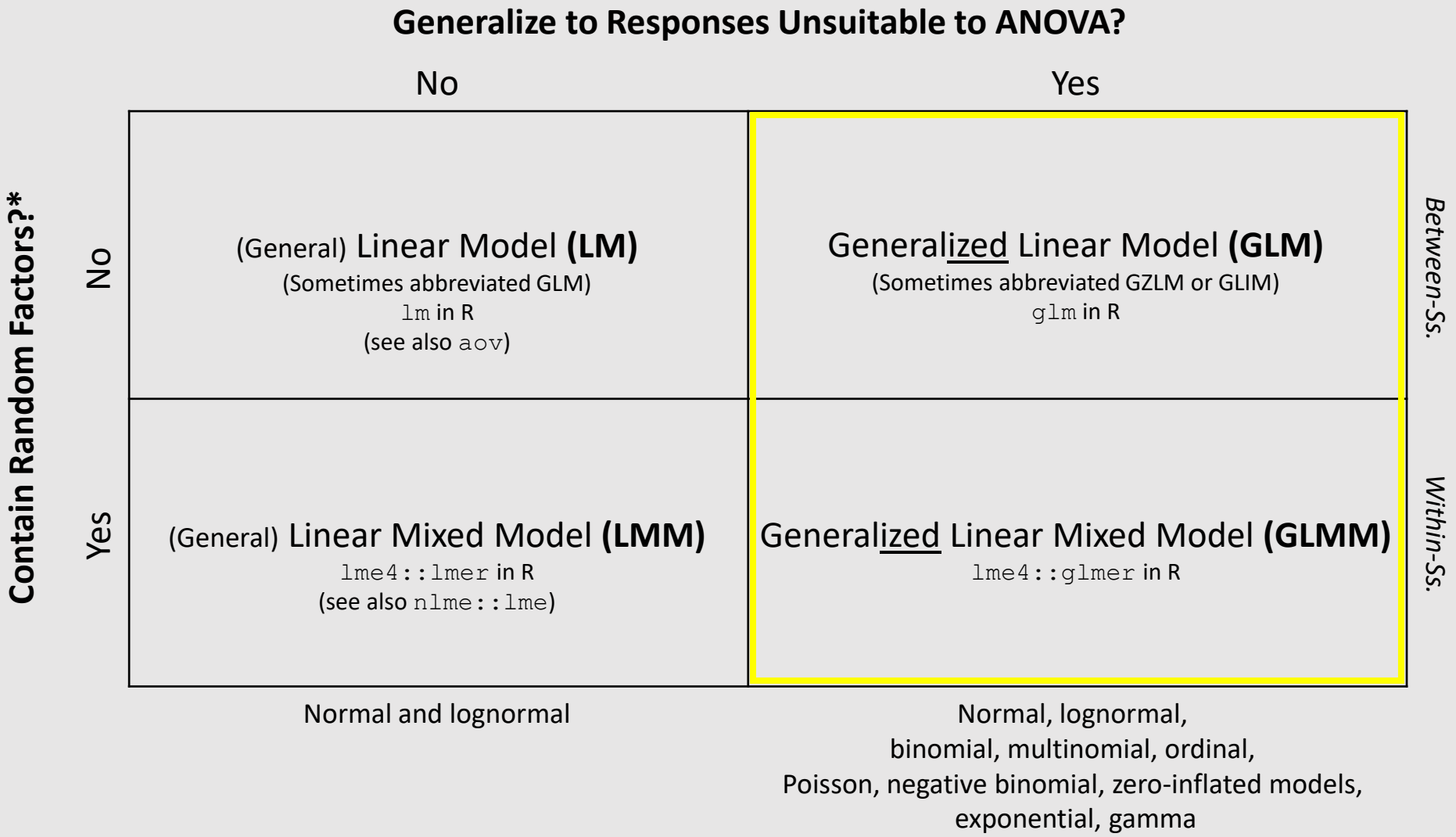
Generalized Linear (Mixed) Models

Terminology



***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
Gaussian	`lm()`[1] `glm() family=gaussian`	`lme4::lmer()`[2] `lme4::glmer() family=gaussian`
Binomial	`glm() family=binomial`	`lme4::glmer() family=binomial`

Multinomial[3]	`nnet::multinom()` or
	`multpois::glm.mp()`
	`multpois::Anova.mp()`
		`multpois::glmer.mp()`
		`multpois::Anova.mp()`

Ordinal	`MASS::polr()`	`ordinal::clmm()` `RVAideMemoire::Anova.clmm()`
Poisson	`glm() family=poisson`	`lme4::glmer() family=poisson`
Quasi-Poisson[4]	`glm() family=quasipoisson`	N/A
Zero-inflated Poisson (ZIP)[5]	`glmmTMB::glmmTMB() family=poisson ziformula=~1`	`glmmTMB::glmmTMB() family=poisson ziformula=~1 REML=TRUE`
Negative binomial	`MASS::glm.nb()`	`lme4::glmer.nb()`
Zero-inflated negative binomial (ZINB)[5]	`glmmTMB::glmmTMB() family=nbinom2 ziformula=~1`	`glmmTMB::glmmTMB() family=nbinom2 ziformula=~1 REML=TRUE`
Exponential	`glm() family=Gamma(link="log")`	`lme4::glmer() family=Gamma(link="log")`
Gamma[6]	`glm() family=Gamma`	`lme4::glmer() family=Gamma`

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 overdisperson, 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	*Linear regression:* Normally distributed responses; equivalent to the linear model (LM) or linear mixed model (LMM)	`library(car) # for Anova`
			`library(effectsize) # for eta_squared`
			`library(performance) # for check_*`
			`df$PId = factor(df$PId)`
			`df$X1 = factor(df$X1)`
			`df$X2 = factor(df$X2)`
			`contrasts(df$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			
			`m = lm(Y ~ X1*X2, data=df)`
			`check_normality(m)`
			`check_homogeneity(m)`
			
			`Anova(m, type=3, test.statistic="F")`
			`eta_squared(m, generalized=TRUE)`
				`library(lme4) # for lmer`
				`library(lmerTest)`
				`library(car) # for Anova`
				`library(effectsize) # for eta_squared`
				`library(performance) # for check_*`
				`df$PId = factor(df$PId)`
				`df$X1 = factor(df$X1)`
				`df$X2 = factor(df$X2)`
				`contrasts(df$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = lmer(Y ~ X1*X2 + (1|PId), data=df)`
				`check_normality(m)`
				`check_homogeneity(m)`
				
				`Anova(m, type=3, test.statistic="F")`
				`eta_squared(m, partial=TRUE)`

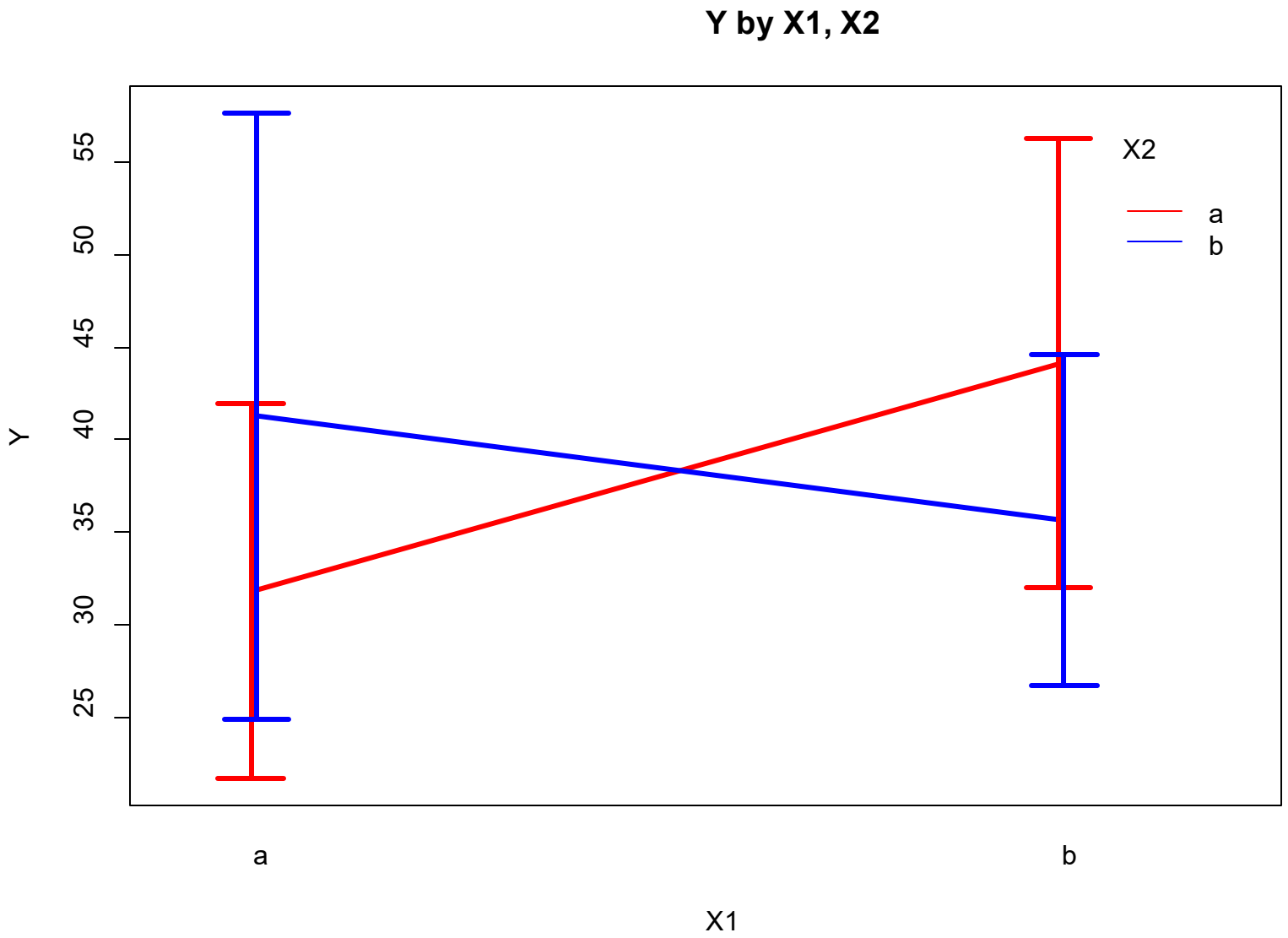
NB. A normal distribution is also known as a Gaussian distribution. The GLMM sample code uses a random intercept for *participant (PId)*. There are also random slope models, which are used when the response changes at different rates for each subject over the repeated factor(s). A random slope example 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	*Linear regression:* Normally distributed responses; equivalent to the linear model (LM) or linear mixed model (LMM)	"Figure 12 shows an interaction plot with ±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 ($F(1, 56) = 8.05$, $p = .006$, $\eta_G^2 = 0.13$)."	"Figure 12 shows an interaction plot with ±1 standard deviation error bars for X1 and X2. An analysis of variance based on a linear **mixed** model indicated a statistically significant X1×X2 interaction ($F(1, 42) = 8.05$, $p = .007$, $\eta_p^2 = 0.13$)."

Figure 12



GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)

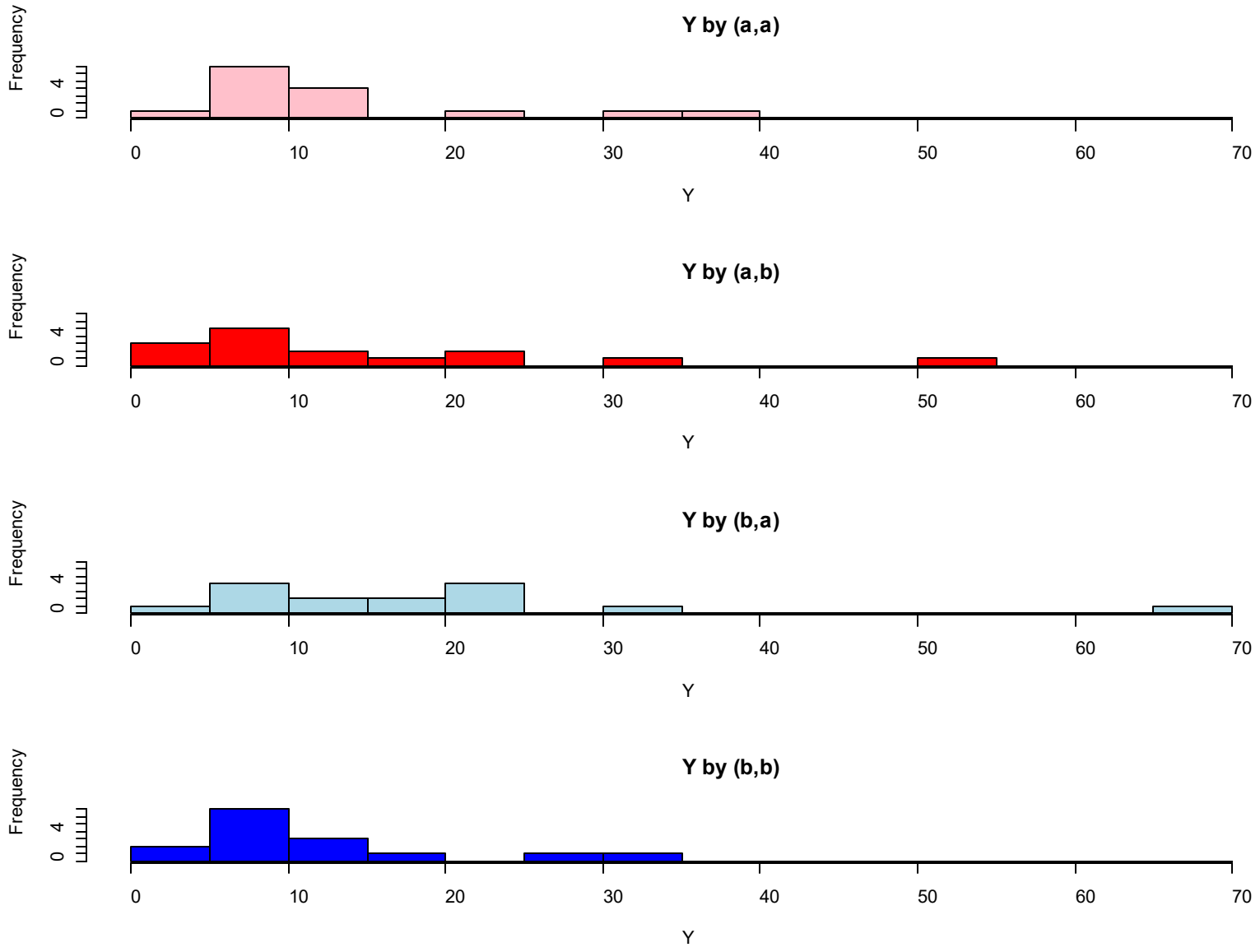
Lognormal	identity	*Linear regression:* Lognormally distributed responses (e.g., time measurements)	`library(car) # for Anova`
			`library(effectsize) # for eta_squared`
			`library(performance) # for check_*`
			`df$PId = factor(df$PId)`
			`df$X1 = factor(df$X1)`
			`df$X2 = factor(df$X2)`
			`contrasts(df$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			
			`m = lm(log(Y) ~ X1*X2, data=df)`
			`check_normality(m)`
			`check_homogeneity(m)`
			
			`Anova(m, type=3, test.statistic="F")`
			`eta_squared(m, generalized=TRUE)`
				`library(lme4) # for lmer`
				`library(lmerTest)`
				`library(car) # for Anova`
				`library(effectsize) # for eta_squared`
				`library(performance) # for check_*`
				`df$PId = factor(df$PId)`
				`df$X1 = factor(df$X1)`
				`df$X2 = factor(df$X2)`
				`contrasts(df$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = lmer(log(Y) ~ X1*X2 + (1|PId), data=df)`
				`check_normality(m)`
				`check_homogeneity(m)`
				
				`Anova(m, type=3, test.statistic="F")`
				`eta_squared(m, partial=TRUE)`

GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Lognormal	identity	*Linear regression:* 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 **mixed** model indicated no statistically significant effects on *log*(Y) of X1, X2, or the X1×X2 interaction."

Figure 13


Y by (a,a)
Frequency
0
4
0
10
20
30
40
50
60
70
Y
Y by (a,b)
Frequency
0
4
0
10
20
30
40
50
60
70
Y
Y by (b,a)
Frequency
0
4
0
10
20
30
40
50
60
70
Y
Y by (b,b)
Frequency
0
4
0
10
20
30
40
50
60
70
Y

GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)

Binomial	logit	*Logistic regression:* Dichotomous responses (i.e., nominal responses with two categories)	`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$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			`m = glm(Y ~ X1*X2, data=df, family=binomial)`
			`Anova(m, type=3)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				`m = glmer(Y ~ X1*X2 + (1|PId), data=df, family=binomial)`
				`Anova(m, type=3)`

Multinomial	logit	*Multinomial logistic regression:* Polytomous responses (i.e., nominal responses with more than two categories)	`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$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "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)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				`m = glmer.mp(Y ~ X1*X2 + (1|PId), data=df) # *`
				`Anova.mp(m, type=3)`
				
				`# if glmer.mp doesn't converge, change the optimizer.`
				`# see the Note at ?glmer.mp.`
				`m = glmer.mp(Y ~ X1*X2 + (1|PId), data=df,`
				`control=glmerControl(optimizer="bobyqa",`
				`optCtrl=list(maxfun=1e+05)))`

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 much more conservative.

GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Binomial	logit	*Logistic regression:* Dichotomous responses (i.e., nominal responses with two categories)	"Figure 14 shows the number of 'yes' and 'no' responses for each X1×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×X2 condition. An analysis of variance based on **mixed** logistic regression indicated a statistically significant effect of X2 on Y ($\chi^2(1, N=60) = 9.13, p = .003$)."
Multinomial	logit	*Multinomial logistic regression:* 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×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×X2 condition. An analysis of variance based on **mixed** 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

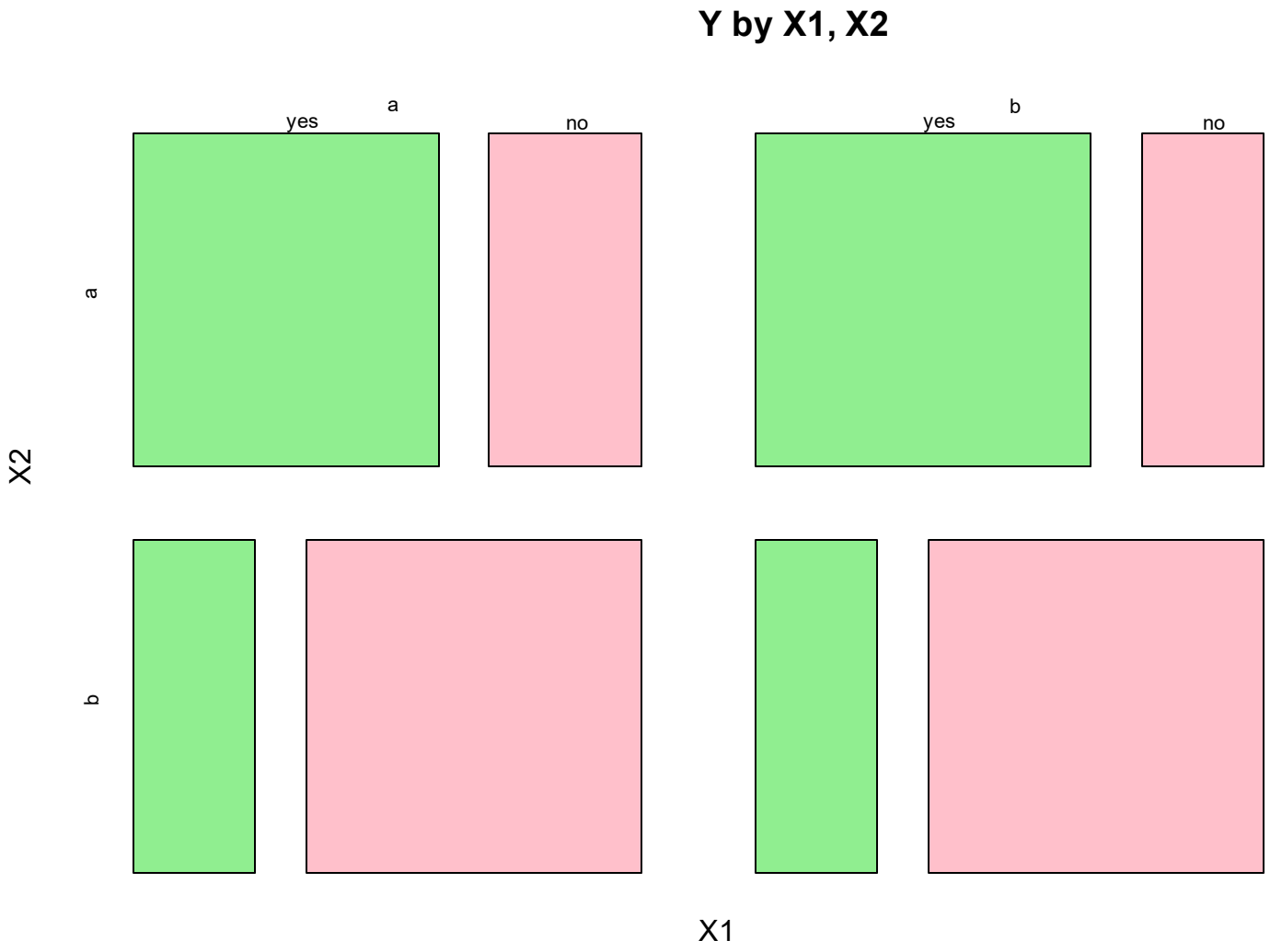
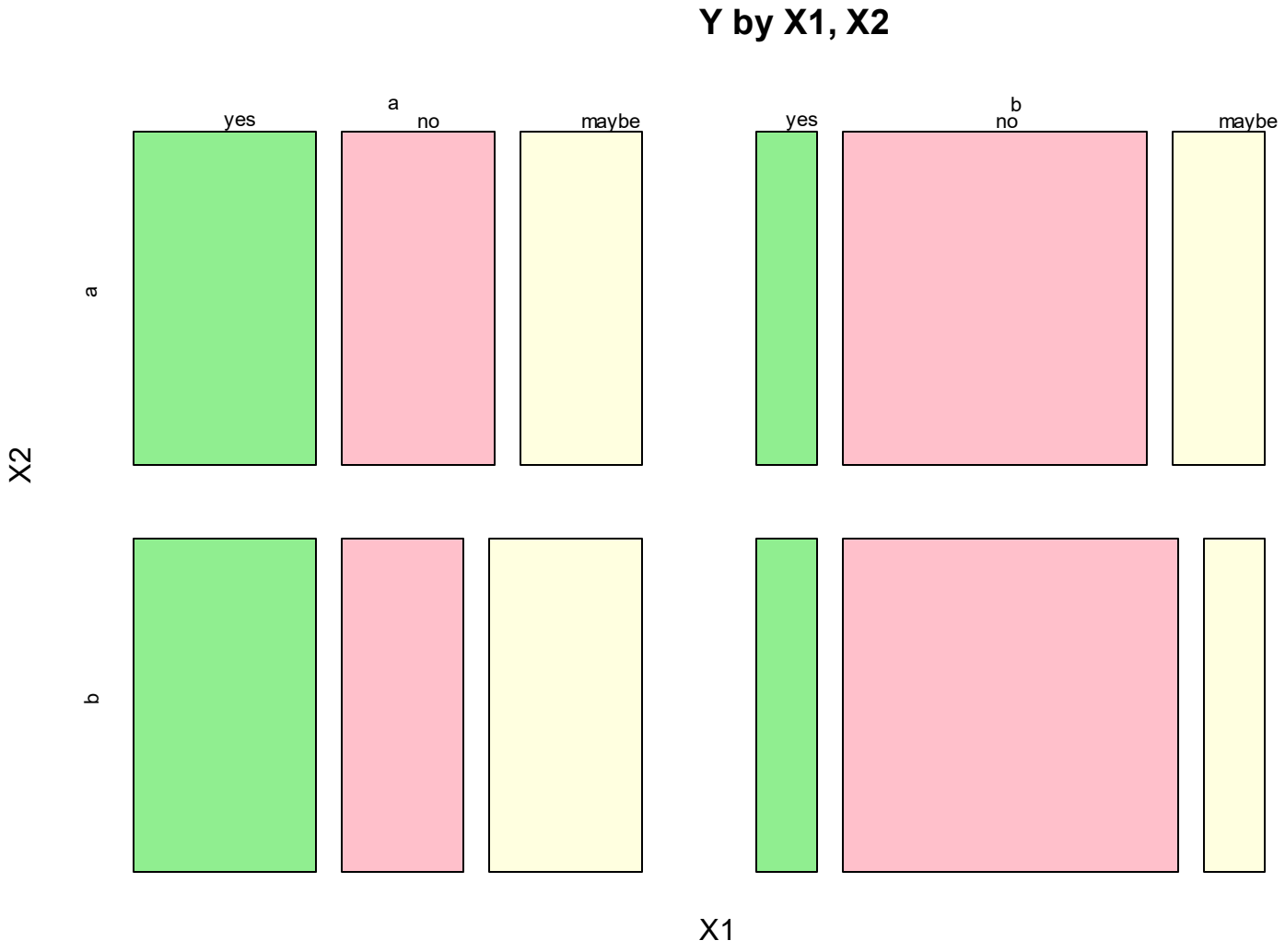


Figure 15



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	*Ordinal logistic regression:* Ordinal responses (e.g., Likert-type scales)	`library(MASS) # for polr`
			`library(car)  # for Anova`
			`df$PId = factor(df$PId)`
			`df$X1 = factor(df$X1)`
			`df$X2 = factor(df$X2)`
			`df$Y = ordered(df$Y) # ordinal response`
			`contrasts(df$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			
			`m = polr(Y ~ X1*X2, data=df, Hess=TRUE)`
			`Anova(m, type=3)`
				`library(ordinal)       # for clmm`
				`library(RVAideMemoire) # for Anova.clmm`
				`dt$PId = factor(dt$PId)`
				`dt$X1 = factor(dt$X1)`
				`dt$X2 = factor(dt$X2)`
				`dt$Y = ordered(dt$Y)   # ordinal response`
				`contrasts(dt$X1) <- "contr.sum"`
				`contrasts(dt$X2) <- "contr.sum"`
				
				`# Anova.clmm fails if data is named 'df'; use 'dt' instead;`
				`# logit, probit, cloglog, loglog, and cauchit links are valid`
				`m = clmm(Y ~ X1*X2 + (1|PId), data=dt, Hess=TRUE, link="logit")`
				`Anova.clmm(m)`

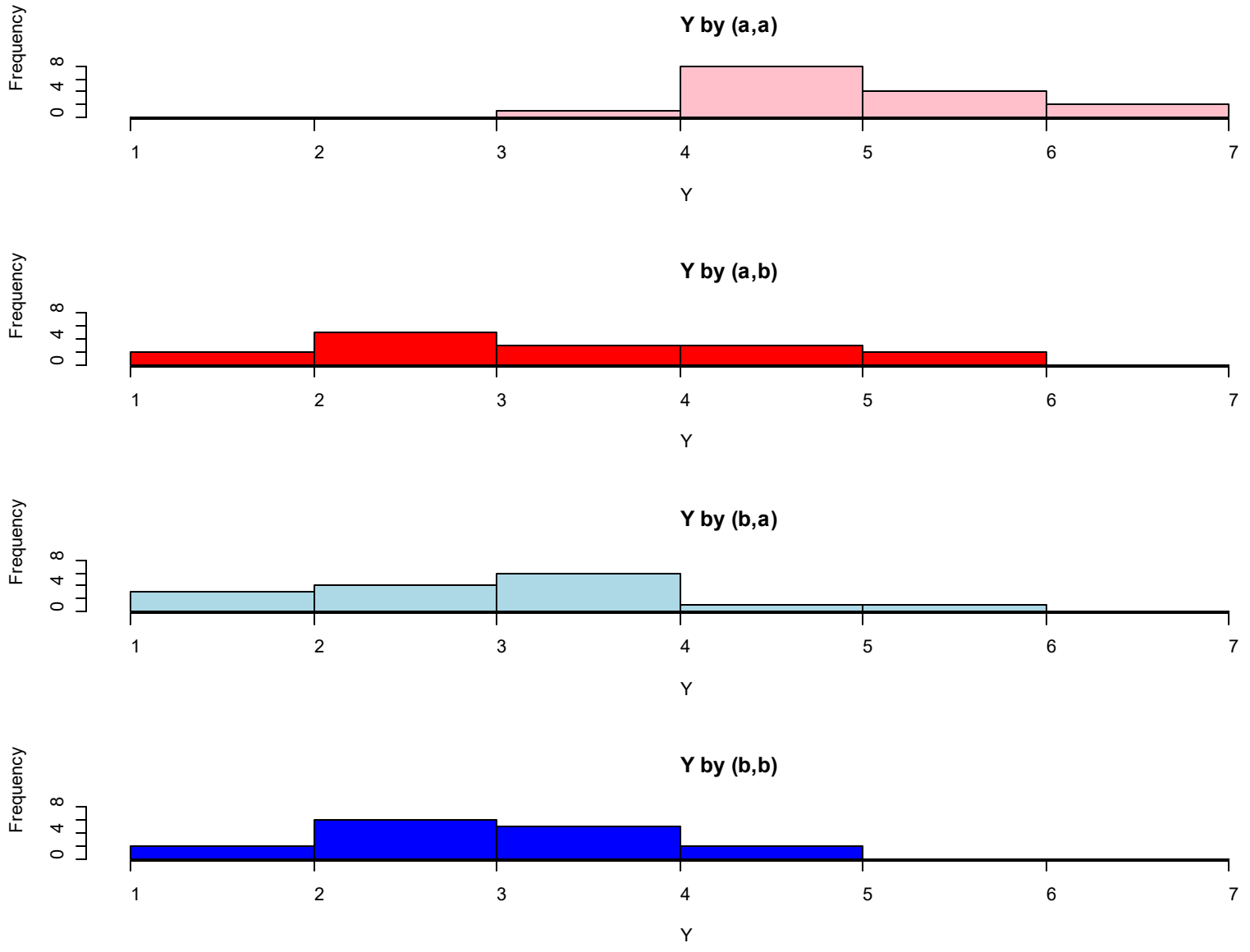
NB. Ordinal logistic regression is also known as cumulative logistic regression.

GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Ordinal	cumulative logit	*Ordinal logistic regression:* 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 **mixed** 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


Y by (a,a)
Frequency
0 4 8
1 2 3 4 5 6 7
Y
Y by (a,b)
Frequency
0 4 8
1 2 3 4 5 6 7
Y
Y by (b,a)
Frequency
0 4 8
1 2 3 4 5 6 7
Y
Y by (b,b)
Frequency
0 4 8
1 2 3 4 5 6 7
Y

GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)

Poisson	log	*Poisson regression:* Count responses	`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$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			`m = glm(Y ~ X1*X2, data=df, family=poisson)`
			`check_overdispersion(m)`
			`# use family=quasipoisson or negative binomial`
			`# regression if overdispersed`
			`Anova(m, type=3)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				`m = glmer(Y ~ X1*X2 + (1|PId), data=df, family=poisson)`
				`check_overdispersion(m)`
				`# use mixed negative binomial regression if overdispersed`
				`Anova(m, type=3)`

Zero-Inflated Poisson	log	*Zero-inflated Poisson regression:* Zero-inflated count responses	`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$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			`m0 = glm(Y ~ X1*X2, data=df, family=poisson)`
			`check_zeroinflation(m0)`
			`m = glmmTMB(Y ~ X1*X2, data=df, family=poisson,`
			`ziformula=~1)`
			`Anova(m, type=3)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				`m0 = glmer(Y ~ X1*X2 + (1|PId), data=df, family=poisson)`
				`check_zeroinflation(m0)`
				`m = glmmTMB(Y ~ X1*X2 + (1|PId), data=df, family=poisson,`
				`ziformula=~1, REML=TRUE)`
				`Anova(m, type=3)`

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	*Poisson regression:* Count responses	"Figure 17 shows histograms of count responses in each X1×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×X2 interaction ($\chi^2(1, N=60) = 5.59, p = .018$)."	"Figure 17 shows histograms of count responses in each X1×X2 condition. An analysis of variance based on **mixed** Poisson regression indicated a statistically significant effect of X1 on Y ($\chi^2(1, N=60) = 4.44, p = .035$) and a significant X1×X2 interaction ($\chi^2(1, N=60) = 5.54, p = .019$)."
Zero-Inflated Poisson	log	*Zero-inflated Poisson regression:* Zero-inflated count responses	"Figure 18 shows histograms of zero-inflated count responses in each X1×X2 condition. An analysis of variance based on zero-inflated Poisson regression indicated a statistically significant X1×X2 interaction ($\chi^2(1, N=60) = 5.63, p = .018$)."	"Figure 18 shows histograms of zero-inflated count responses in each X1×X2 condition. An analysis of variance based on **mixed** zero-inflated Poisson regression indicated a statistically significant X1×X2 interaction ($\chi^2(1, N=60) = 5.63, p = .018$)."

Figure 17

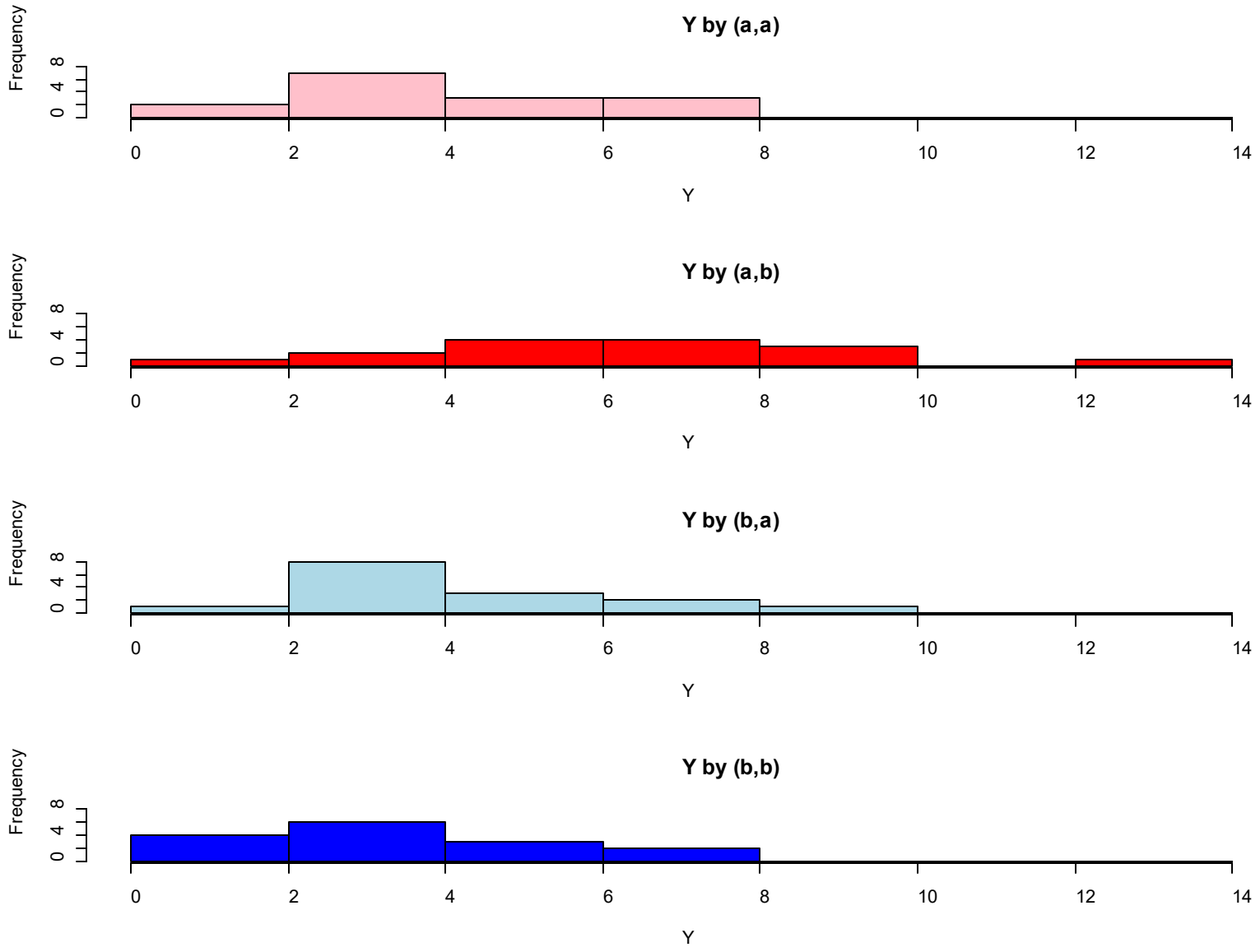
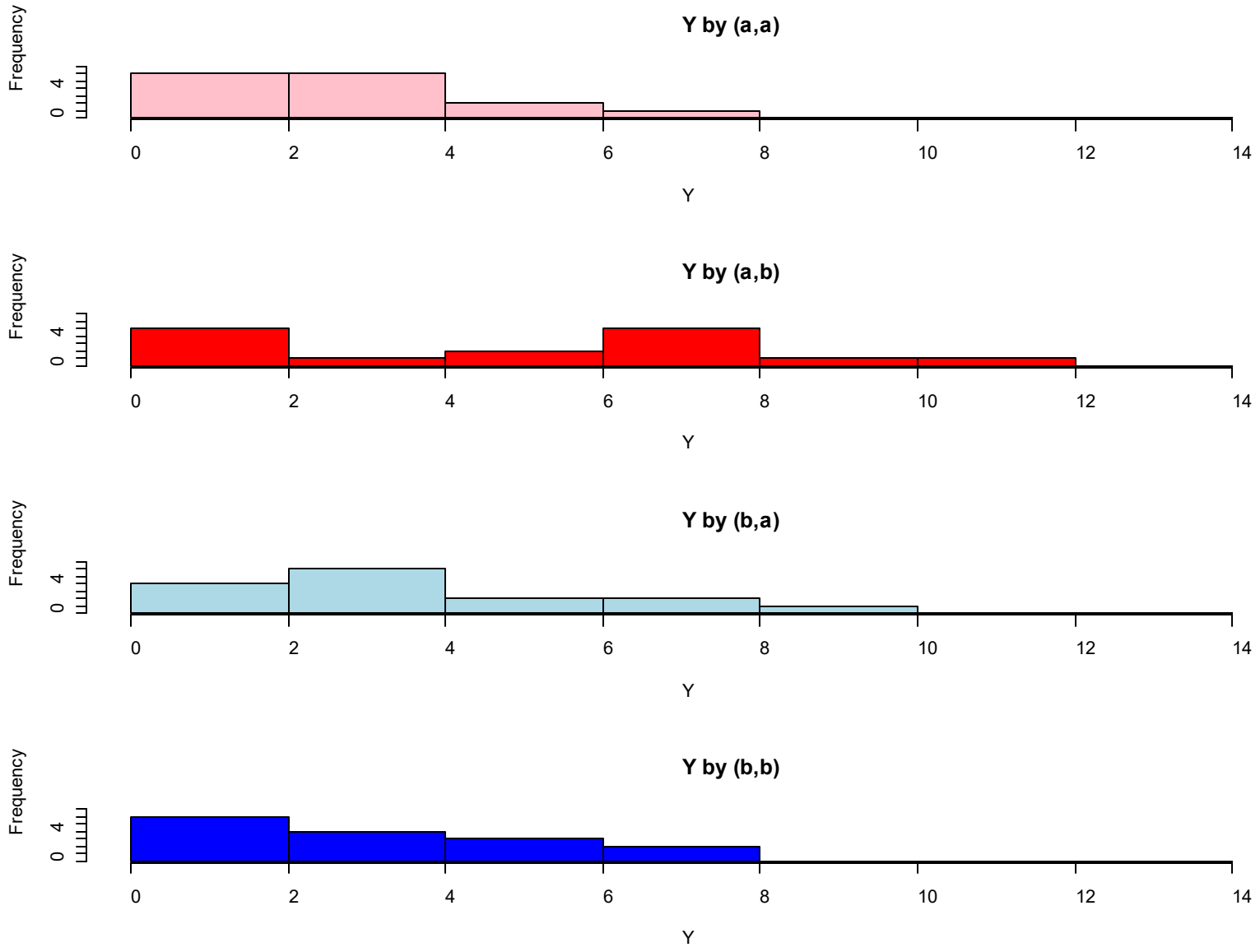

Y by (a,a)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (a,b)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (b,a)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (b,b)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y

Figure 18


Y by (a,a)
Frequency
0
4
0
2
4
6
8
10
12
14
Y
Y by (a,b)
Frequency
0
4
0
2
4
6
8
10
12
14
Y
Y by (b,a)
Frequency
0
4
0
2
4
6
8
10
12
14
Y
Y by (b,b)
Frequency
0
4
0
2
4
6
8
10
12
14
Y

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	*Negative binomial regression:* Overdispersed count responses	`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$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			
			`m = glm.nb(Y ~ X1*X2, data=df)`
			`Anova(m, type=3)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = glmer.nb(Y ~ X1*X2 + (1|PId), data=df)`
				`Anova(m, type=3)`

Zero-Inflated Negative Binomial	log	*Zero-inflated negative binomial regression:* Overdispersed zero-inflated count responses	`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$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			
			`m0 = glm.nb(Y ~ X1*X2, data=df)`
			`check_zeroinflation(m0)`
			
			`m = glmmTMB(Y ~ X1*X2, data=df, family=nbinom2,`
			`ziformula=~1)`
			`Anova(m, type=3)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m0 = glmer.nb(Y ~ X1*X2 + (1|PId), data=df)`
				`check_zeroinflation(m0)`
				
				`m = glmmTMB(Y ~ X1*X2 + (1|PId), data=df, family=nbinom2,`
				`ziformula=~1, REML=TRUE)`
				`Anova(m, type=3)`

GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Negative Binomial	log	*Negative binomial regression:* 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 **mixed** 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	*Zero-inflated negative binomial regression:* 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 ($\chi^2(1, N=60) = 3.90, p = .048$)."	"Figure 20 shows histograms of zero-inflated count responses in each X1×X2 condition. An analysis of variance based on **mixed** zero-inflated negative binomial regression revealed no statistically significant effects."

Figure 19

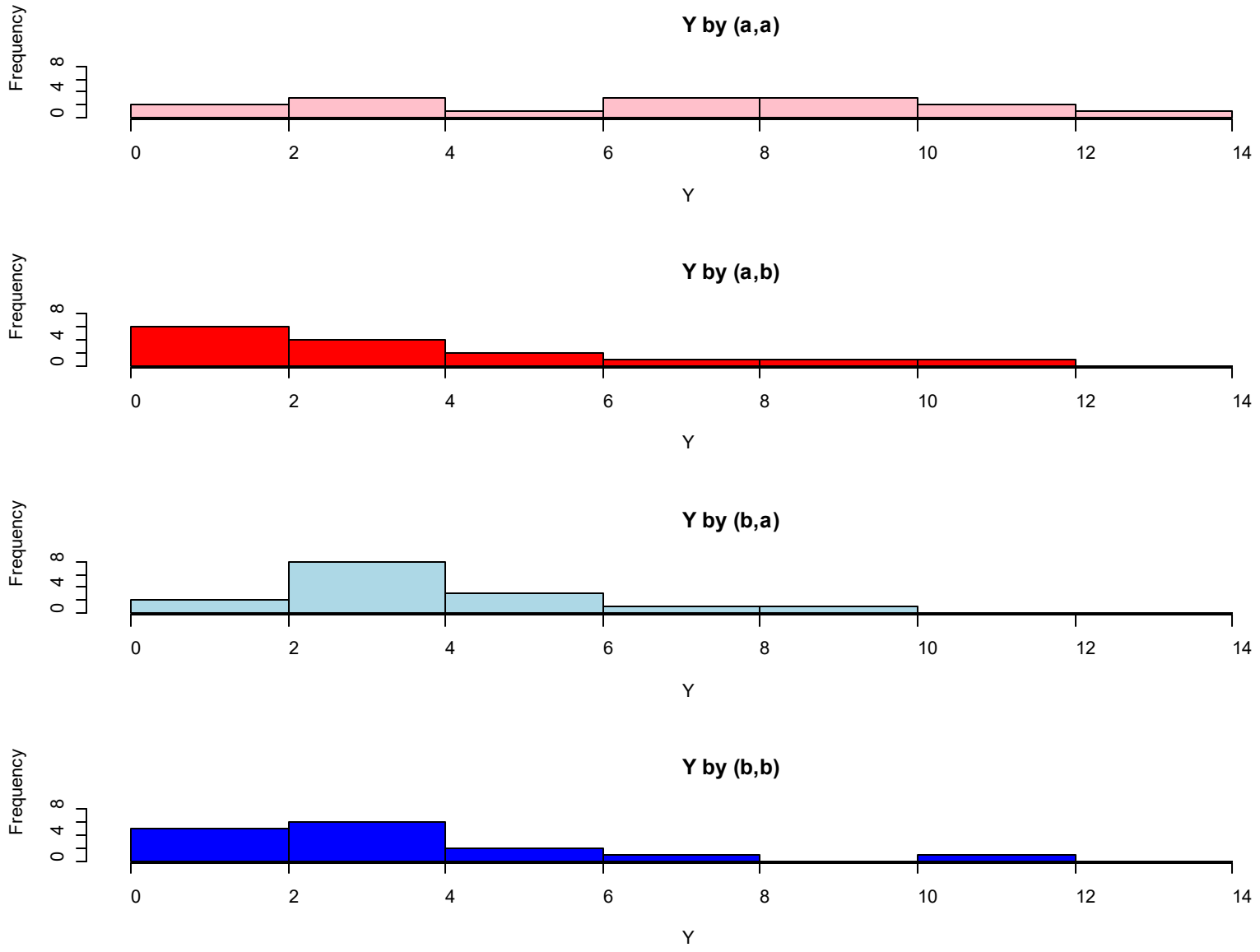
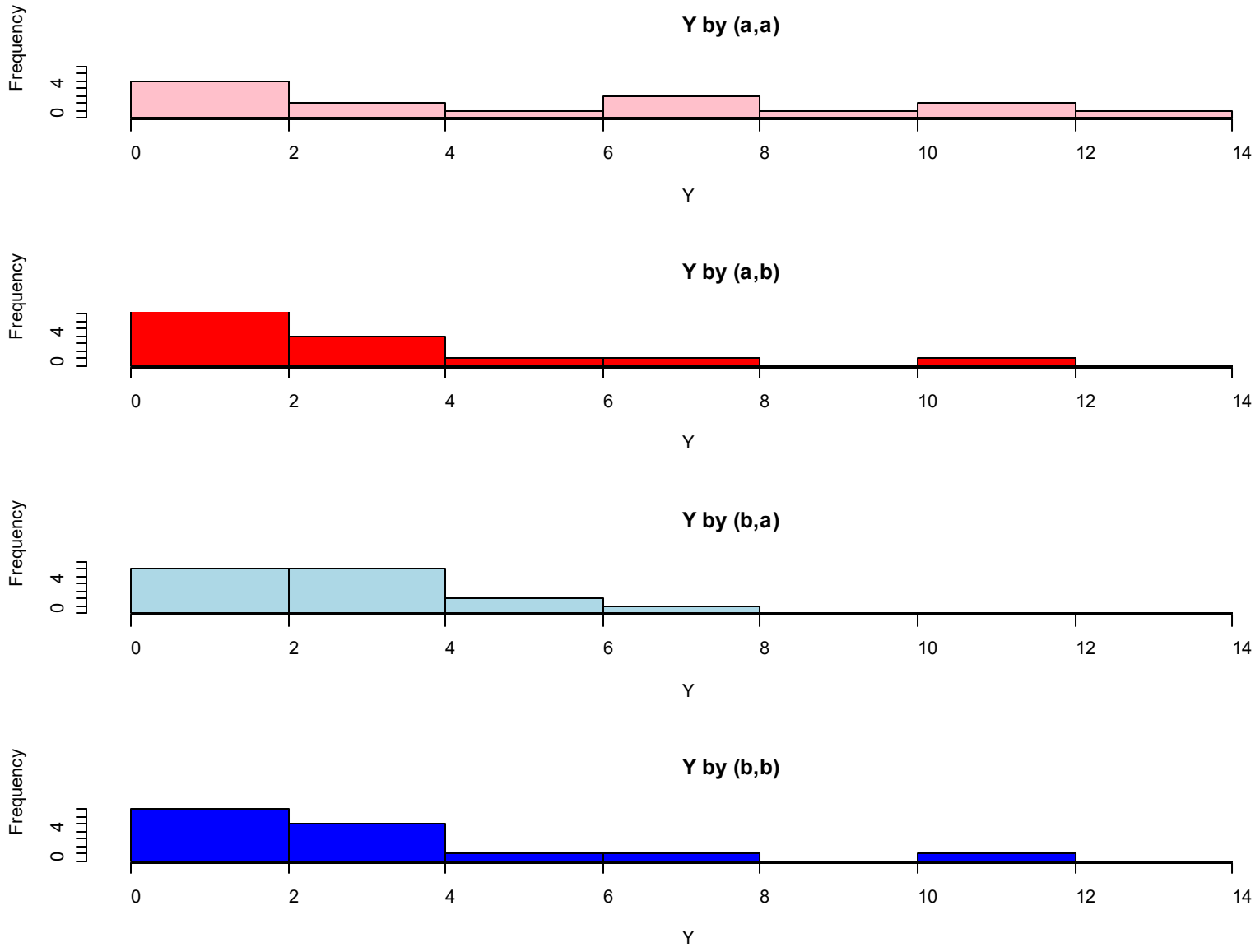

Y by (a,a)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (a,b)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (b,a)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (b,b)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y

Figure 20


Y by (a,a)
Frequency
0
4
0
2
4
6
8
10
12
14
Y
Y by (a,b)
Frequency
0
4
0
2
4
6
8
10
12
14
Y
Y by (b,a)
Frequency
0
4
0
2
4
6
8
10
12
14
Y
Y by (b,b)
Frequency
0
4
0
2
4
6
8
10
12
14
Y

GLM / GLMM

Distributions and canonical links

Distribution	Link	Typical Uses	R code for GLM (between-Ss.)	R code for GLMM (within-Ss.)

Exponential	log	*Exponential regression:* Exponentially distributed responses (e.g., income)	`library(car) # for Anova`
			`df$PId = factor(df$PId)`
			`df$X1 = factor(df$X1)`
			`df$X2 = factor(df$X2)`
			`contrasts(df$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			
			`m = glm(Y ~ X1*X2, data=df,`
			`family=Gamma(link="log"))`
			`Anova(m, type=3)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = glmer(Y ~ X1*X2 + (1|PId), data=df,`
				`family=Gamma(link="log"))`
				`Anova(m, type=3)`

Gamma	inverse	*Gamma regression:* Skewed continuous responses (e.g., time measurements)	`library(car) # for Anova`
			`df$PId = factor(df$PId)`
			`df$X1 = factor(df$X1)`
			`df$X2 = factor(df$X2)`
			`contrasts(df$X1) <- "contr.sum"`
			`contrasts(df$X2) <- "contr.sum"`
			
			`m = glm(Y ~ X1*X2, data=df, family=Gamma)`
			`Anova(m, type=3)`
				`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$X1) <- "contr.sum"`
				`contrasts(df$X2) <- "contr.sum"`
				
				`m = glmer(Y ~ X1*X2 + (1|PId), data=df, family=Gamma)`
				`Anova(m, type=3)`

NB. Gamma distributions are parameterized by *shape* and *scale* (or sometimes *rate*, which is 1/*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	*Exponential regression:* Exponentially distributed responses (e.g., income)	"Figure 21 shows exponential histograms for each X1×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×X2 condition. An analysis of variance based on **mixed** exponential regression indicated a statistically significant effect of X2 on Y ($\chi^2(1, N=60) = 31.00, p < .0001$)."
Gamma	inverse	*Gamma regression:* Skewed continuous responses (e.g., time measurements)	"Figure 22 shows gamma histograms for each X1×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×X2 interaction ($\chi^2(1, N=60) = 7.97, p = .005$)."	"Figure 22 shows gamma histograms for each X1×X2 condition. An analysis of variance based on **mixed** gamma regression indicated a statistically significant effect of X2 on Y ($\chi^2(1, N=60) = 25.36, p < .0001$) and an X1×X2 interaction ($\chi^2(1, N=60) = 8.86, p = .003$)."

Figure 21

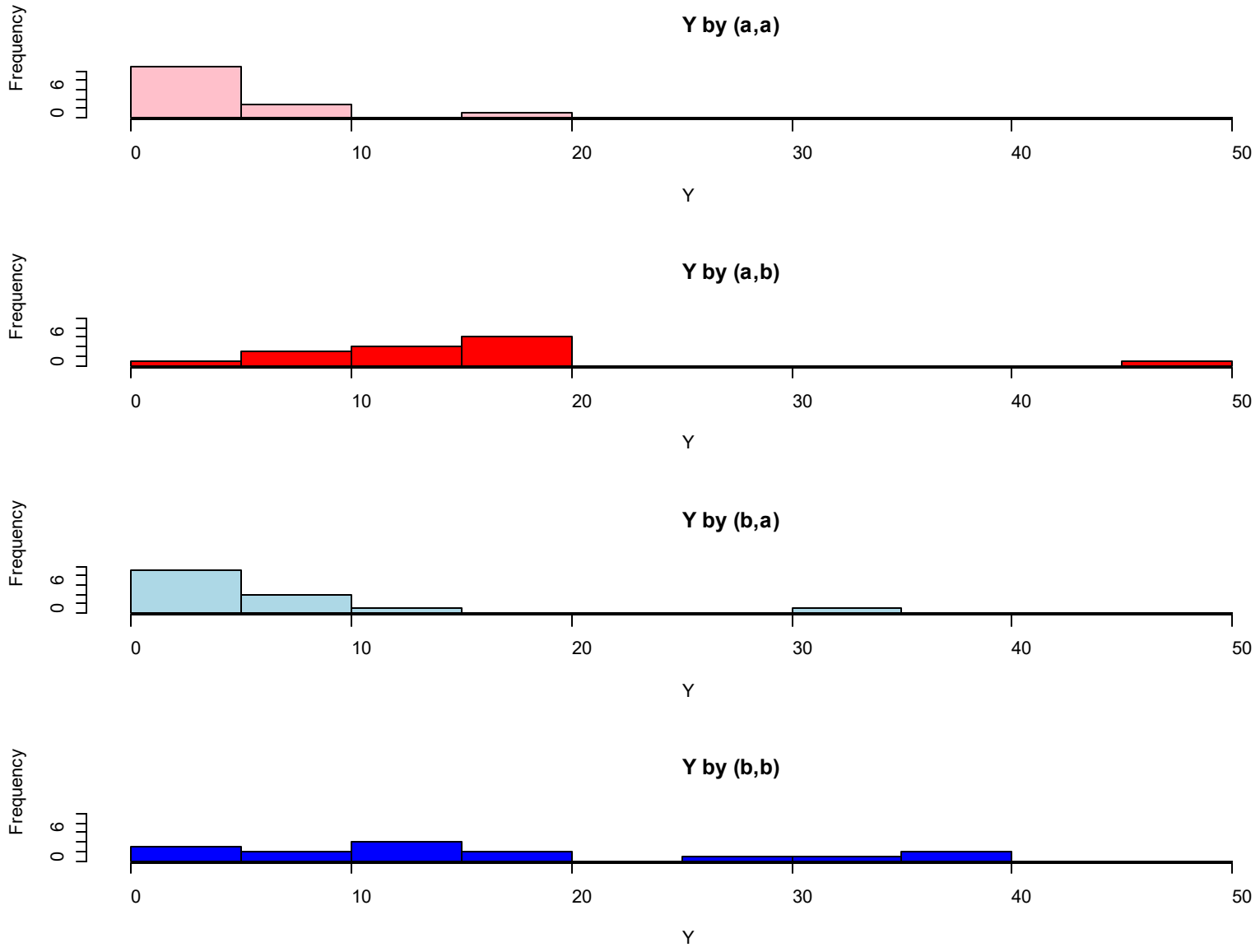
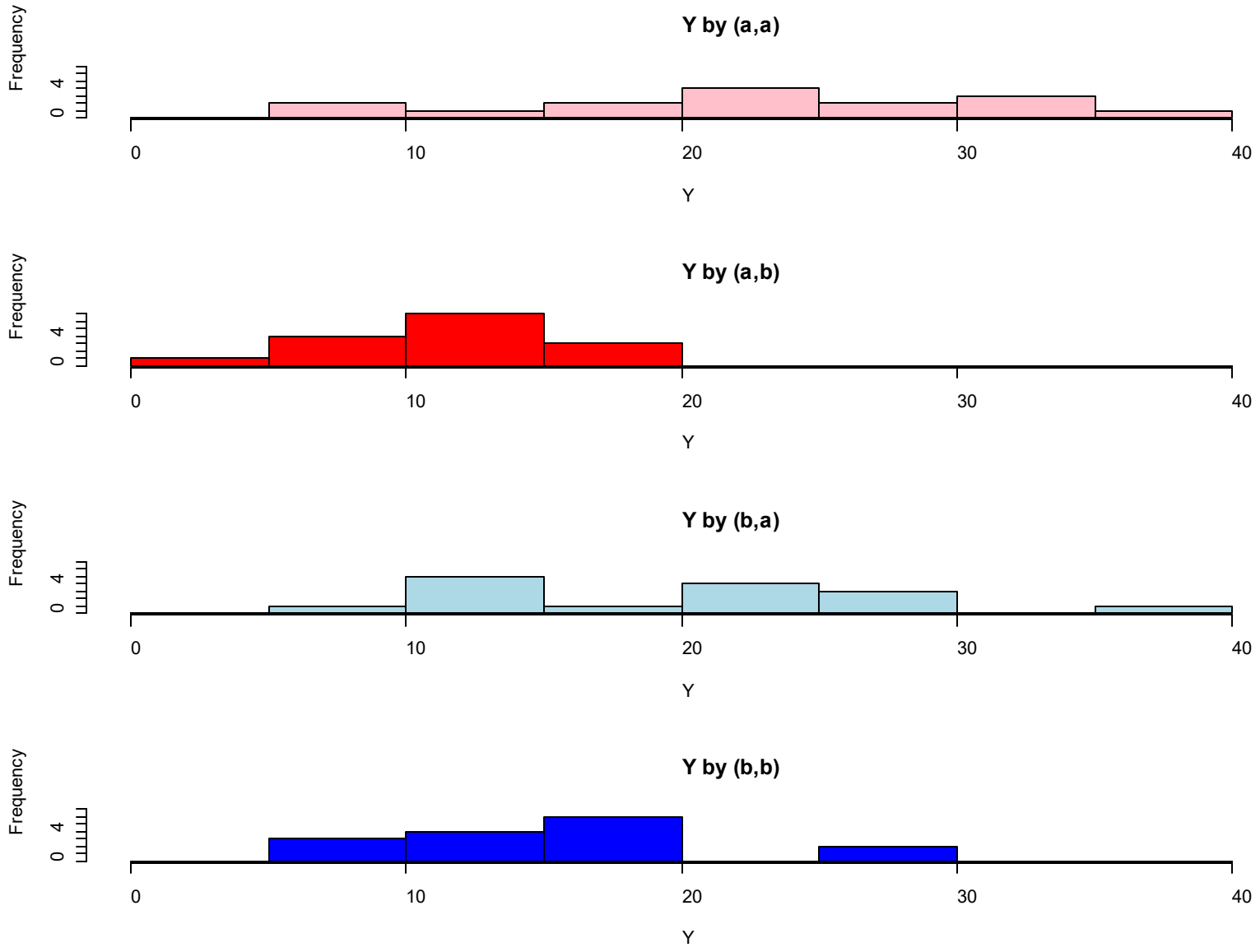

Y by (a,a)
Frequency
0
6
0
10
20
30
40
50
Y
Y by (a,b)
Frequency
0
6
0
10
20
30
40
50
Y
Y by (b,a)
Frequency
0
6
0
10
20
30
40
50
Y
Y by (b,b)
Frequency
0
6
0
10
20
30
40
50
Y

Figure 22


Y by (a,a)
Frequency
0
4
0
10
20
30
40
Y
Y by (a,b)
Frequency
0
4
0
10
20
30
40
Y
Y by (b,a)
Frequency
0
4
0
10
20
30
40
Y
Y by (b,b)
Frequency
0
4
0
10
20
30
40
Y

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	`# df has one factor (X) w/levels (a,b,c) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X, adjust="holm") # m is from lm or lme4::lmer`
					`emm$contrasts`
					`eff_size(emm$emmeans, sigma=sigma(m), edf=df.residual(m)) # Cohen's d`

1	≥2	Logistic regression	*Z*-test	Btwn, Within	`# 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`

1	≥2	Multinomial logistic regression	Chi-squared test	Btwn	`# 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`
					
					`# or, 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"`
					`)`

				Within	`# 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`
					
					`# if glmer.mp.con doesn't converge, change the optimizer. see the Note at ?glmer.mp.con.`
					`glmer.mp.con(m, pairwise ~ X, adjust="holm",`
					`  control=glmerControl(optimizer="bobyqa", optCtrl=list(maxfun=1e+05))`
					`)`

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 *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' ($t(57) = -3.16$, $p = .008$, $d = -1.00$) and 'a' *vs.* 'c' ($t(57) = -2.47$, $p = .033$, $d = -0.78$) were significantly different, but not 'b' *vs.* 'c'."
				Within	"Three *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' ($t(38) = -3.16$, $p = .009$, $d = -1.00$) and 'a' *vs.* 'c' ($t(38) = -2.47$, $p = .036$, $d = -0.78$) were significantly different, but not 'b' *vs.* 'c'."
1	≥2	Logistic regression	*Z*-test	Btwn	"Three *post hoc* 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 *post hoc* 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 *post hoc* 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' ($\chi^2(2, N=40) = 10.46$, $p = .016$) and 'b' *vs.* 'c' ($\chi^2(2, N=40) = 7.94$, $p = .038$) were significantly different, but not 'a' *vs.* 'b'."
				Within	"Three *post hoc* 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' were significantly different ($\chi^2(2, N=40) = 12.22$, $p = .007$) but not 'a' *vs.* 'b' or 'b' *vs.* 'c'."

GLM / GLMM

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	R Code

1	≥2	Ordinal logistic regression	*Z*-test	Btwn, Within	`# 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`

1	≥2	Poisson regression	*Z*-test	Btwn, Within	`# 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`

1	≥2	Zero-inflated Poisson regression	*Z*-test	Btwn, Within	`# 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`

1	≥2	Negative binomial regression	*Z*-test	Btwn, Within	`# 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`

1	≥2	Zero-inflated negative binomial regression	*Z*-test	Btwn, Within	`# 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`

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	Ordinal logistic regression	*Z*-test	Btwn, Within	"Three *post hoc* 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'."
1	≥2	Poisson regression	*Z*-test	Btwn, Within	"Three *post hoc* 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, Within	"Three *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' ($Z = -2.66$, $p = .018$) and 'b' *vs.* 'c' ($Z = 2.75$, $p = ..018$) were significantly different, but not 'a' *vs.* 'c'."
1	≥2	Negative binomial regression	*Z*-test	Btwn, Within	"Three *post hoc* 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 *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' ($Z = -5.18$, $p < .0001$) and 'b' *vs.* 'c' ($Z = 4.63$, $p < .0001$) were significantly different, but not 'a' *vs.* 'c'."
				Within	"Three *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' ($Z = -5.04$, $p < .0001$) and 'b' *vs.* 'c' ($Z = 4.48$, $p < .0001$) 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	`# 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")`

1	≥2	Gamma regression	*Z*-test	Btwn, Within	`# 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`

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 *post hoc* 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 *post hoc* 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 *post hoc* 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 *post hoc* 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	`# df has two factors (X1,X2) each w/levels (a,b) and continuous response (Y)`
					`library(emmeans) # for emmeans, eff_size`
					`emm = emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from lm or lme4::lmer`
					`emm$contrasts`
					`eff_size(emm$emmeans, sigma=sigma(m), edf=df.residual(m)) # Cohen's d`

≥2	≥2	Logistic regression	*Z*-test	Btwn, Within	`# 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`

≥2	≥2	Multinomial logistic regression	Chi-squared test	Btwn	`# 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`
					
					`# or, 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"`
					`)`

				Within	`# 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`
					
					`# If glmer.mp.con doesn't converge, change the optimizer. See the Note at ?glmer.mp.con.`
					`glmer.mp.con(m, pairwise ~ X1*X2, adjust="holm",`
					`  control=glmerControl(optimizer="bobyqa", optCtrl=list(maxfun=1e+05))`
					`)`

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 *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {b,a} was significantly different ($t(56) = -2.75$, $p = .048$, $d = -1.01$). All other pairwise comparisons were not detectably different."
				Within	"Six *post hoc* 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 *post hoc* 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 *post hoc* 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."

GLM / GLMM

Post hoc pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	R Code

≥2	≥2	Ordinal logistic regression	*Z*-test	Btwn, Within	`# 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`

≥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`

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	Ordinal logistic regression	*Z*-test	Btwn, Within	"Six *post hoc* 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."
≥2	≥2	Poisson regression	*Z*-test	Btwn, Within	"Six *post hoc* 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 *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {a,b} was significantly different ($Z = -2.68$, $p = .045$). All other pairwise comparisons were not detectably different."
				Within	"Six *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {a,b} were significantly different ($Z = -2.68$, $p = .044$) . 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	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	Negative binomial regression	*Z*-test	Btwn	"Six *post hoc* 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 *post hoc* 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 *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {b,a} was significantly different ($Z = 2.78$, $p = .033$). All other pairwise comparisons were not detectably different."
				Within	"Six *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {b,a} was significantly different ($Z = 2.64$, $p < .05$). 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	`# 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")`

≥2	≥2	Gamma regression	*Z*-test	Btwn, Within	`# 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`

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 *post hoc* 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 *post hoc* 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 *post hoc* 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 *post hoc* 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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