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#Rstats

Statistical Analysis & Reporting in R

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Table of Analyses

Proportions & Association

Samples	Categories	Tests
1	2	One-sample χ^2 test, binomial test
1	≥2	One-sample χ^2 test, multinomial test
2	≥2	Two-sample χ^2 test, *G*-test, Fisher's exact test
2*	≥2	Symmetry test

Assumptions

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

Distributions

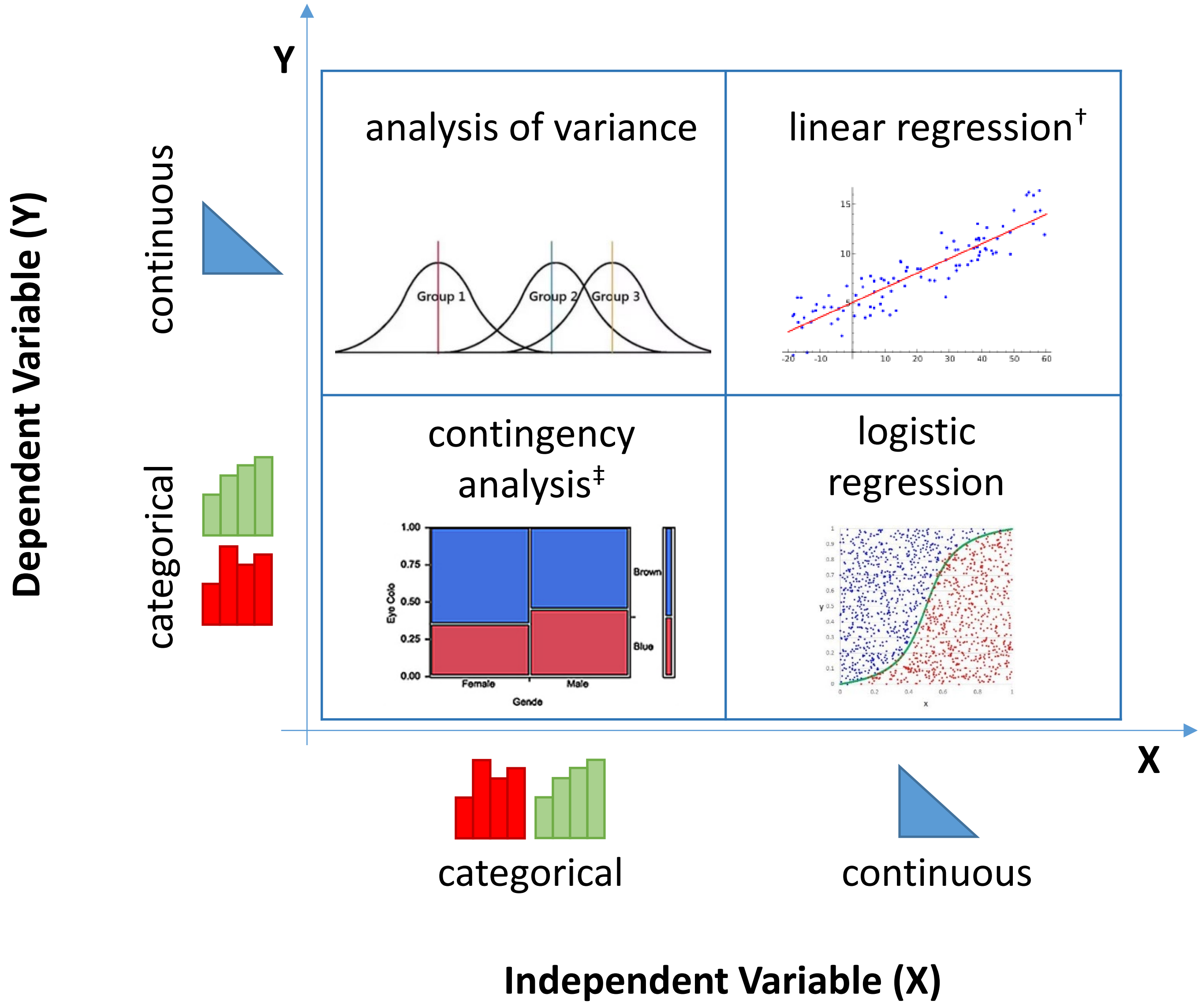
Shapiro-Wilk test
χ^2 goodness-of-fit test

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)	

*Dependent samples

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

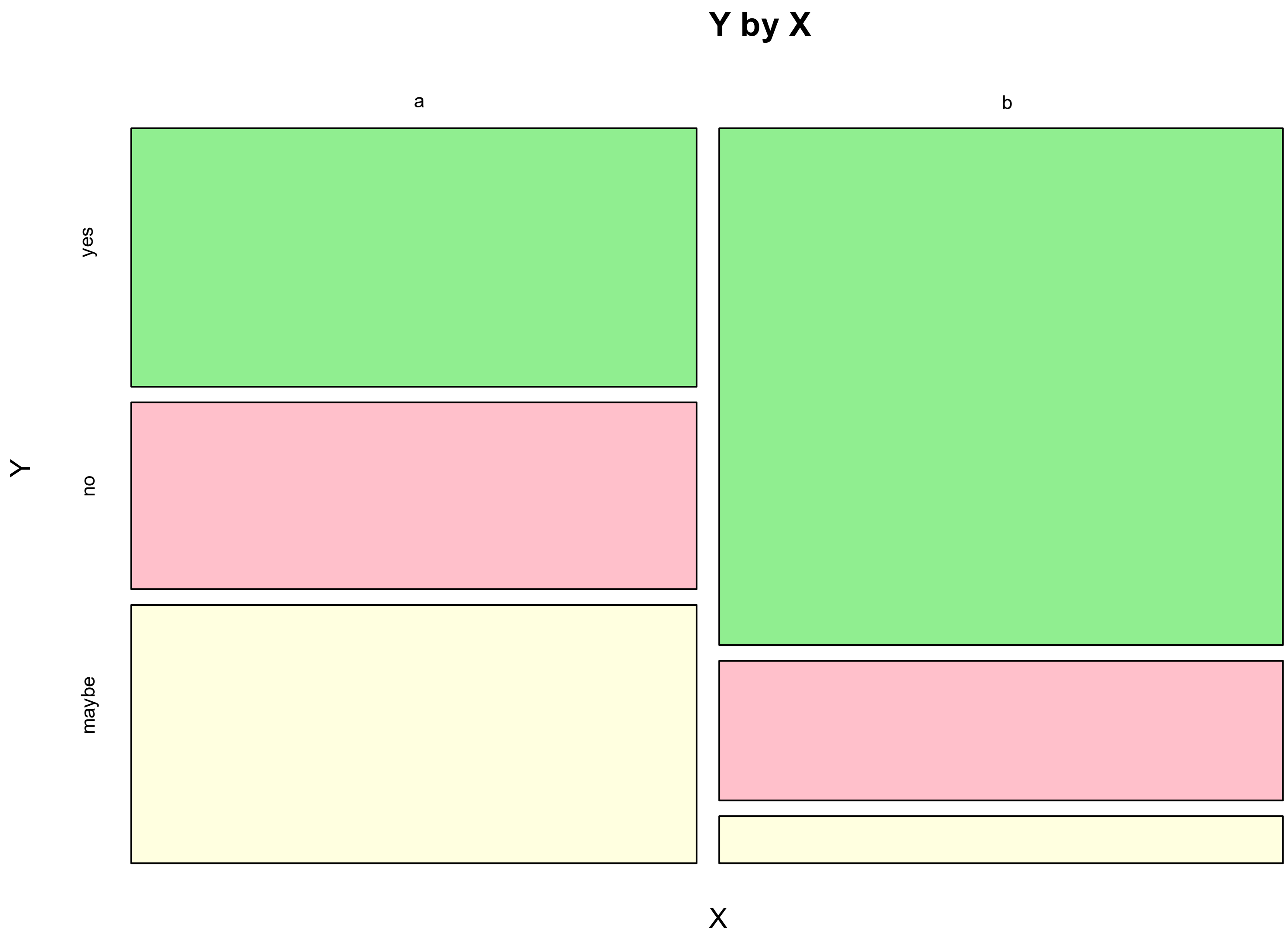
Two samples

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≥200	"Table 1 shows the counts of 'yes', 'no', and 'maybe' responses (Y) for each of 'a' and 'b' (X). Figure 1 plots these proportions. A two-sample Pearson chi-squared test indicated a statistically significant association between X and Y ($\chi^2(2, N{=}60) = 10.18$, p = .006)."

Table 1

		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)`

Association

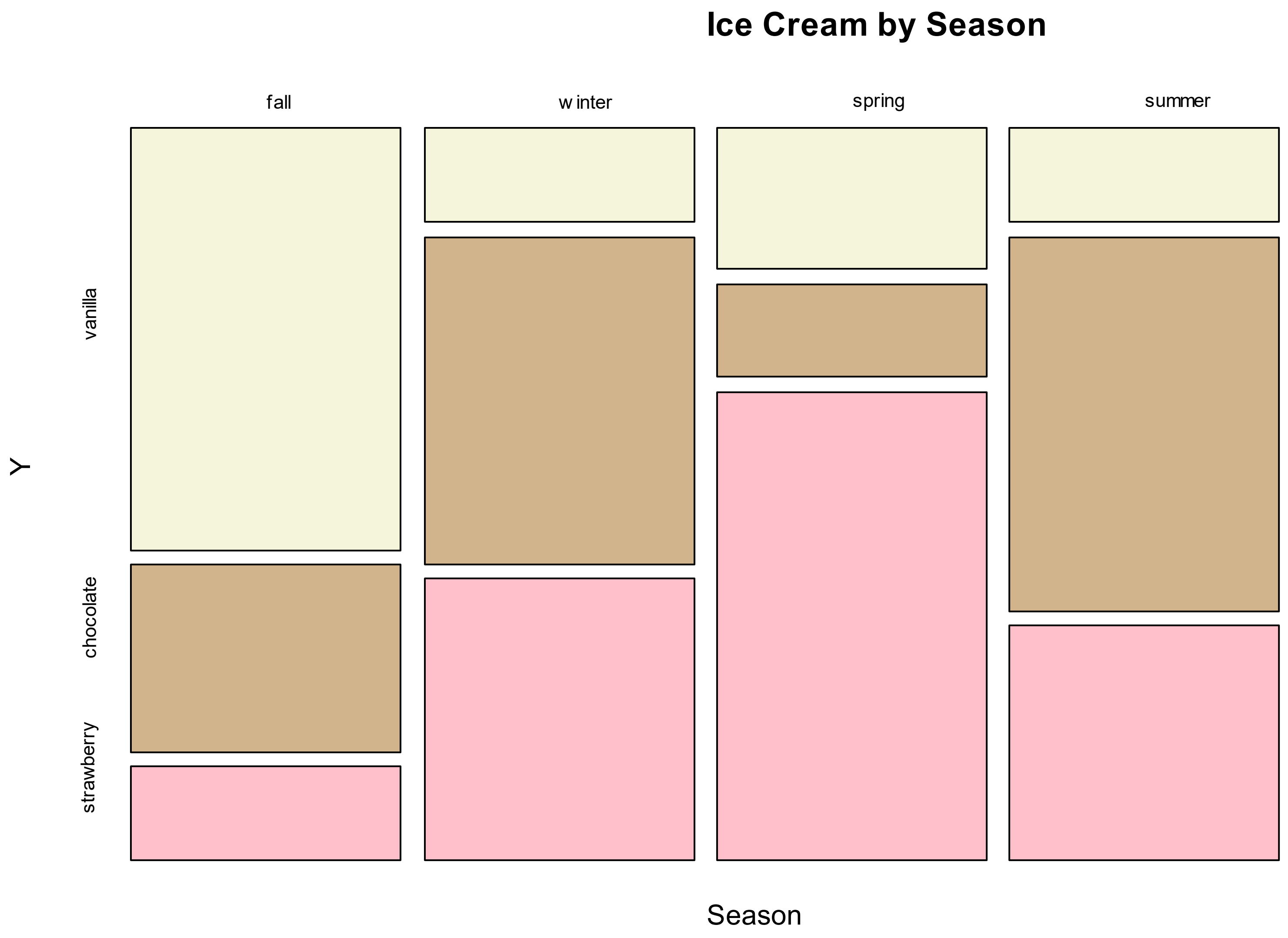
Dependent samples

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)."

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
w inter
spring
summer
vanilla
chocolate
strawberry
Y
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:`
				`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:`
				`exp = G.test(xt)$expected[,1] # expected 'yes'`
				`y = G.test(xt[,1], p=exp/sum(exp))`
				`exp = G.test(xt)$expected[,2] # expected 'no'`
				`n = G.test(xt[,2], p=exp/sum(exp))`
				`exp = G.test(xt)$expected[,3] # expected 'maybe'`
				`m = G.test(xt[,3], p=exp/sum(exp))`
				`p.adjust(c(y$p.value, n$p.value, m$p.value), method="holm")`
				
				`# test row proportions:`
				`exp = G.test(xt)$expected[1,] # expected 'a'`
				`a = G.test(xt[1,], p=exp/sum(exp))`
				`exp = G.test(xt)$expected[2,] # expected 'b'`
				`b = G.test(xt[2,], p=exp/sum(exp))`
				`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:`
				`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:`
				`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

<table>
<tr><th>Samples</th><th>Response Categories</th><th>Omnibus Test</th><th>Contrast Test</th><th>R Code</th></tr>
<tr><td rowspan="2">2</td><td rowspan="2">≥2</td><td rowspan="2">chi-squared test</td><td>chi-squared tests on each table column (or row) against chance</td><td>

```
# 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")
```

</td></tr>
<tr><td>chi-squared tests on each table column (or row) against expected frequencies</td><td>

```
# xt is the m×n crosstabs created for the chi-squared test
# test column proportions:
exp = chisq.test(xt)$expected[,1] # expected 'yes'
y = chisq.test(xt[,1], p=exp/sum(exp))
exp = chisq.test(xt)$expected[,2] # expected 'no'
n = chisq.test(xt[,2], p=exp/sum(exp))
exp = chisq.test(xt)$expected[,3] # expected 'maybe'
m = chisq.test(xt[,3], p=exp/sum(exp))
p.adjust(c(y$p.value, n$p.value, m$p.value), method="holm")

# test row proportions:
exp = chisq.test(xt)$expected[1,] # expected 'a'
a = chisq.test(xt[1,], p=exp/sum(exp))
exp = chisq.test(xt)$expected[2,] # expected 'b'
b = chisq.test(xt[2,], p=exp/sum(exp))
p.adjust(c(a$p.value, b$p.value), method="holm")
```

</td></tr>
</table>

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

<table>
<tr><th>Samples</th><th>Response Categories</th><th>Omnibus Test</th><th>Contrast Test</th><th>R Code</th></tr>
<tr><td>2</td><td>≥2</td><td>Symmetry test</td><td>Pairwise symmetry tests</td><td><pre>
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")
</pre></td></tr>
<tr><td>2</td><td>≥2</td><td>Symmetry test</td><td>Pairwise sign tests</td><td><pre>
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")
</pre></td></tr>
</table>

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 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."

Bibliography (contingency tables, tests of proportion and association)

- Conover, W.J. (1999). The sign test. In *Practical Nonparametric Statistics* (3rd ed.). New York, NY: John Wiley & Sons, pp. 157-165. https://www.wiley.com/en-us/Practical+Nonparametric+Statistics%2C+3rd+Edition-p-9780471160687
- Fisher, R.A. (1922). On the interpretation of χ^2 from contingency tables, and the calculation of P. *Journal of the Royal Statistical Society 85* (1), pp. 87-94. https://doi.org/10.2307/2340521
- Mehta, C.R. and Patel, N.R. (1983). A network algorithm for performing Fisher's exact test in r×c contingency tables. *Journal of the American Statistical Association 78* (382), pp. 427-434. https://doi.org/10.2307/2288652
- Pearson, K. (1900). On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling. *The London, Edinburgh, and Dublin Philosophical Magazine and Journal of Science, Series 5, vol. 50* (302), pp. 157-175. https://doi.org/10.1080/14786440009463897
- Sokal, R.R. and Rohlf, F.J. (1969). *Biometry: The Principles and Practice of Statistics in Biological Research*. San Francisco, CA: W. H. Freeman & Co. https://books.google.com/books?id=C-OTQgAACAAJ
- Strasser, H. and Weber, C. (1999). On the asymptotic theory of permutation statistics. *Mathematical Methods of Statistics 8* (2), pp. 220-250. https://doi.org/10.57938/ff565ba0-aa64-4fe0-a158-86fd331bee78

Assumptions

ANOVA Assumptions

Normality

Assumption	Test Name	Context of Use	R Code

Normality	Shapiro-Wilk test (on the response in each condition)	*t*-test, ANOVA	`# 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`
			`library(performance) # for check_normality`
			`m = aov_ez(dv="Y", between=c("X1","X2"), id="PId", type=3, data=df) # make model`
			`r = residuals(m$lm) # extract residuals`
			`mean(r); sum(r) # both should be ~0`
			`plot(r[1:length(r)], main="Residual plot"); abline(h=0) # should look random`
			`hist(r, main="Histogram of residuals") # should look normal`
			`qqnorm(r); qqline(r) # Q-Q plot`
			`shapiro.test(r) # Shapiro-Wilk test`
			`print(check_normality(m)) # same`

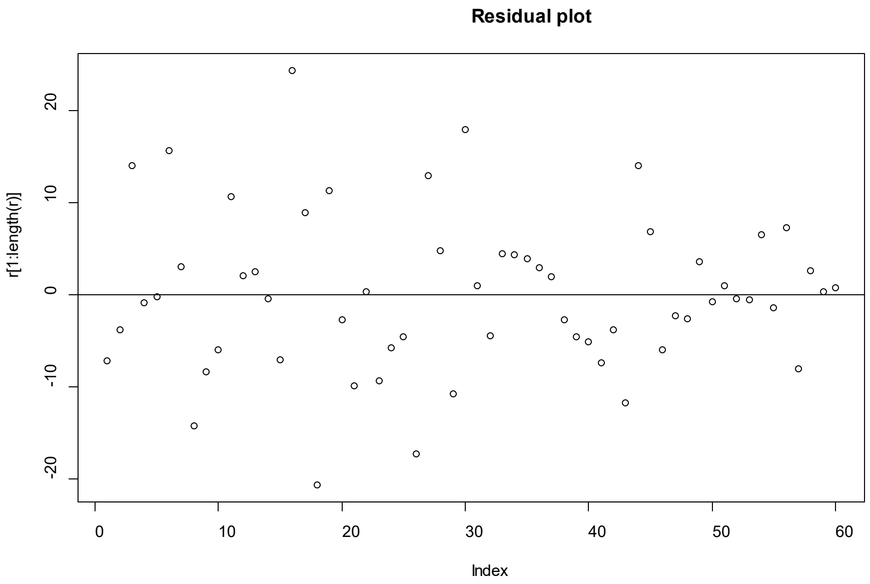
Normality	Shapiro-Wilk test (on residuals)	Linear mixed model (LMM)	`# df has two factors (X1,X2) each w/two levels (a,b) and continuous response (Y)`
			`library(lme4) # for lmer`
			`library(lmerTest)`
			`library(performance) # for check_normality`
			`m = lmer(Y ~ X1*X2 + (1|PId), data=df) # make linear mixed model`
			`r = residuals(m) # extract model residuals`
			`mean(r); sum(r) # both should be ~0`
			`plot(r[1:length(r)], main="Residual plot"); abline(h=0) # should look random`
			`hist(r, main="Histogram of residuals") # should look normal`
			`qqnorm(r); qqline(r) # Q-Q plot`
			`shapiro.test(r) # Shapiro-Wilk test`
			`print(check_normality(m)) # same`

ANOVA Assumptions

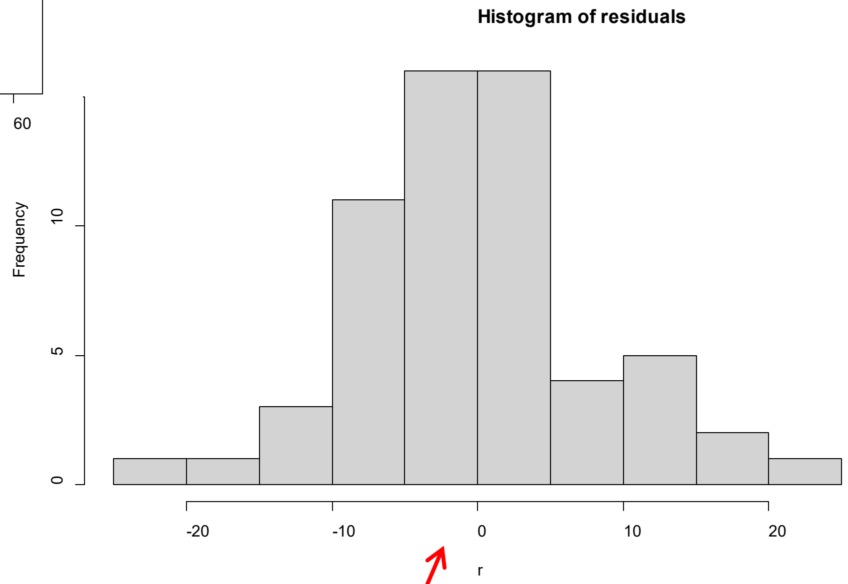
Normality

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

Figure 3

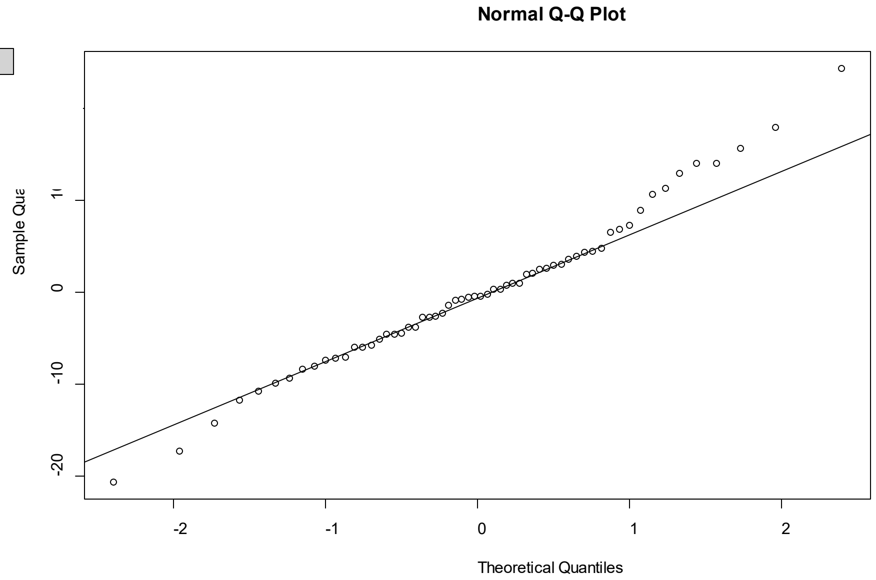


should look random



should look normal

points should fall near line



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(car)  # for Anova`
			`m = aov_ez(dv="Y", between="X1", within="X2", id="PId", type=3, data=df)`
			`print(check_homogeneity(m)) # Levene's test`
			
			`# if a violation occurs (p<.05), use a Welch t-test for one factor of two levels...`
			`t.test(Y ~ X1, data=df, var.equal=FALSE)`
			
			`# ...or a White-adjusted ANOVA for >1 factor or >2 levels`
			`Anova(m$lm, type=3, white.adjust=TRUE) # shows between-Ss. factors only`

Sphericity	Mauchly's test	Any ANOVA model with at least one within-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_sphericity`
			`m = aov_ez(dv="Y", between="X1", within="X2", id="PId", type=3, data=df)`
			`print(check_sphericity(m))`
			
			`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
Homogeneity of variance	Levene's test	Any ANOVA model with at least one between-subjects factor	"To test the homogeneity of variance assumption, Levene's test was run on a mixed factorial ANOVA with a between-subjects factor X1 and a within-subjects factor X2. The test was statistically non-significant (p = .753), indicating no violation."
Sphericity	Mauchly's test	Any ANOVA model with at least one within-subjects factor	"To test the sphericity assumption, Mauchly's test of sphericity was run on a mixed factorial ANOVA with a between-subjects factor X1 and a within-subjects factor X2. The test was statistically non-significant (p = .999), indicating no sphericity violation."

Bibliography (ANOVA assumptions of normality, homogeneity of variance, sphericity)

- Bartlett, M.S. (1937). Properties of sufficiency and statistical tests. *Proceedings of the Royal Society of London, Series A 160* (901), pp. 268-282. https://www.jstor.org/stable/96803
- Brown, M.B. and Forsythe, A.B. (1974). Robust tests for the equality of variances. *Journal of the American Statistical Association 69* (346), pp. 364-367. https://doi.org/10.2307/2285659
- Fligner, M.A. and Killeen, T.J. (1976). Distribution-free two-sample tests for scale. *Journal of the American Statistical Association 71* (353), pp. 210-213. https://www.jstor.org/stable/2285771
- Greenhouse, S.W. and Geisser, S. (1959). On methods in the analysis of profile data. *Psychometrika 24* (2), pp. 95-112. https://doi.org/10.1007/BF02289823
- Levene, H. (1960). Robust tests for equality of variances. In *Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling*, I. Olkin, S.G. Ghurye, H. Hoeffding, W.G. Madow and H.B. Mann (eds.). Palo Alto, CA: Stanford University Press, pp. 278-292.
- Mauchly, J.W. (1940). Significance test for sphericity of a normal n-variate distribution. *The Annals of Mathematical Statistics 11* (2), pp. 204-209. https://www.jstor.org/stable/2235878
- Shapiro, S.S. and Wilk, M.B. (1965). An analysis of variance test for normality (complete samples). *Biometrika 52* (3/4), pp. 591-611. https://doi.org/10.2307/2333709
- Welch, B.L. (1951). On the comparison of several mean values: An alternative approach. *Biometrika 38* (3/4), pp. 330-336. https://doi.org/10.2307/2332579
- White, H. (1980). A heteroskedasticity-consistent covariance matrix estimator and a direct test for heteroskedasticity. *Econometrica 48* (4), pp. 817-838. https://doi.org/10.2307/1912934

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`
			`fa = gofTest(df[df$X == "a",]$Y, distribution="norm") # create fit for X=a`
			`print(fa) # Shapiro-Wilk GOF`
			`fb = gofTest(df[df$X == "b",]$Y, distribution="norm") # create fit for X=b`
			`print(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`
			`fa = gofTest(df[df$X == "a",]$Y, distribution="lnorm") # create fit for X=a`
			`print(fa) # Shapiro-Wilk GOF`
			`fb = gofTest(df[df$X == "b",]$Y, distribution="lnorm") # create fit for X=b`
			`print(fb) # Shapiro-Wilk GOF`

Poisson	lambda (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`
			`fa = fitdist(df[df$X == "a",]$Y, distr="pois") # create fit for X=a`
			`gofstat(fa) # chi-squared GOF`
			`fb = fitdist(df[df$X == "b",]$Y, distr="pois") # create fit for X=b`
			`gofstat(fb) # chi-squared GOF`
			
			`# if var/mean > 1.15, we have overdispersion; if so, use quasipoisson or an nbinom GL(M)M`
			`abs(var(df[df$X == "a",]$Y) / mean(df[df$X == "a",]$Y)) > 1.15`
			`abs(var(df[df$X == "b",]$Y) / mean(df[df$X == "b",]$Y)) > 1.15`

Negative Binomial	theta (θ): `size`
	mu (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`
			`fa = fitdist(df[df$X == "a",]$Y, distr="nbinom") # create fit for X=a`
			`gofstat(fa) # chi-squared GOF`
			`fb = fitdist(df[df$X == "b",]$Y, distr="nbinom") # create fit for X=b`
			`gofstat(fb) # chi-squared 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."

Poisson	lambda (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."

Negative Binomial	theta (θ): `size`
	mu (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 4

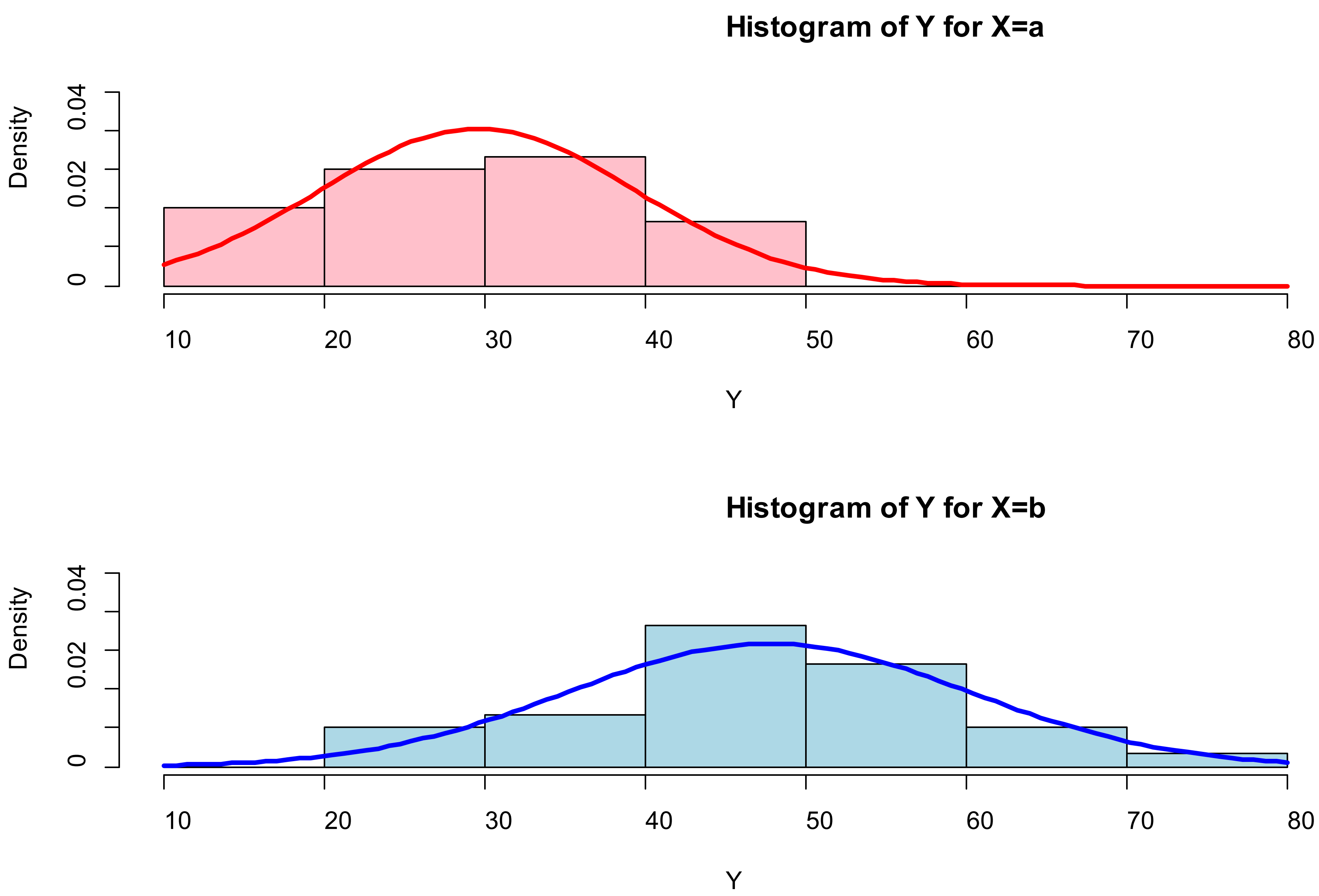
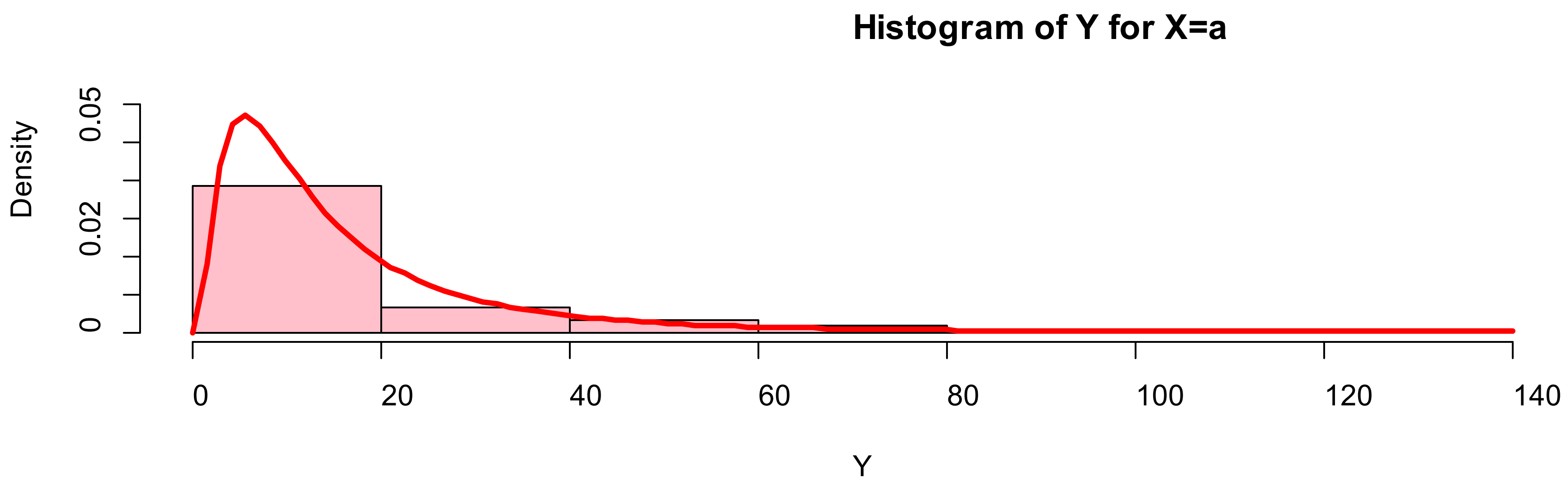

Histogram of Y for X=a
Density
0
0.02
0.04
10
20
30
40
50
60
70
80
Y
Histogram of Y for X=b
Density
0
0.02
0.04
10
20
30
40
50
60
70
80
Y

Figure 5


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

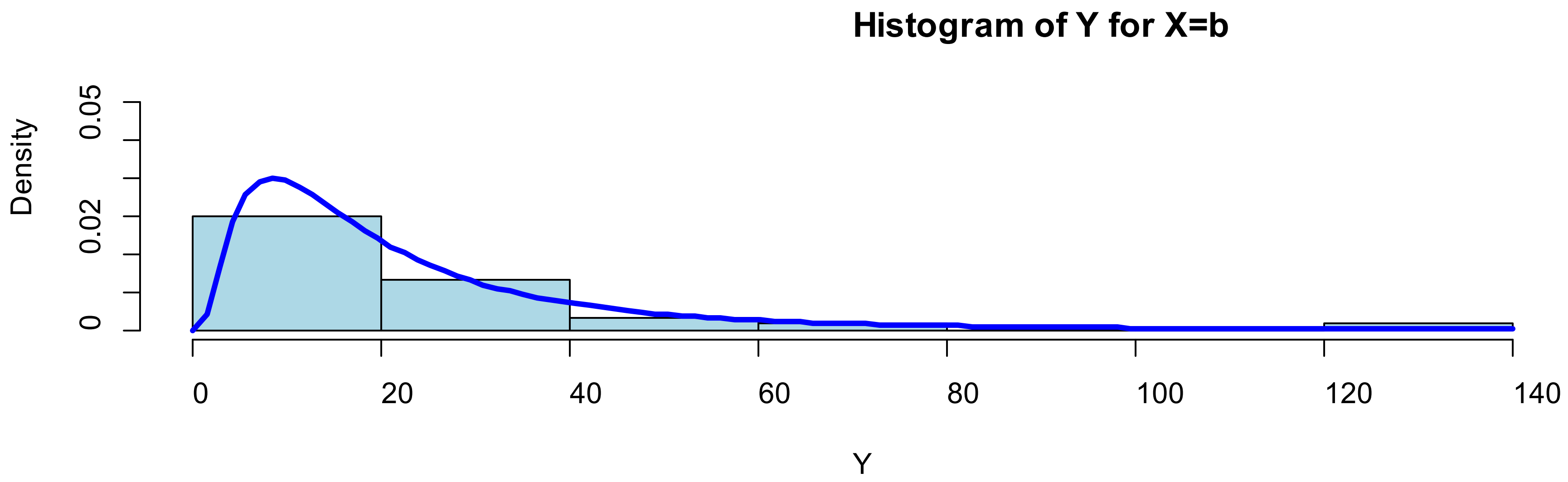

Histogram of Y for X=b
Density
0
0.02
0.05
0
20
40
60
80
100
120
140
Y

Figure 6

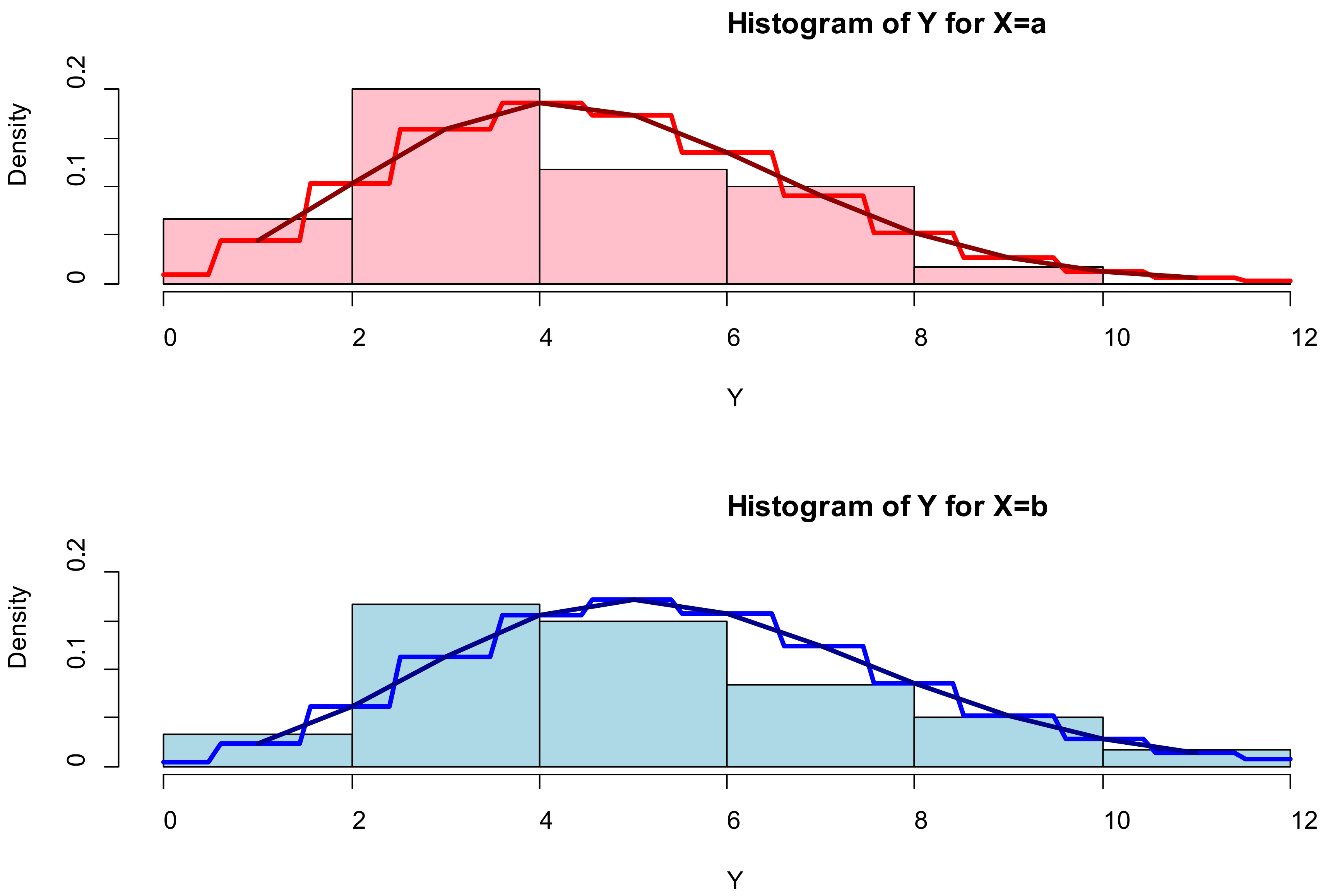
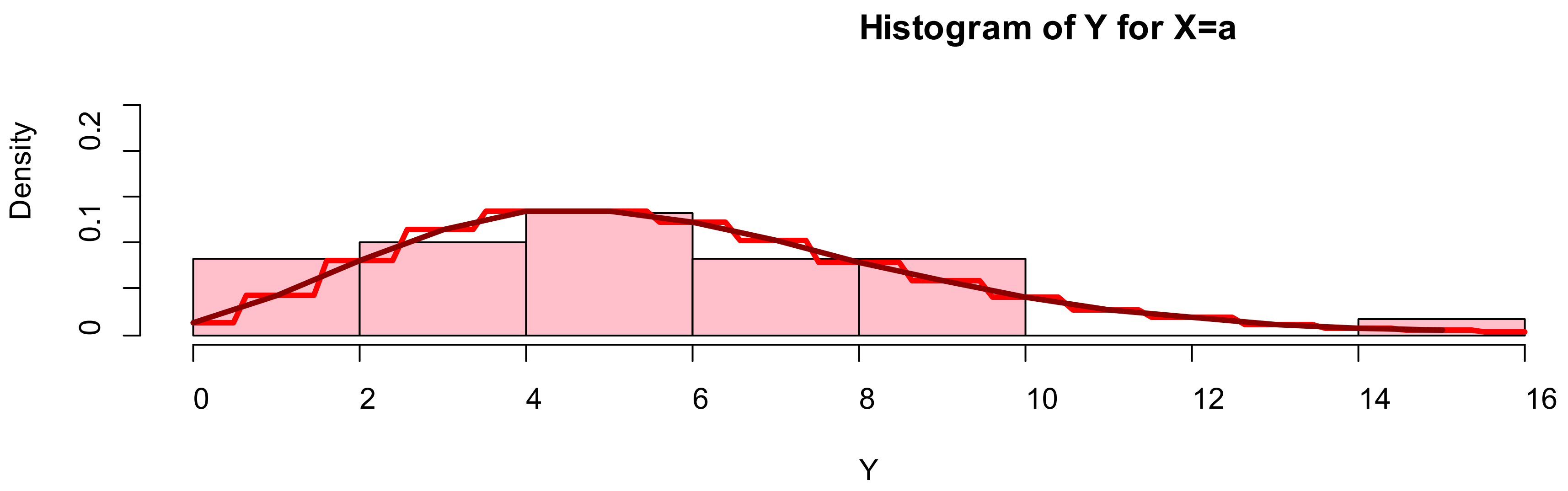
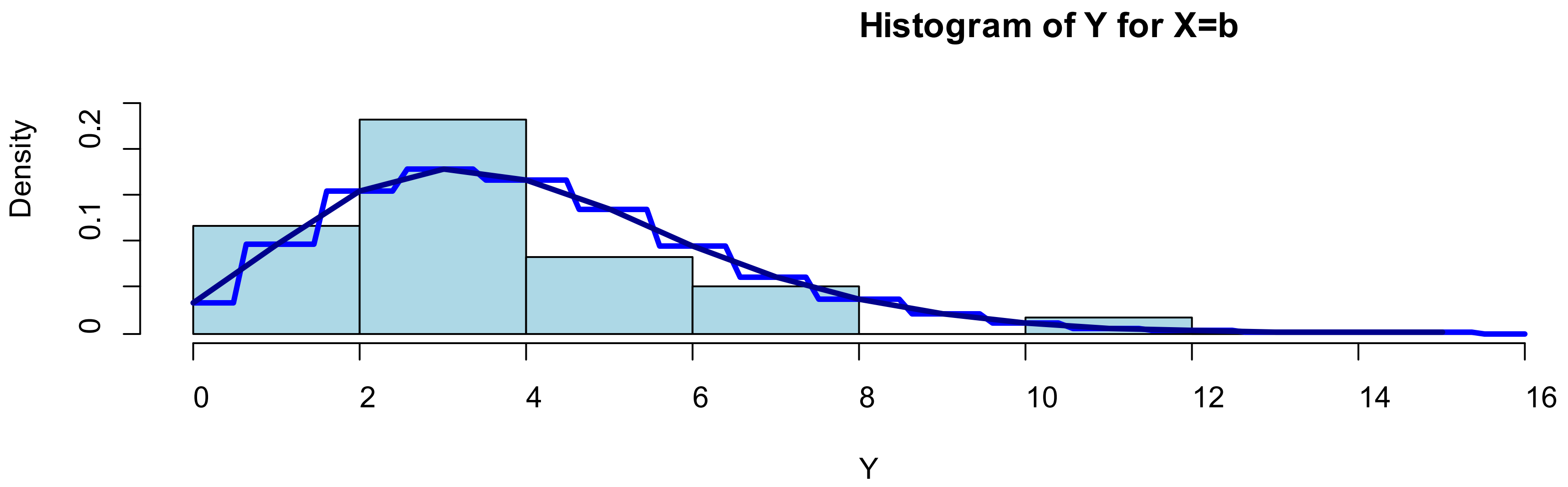

Histogram of Y for X=a
Density
0
0.1
0.2
0
2
4
6
8
10
12
Y
Histogram of Y for X=b
Density
0
0.1
0.2
0
2
4
6
8
10
12
Y

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`
			`fa = gofTest(df[df$X == "a",]$Y, distribution="exp") # create fit for X=a`
			`print(fa) # Shapiro-Wilk GOF`
			`fb = gofTest(df[df$X == "b",]$Y, distribution="exp") # create fit for X=b`
			`print(fb) # Shapiro-Wilk 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`
			`fa = gofTest(df[df$X == "a",]$Y, distribution="gamma") # create fit for X=a`
			`print(fa) # Shapiro-Wilk GOF`
			`fb = gofTest(df[df$X == "b",]$Y, distribution="gamma") # create fit for X=b`
			`print(fb) # Shapiro-Wilk 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

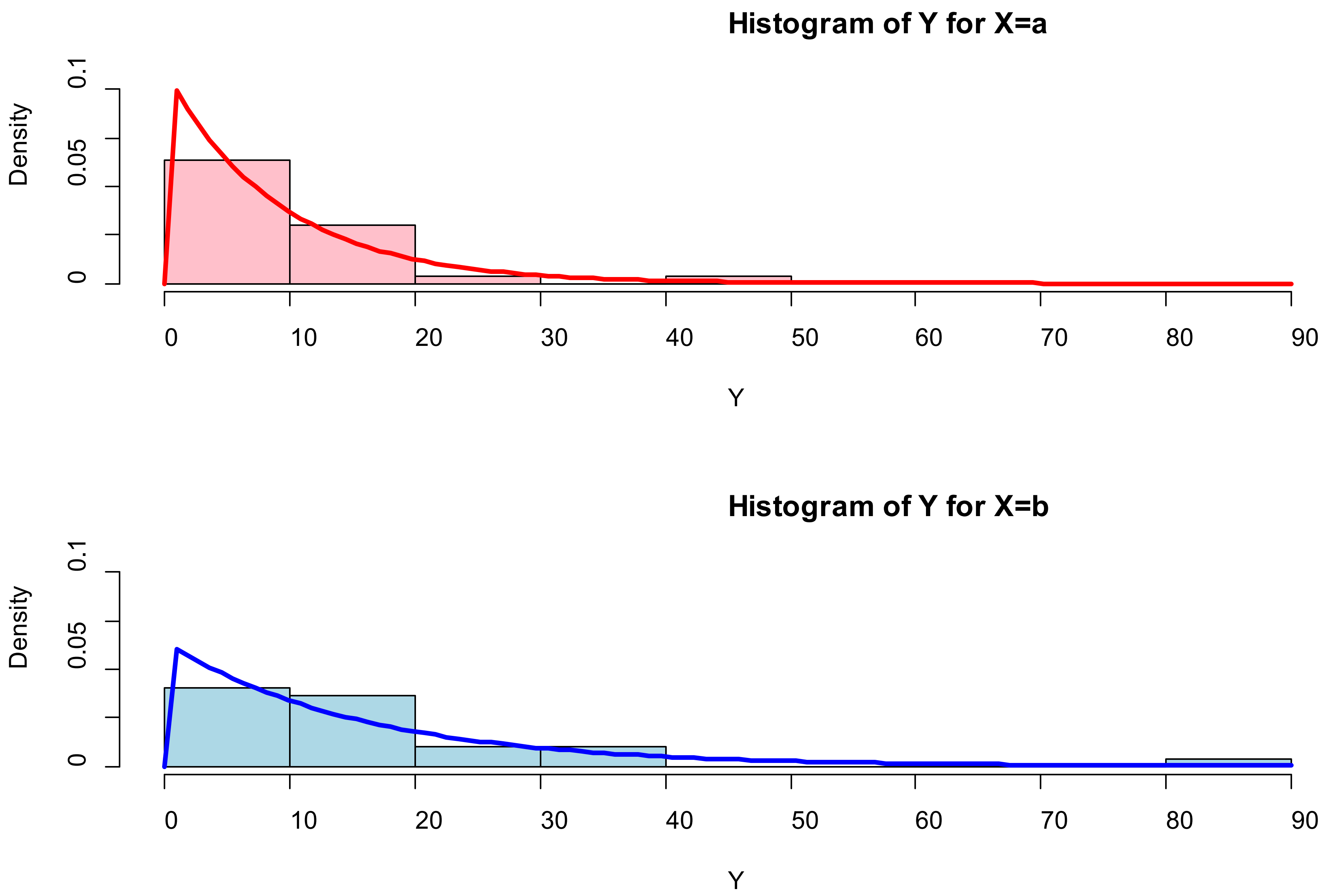
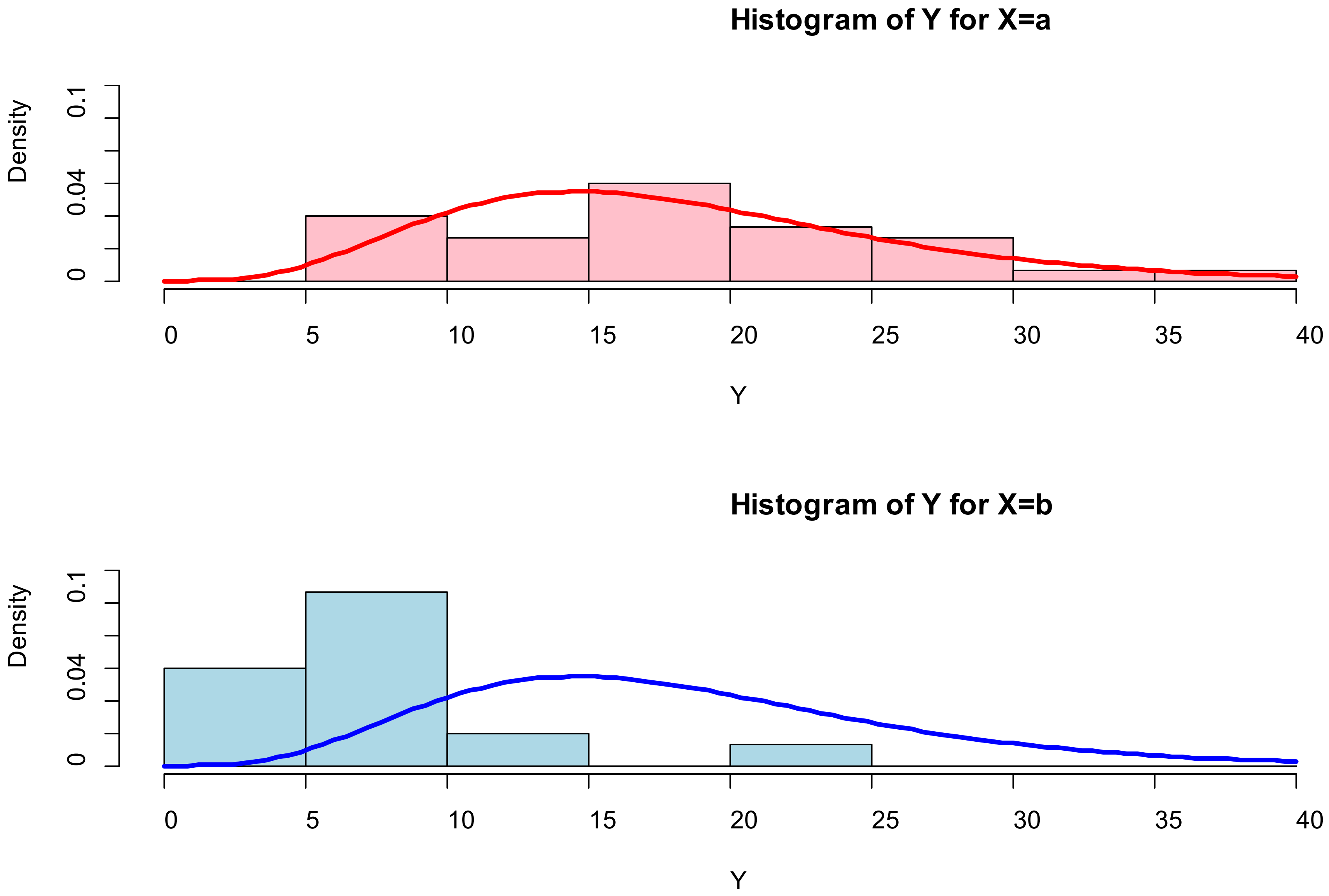

Histogram of Y for X=a
Density
0
0.05
0.1
0
10
20
30
40
50
60
70
80
90
Y
Histogram of Y for X=b
Density
0
0.05
0.1
0
10
20
30
40
50
60
70
80
90
Y

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

Bibliography (data distributions)

- Aitchison, J. and Brown, J.A.C. (1957). *The Lognormal Distribution*. Cambridge, UK: Cambridge University Press. http://www.jstor.org/stable/2227716
- Hilbe, J.M. (2011). *Negative Binomial Regression*. Cambridge, UK: Cambridge University Press. https://doi.org/10.1017/CBO9780511973420
- Hilbe, J.M. (2014). *Modeling Count Data*. New York, NY: Cambridge University Press. https://books.google.com/books?id=aZLfAwAAQBAJ
- Lawless, J.F. (1987). Negative binomial and mixed Poisson regression. *The Canadian Journal of Statistics 15* (3), pp. 209-225. https://doi.org/10.2307/3314912
- Ng, V.K.Y. and Cribbie, R.A. (2017). Using the gamma generalized linear model for modeling continuous, skewed and heteroscedastic outcomes in psychology. *Current Psychology 36* (2), pp. 225-235. https://doi.org/10.1007/s12144-015-9404-0
- Pearson, K. (1900). On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling. *The London, Edinburgh, and Dublin Philosophical Magazine and Journal of Science, Series 5, vol. 50* (302), pp. 157-175. https://doi.org/10.1080/14786440009463897
- Shapiro, S.S. and Wilk, M.B. (1965). An analysis of variance test for normality (complete samples). Biometrika 52 (3/4), pp. 591-611. https://doi.org/10.2307/2333709
- Vermunt, J.K. (1997). *Log-linear Models for Event Histories*. Thousand Oaks, CA: Sage Publications. https://books.google.com/books?id=apI_AQAAIAAJ
- von Bortkiewicz, L. (1898). *Das Gesetz der Kleinen Zahlen (The Law of Small Numbers)*. Leipzig, Germany: Druck und Verlag von B.G. Teubner. https://books.google.com/books?id=o_k3AAAAMAAJ

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 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 t.test(Y ~ X, data=df, var.equal=FALSE) # if p<.05, violation of homogeneity
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 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 print(check_homogeneity(m)) # Levene's test leveneTest(Y ~ X, data=df, center=mean) # same anova(m) # if p≥.05, no violation of homogeneity Anova(m\$lm, type=3, white.adjust=TRUE) # if p<.05, violation of homogeneity

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 ($t(58) = -5.21$, $p < .0001$)."
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 ($F(2, 57) = 4.24$, $p = .019$)."

Note: "*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`
				`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 homogeneity nor sphericity applies to a paired t-test`

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`
				`print(check_sphericity(m))  # Mauchly's test`
				
				`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 ($t(29) = -4.85$, $p < .0001$)."
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 ($F(2, 38) = 4.06$, $p = .025$)."

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

Parametric Tests

Multiple between-Ss. factors

<table>
<tr><th>Factors</th><th>Levels</th><th>Between or Within Subjects</th><th>Test Name</th><th>R Code</th></tr>
<tr><td rowspan="2">≥2</td><td rowspan="2">≥2</td><td rowspan="2">Between</td><td>Factorial ANOVA</td><td><code># df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)
library(afex) # for aov_ez
library(performance) # for check_homogeneity
library(car) # for Anova
df$PId = factor(df$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
print(check_homogeneity(m)) # Levene's test
leveneTest(Y ~ X1*X2, data=df, center=mean) # same

anova(m) # if p≥.05, no violation of homogeneity
Anova(m$lm, type=3, white.adjust=TRUE) # if p<.05, violation of homogeneity</code></td></tr>
<tr><td>Linear model (LM)</td><td><code># df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)
library(car) # for Anova
df$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
print(check_homogeneity(m)) # Levene's test
leveneTest(Y ~ X1*X2, data=df, center=mean) # same

anova(m) # if p≥.05, no violation of homogeneity
Anova(m, type=3, white.adjust=TRUE) # if p<.05, violation of homogeneity</code></td></tr>
</table>

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 ($F(1, 56) = 20.51$, $p < .0001$), no significant effect of X2 ($F(1, 56) = 0.09$, $p = .766$), and a significant X1×X2 interaction ($F(1, 56) = 7.15$, $p = .010$)."
			Linear Model (LM)	"Figure 10 shows an interaction plot with ±1 standard deviation error bars for X1 and X2. Levene's test indicated a violation of the assumption of homogeneity of variance ($F(3, 56) = 6.86$, $p = .001$). Therefore, a White-adjusted factorial ANOVA was used. It indicated a significant effect on Y of X1 ($F(1, 56) = 20.51$, $p < .0001$), no significant effect of X2 ($F(1, 56) = 0.09$, $p = .766$), and a significant X1×X2 interaction ($F(1, 56) = 7.15$, $p = .010$)."

Parametric Tests

Multiple within-Ss. factors

<table>
<tr><th>Factors</th><th>Levels</th><th>Between or Within Subjects</th><th>Test Name</th><th>R Code</th></tr>
<tr><td>≥2</td><td>≥2</td><td>Within</td><td>Factorial repeated measures ANOVA</td><td><code># 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
print(check_sphericity(m)) # Mauchly's test

anova(m, correction="none") # use if p≥.05, no violation of sphericity
anova(m, correction="GG")   # use if p<.05, sphericity violation</code></td></tr>
<tr><td>≥2</td><td>≥2</td><td>Within</td><td>Linear mixed model (LMM)*</td><td><code># df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)
library(lme4) # for lmer
library(lmerTest)
library(car) # for Anova
df$PId = factor(df$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")</code></td></tr>
</table>

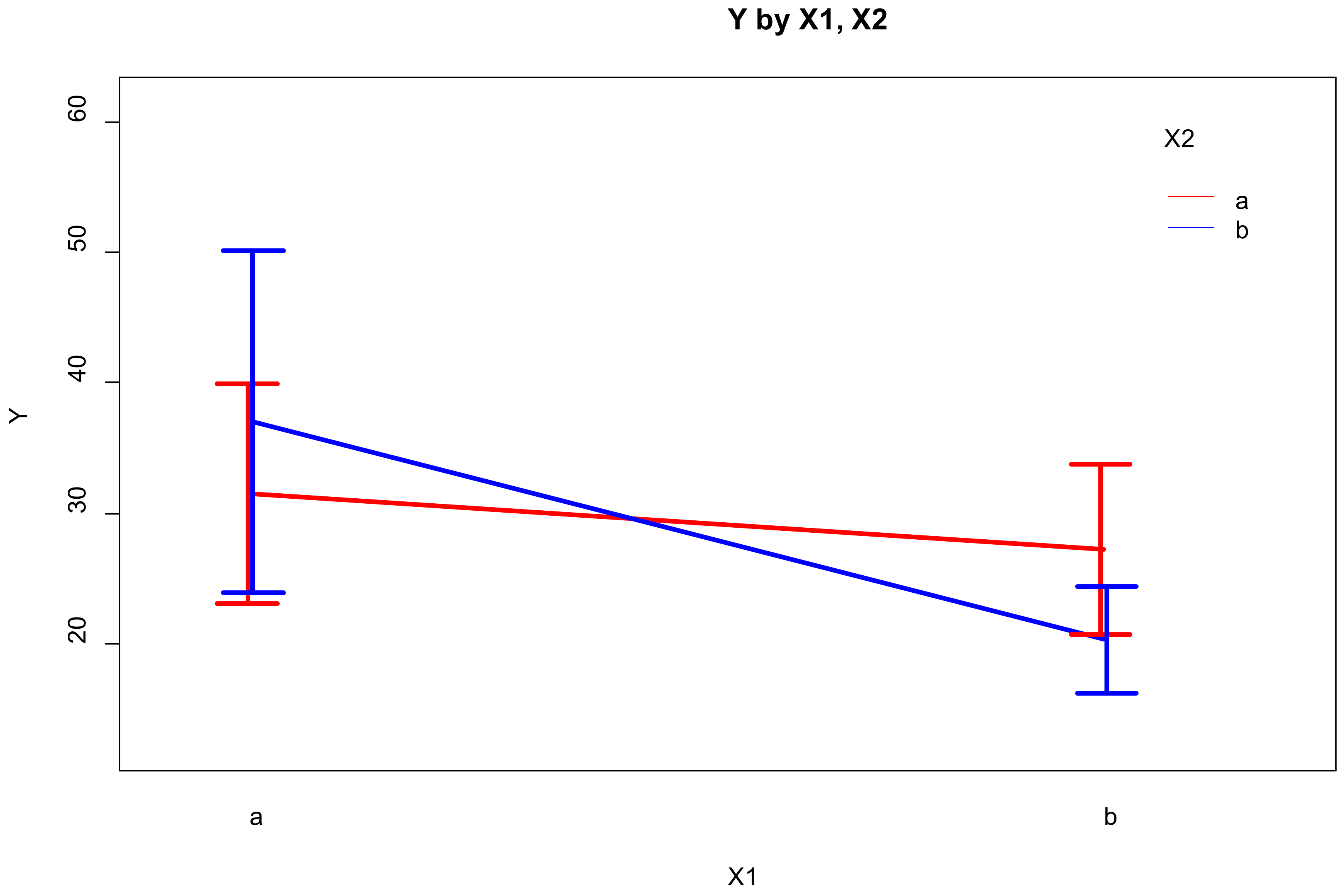
*The LMM sample code uses a random intercept for *participant (PId)*. There are also random slope models, which are used when the response changes at different rates for each *PId* over a repeated factor. A 2-minute random slope example of county population growth over time can be seen here (https://www.youtube.com/watch?v=YDe6F7CXjWw).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

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 ($F(1, 14) = 29.58$, $p < .0001$), no significant effect of X2 ($F(1, 14) = 0.08$, $p = .785$), and a significant X1×X2 interaction ($F(1, 14) = 5.11$, $p = .040$)."
≥2	≥2	Within	Linear Mixed Model (LMM)	"Figure 10 shows an interaction plot with ±1 standard deviation error bars for X1 and X2. An analysis of variance based on a linear mixed model (LMM) indicated a significant effect on Y of X1 ($F(1, 42) = 21.98$, $p < .0001$), no significant effect of X2 ($F(1, 42) = 0.10$, $p = .758$), and a significant X1×X2 interaction ($F(1, 42) = 7.66$, $p = .008$)."

Figure 10



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`
					`emmeans(m, pairwise ~ X, adjust="holm") # m is from afex::aov_ez`

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`
					`emmeans(m, pairwise ~ X, adjust="holm") # m is from afex::aov_ez`

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 ($t(57) = -2.77$, $p = .023$), 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 independent-samples *t*-tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' was significantly different ($t(19) = -2.70$, $p = .042$), but 'a' *vs.* 'c' and 'b' *vs.* 'c' were not."

Parametric Tests

Post hoc pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Test	Test Name	B/W	R Code

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

≥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`
					`emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from afex::aov_ez`

≥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`
					`emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from lme4::lmer`

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} ($t(56) = 3.53$, $p = .004$), {b,a} *vs.* {a,b} ($t(56) = -3.10$, $p = .012$), and {a,b} *vs.* {b,b} ($t(56) = 5.27$, $p < .0001$) were significantly different. The other three pairwise comparisons were not detectably different."
≥2	≥2	Factorial repeated measures ANOVA	Paired samples *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} ($t(14) = 4.82$, $p = .002$), {b,a} *vs.* {b,b} ($t(14) = 3.27$, $p = .023$), {a,b} *vs.* {b,b} ($t(14) = 4.25$, $p = .004$) were significantly different. The other three pairwise comparisons were not detectably different."
≥2	≥2	Linear mixed model (LMM)	Paired samples *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} ($t(42) = 3.53$, $p = .005$), {b,a} *vs.* {a,b} ($t(42) = -3.10$, $p = .014$), and {a,b} *vs.* {b,b} ($t(42) = 5.27$, $p < .0001$) were significantly different. The other three pairwise comparisons were not detectably different."

Bibliography (parametric *t*-tests, F-tests, and effect sizes)

- Cohen, J. (1973). Eta-squared and partial eta-squared in fixed factor ANOVA designs. *Educational and Psychological Measurement 33* (1), pp. 107-112. https://doi.org/10.1177/001316447303300111
- Cohen, J. (1988). *Statistical Power Analysis for the Behavioral Sciences*. Hillsdale, NJ: Lawrence Erlbaum Associates, pp. 20-27.
- Fisher, R.A. (1921). On the "probable error" of a coefficient of correlation deduced from a small sample. *Metron 1* (4), pp. 3-32.
- Fisher, R.A. (1925). *Statistical methods for research workers*. Edinburgh, Scotland: Oliver and Boyd. https://en.wikipedia.org/wiki/Statistical_Methods_for_Research_Workers
- Greenhouse, S.W. and Geisser, S. (1959). On methods in the analysis of profile data. *Psychometrika 24* (2), pp. 95-112. https://doi.org/10.1007/BF02289823
- Kenward, M.G. and Roger, J.H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics 53* (3), pp. 983-997. https://doi.org/10.2307/2533558
- Levene, H. (1960). Robust tests for equality of variances. In *Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling*, I. Olkin, S.G. Ghurye, H. Hoeffding, W.G. Madow and H.B. Mann (eds.). Palo Alto, CA: Stanford University Press, pp. 278-292.
- Mauchly, J.W. (1940). Significance test for sphericity of a normal n-variate distribution. *The Annals of Mathematical Statistics 11* (2), pp. 204-209. https://www.jstor.org/stable/2235878
- Olejnik, S. and Algina, J. (2003). Generalized eta and omega squared statistics: Measures of effect size for some common research designs. *Psychological Methods 8* (4), pp. 434-447. https://doi.org/10.1037/1082-989X.8.4.434

Bibliography (parametric *t*-tests, F-tests, and effect sizes)

- Student. (1908). The probable error of a mean. *Biometrika 6* (1), pp. 1-25. https://doi.org/10.2307/2331554
- Wald, A. (1943). Tests of statistical hypotheses concerning several parameters when the number of observations is large. *Transactions of the American Mathematical Society 54* (3), pp. 426-482. https://doi.org/10.2307/1990256
- Welch, B.L. (1951). On the comparison of several mean values: An alternative approach. *Biometrika 38* (3/4), pp. 330-336. https://doi.org/10.2307/2332579
- White, H. (1980). A heteroskedasticity-consistent covariance matrix estimator and a direct test for heteroskedasticity. *Econometrica 48* (4), pp. 817-838. https://doi.org/10.2307/1912934

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`
			`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`
			`Anova(m, type=3, test.statistic="Chisq") # for chisq test`
			`emmeans(m, pairwise ~ X, adjust="holm", mode="containment") # post hoc tests`

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`

Note: The `lme4::lmer` function does not allow specifying common variance-covariance (VCV) structures for repeated factors or residuals. Therefore, we must use `nlme::lme` for this. For a list of common VCV structures, see https://www.ibm.com/docs/en/spss-statistics/26.0.0?topic=mixed-covariance-structure-list-command. For their matrix formulations, see https://www.ibm.com/docs/en/spss-statistics/26.0.0?topic=statistics-covariance-structures. For a treatment in R, see https://rpubs.com/samuelkn/CovarianceStructuresInR.

Note: 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`

Note: 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.

Bibliography (variance-covariance structures, linear mixed models, random effects)

- Frederick, B.N. (1999). Fixed-, random-, and mixed-effects ANOVA models: A user-friendly guide for increasing the generalizability of ANOVA results. In *Advances in Social Science Methodology*, B. Thompson (ed.). Stamford, CT: JAI Press, pp. 111-122. http://eric.ed.gov/?id=ED426098
- Krueger, C. and Tian, L. (2004). A comparison of the general linear mixed model and repeated measures ANOVA using a dataset with multiple missing data points. *Biological Research for Nursing 6* (2), pp. 151-157. https://doi.org/10.1177/1099800404267682
- Laird, N.M. and Ware, J.H. (1982). Random-effects models for longitudinal data. *Biometrics 38* (4), pp. 963-974. https://www.jstor.org/stable/2529876
- Littell, R.C., Henry, P.R. and Ammerman, C.B. (1998). Statistical analysis of repeated measures data using SAS procedures. *Journal of Animal Science 76* (4), pp. 1216-1231. https://doi.org/10.2527/1998.7641216x
- Littell, R.C., Pendergast, J. and Natarajan, R. (2000). Modelling covariance structure in the analysis of repeated measures data. *Statistics in Medicine 19* (13), pp. 1793-1819. https://doi.org/10.1002/1097-0258(20000715)19:13<1793::AID-SIM482>3.0.CO;2-Q
- Pinheiro, J.C. and Bates, D.M. (2000). *Mixed-Effects Models in S and S-PLUS*. New York, NY: Springer. https://link.springer.com/book/10.1007/b98882
- Schuster, C. and von Eye, A. (2001). The relationship of ANOVA models with random effects and repeated measurement designs. *Journal of Adolescent Research 16* (2), pp. 205-220. https://doi.org/10.1177/0743558401162006
- Ware, J.H. (1985). Linear models for the analysis of serial measurements in longitudinal studies. *American Statistician 39* (2), pp. 95-101. https://doi.org/10.2307/2682803
- West, B.T., Welch, K.B. and Gałecki, A.T. (2015). *Linear Mixed Models*. Boca Raton, FL: CRC Press.

Nonparametric Tests

Nonparametric Tests

One factor with 2 levels

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

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

Nonparametric Tests

One factor with 2 levels

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

Note: "*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 ($\chi^2(2, N{=}60) = 12.90$, $p = .002$)."

Note: "*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)`

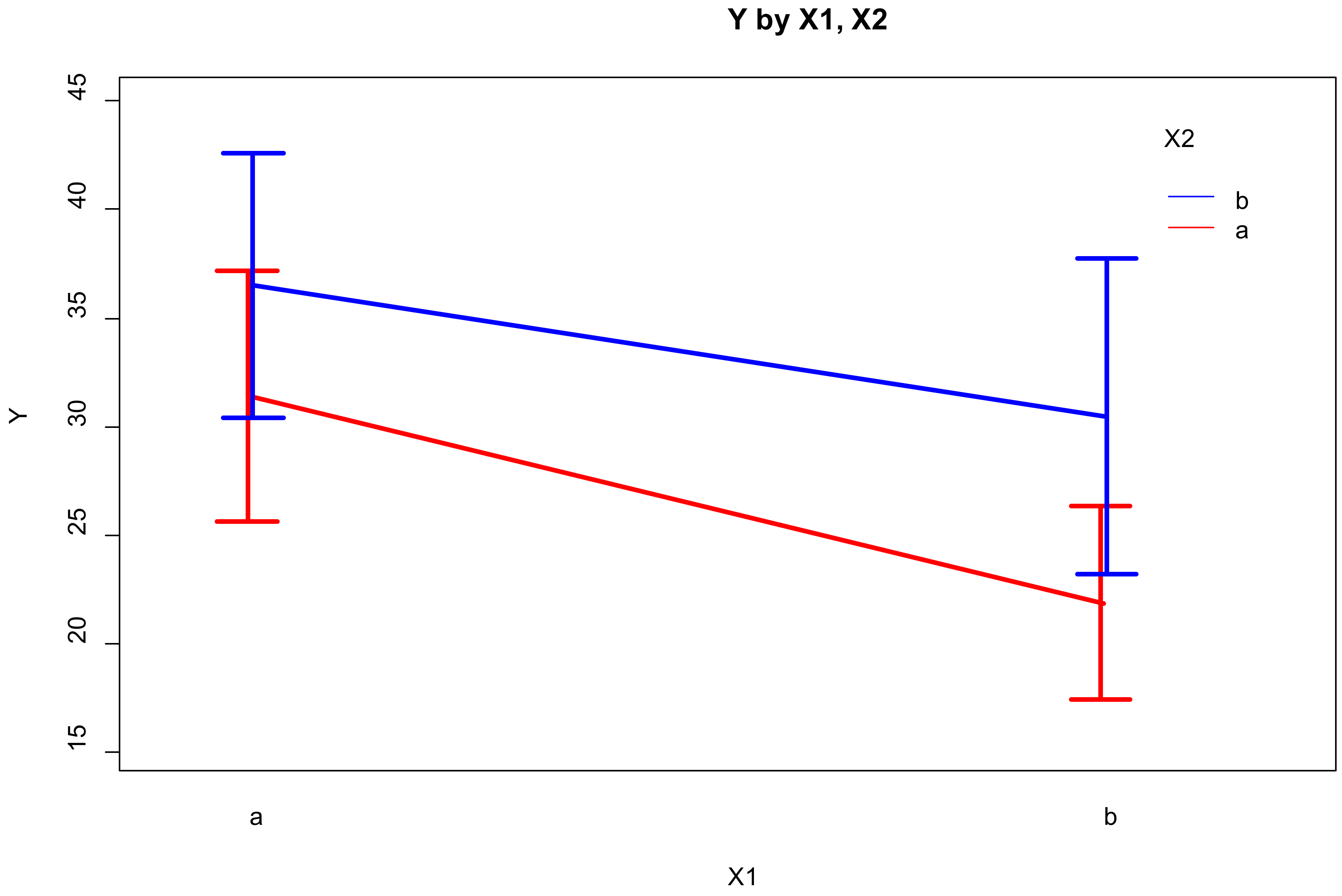
*The Aligned Rank Transform within-subjects sample code uses a random <u>intercept</u> for *participant (PId)*. There are also random <u>slope</u> models, which are used when the response changes at different rates for each participant over a repeated factor. A 2-minute random slope example of county 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://thecraftofstatisticalanalysis.com/random-intercept-random-slope-models/).

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-scores`
					`wilcoxonZ(df[df$X == "a",]$Y, df[df$X == "c",]$Y)`
					`wilcoxonZ(df[df$X == "b",]$Y, df[df$X == "c",]$Y)`

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-scores`
					`wilcoxonZ(df2$a, df2$c, paired=TRUE)`
					`wilcoxonZ(df2$b, df2$c, paired=TRUE)`

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."

Bibliography (one-way nonparametric tests, aligned rank transform)

- Brown, G.W. and Mood, A.M. (1948). Homogeneity of several samples. *The American Statistician 2* (3), p. 22. https://doi.org/10.2307/2682087
- Brown, G.W. and Mood, A.M. (1951). On median tests for linear hypotheses. In *Proceedings of the Second Berkeley Symposium on Mathematical Statistics and Probability*. Berkeley, CA: University of California Press, pp. 159-166. https://projecteuclid.org/ebooks/berkeley-symposium-on-mathematical-statistics-and-probability/Proceedings-of-the-Second-Berkeley-Symposium-on-Mathematical-Statistics-and/chapter/On-Median-Tests-for-Linear-Hypotheses/bsmsp/1200500226
- Conover, W.J. (1999). The sign test. In *Practical Nonparametric Statistics (3rd ed.)*. New York, NY: John Wiley & Sons, pp. 157-165. https://www.wiley.com/en-us/Practical+Nonparametric+Statistics%2C+3rd+Edition-p-9780471160687
- Elkin, L.A., Kay, M., Higgins, J. and Wobbrock, J.O. (2021). An aligned rank transform procedure for multifactor contrast tests. *Proceedings of the ACM Symposium on User Interface Software and Technology (UIST '21)*. New York, NY: ACM Press, pp. 754-768. https://doi.org/10.1145/3472749.3474784
- Friedman, M. (1937). The use of ranks to avoid the assumption of normality implicit in the analysis of variance. *Journal of the American Statistical Association 32* (200), pp. 675-701. https://doi.org/10.2307/2279372
- Higgins, J.J., Blair, R.C. and Tashtoush, S. (1990). The aligned rank transform procedure. *Proceedings of the Conference on Applied Statistics in Agriculture*. Manhattan, Kansas: New Prairie Press, pp. 185-195. http://newprairiepress.org/agstatconference/1990/proceedings/18/
- Higgins, J.J. and Tashtoush, S. (1994). An aligned rank transform test for interaction. *Nonlinear World 1* (2), pp. 201-211.
- Hodges, J.L. and Lehmann, E.L. (1962). Rank methods for combination of independent experiments in the analysis of variance. *Annals of Mathematical Statistics 33* (2), pp. 482-497. https://www.jstor.org/stable/2237528

Bibliography (one-way nonparametric tests, aligned rank transform)

- Kruskal, W.H. and Wallis, W.A. (1952). Use of ranks in one-criterion variance analysis. *Journal of the American Statistical Association 47* (260), pp. 583-621. https://doi.org/10.2307/2280779
- Mann, H.B. and Whitney, D.R. (1947). On a test of whether one of two random variables is stochastically larger than the other. *Annals of Mathematical Statistics 18* (1), pp. 50-60. https://www.jstor.org/stable/2236101
- Salter, K.C. and Fawcett, R.F. (1985). A robust and powerful rank test of treatment effects in balanced incomplete block designs. *Communications in Statistics: Simulation and Computation 14* (4), pp. 807-828. https://doi.org/10.1080/03610918508812475
- Salter, K.C. and Fawcett, R.F. (1993). The ART test of interaction: A robust and powerful rank test of interaction in factorial models. *Communications in Statistics: Simulation and Computation 22* (1), pp. 137-153. https://doi.org/10.1080/03610919308813085
- Wilcoxon, F. (1945). Individual comparisons by ranking methods. *Biometrics Bulletin 1* (6), pp. 80-83. https://doi.org/10.2307/3001968
- Wobbrock, J.O., Findlater, L., Gergle, D. and Higgins, J.J. (2011). The aligned rank transform for nonparametric factorial analyses using only ANOVA procedures. *Proceedings of the ACM Conference on Human Factors in Computing Systems (CHI '11)*. New York, NY: ACM Press, pp. 143-146. https://doi.org/10.1145/1978942.1978963

Generalized Linear (Mixed) Models

Terminology

Generalize to Responses Unsuitable to ANOVA?

Contain Random Factors?*		No	Yes	
	No	(General) Linear Model **(LM)** (Sometimes abbreviated GLM) `lm` in R (see also `aov`)	Generalized Linear Model **(GLM)** (Sometimes abbreviated GZLM or GLIM) `glm` in R	*Between-Ss.*
	Yes	(General) Linear Mixed Model **(LMM)** `lme4::lmer` in R (see also `nlme::lme`)	Generalized Linear Mixed Model **(GLMM)** `lme4::glmer` in R	*Within-Ss.*
		Normal only	Normal, binomial, multinomial, ordinal, Poisson, zero-inflated Poisson, negative binomial, zero-inflated negative binomial, exponential, gamma	

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

Distribution	GLM	GLMM
Normal	`lm()`[1]	`lme4::lmer()`[2]
Lognormal[3]	`lm(log(Y) ~ ...)`	`lme4::lmer(log(Y) ~ ...)`
Binomial	`glm() family=binomial`	`lme4::glmer() family=binomial`
Multinomial[4]	`multpois::glm.mp()` `multpois::Anova.mp()`	`multpois::glmer.mp()` `multpois::Anova.mp()`
Ordinal	`MASS::polr()`	`ordinal::clmm()` `RVAideMemoire::Anova.clmm()`
Poisson	`glm() family=poisson` `#or family=quasipoisson`[5]	`lme4::glmer() family=poisson`
Zero-inflated Poisson[6]	`glmmTMB::glmmTMB() family=poisson ziformula=~1`	`glmmTMB::glmmTMB() family=poisson ziformula=~1 REML=TRUE`[7]
Negative binomial	`MASS::glm.nb()`	`lme4::glmer.nb()`
Zero-inflated negative binomial[6]	`glmmTMB::glmmTMB() family=nbinom2 ziformula=~1`	`glmmTMB::glmmTMB() family=nbinom2 ziformula=~1 REML=TRUE`[7]
Exponential	`glm() family=Gamma(link="log")`	`lme4::glmer() family=Gamma(link="log")`
Gamma[8]	`glm() family=Gamma`	`lme4::glmer() family=Gamma`

Footnotes [1] – [8] appear on next slide.

Footnotes

[1] `lm` and `glm` are from the base `stats` package in R. A call to `glm` with `family=gaussian` is the same as a call to `lm`.

[2] An `lme4::glmer` call with `family=gaussian` will produce a message that one should just use `lme4::lmer`, which is equivalent.

[3] A lognormal distribution is just a log-transform of the response *Y* and otherwise a linear (mixed) model.

[4] The `multpois` functions use the multinomial-Poisson transformation (Baker 1994). See **NB**, below.

[5] Use `family=quasipoisson` when mild overdispersion is present. If overdisperson is large, use negative binomial regression. Note that `family=quasipoisson` cannot be used with `lme4::glmer`.

[6] Use zero-inflated variants of Poisson regression or negative binomial regression when distributions show large numbers of zeros relative to other counts. Use `print(performance::check_zeroinflation(m))` to test whether a regular Poisson or negative binomial model `m` is zero-inflated. The `glmmTMB` function takes a `ziformula` parameter that can be set to `~1` to fit a single zero-inflation parameter applying to all observations. (The `glmmTMB` vignette offers more detail.)

[7] `glmmTMB` models with random factors should set `REML` to `TRUE` to use restricted maximum likelihood estimation.

[8] Gamma models use the inverse function as their canonical link, $f(x) = x^{-1}$. Sometimes this fails; in such cases, it is reasonable to try the log link function, $f(x) = \log(x)$. Set the `family` parameter to `Gamma(link="log")`.

NB: Unfortunately, there is no `family=multinomial` option for `glm` or `lme4::glmer`. Also, the `nnet::multinom` function produces models that are difficult to use with `emmeans`. Moreover, `multinom` cannot accept random factors to handle repeated measures. Some other functions *do* offer multinomial regression modeling, such as `mclogit::mblogit`, but do not enable ANOVA-style output. Markov chain Monte Carlo (MCMC) methods in the `MCMCglmm` package also exist, but these methods utilize Bayesian approaches distinct from the other models presented here. Fortunately, Baker (1994) illustrated how multinomial models can be treated as Poisson models using the multinomial-Poisson transformation. By analyzing our data as counts for each categorical alternative, we can use `glm` or `lme4::glmer` with `family=poisson` to obtain the equivalent results as if they had a `family=multinomial` option. The `multpois` package offers such models, and the `multpois::Anova.mp` function produces ANOVA-style output. The `*.mp.con` functions carry out *post hoc* pairwise comparisons.

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(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)
			print(check_normality(m))
			print(check_homogeneity(m))
			Anova(m, type=3, test.statistic="F")
				library(lme4) # for lmer
				library(lmerTest)
				library(car) # for Anova
				library(performance) # for check_*
				df$PId = factor(df$PId)
				df$X1 = factor(df$X1)
				df$X2 = factor(df$X2)
				contrasts(df$X1) <- "contr.sum"
				contrasts(df$X2) <- "contr.sum"
				m = lmer(Y ~ X1*X2 + (1|PId), data=df)
				print(check_normality(m))
				print(check_homogeneity(m))
				Anova(m, type=3, test.statistic="F")

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

Note: 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://thecraftofstatisticalanalysis.com/random-intercept-random-slope-models/).

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 ($F(1, 56) = 8.05$, $p = .006$)."	"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 ($F(1, 42) = 8.05$, $p = .007$)."
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 12

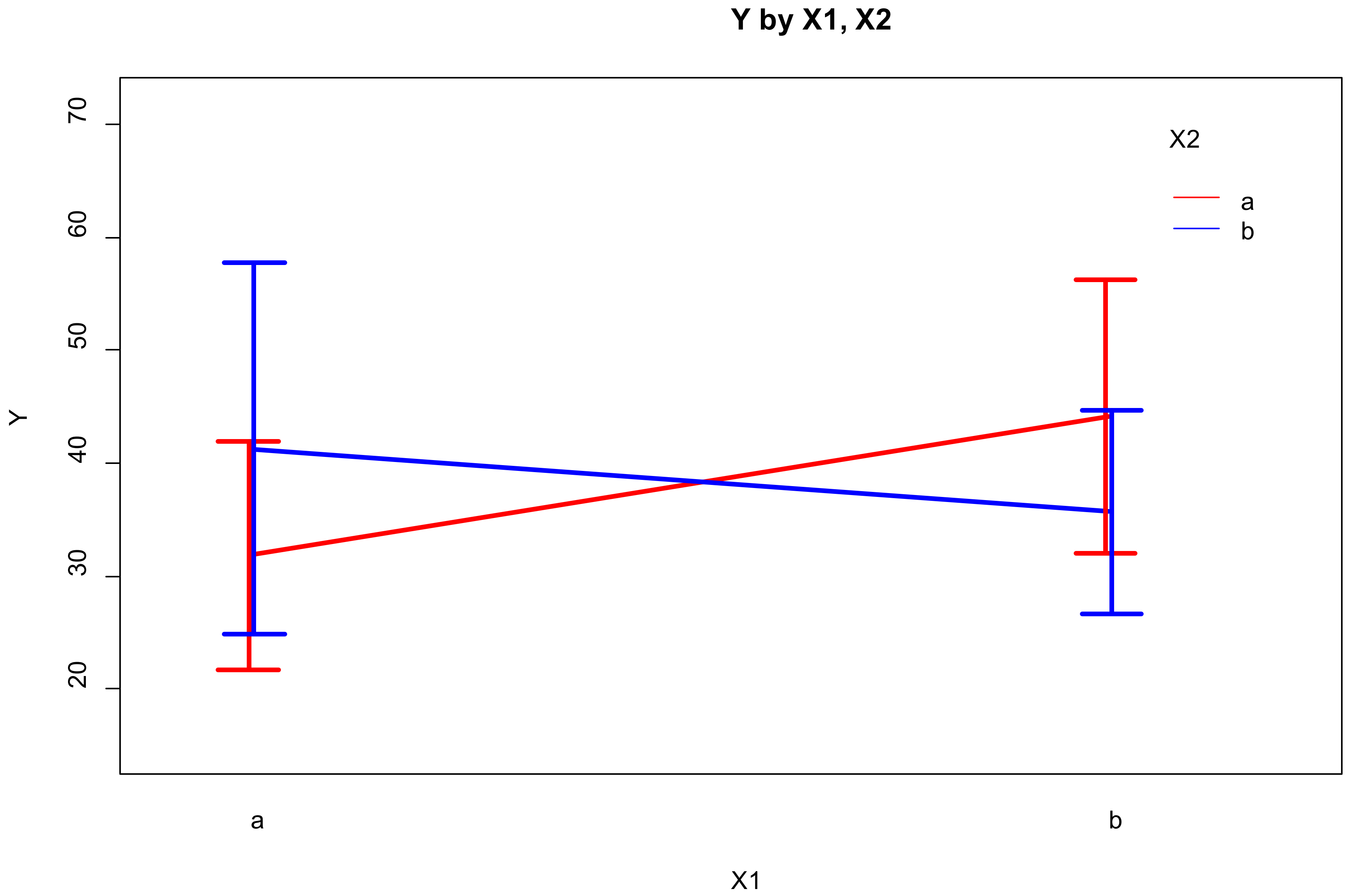
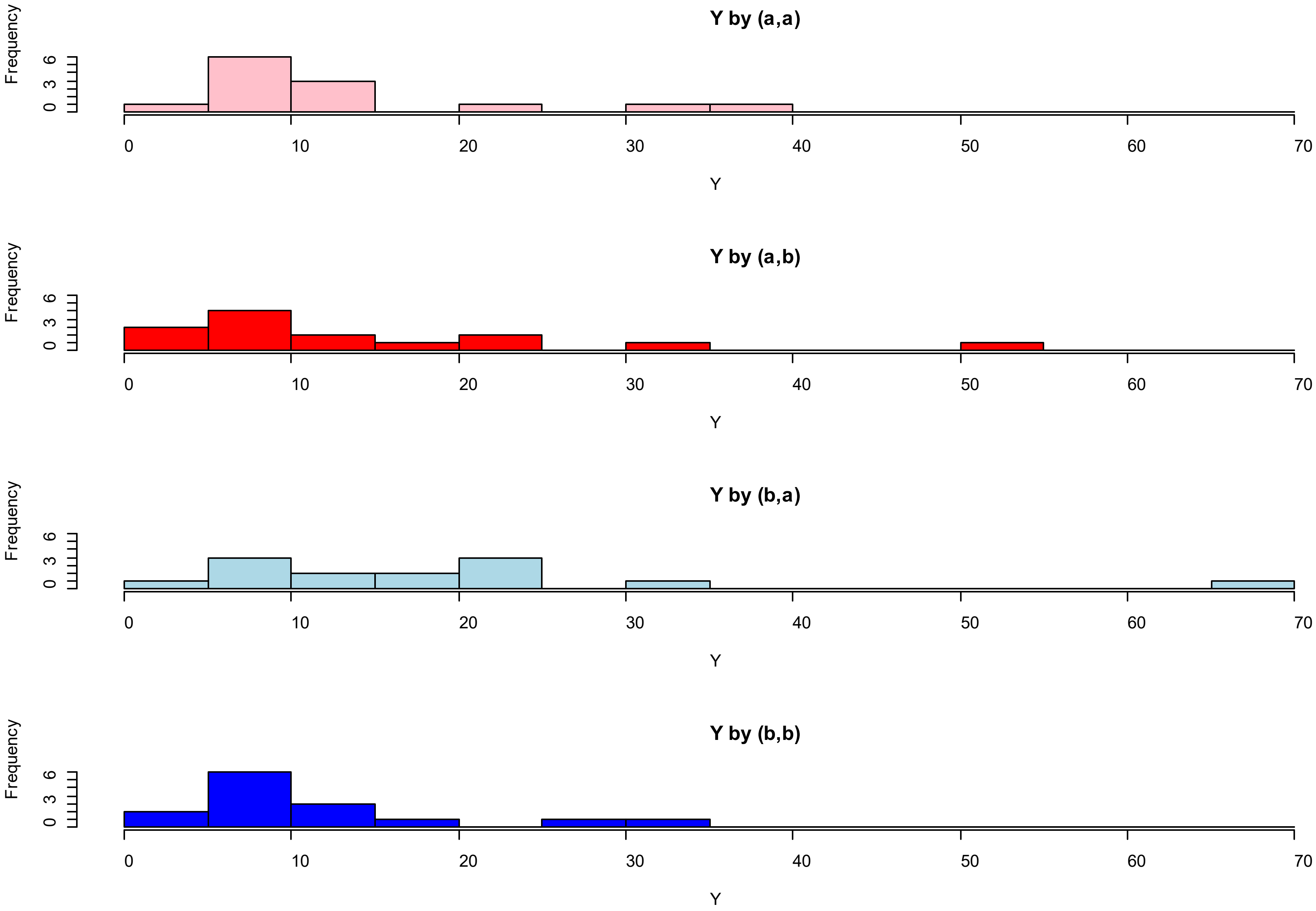


Figure 13


Y by (a,a)
Frequency
0 3 6
0 10 20 30 40 50 60 70
Y
Y by (a,b)
Frequency
0 3 6
0 10 20 30 40 50 60 70
Y
Y by (b,a)
Frequency
0 3 6
0 10 20 30 40 50 60 70
Y
Y by (b,b)
Frequency
0 3 6
0 10 20 30 40 50 60 70
Y

GLM / GLMM

Distributions and canonical links

<table>
<tr><th>Distribution</th><th>Link</th><th>Typical Uses</th><th>R code for GLM (between-Ss.)</th><th>R code for GLMM (within-Ss.)</th></tr>
<tr><td>Binomial</td><td>logit</td><td>Logistic regression:
Dichotomous responses (i.e., nominal responses with two categories)</td><td><pre>library(car) # for Anova
df$PId = factor(df$PId)
df$X1 = factor(df$X1)
df$X2 = factor(df$X2)
df$Y = factor(df$Y) # dichotomous response
contrasts(df$X1) <- "contr.sum"
contrasts(df$X2) <- "contr.sum"
m = glm(Y ~ X1*X2, data=df, family=binomial)
Anova(m, type=3)</pre></td><td><pre>library(lme4) # for glmer
library(lmerTest)
library(car) # for Anova
df$PId = factor(df$PId)
df$X1 = factor(df$X1)
df$X2 = factor(df$X2)
df$Y = factor(df$Y) # dichotomous response
contrasts(df$X1) <- "contr.sum"
contrasts(df$X2) <- "contr.sum"
m = glmer(Y ~ X1*X2 + (1|PId), data=df, family=binomial)
Anova(m, type=3)</pre></td></tr>
<tr><td>Multinomial</td><td>logit</td><td>Multinomial logistic regression:
Polytomous responses (i.e., nominal responses with more than two categories)</td><td><pre>library(multpois) # for glm.mp, Anova.mp
df$PId = factor(df$PId)
df$X1 = factor(df$X1)
df$X2 = factor(df$X2)
df$Y = factor(df$Y) # polytomous response
contrasts(df$X1) <- "contr.sum"
contrasts(df$X2) <- "contr.sum"
m = glm.mp(Y ~ X1*X2, data=df)
Anova.mp(m, type=3)</pre></td><td><pre>library(multpois) # for glmer.mp, Anova.mp
df$PId = factor(df$PId)
df$X1 = factor(df$X1)
df$X2 = factor(df$X2)
df$Y = factor(df$Y) # polytomous response
contrasts(df$X1) <- "contr.sum"
contrasts(df$X2) <- "contr.sum"
m = glmer.mp(Y ~ X1*X2 + (1|PId), data=df)
Anova.mp(m, type=3)</pre></td></tr>
</table>

Notes: 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).

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 (χ^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 (χ^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 (χ^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 (χ^2(2, *N*=60) = 9.28, *p* = .010)."

Figure 14

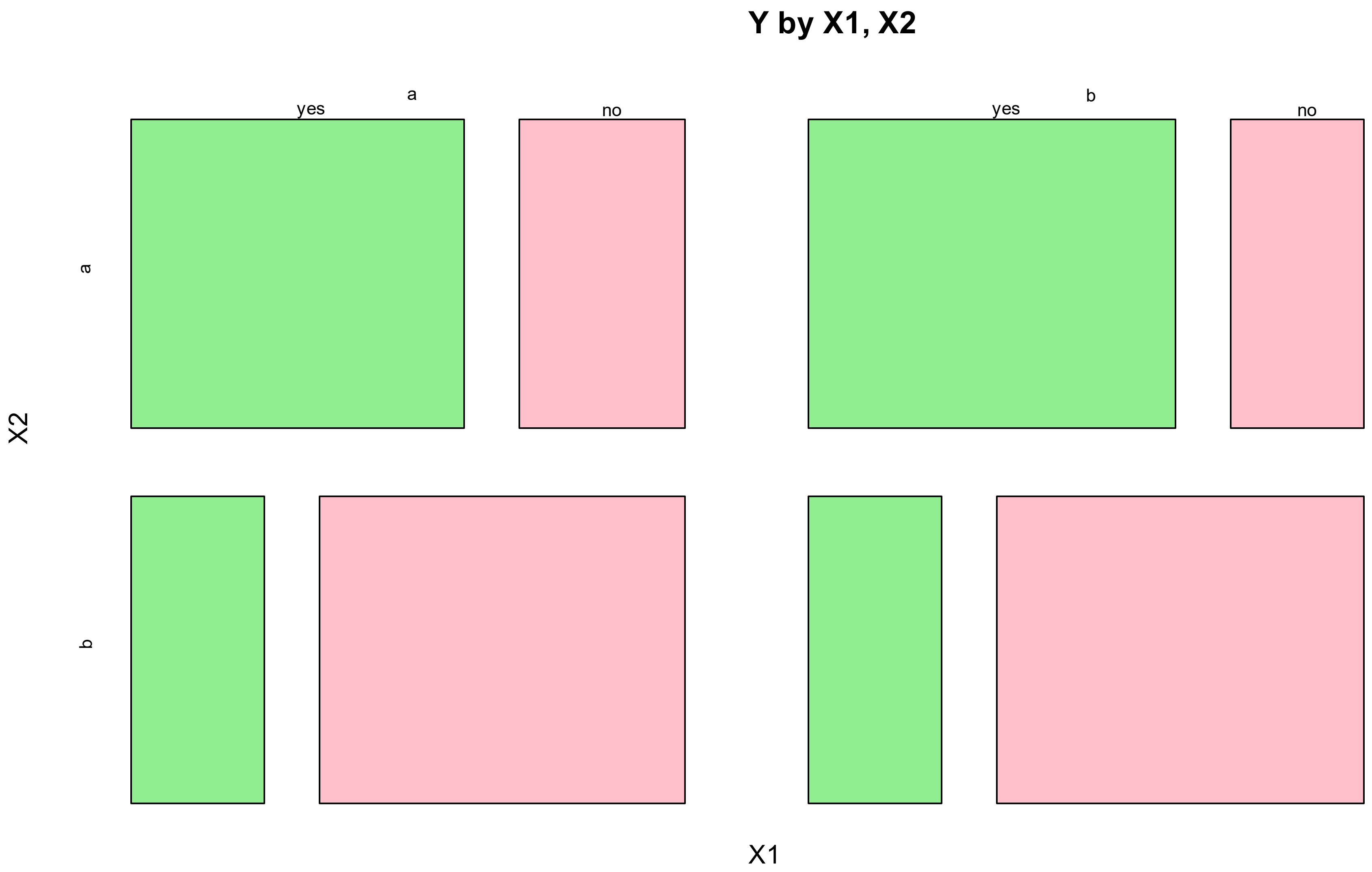
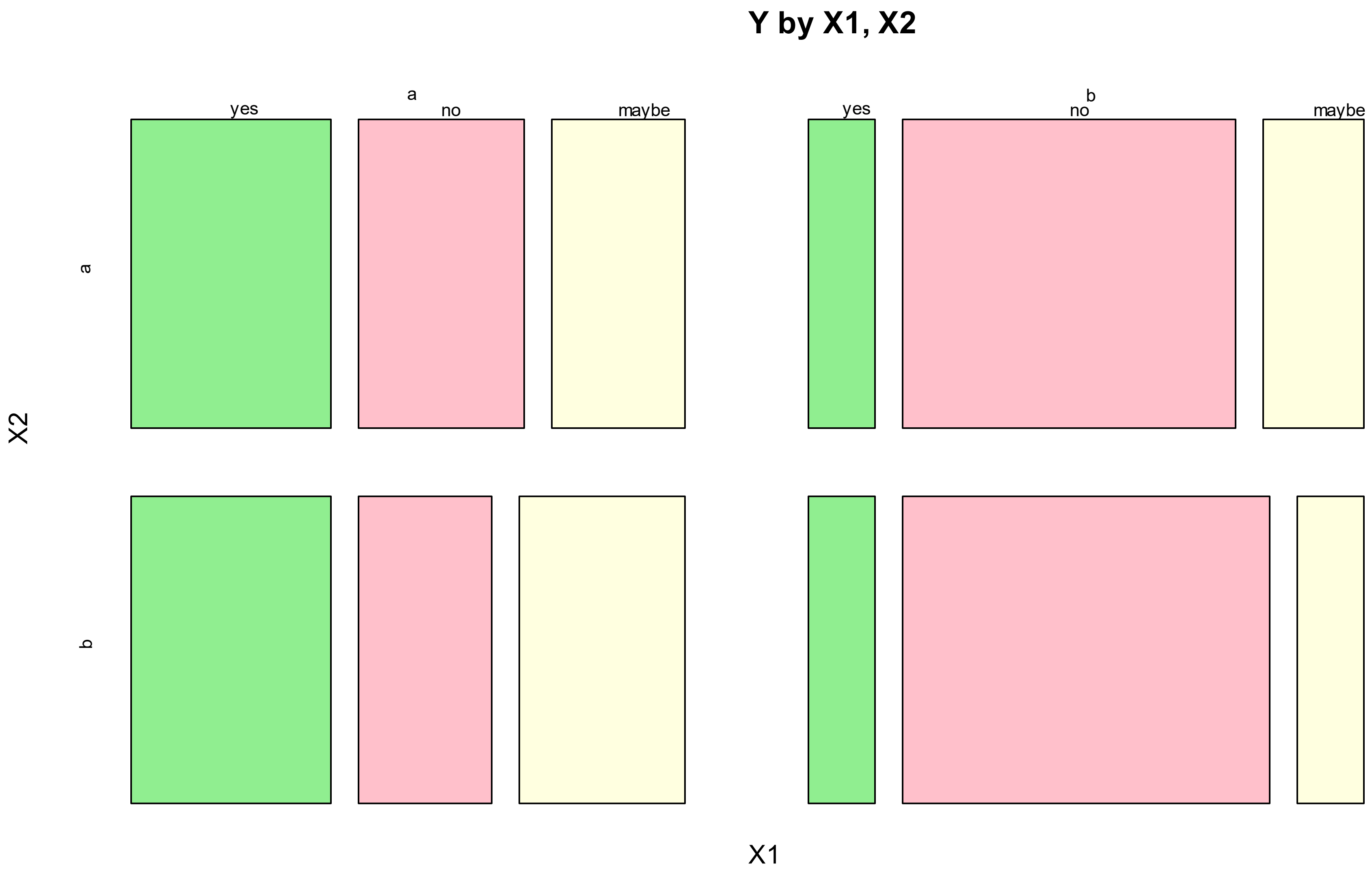


Figure 15



GLM / GLMM

Distributions and canonical links

<table>
<tr><th>Distribution</th><th>Link</th><th>Typical Uses</th><th>R code for GLM (between-Ss.)</th><th>R code for GLMM (within-Ss.)</th></tr>
<tr><td>Ordinal</td><td>cumulative logit</td><td>Ordinal logistic regression: Ordinal responses (e.g., Likert-type scales)</td><td>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)</td><td>library(ordinal) # for clmm
library(RVAideMemoire) # for Anova.clmm
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"
df2 <- as.data.frame(df) # Anova.clmm fails without this
m = clmm(Y ~ X1*X2 + (1|PId), data=df2, Hess=TRUE, link="logit")
# logit, probit, cloglog, loglog, cauchit links are valid
Anova.clmm(m)</td></tr>
</table>

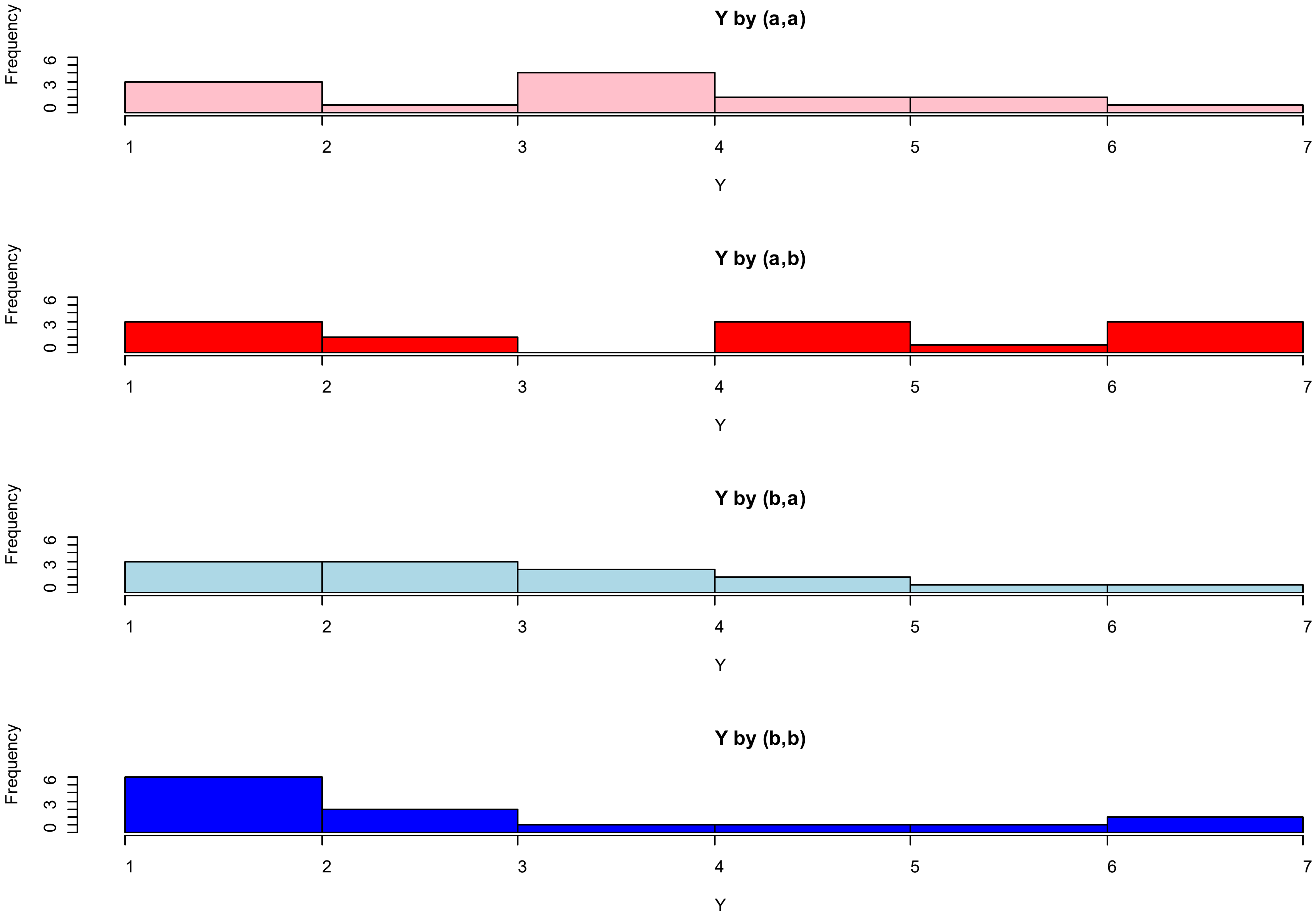
Note: Ordinal logistic regression is also known as cumulative logistic regression.

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 no statistically significant effects on Y of X1, X2, or the X1×X2 interaction."	"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 no statistically significant effects on Y of X1, X2, or the X1×X2 interaction."

Figure 16



GLM / GLMM

Distributions and canonical links

<table>
<tr><th>Distribution</th><th>Link</th><th>Typical Uses</th><th>R code for GLM (between-Ss.)</th><th>R code for GLMM (within-Ss.)</th></tr>
<tr><td>Poisson</td><td>log</td><td>Poisson regression:
Count responses</td><td>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)
print(check_overdispersion(m))
# use family=quasipoisson or negative binomial
# regression if overdispersed
Anova(m, type=3)</td><td>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)
print(check_overdispersion(m))
# use mixed negative binomial regression if overdispersed
Anova(m, type=3)</td></tr>
<tr><td>Zero-Inflated Poisson</td><td>log</td><td>Zero-inflated Poisson regression:
Zero-inflated count responses</td><td>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)
print(check_zeroinflation(m0))
m = glmmTMB(Y ~ X1*X2, data=df, family=poisson,
            ziformula=~1)
Anova(m, type=3)</td><td>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)
print(check_zeroinflation(m0))
m = glmmTMB(Y ~ X1*X2 + (1|PId), data=df, family=poisson,
            ziformula=~1, REML=TRUE)
Anova(m, type=3)</td></tr>
</table>

Notes: 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 `abs(var(Y)/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 ($\chi^2(1, N{=}60) = 7.34$, $p = .007$)."	"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 ($\chi^2(1, N{=}60) = 7.34$, $p = .007$)."

Figure 17

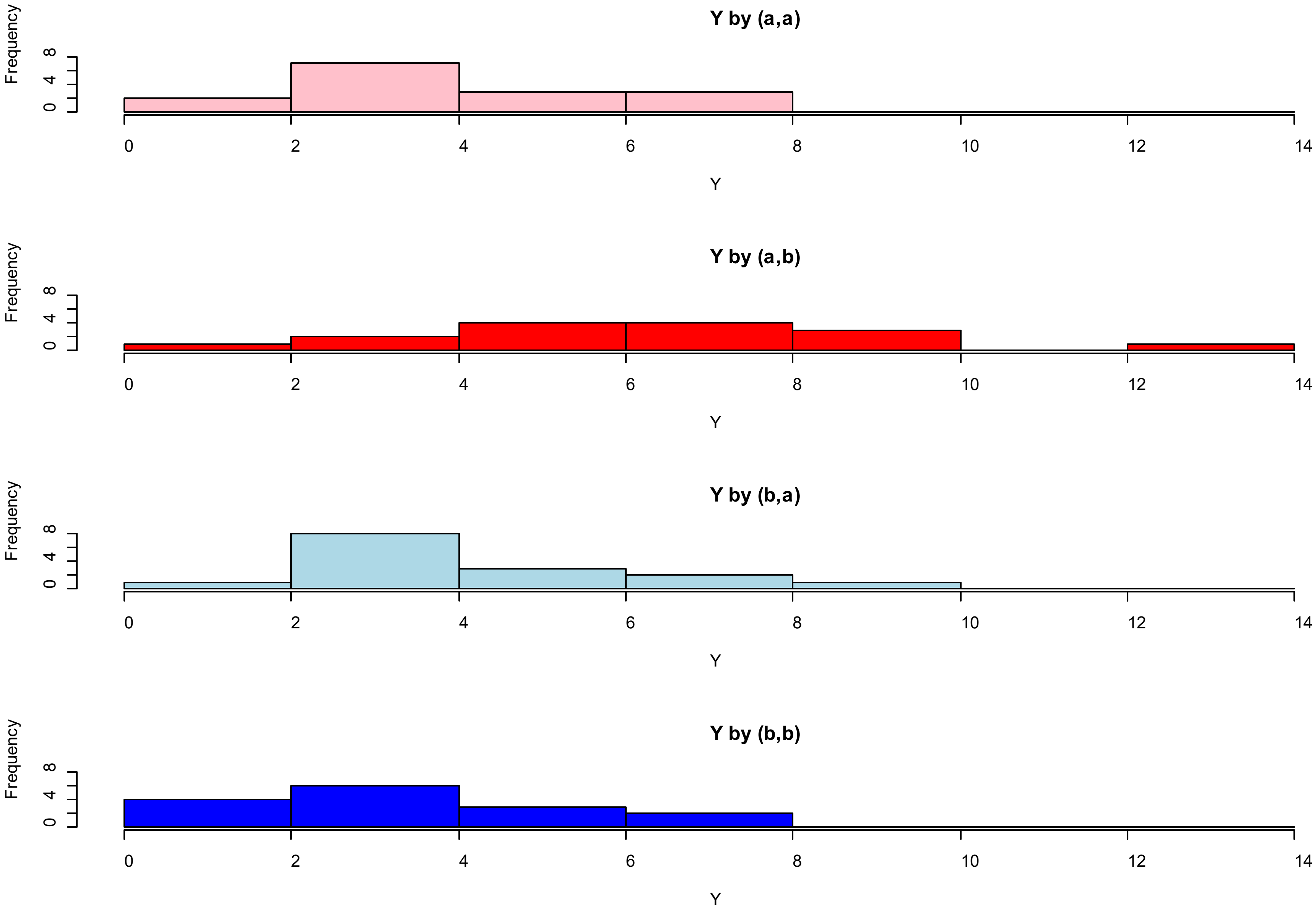
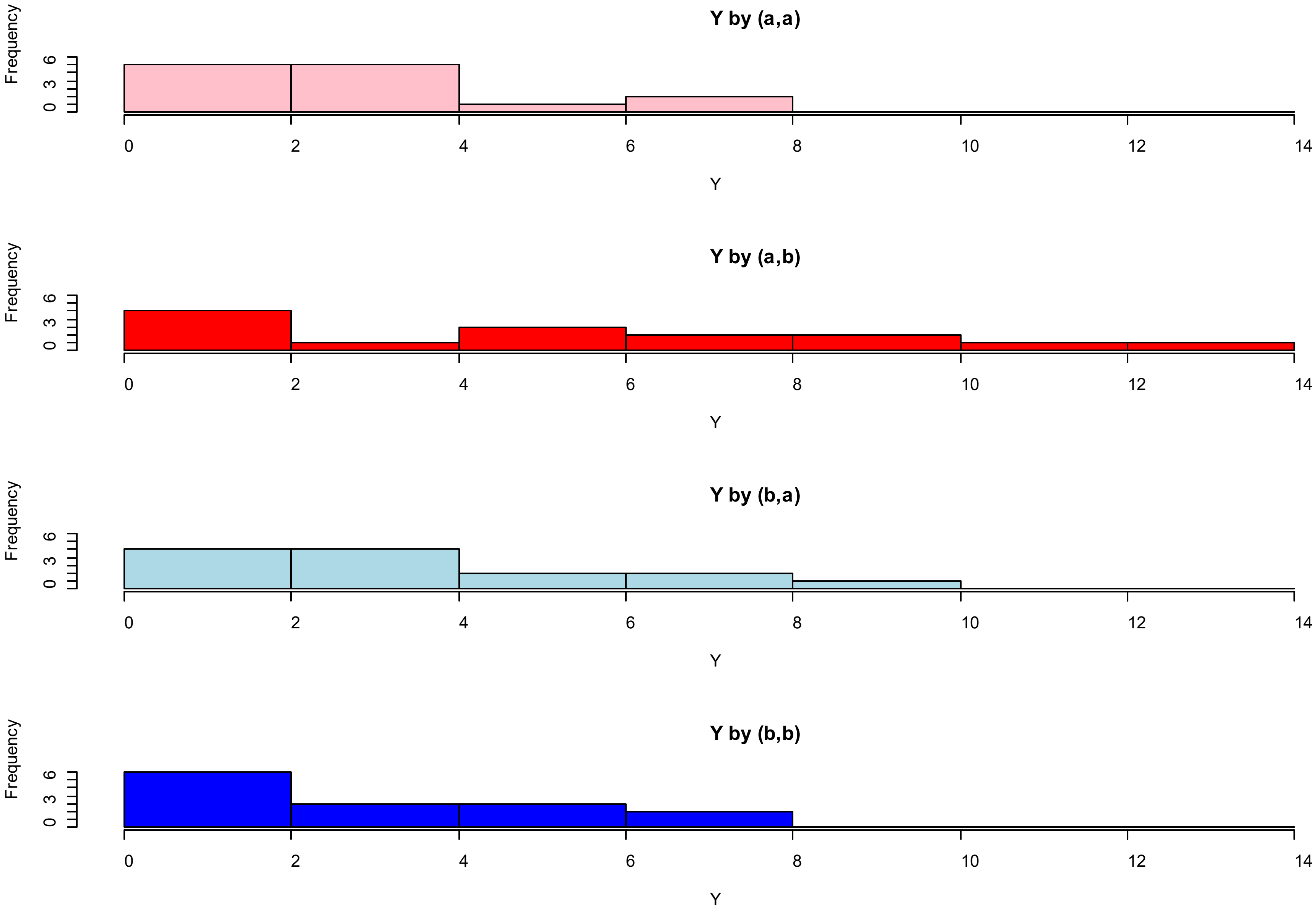

Y by (a,a)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (a,b)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (b,a)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y
Y by (b,b)
Frequency
0 4 8
0 2 4 6 8 10 12 14
Y

Figure 18


Y by (a,a)
Frequency
0 3 6
0 2 4 6 8 10 12 14
Y
Y by (a,b)
Frequency
0 3 6
0 2 4 6 8 10 12 14
Y
Y by (b,a)
Frequency
0 3 6
0 2 4 6 8 10 12 14
Y
Y by (b,b)
Frequency
0 3 6
0 2 4 6 8 10 12 14
Y

GLM / GLMM

Distributions and canonical links

<table>
<tr><th>Distribution</th><th>Link</th><th>Typical Uses</th><th>R code for GLM (between-Ss.)</th><th>R code for GLMM (within-Ss.)</th></tr>
<tr><td>Negative Binomial</td><td>log</td><td>Negative binomial regression:
Overdispersed count responses</td><td>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)</td><td>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)</td></tr>
<tr><td>Zero-Inflated Negative Binomial</td><td>log</td><td>Zero-inflated negative binomial regression:
Overdispersed zero-inflated count responses</td><td>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)
print(check_zeroinflation(m0))
m = glmmTMB(Y ~ X1*X2, data=df, family=nbinom2,
ziformula=~1)
Anova(m, type=3)</td><td>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)
print(check_zeroinflation(m0))
m = glmmTMB(Y ~ X1*X2 + (1|PId), data=df, family=nbinom2,
ziformula=~1, REML=TRUE)
Anova(m, type=3)</td></tr>
</table>

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 ($\chi^2(1, N=60) = 6.25$, $p = .012$)."	"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 indicated a statistically significant effect of X1 on Y ($\chi^2(1, N=60) = 5.52$, $p = .019$)."

Figure 19

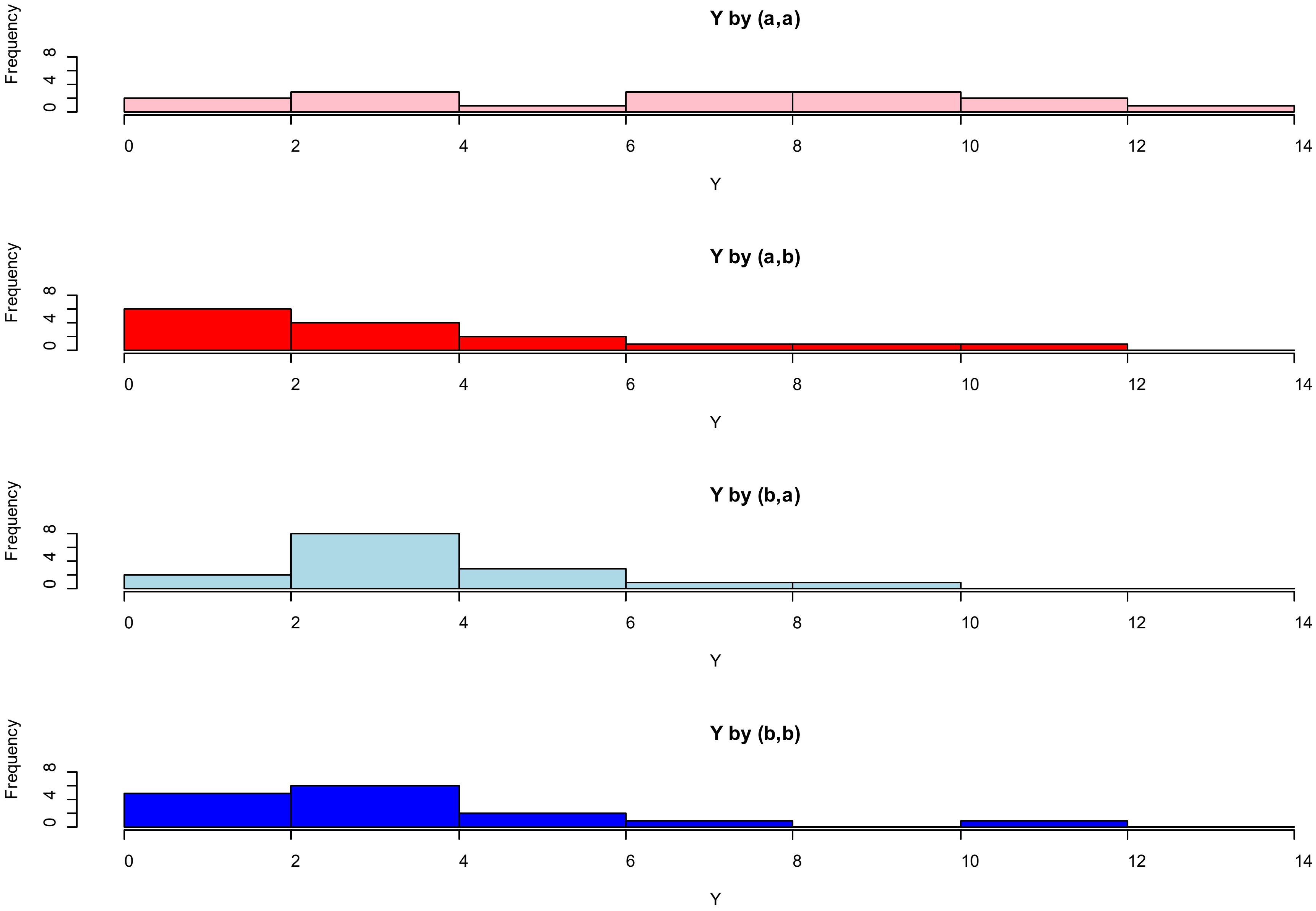
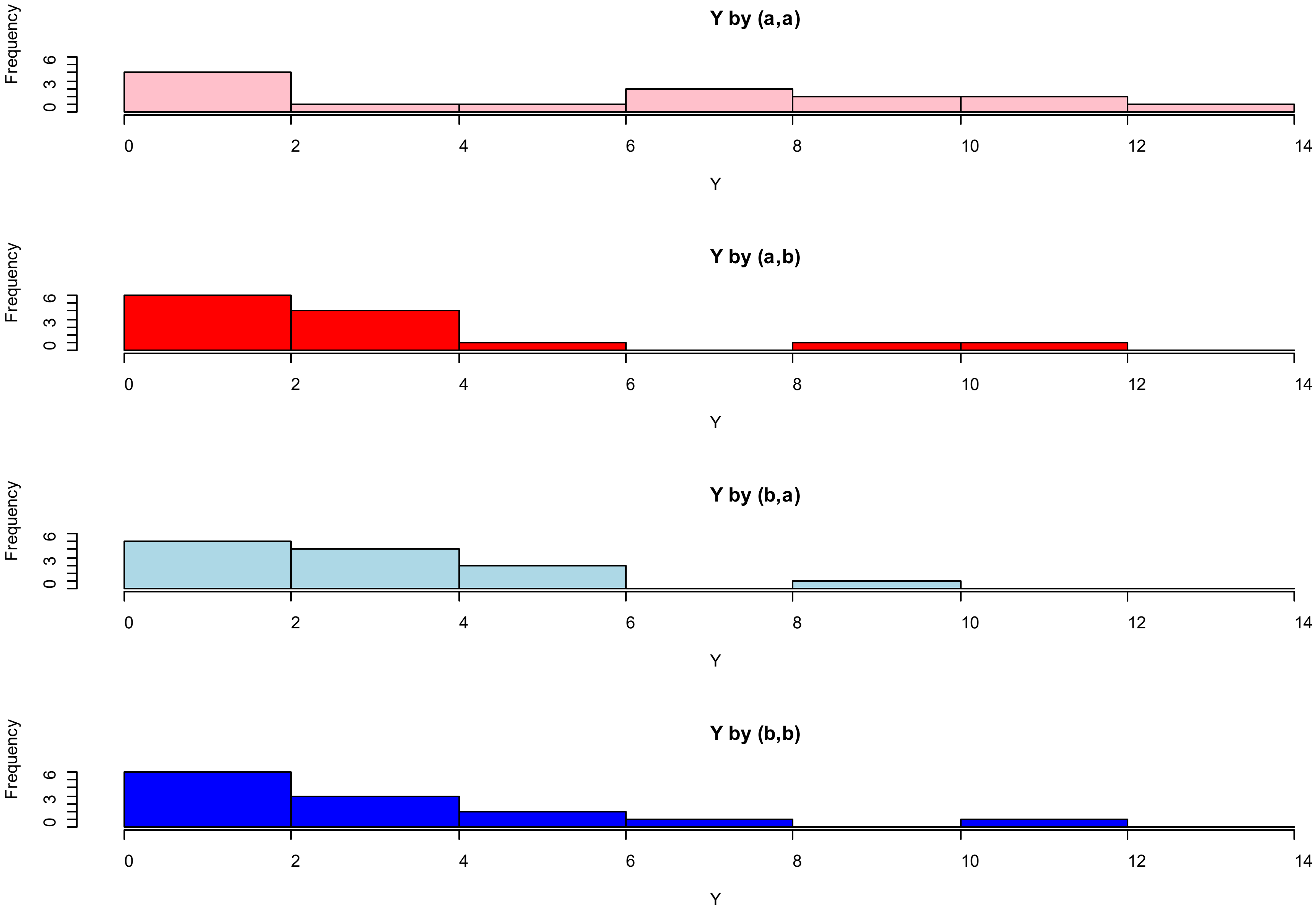

Y by (a,a)
Frequency
0
4
8
0
2
4
6
8
10
12
14
Y
Y by (a,b)
Frequency
0
4
8
0
2
4
6
8
10
12
14
Y
Y by (b,a)
Frequency
0
4
8
0
2
4
6
8
10
12
14
Y
Y by (b,b)
Frequency
0
4
8
0
2
4
6
8
10
12
14
Y

Figure 20


Y by (a,a)
Frequency
0 3 6
0 2 4 6 8 10 12 14
Y
Y by (a,b)
Frequency
0 3 6
0 2 4 6 8 10 12 14
Y
Y by (b,a)
Frequency
0 3 6
0 2 4 6 8 10 12 14
Y
Y by (b,b)
Frequency
0 3 6
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)`

Notes: 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

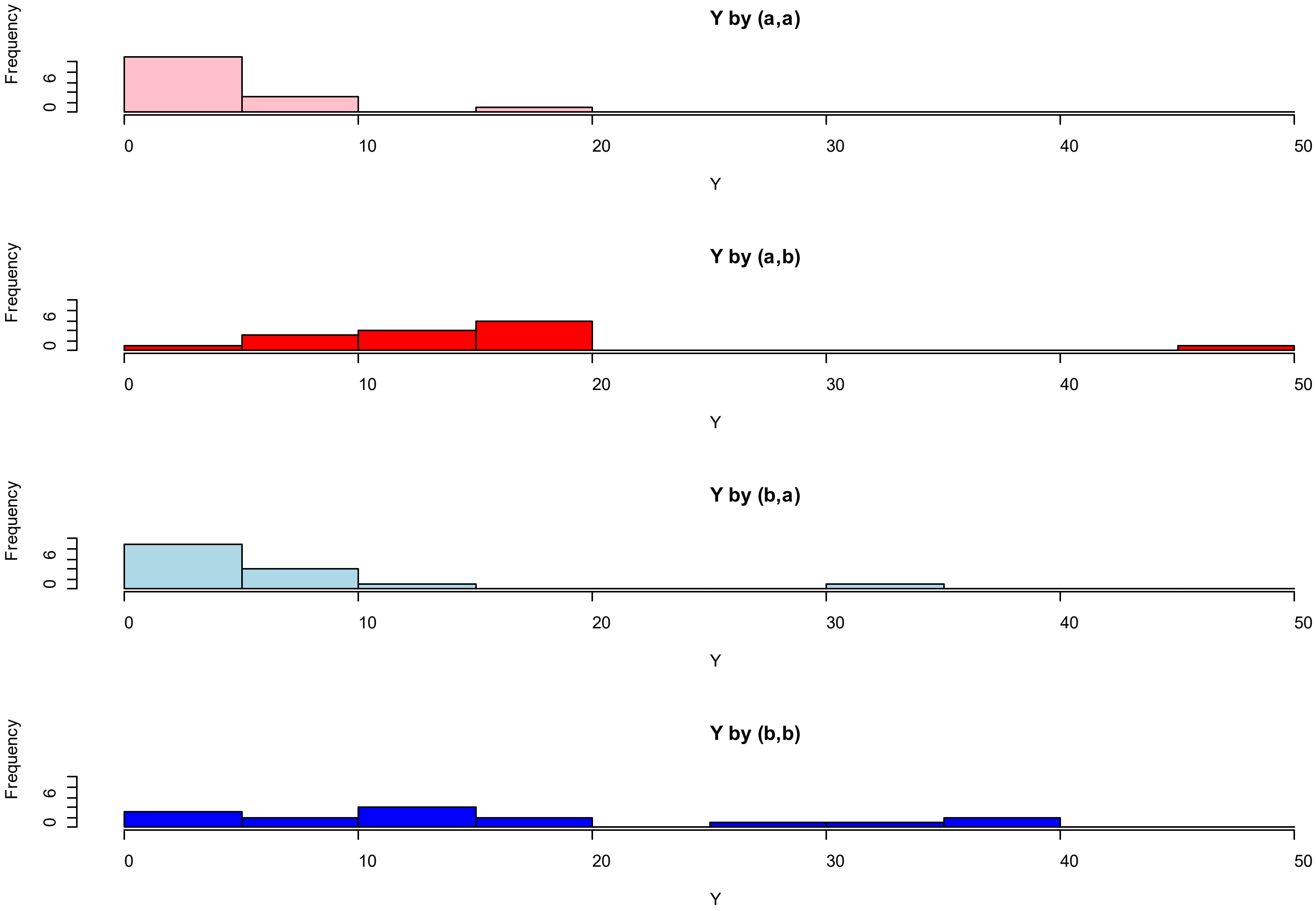
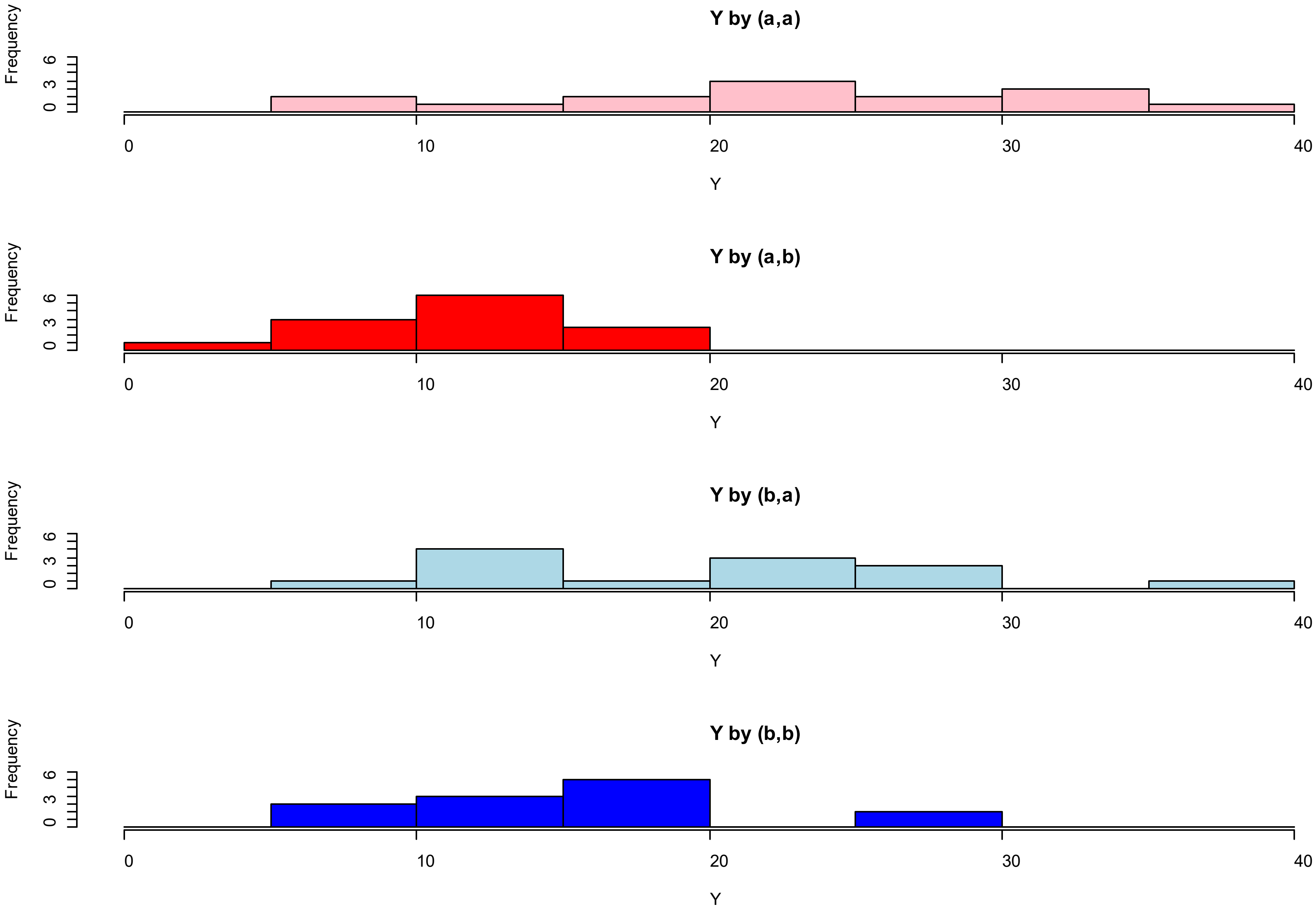

Y by (a,a)
Frequency
0
6
0
10
20
30
40
50
Y
Y by (a,b)
Frequency
0
6
0
10
20
30
40
50
Y
Y by (b,a)
Frequency
0
6
0
10
20
30
40
50
Y
Y by (b,b)
Frequency
0
6
0
10
20
30
40
50
Y

Figure 22


Y by (a,a)
Frequency
0
3
6
0
10
20
30
40
Y
Y by (a,b)
Frequency
0
3
6
0
10
20
30
40
Y
Y by (b,a)
Frequency
0
3
6
0
10
20
30
40
Y
Y by (b,b)
Frequency
0
3
6
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`
					`emmeans(m, pairwise ~ X, adjust="holm") # m is from lm or lme4::lmer`

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`

				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`

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`

Notes: 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' ($t(57) = -3.16$, $p = .008$) and 'a' *vs.* 'c' ($t(57) = -2.47$, $p = .033$) 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' ($t(38) = -3.16$, $p = .009$) and 'a' *vs.* 'c' ($t(38) = -2.47$, $p = .036$) were significantly different, but not 'b' *vs.* 'c'."
1	≥2	Logistic regression	*Z*-test	Btwn	"Three *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' ($\chi^2(2, N=40) = 14.71$, $p = .001$) and 'b' *vs.* 'c' ($\chi^2(2, N=40) = 17.65$, $p < .001$) were significantly different, but not 'a' *vs.* 'b'."
				Within	"Three *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' ($\chi^2(2, N=40) = 12.22$, $p = .007$) and 'b' *vs.* 'c' ($\chi^2(2, N=40) = 10.73$, $p = .009$) were significantly different, but not 'a' *vs.* 'b'."
1	≥2	Ordinal logistic regression	*Z*-test	Btwn, Within	"Three *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'b' *vs.* 'c' was significantly different ($Z = -2.72$, $p = .020$), but not 'a' *vs.* 'b' or 'a' *vs.* 'c'."

GLM / GLMM

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	R Code

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

Notes: Between-subjects models are from GLMs, within-subjects models are from GLMMs.

GLM / GLMM

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	Report
1	≥2	Poisson regression	*Z*-test	Btwn, Within	"Three *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	"Three *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' (Z = -2.81, p = .010) and 'b' *vs.* 'c' (Z = 2.98, p = .009) were significantly different, but not 'a' *vs.* 'c'."
				Within	"Three *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that 'a' *vs.* 'b' (Z = -2.81, p = .010) and 'b' *vs.* 'c' (Z = 2.99, p = .009) were significantly different, but not 'a' *vs.* 'c'."
1	≥2	Negative binomial regression	*Z*-test	Btwn, Within	"Three *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 = -4.37, p < .0001) and 'b' *vs.* 'c' (Z = 4.47, 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 = -4.24, p < .0001) and 'b' *vs.* 'c' (Z = 4.32, p < .0001) were significantly different, but not 'a' *vs.* 'c'."

GLM / GLMM

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	R Code

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

Notes: 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`
					`emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from lm or lme4::lmer`

≥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`

				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`

≥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`

Notes: 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 ($t(56) = -2.75$, $p = .048$). 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."
≥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 no individual pairwise comparison was detectably different."

GLM / GLMM

Post hoc pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	R Code

≥2	≥2	Poisson regression	*Z*-test	Btwn, Within	`# df has two factors (X1,X2) each w/levels (a,b) and count response (Y)`
					`library(emmeans) # for emmeans`
					`emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glm or lme4::glmer with family=poisson`

≥2	≥2	Zero-inflated Poisson regression	*Z*-test	Btwn, Within	`# df has two factors (X1,X2) each w/levels (a,b) and zero-inflated count response (Y)`
					`library(emmeans) # for emmeans`
					`emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glmmTMB::glmmTMB with family=poisson`

≥2	≥2	Negative binomial regression	*Z*-test	Btwn, Within	`# df has two factors (X1,X2) each w/levels (a,b) and overdispersed count response (Y)`
					`library(emmeans) # for emmeans`
					`emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from MASS::glm.nb or lme4::glmer.nb`

≥2	≥2	Zero-inflated negative binomial regression	*Z*-test	Btwn, Within	`# df has two factors (X1,X2) each w/levels (a,b) and zero-inflated overdispersed count response (Y)`
					`library(emmeans) # for emmeans`
					`emmeans(m, pairwise ~ X1*X2, adjust="holm") # m is from glmmTMB::glmmTMB with family=nbinom2`

Notes: Between-subjects models are from GLMs, within-subjects models are from GLMMs.

GLM / GLMM

Post hoc pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	Report
≥2	≥2	Poisson regression	*Z*-test	Btwn, Within	"Six *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} (Z = -3.10, p = .012) and {a,b} *vs.* {b,b} (Z = 3.01, p = .013) were significantly different. Other pairwise comparisons were not detectably different."
				Within	"Six *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {a,b} (Z = -3.10, p = .011) and {a,b} *vs.* {b,b} (Z = 3.01, p = .013) were significantly different. Other pairwise comparisons were not detectably different."
≥2	≥2	Negative binomial regression	*Z*-test	Btwn	"Six *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} (Z = 2.99, p = .017) and {a,a} *vs.* {b,b} (Z = 2.66, p = .040) were significantly different. Other pairwise comparisons were not detectably different."
				Within	"Six *post hoc* pairwise comparisons, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {a,a} *vs.* {b,a} was significantly different (Z = 2.82, p = .029). All other pairwise comparisons were not detectably different."

GLM / GLMM

Post hoc pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Model	Test	B/W	R Code

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

Notes: 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."

Bibliography

Generalized linear (mixed) models

- Breslow, N.E. and Clayton, D.G. (1993). Approximate inference in generalized linear mixed models. *Journal of the American Statistical Association 88* (421), pp. 9-25. https://doi.org/10.2307/2290687
- Nelder, J.A. and Wedderburn, R.W.M. (1972). Generalized linear models. *Journal of the Royal Statistical Society, Series A 135* (3), pp. 370-384. https://doi.org/10.2307/2344614
- Wald, A. (1943). Tests of statistical hypotheses concerning several parameters when the number of observations is large. *Transactions of the American Mathematical Society 54* (3), pp. 426-482. https://doi.org/10.2307/1990256

Lognormal models

- Aitchison, J. and Brown, J.A.C. (1957). *The Lognormal Distribution*. Cambridge, UK: Cambridge University Press. http://www.jstor.org/stable/2227716
- Berry, D.A. (1987). Logarithmic transformations in ANOVA. *Biometrics 43* (2), pp. 439-456. https://doi.org/10.2307/2531826
- Lawrence, R.J. (1988). The log-normal as event-time distribution. In *Log-normal Distributions: Theory and Application*, E.L. Crow and K. Shimizu (eds.). New York, NY: Dekker, pp. 211-228.
- Limpert, E., Stahel, W.A. and Abbt, M. (2001). Log-normal distributions across the sciences: Keys and clues. *BioScience 51* (5), pp. 341-352. https://doi.org/10.1641/0006-3568(2001)051[0341:LNDATS]2.0.CO;2

Binomial models

- Berkson, J. (1944). Application of the logistic function to bio-assay. *Journal of the American Statistical Association 39* (227), pp. 357-365. https://doi.org/10.2307/2280041
- Gilmour, A.R., Anderson, R.D. and Rae, A.L. (1985). The analysis of binomial data by a generalized linear mixed model. *Biometrika 72* (3), pp. 593-599. https://doi.org/10.2307/2336731
- Stiratelli, R., Laird, N. and Ware, J.H. (1984). Random-effects models for serial observations with binary response. *Biometrics 40* (4), pp. 961-971. https://doi.org/10.2307/2531147

Bibliography

Multinomial models

- Begg, C.B. and Gray, R. (1984). Calculation of polychotomous logistic regression parameters using individualized regressions. *Biometrika 71* (1), pp. 11-18. https://www.jstor.org/stable/2336391
- Cox, D.R. (1966). Some procedures connected with the logistic qualitative response curve. In *Research Papers in Probability and Statistics (Festschrift for J. Neyman)*, F.N. David (ed.). London, UK: John Wiley & Sons, pp. 55-71.
- Daniels, M.J. and Gatsonis, C. (1997). Hierarchical polytomous regression models with applications to health services research. *Statistics in Medicine 16* (20), pp. 2311-2325. https://doi.org/10.1002/(SICI)1097-0258(19971030)16:20%3C2311::AID-SIM654%3E3.0.CO;2-E
- Hartzel, J., Agresti, A. and Caffo, B. (2001). Multinomial logit random effects models. *Statistical Modelling 1* (2), pp. 81-102. https://doi.org/10.1177/1471082X0100100201
- Hedeker, D. (2003). A mixed-effects multinomial logistic regression model. *Statistics in Medicine 22* (9), pp. 1433-1446. https://doi.org/10.1002/sim.1522
- Theil, H. (1969). A multinomial extension of the linear logit model. *International Economic Review 10* (3), pp. 251-259. https://doi.org/10.2307/2525642

Bibliography

Multinomial-Poisson trick

- Baker, S.G. (1994). The multinomial-Poisson transformation. *The Statistician 43* (4), pp. 495-504. https://doi.org/10.2307/2348134
- Chen, Z. and Kuo, L. (2001). A note on the estimation of the multinomial logit model with random effects. *The American Statistician 55* (2), pp. 89-95. https://www.jstor.org/stable/2685993
- Guimaraes, P. (2004). Understanding the multinomial-Poisson transformation. *The Stata Journal 4* (3), pp. 265-273. https://www.stata-journal.com/article.html?article=st0069
- Lee, J.Y.L., Green, P.J. and Ryan, L.M. (2017). On the "Poisson trick" and its extensions for fitting multinomial regression models. arXiv:1707.08538v1 [stat.ME], 25 pages. https://arxiv.org/abs/1707.08538

Ordinal models

- Agresti, A. (2010). *Analysis of Ordinal Categorical Data (2nd Ed)*. Hoboken, NJ : John Wiley & Sons, Inc. https://onlinelibrary.wiley.com/doi/book/10.1002/9780470594001
- Hedeker, D. and Gibbons, R.D. (1994). A random-effects ordinal regression model for multilevel analysis. *Biometrics 50* (4), pp. 933-944. https://www.jstor.org/stable/2533433
- McCullagh, P. (1980). Regression models for ordinal data. *Journal of the Royal Statistical Society, Series B 42* (2), pp. 109-142. https://www.jstor.org/stable/2984952
- McKelvey, R.D. and Zavoina, W. (1975). A statistical model for the analysis of ordinal level dependent variables. *Journal of Mathematical Sociology 4* (1), pp. 103-120. https://doi.org/10.1080/0022250X.1975.9989847
- Winship, C. and Mare, R.D. (1984). Regression models with ordinal variables. *American Sociological Review 49* (4), pp. 512-525. https://doi.org/10.2307/2095465

Bibliography

Count models – Poisson and negative binomial

- Cox, D.R. (1983). Some remarks on overdispersion. *Biometrika 70* (1), pp. 269-274. https://doi.org/10.2307/2335966
- Gardner, W., Mulvey, E.P. and Shaw, E.C. (1995). Regression analyses of counts and rates: Poisson, overdispersed Poisson, and negative binomial models. *Psychological Bulletin 118* (3), pp. 392-404. https://doi.org/10.1037/0033-2909.118.3.392
- Hilbe, J.M. (2011). *Negative Binomial Regression*. Cambridge, UK: Cambridge University Press. https://doi.org/10.1017/CBO9780511973420
- Hilbe, J.M. (2014). *Modeling Count Data*. New York, NY: Cambridge University Press. https://books.google.com/books?id=aZLfAwAAQBAJ
- Lawless, J.F. (1987). Negative binomial and mixed Poisson regression. *The Canadian Journal of Statistics 15* (3), pp. 209-225. https://doi.org/10.2307/3314912
- Ver Hoef, J.M. and Boveng, P.L. (2007). Quasi-Poisson vs. negative binomial regression: How should we model overdispersed count data? *Ecology 88* (11), pp. 2766-2772. https://doi.org/10.1890/07-0043.1
- Vermunt, J.K. (1997). *Log-linear Models for Event Histories*. Thousand Oaks, CA: Sage Publications. Retrieved from https://books.google.com/books?id=apI_AQAAIAAJ
- von Bortkiewicz, L. (1898). *Das Gesetz der Kleinen Zahlen (The Law of Small Numbers)*. Leipzig, Germany: Druck und Verlag von B.G. Teubner. https://books.google.com/books?id=o_k3AAAAMAAJ

Bibliography

Zero-inflated count models – Poisson and negative binomial

- Hall, D.B. (2000). Zero-inflated Poisson and binomial regression with random effects: A case study. *Biometrics 56* (4), pp. 1030-1039. https://doi.org/10.1111/j.0006-341X.2000.01030.x
- Heilbron, D.C. (1994). Zero-altered and other regression models for count data with added zeros. *Biometrical Journal 36* (5), pp. 531-547. https://doi.org/10.1002/bimj.4710360505
- Lambert, D. (1992). Zero-inflated Poisson regression, with an application to defects in manufacturing. *Technometrics 34* (1), pp. 1-14. https://doi.org/10.2307/1269547

Gamma models

- Nelder, J.A. and Wedderburn, R.W.M. (1972). Generalized linear models. *Journal of the Royal Statistical Society, Series A 135* (3), pp. 370-384. https://doi.org/10.2307/2344614
- Ng, V.K.Y. and Cribbie, R.A. (2017). Using the gamma generalized linear model for modeling continuous, skewed and heteroscedastic outcomes in psychology. *Current Psychology 36* (2), pp. 225-235. https://doi.org/10.1007/s12144-015-9404-0
- Stroup, W.W., Ptukhina, M. and Garai, J. (2024). *Generalized Linear Mixed Models: Modern Concepts, Methods and Applications*. Boca Raton, FL: CRC Press, pp. 453-472. https://doi.org/10.1201/9780429092060

Bibliography

Post hoc comparisons

- Boik, R.J. (1979). Interactions, partial interactions, and interaction contrasts in the analysis of variance. *Psychological Bulletin 86* (5), pp. 1084-1089. https://doi.org/10.1037/0033-2909.86.5.1084
- Holm, S. (1979). A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics 6* (2), pp. 65-70. http://www.jstor.org/stable/4615733
- Kenward, M.G. and Roger, J.H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics 53* (3), pp. 983-997. https://doi.org/10.2307/2533558
- Kramer, C.Y. (1956). Extension of multiple range tests to group means with unequal numbers of replications. *Biometrics 12* (3), pp. 307-310. https://doi.org/10.2307/3001469
- Marascuilo, L.A. and Levin, J.R. (1970). Appropriate post hoc comparisons for interaction and nested hypotheses in analysis of variance designs: The elimination of Type IV errors. *American Educational Research Journal 7* (3), pp. 397-421. https://doi.org/10.3102/00028312007003397
- Satterthwaite, F.E. (1946). An approximate distribution of estimates of variance components. *Biometrics Bulletin 2* (6), pp. 110-114. https://doi.org/10.2307/3002019
- Tukey, J.W. (1949). Comparing individual means in the analysis of variance. *Biometrics 5* (2), pp. 99-114. https://doi.org/10.2307/3001913
- Tukey, J.W. (1953). *The Problem of Multiple Comparisons*. Princeton, NJ: Princeton University.