`#Rstats`

Statistical Analysis & Reporting in R

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Table of Analyses

Proportion & 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 (dep.)	≥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	<u>B</u>etween or <u>W</u>ithin	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)	

Analysis Categories
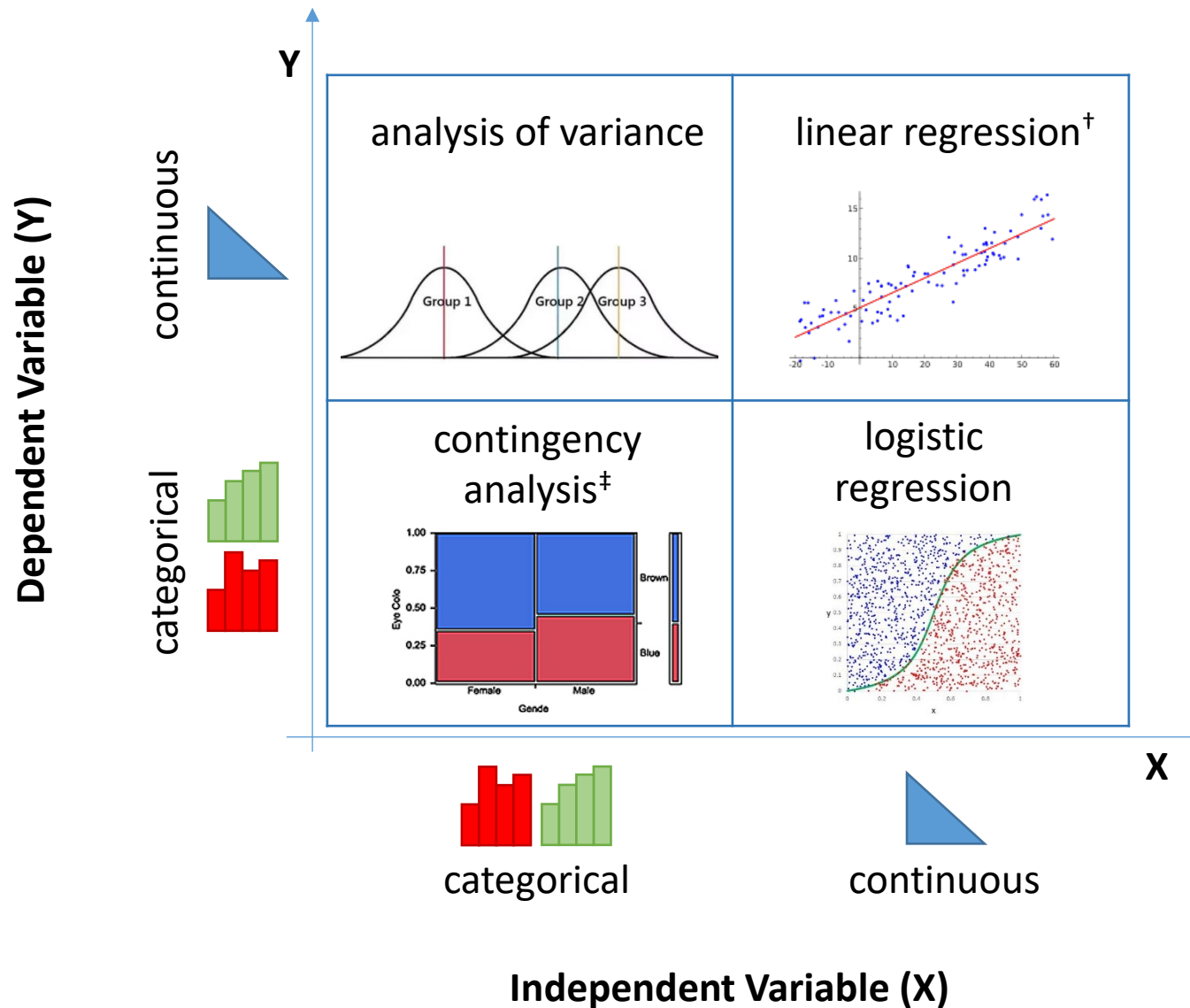
Proportion & Association

Proportion & Association

One independent sample

Samples	Response Categories	Test Name	Exact Test?	R Code

1	2	Binomial test	Yes, use with $N \leq 200$	```# 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 $N \leq 200$	```# 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")
				
				# the following gives the same result
				library(RVAideMemoire) # for multinomial.test
				multinomial.test(df$Y)```

		One-sample Pearson 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)```

Proportion & Association

One independent sample

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

Proportion & Association

Two independent samples

Samples	Response Categories	Test Name	Exact Test?	R Code
2	≥2	Fisher's exact test	Yes, use with $N \le 200$	```# 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 Pearson 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
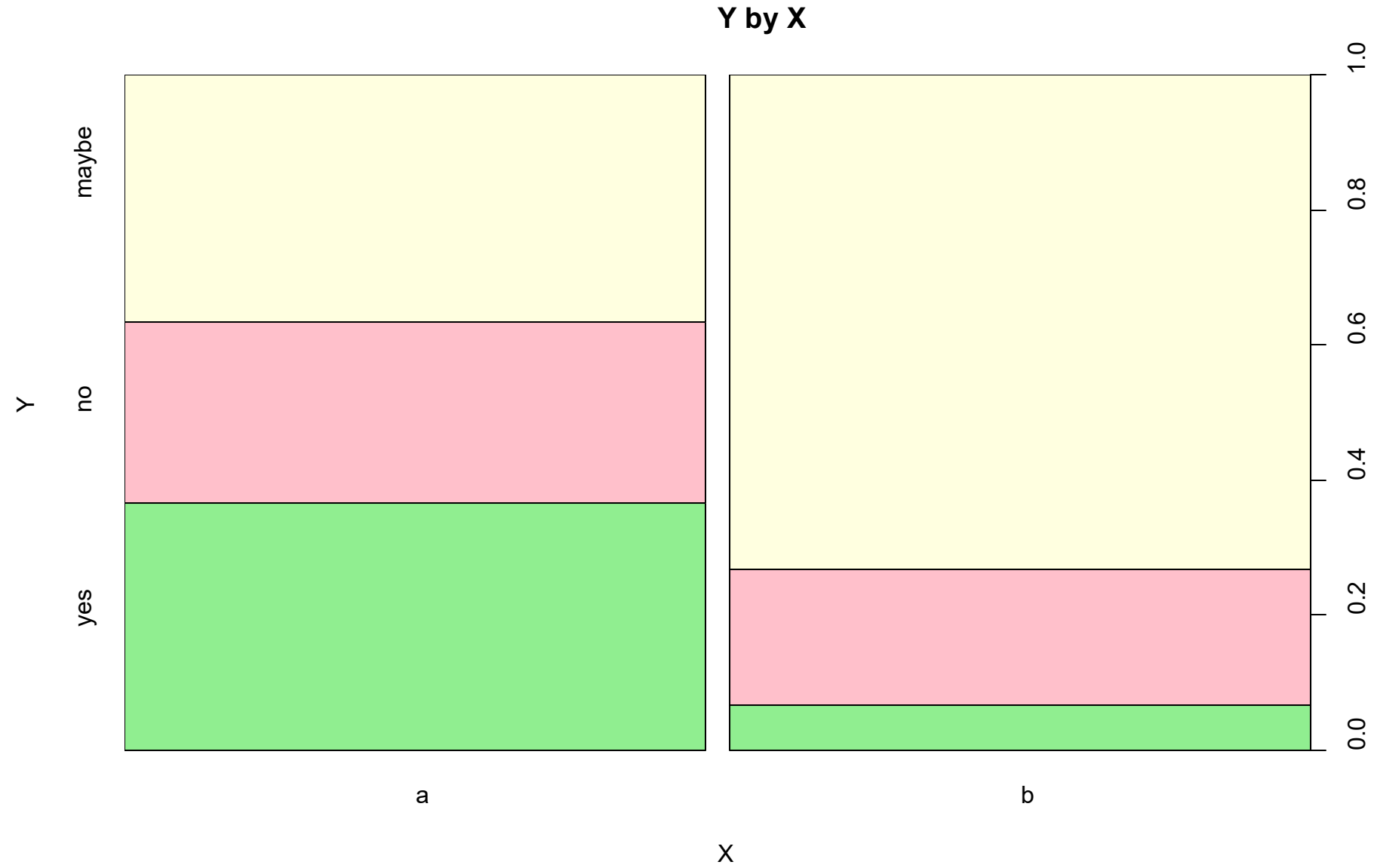chisq.test(xt)```

Proportion & Association

Two independent samples

Samples	Response Categories	Test Name	Exact Test?	Report
2	≥2	Fisher's exact test	Yes, use with $N{\le}200$	"Table 1 shows the counts of 'maybe', 'no', and 'yes' 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 'maybe', 'no', and 'yes' 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 Pearson chi-squared test	No, use with $N{>}200$	"Table 1 shows the counts of 'maybe', 'no', and 'yes' 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		
		maybe	**no**	**yes**
X	**a**	11	8	11
	b	22	6	2

Figure 1

Y by X

Proportion & Association

Two 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)```
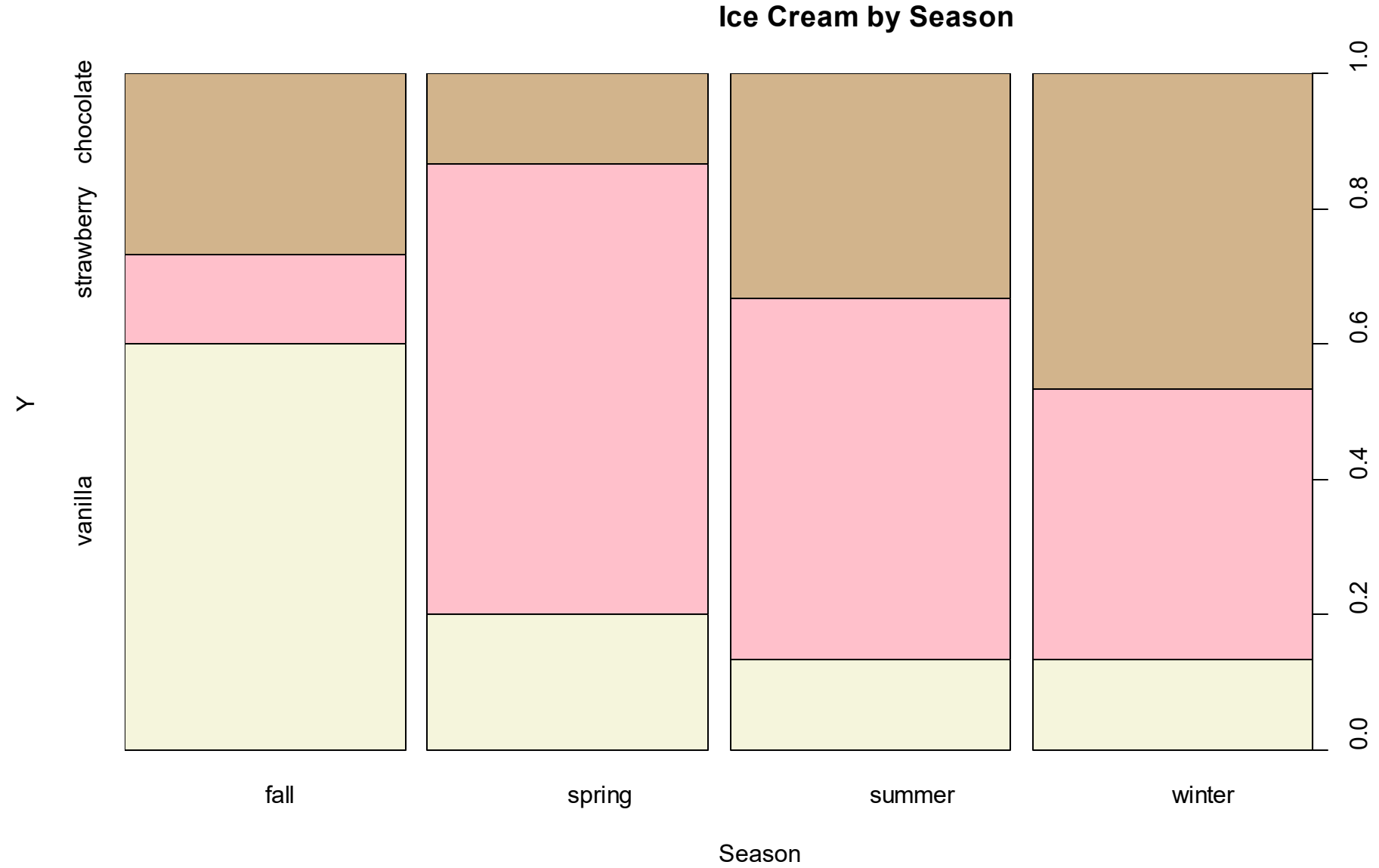
Proportion & Association

Two 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, 18 were 'chocolate', 26 were 'strawberry', and 16 were 'vanilla'. A symmetry test shows that the ice cream proportions across seasons were significantly different ($p = .013$)."

Table 2

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

Figure 2

Ice Cream by Season

Proportion & Association

Post hoc comparisons

Proportion & Association

Post hoc tests – One independent sample

Samples	Response Categories	Omnibus Test	Contrast Test	R Code

1	≥2	Multinomial test	Pairwise binomial tests	```# For Y's response categories, test each in pairwise fashion against 50/50.```
				```mn = binom.test(c(sum(df$Y == "maybe"), sum(df$Y == "no")), p=1/2) # maybe vs. no```
				```my = binom.test(c(sum(df$Y == "maybe"), sum(df$Y == "yes")), p=1/2) # maybe vs. yes```
				```ny = binom.test(c(sum(df$Y == "no"), sum(df$Y == "yes")), p=1/2) # no vs. yes```
				```p.adjust(c(mn$p.value, my$p.value, ny$p.value), method="holm")```
				
				```# or, equivalently, if xt is a table of counts for each category in Y```
				```library(RVAideMemoire) # for multinomial.multcomp```
				```multinomial.multcomp(xt, p.method="holm") # same results as above```

1	≥2	One-sample Pearson chi-squared test	Pairwise chi-squared tests	```# xt is a table of counts for each category of Y```
				```library(RVAideMemoire) # for chisq.multcomp```
				```chisq.multcomp(xt, p.method="holm") # xt shows levels```
				```# for the chi-squared values, use qchisq(1-p, df=1), where p is the pairwise p-value:```
				```qchisq(1 - .011, df=1) # 6.465```

1	≥2	Multinomial test, one-sample Pearson chi-squared test	Individual binomial tests against chance	```# A different kind of post hoc test for one sample. For Y's response categories,```
				```# test each proportion against chance.```
				```# df is a long-format data table w/participant (PId) and N-category outcome (Y)```
				```m = binom.test(sum(df$Y == "maybe"), nrow(df), p=1/3) # maybe```
				```n = binom.test(sum(df$Y == "no"), nrow(df), p=1/3) # no```
				```y = binom.test(sum(df$Y == "yes"), nrow(df), p=1/3) # yes```
				```p.adjust(c(m$p.value, n$p.value, y$p.value), method="holm")```

Proportion & Association

Post hoc tests – One independent 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 'maybe' *vs.* 'yes' and 'maybe' *vs.* 'no' were not significantly different, but that the proportions of 'no' *vs.* 'yes' were ($p = .016$)."
1	≥2	One-sample Pearson 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.* 'yes' were significantly different ($\chi^2(1, N=43) = 6.47, p = .011$)."
1	≥2	Multinomial test, one-sample Pearson 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 'yes' responses was significantly different from chance ($p = .011$)."

Proportion & Association

Post hoc tests – Two independent samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code

2	≥2	Fisher's exact test	Pairwise Fisher's exact tests	```# xt is an m × n crosstabs with categories X and Y```
				```library(RVAideMemoire) # for fisher.multcomp```
				```fisher.multcomp(xt, p.method="holm") # xt shows levels```

2	≥2	*G*-test	Pairwise *G*-tests	```# xt is an m × n crosstabs with categories X and Y```
				```library(RVAideMemoire) # for G.multcomp```
				```G.multcomp(xt, p.method="holm") # xt shows levels```

2	≥2	Two-sample Pearson chi-squared test	Pairwise chi-squared tests	```# xt is an m × n crosstabs with categories X and Y```
				```library(RVAideMemoire) # for chisq.multcomp```
				```chisq.multcomp(xt, p.method="holm") # xt shows levels```
				```# for the chi-squared values, use qchisq(1-p, df=1), where p is the pairwise p-value:```
				```qchisq(1 - .00067, df=1) # 11.571```

2	≥2	Fisher's exact test, *G*-test, two-sample Pearson chi-squared test	Individual binomial tests against chance	```# A different kind of post hoc test for two samples. For X's categories (a,b) and Y's```
				```# response categories (maybe, no, yes), test each proportion of Y within each level of X```
				```# against chance.```
				```# df is a long-format data table w/participant (PId), factor (X), and N-category outcome (Y)```
				```am = binom.test(sum(df[df$X == "a",]$Y == "maybe"), nrow(df[df$X == "a",]), p=1/3)```
				```an = binom.test(sum(df[df$X == "a",]$Y == "no"), nrow(df[df$X == "a",]), p=1/3)```
				```ay = binom.test(sum(df[df$X == "a",]$Y == "yes"), nrow(df[df$X == "a",]), p=1/3)```
				```p.adjust(c(am$p.value, an$p.value, ay$p.value), method="holm")```
				
				```bm = binom.test(sum(df[df$X == "b",]$Y == "maybe"), nrow(df[df$X == "b",]), p=1/3)```
				```bn = binom.test(sum(df[df$X == "b",]$Y == "no"), nrow(df[df$X == "b",]), p=1/3)```
				```by = binom.test(sum(df[df$X == "b",]$Y == "yes"), nrow(df[df$X == "b",]), p=1/3)```
				```p.adjust(c(bm$p.value, bn$p.value, by$p.value), method="holm")```

Proportion & Association
Post hoc tests – Two independent samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	≥2	Fisher's exact test	Pairwise Fisher's exact tests	"Three *post hoc* Fisher's exact tests of association, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that there was a significant association for {a, b}:{maybe, yes} (p = .008), but not for {a, b}:{maybe, no} or {a, b}:{no, yes}."
2	≥2	*G*-test	Pairwise *G*-tests	"Fifteen *post hoc* pairwise comparisons using *G*-tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {b, maybe} *vs*. {b, yes} was statistically significant (p < .001), as was {b, maybe} *vs*. {b, no} (p = .026). The other pairwise comparisons were not statistically significant."
2	≥2	Two-sample Pearson chi-squared test	Pairwise chi-squared tests	"Fifteen *post hoc* pairwise comparisons using Pearson chi-squared tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that {b, maybe} *vs*. {b, yes} was statistically significant (p = .001), as was {b, maybe} *vs*. {b, no} (p = .035). The other pairwise comparisons were not statistically significant."
2	≥2	Fisher's exact test, *G*-test, two-sample Pearson chi-squared test	Individual binomial tests against chance	"Three *post hoc* binomial tests, corrected with Holm's sequential Bonferroni procedure (Holm 1979), indicated that, for X='a', the proportions of 'maybe', 'no', and 'yes' were not significantly different from chance (*i.e.*, 10 each). Three similar *post hoc* binomial tests for X='b' indicated that the proportion of 'maybe' responses was significantly different from chance (p < .0001), as was the proportion of 'yes' responses (p = .003), but not the proportion of 'no' responses (p = .174)."

Proportion & Association

Post hoc tests – Two dependent samples

Samples	Response Categories	Omnibus Test	Contrast Test	R Code
2	≥2	Symmetry test	Sign test	```# 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

Post hoc sign tests for the "fall" season, with obvious replication to other seasons.
add new columns to the data table:
df$chose.chocolate.in.fall = ifelse(df$Y == "chocolate" & df$X == "fall", 1, 0)
df$chose.strawberry.in.fall = ifelse(df$Y == "strawberry" & df$X == "fall", 1, 0)
df$chose.vanilla.in.fall = ifelse(df$Y == "vanilla" & df$X == "fall", 1, 0)

# chocolate vs. strawberry:
cs = pvalue(sign_test(chose.chocolate.in.fall ~ chose.strawberry.in.fall, data=df))
# chocolate vs. vanilla:
cv = pvalue(sign_test(chose.chocolate.in.fall ~ chose.vanilla.in.fall, data=df))
# strawberry vs. vanilla:
sv = pvalue(sign_test(chose.strawberry.in.fall ~ chose.vanilla.in.fall, data=df))

p.adjust(c(cs, cv, sv), method="holm")``` |

Proportion & Association

Post hoc tests – Two dependent samples

Samples	Response Categories	Omnibus Test	Contrast Test	Report
2	≥2	Symmetry test	Sign test	"The proportions of each ice cream flavor chosen in the fall were compared using three *post hoc* sign tests corrected with Holm's sequential Bonferroni procedure (Holm 1979). The proportions of 'chocolate', 'strawberry', and 'vanilla' flavors chosen in the fall did not significantly differ."

Bibliography (contingency tables, tests of proportion and association)

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Assumptions

ANOVA Assumptions

Normality

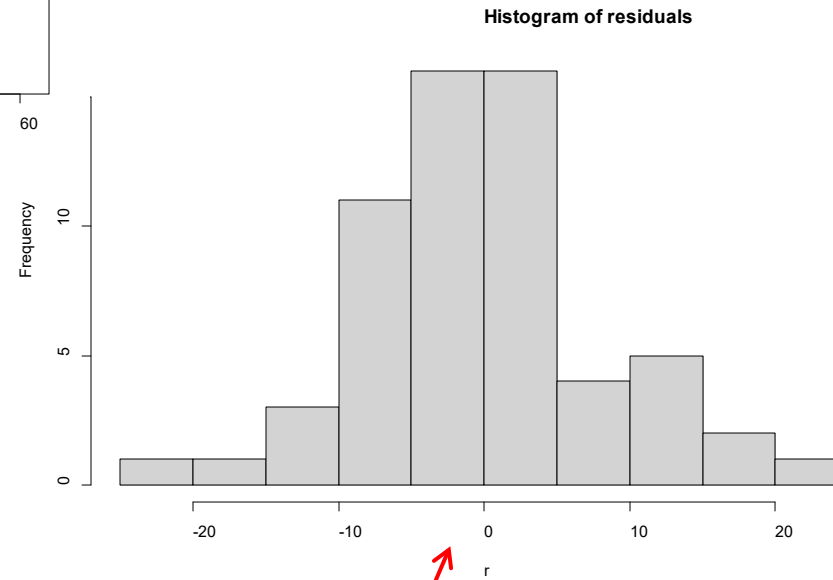| Assumption	Test Name	Context of Use	R Code

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

Normality	Shapiro-Wilk test (on residuals)	*t*-test, ANOVA	<pre># df has two factors (X1,X2) each w/two levels (a,b) and continuous response (Y)
			library(afex) # for aov_ez
			library(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</pre>

Normality	Shapiro-Wilk test (on residuals)	Linear mixed model (LMM)	<pre># df has two factors (X1,X2) each w/two levels (a,b) and continuous response (Y)
			library(lme4) # for lmer
			library(lmerTest)
			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</pre>

ANOVA Assumptions

Normality

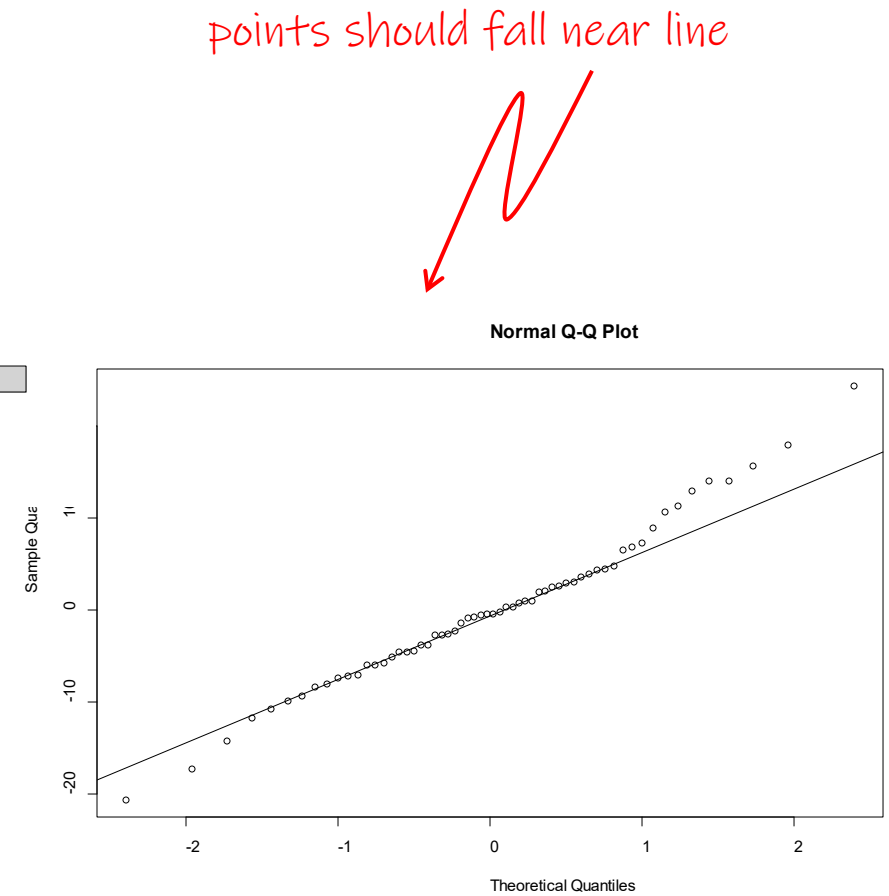| Assumption	Test Name	Context of Use	Report
Normality	Shapiro-Wilk test (on the response in each condition)	t-test, ANOVA	"To test the normality assumption, a Shapiro-Wilk test was run on the response Y for each combination of levels of factors X1 and X2. All combinations were found to be statistically 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

ANOVA Assumptions

Homoscedasticity & sphericity

Assumption	Test Name	Context of Use	R Code

Homogeneity of variance	Levene's test	Any ANOVA model with at least one between-subjects factor	<pre># df has one between-Ss factor (X1), one within-Ss factor (X2), and continuous response (Y)
			library(afex) # for aov_ez
			library(performance) # for check_homogeneity
			library(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</pre>

Sphericity	Mauchly's test	Any ANOVA model with at least one within-subjects factor	<pre># df has one between-Ss factor (X1), one within-Ss factor (X2), and continuous response (Y)
			library(afex) # for aov_ez
			library(performance) # for check_sphericity
			m = aov_ez(dv="Y", between="X1", within="X2", id="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</pre>

ANOVA Assumptions
Homoscedasticity & sphericity

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

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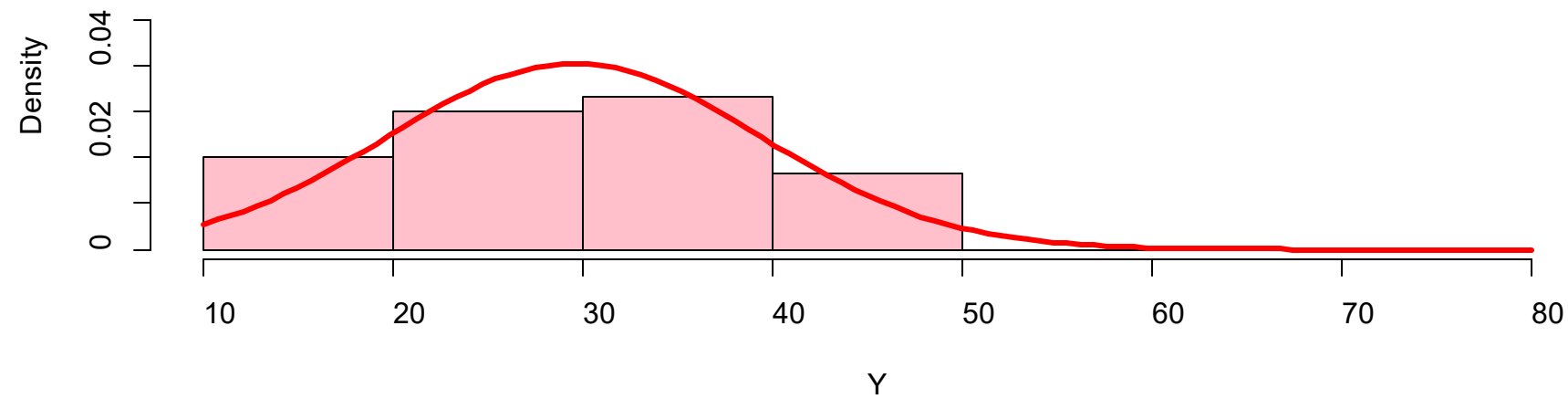
Distributions

Distributions

Distribution	Parameterization	R Distribution Fns	R Code

Normal	mean (μ): `mean`
	standard deviation (σ): `sd`
		`_norm:`
		  `dnorm`
		  `pnorm`
		  `qnorm`
		  `rnorm`
			```# df has one factor (X) w/two levels (a,b) and continuous response Y```
			```library(EnvStats) # for gofTest```
			```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-square GOF```
			```fb = fitdist(df[df$X == "b",]$Y, distr="pois") # create fit for X=b```
			```gofstat(fb) # chi-square 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-square GOF```
			```fb = fitdist(df[df$X == "b",]$Y, distr="nbinom") # create fit for X=b```
			```gofstat(fb) # chi-square 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
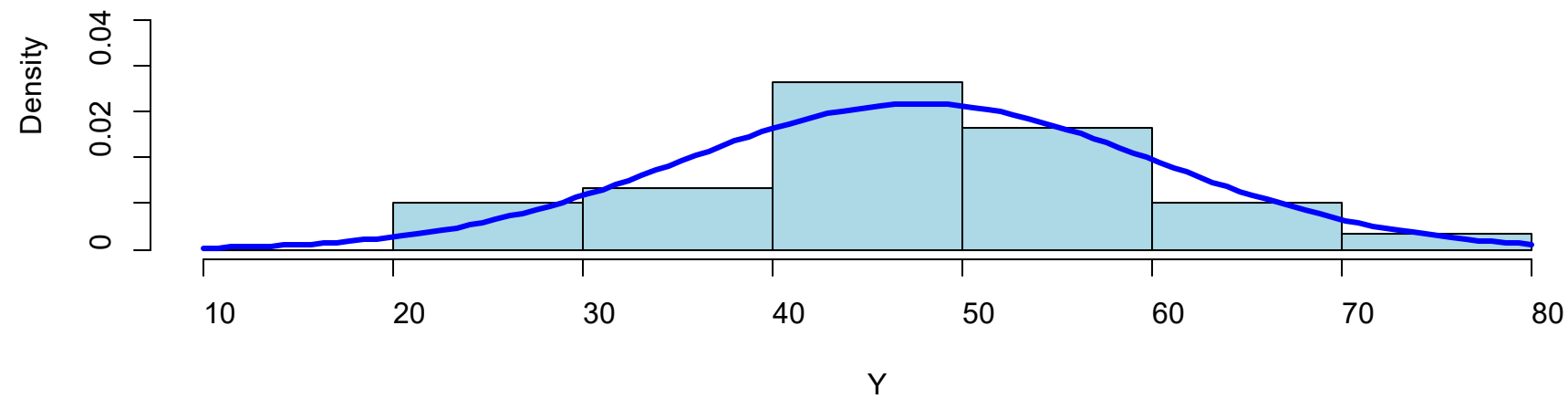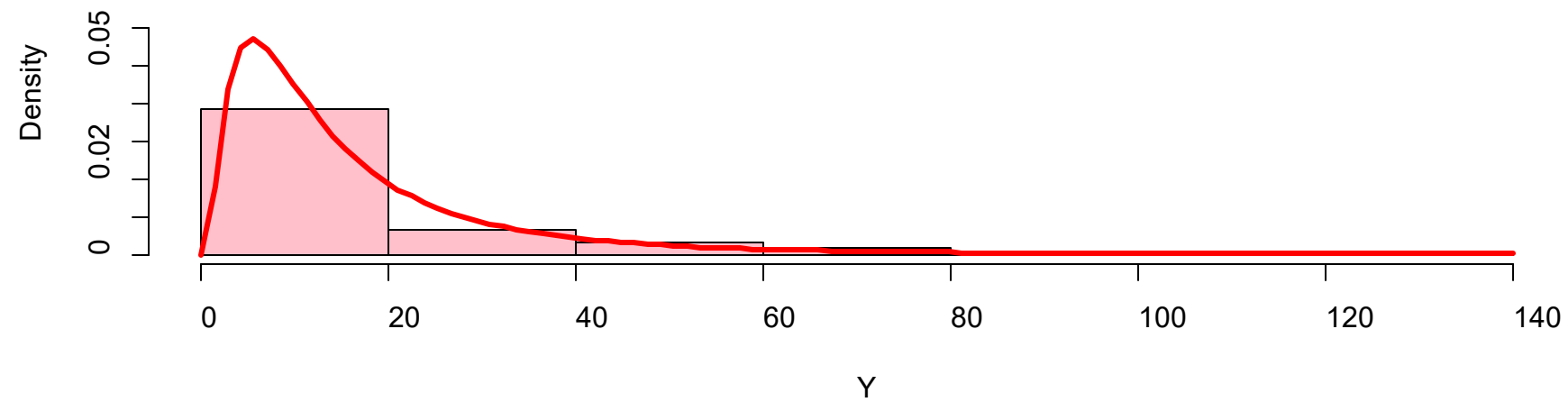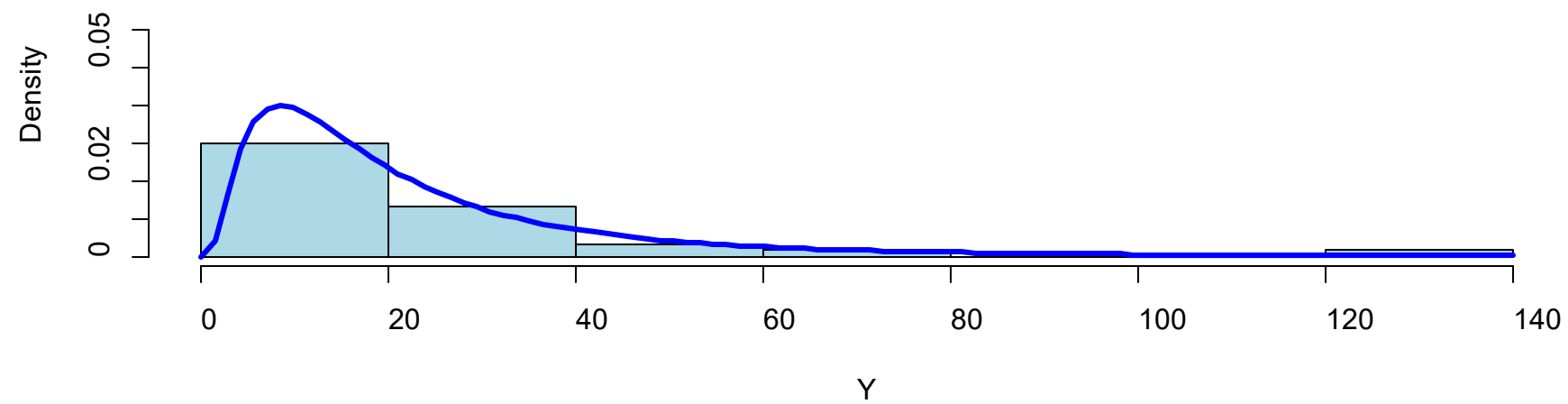
Figure 5

Figure 6

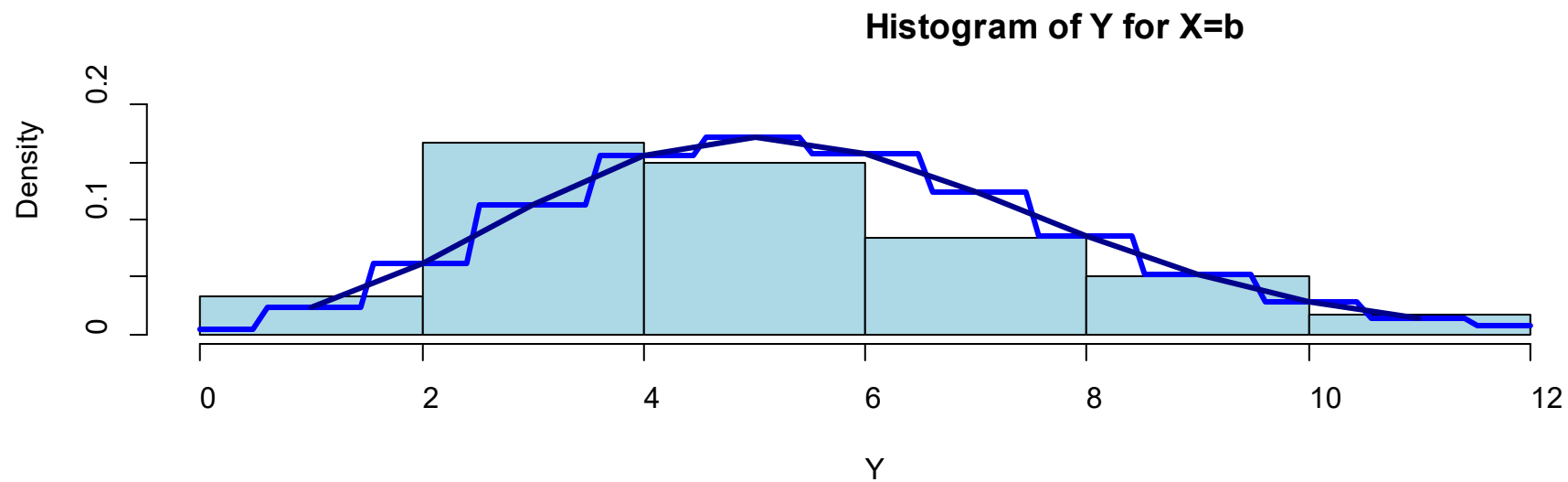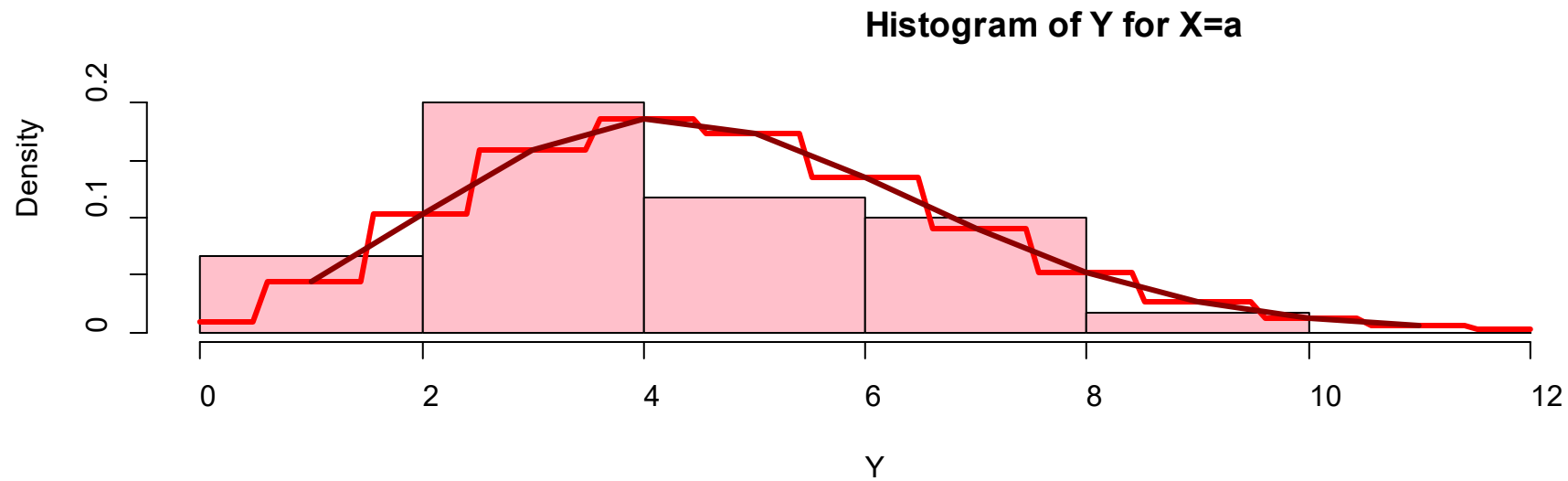# Figure 7

Histogram of Y for X=a
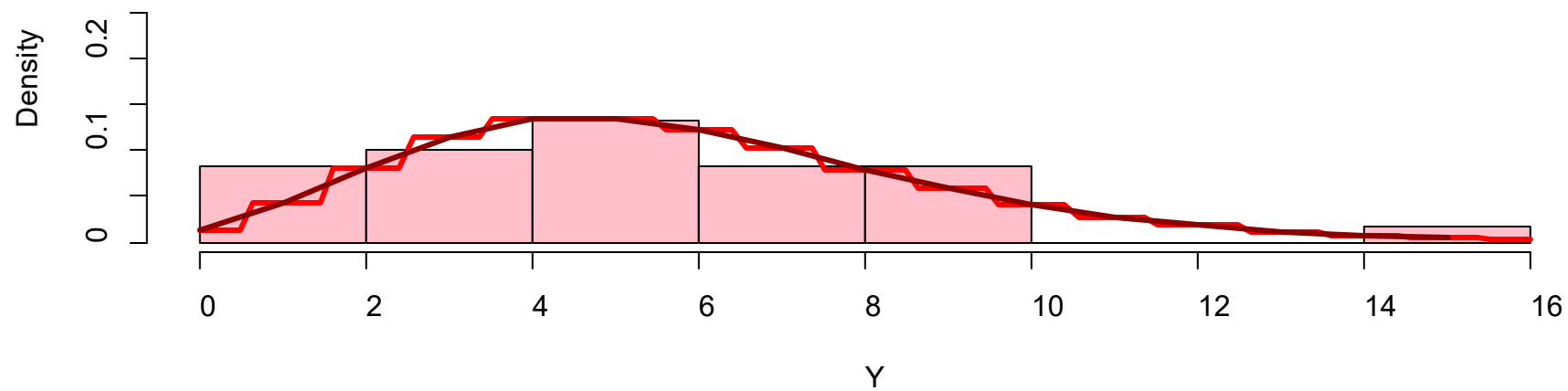
Histogram of Y for X=b

Distribution Tests

Distribution	Parameterization	R Distribution Fns	R Code

Exponential	rate (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

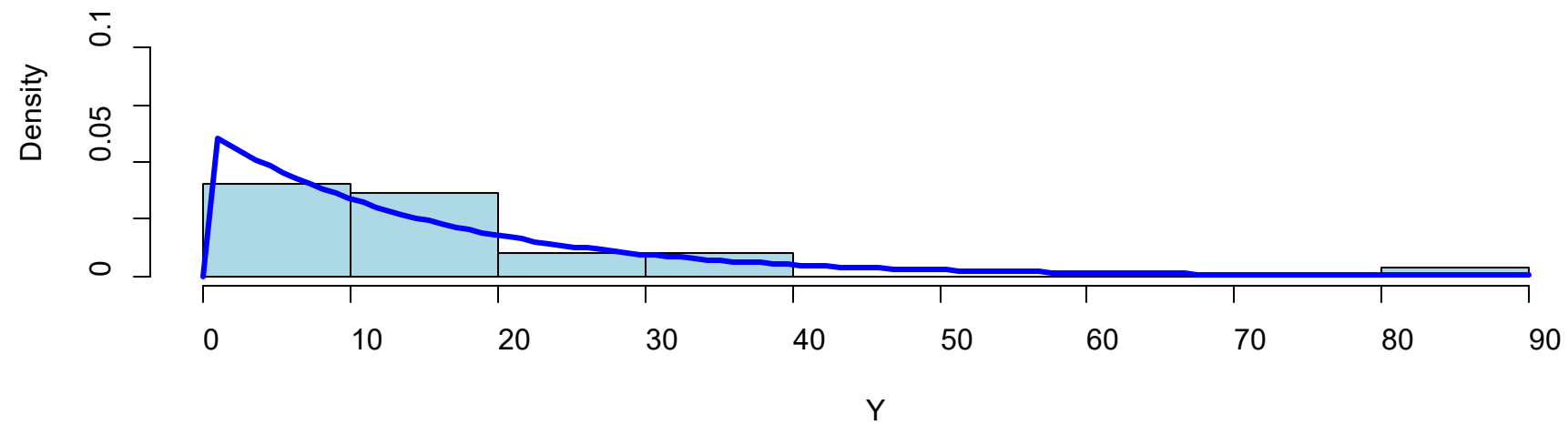**Histogram of Y for X=a**
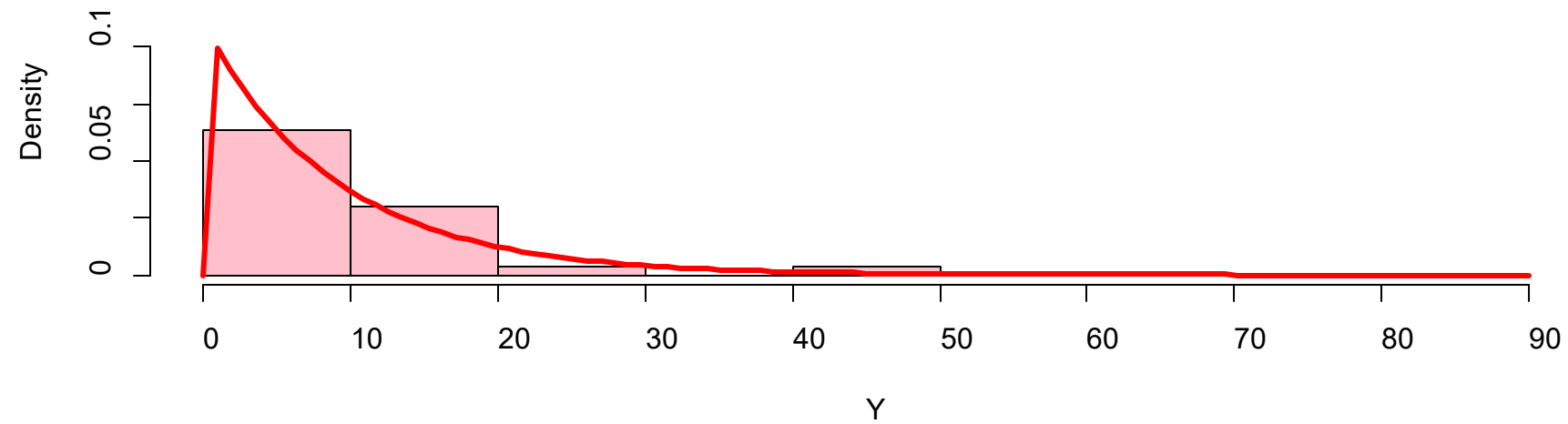
Histogram of Y for X=b

Figure 9
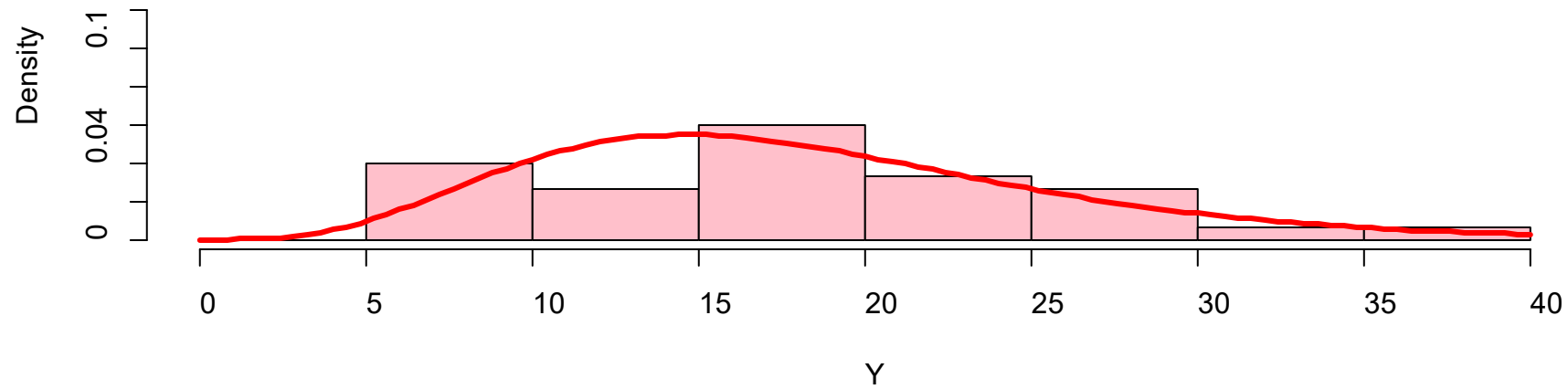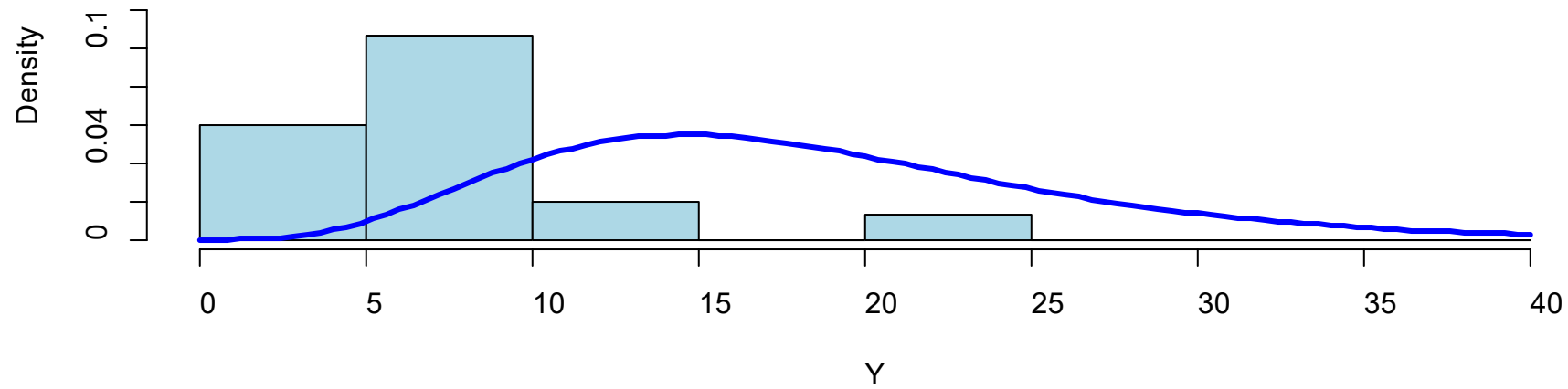
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Parametric Tests

Parametric Tests

One between-Ss. factor

Factors	Levels	Between or Within Subjects	Test Name	R Code
1	2	Between	Independent-samples *t*-test	```# df has one between-Ss. factor (X) w/levels (a,b) and continuous response (Y)
library(car) # for leveneTest
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

Factors	Levels	Between or Within Subjects	Test Name	R Code
| ≥2 | ≥2 | Between | Factorial ANOVA | ```r
# 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$lm, type=3, white.adjust=TRUE) # if p<.05, violation of homogeneity
``` |
| | | | Linear model (LM) | ```r
# df has two between-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)
library(car) # for Anova
df$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
``` |

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

Factors	Levels	Between or Within Subjects	Test Name	R Code
≥2	≥2	Within	Factorial repeated measures ANOVA	```# df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)
library(afex) # for aov_ez
library(performance) # for check_sphericity
df$PId = factor(df$PId) # participant is nominal
df$X1 = factor(df$X1) # X1 is a 2-level factor
df$X2 = factor(df$X2) # X2 is a 2-level factor
contrasts(df$X1) <- "contr.sum"
contrasts(df$X2) <- "contr.sum"

m = aov_ez(dv="Y", within=c("X1","X2"), id="PId", type=3, data=df) # fit model
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``` |
| ≥2 | ≥2 | Within | Linear mixed model (LMM)* | ```# df has two within-Ss. factors (X1,X2) each w/levels (a,b) and continuous response (Y)
library(lme4) # for lmer
library(lmerTest)
library(car) # for Anova
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")``` |

*The LMM 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 *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

Y by X1, X2

Parametric Tests

Post hoc pairwise comparisons

Parametric Tests

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Test	Test Name	B/W	R Code

1	>2	One-way ANOVA	Independent samples *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."

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Variance-Covariance Structures

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

Covariance Structures

Optional when fitting linear mixed models (LMMs)

Abbreviation	Name	Description	R Code

ID	Scaled identity	All variances are equal, and all covariances are zero.	```# df has one within-Ss. factor (X) w/levels (a,b,c) and continuous response (Y)```
			```library(nlme) # for lme```
			```library(car) # for Anova```
			```library(emmeans) # for emmeans```
			```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.

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Nonparametric Tests

Nonparametric Tests

One factor with 2 levels

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

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

Y by X1, X2

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	<pre># df has one between-Ss. factor (X) w/levels (a,b,c) and continuous response (Y)
					library(rcompanion) # for wilcoxonZ
					ab = wilcox.test(df[df$X == "a",]$Y, df[df$X == "b",]$Y, exact=FALSE) # a vs. b
					ac = wilcox.test(df[df$X == "a",]$Y, df[df$X == "c",]$Y, exact=FALSE) # a vs. c
					bc = wilcox.test(df[df$X == "b",]$Y, df[df$X == "c",]$Y, exact=FALSE) # b vs. c
					p.adjust(c(ab$p.value, ac$p.value, bc$p.value), method="holm") # p-values
					
					wilcoxonZ(df[df$X == "a",]$Y, df[df$X == "b",]$Y) # Z-scores
					wilcoxonZ(df[df$X == "a",]$Y, df[df$X == "c",]$Y)
					wilcoxonZ(df[df$X == "b",]$Y, df[df$X == "c",]$Y)</pre>

1	≥2	Friedman test	Wilcoxon signed-rank test	Within	<pre># df has one within-Ss. factor (X) w/levels (a,b,c) and continuous response (Y)
					library(reshape2) # for dcast
					library(rcompanion) # for wilcoxonZ
					df2 <- dcast(df, PId ~ X, value.var="Y") # make wide-format table
					ab = wilcox.test(df2$a, df2$b, paired=TRUE, exact=FALSE) # a vs. b
					ac = wilcox.test(df2$a, df2$c, paired=TRUE, exact=FALSE) # a vs. c
					bc = wilcox.test(df2$b, df2$c, paired=TRUE, exact=FALSE) # b vs. c
					p.adjust(c(ab$p.value, ac$p.value, bc$p.value), method="holm") # p-values
					
					wilcoxonZ(df2$a, df2$b, paired=TRUE) # Z-scores
					wilcoxonZ(df2$a, df2$c, paired=TRUE)
					wilcoxonZ(df2$b, df2$c, paired=TRUE)</pre>

Nonparametric Tests

Post hoc pairwise comparisons – One factor

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

Nonparametric Tests

Post hoc pairwise comparisons – Multiple factors

Factors	Levels	Omnibus Test	Test Name	B/W	R Code

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

Nonparametric Tests
Post hoc pairwise comparisons – Multiple factors

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

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General<u>ized</u> Linear (Mixed) Models

Terminology

Generalize to Responses Unsuitable to ANOVA?

	No	Yes

Contain Random Factors?*

Between-Ss.

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

Within-Ss.

Yes

(General) Linear Mixed Model **(LMM)**
`lme4::lmer` in R
(see also `nlme::lme`)

Generalized Linear Mixed Model **(GLMM)**
`lme4::glmer` in R

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` `REML=TRUE`[7] `ziformula=~1`
Negative binomial	`MASS::glm.nb()`	`lme4::glmer.nb()`
Zero-inflated negative binomial[6]	`glmmTMB::glmmTMB() family=nbinom2` `ziformula=~1`	`glmmTMB::glmmTMB() family=nbinom2` `REML=TRUE`[7] `ziformula=~1`
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 <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 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

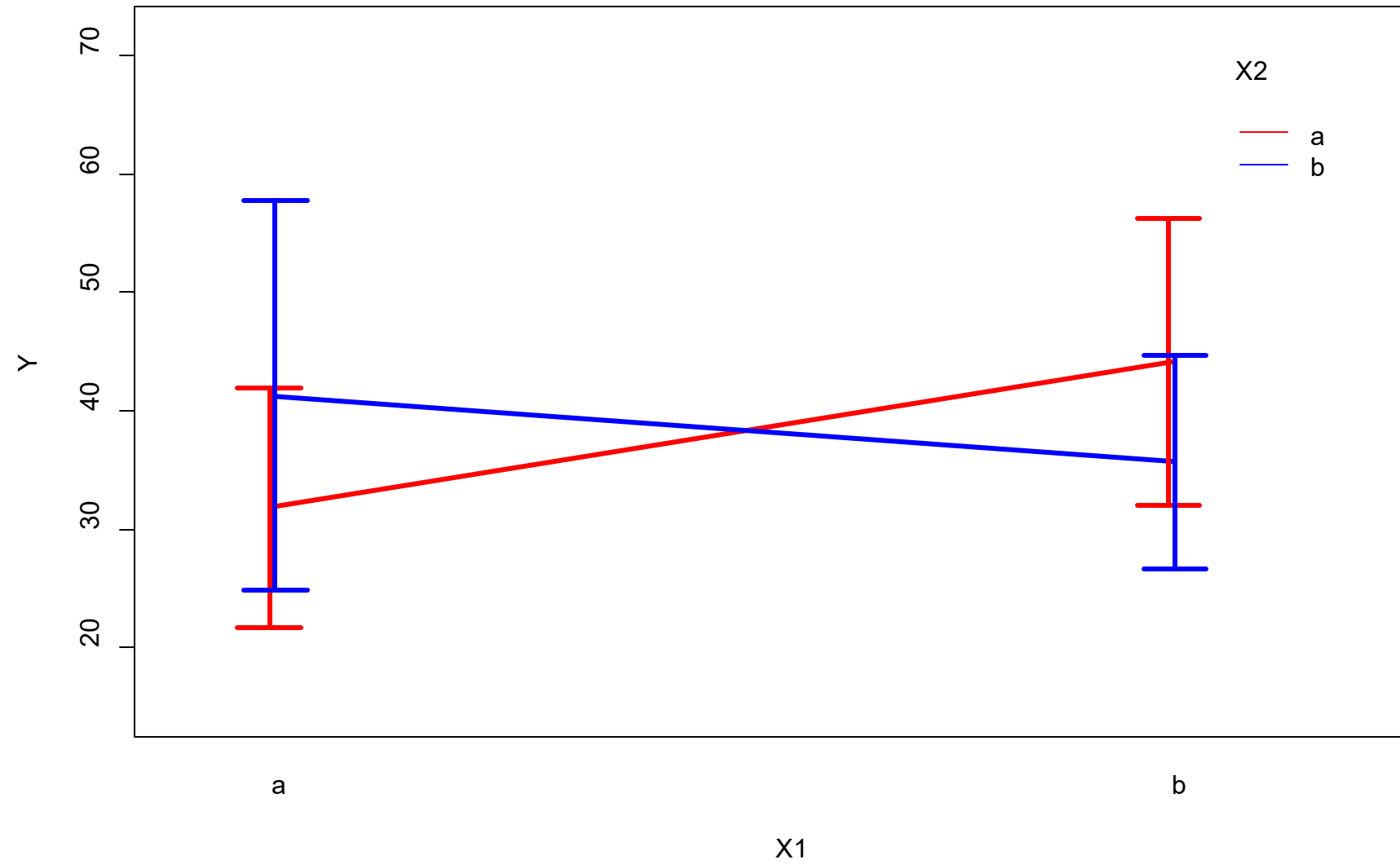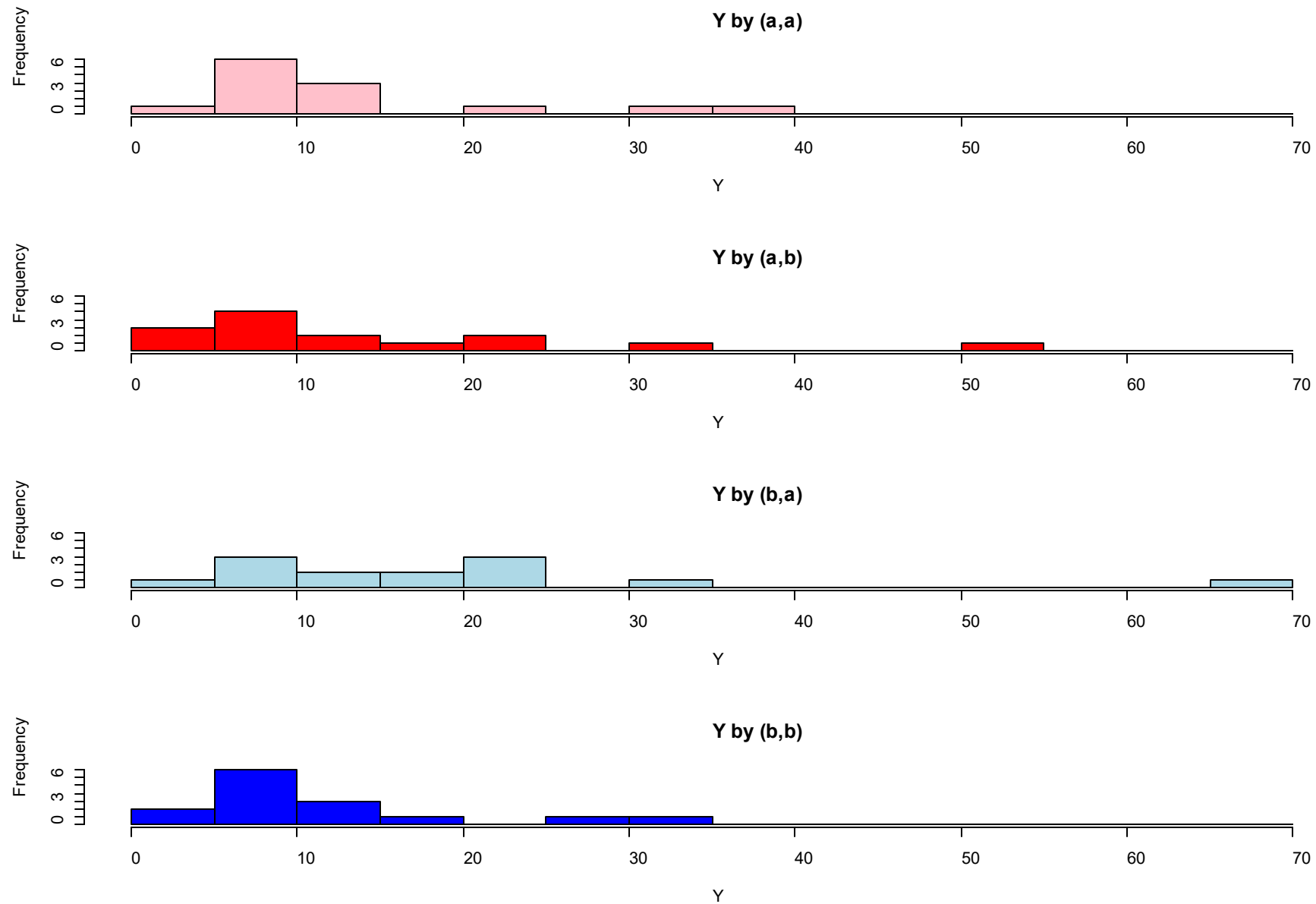| Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Normal	identity	*Linear regression:* Normally distributed responses; equivalent to the linear model (LM) or linear mixed model (LMM)	"Figure 12 shows an interaction plot with ±1 standard deviation error bars for 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

GLM / GLMM
Distributions and canonical links

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

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

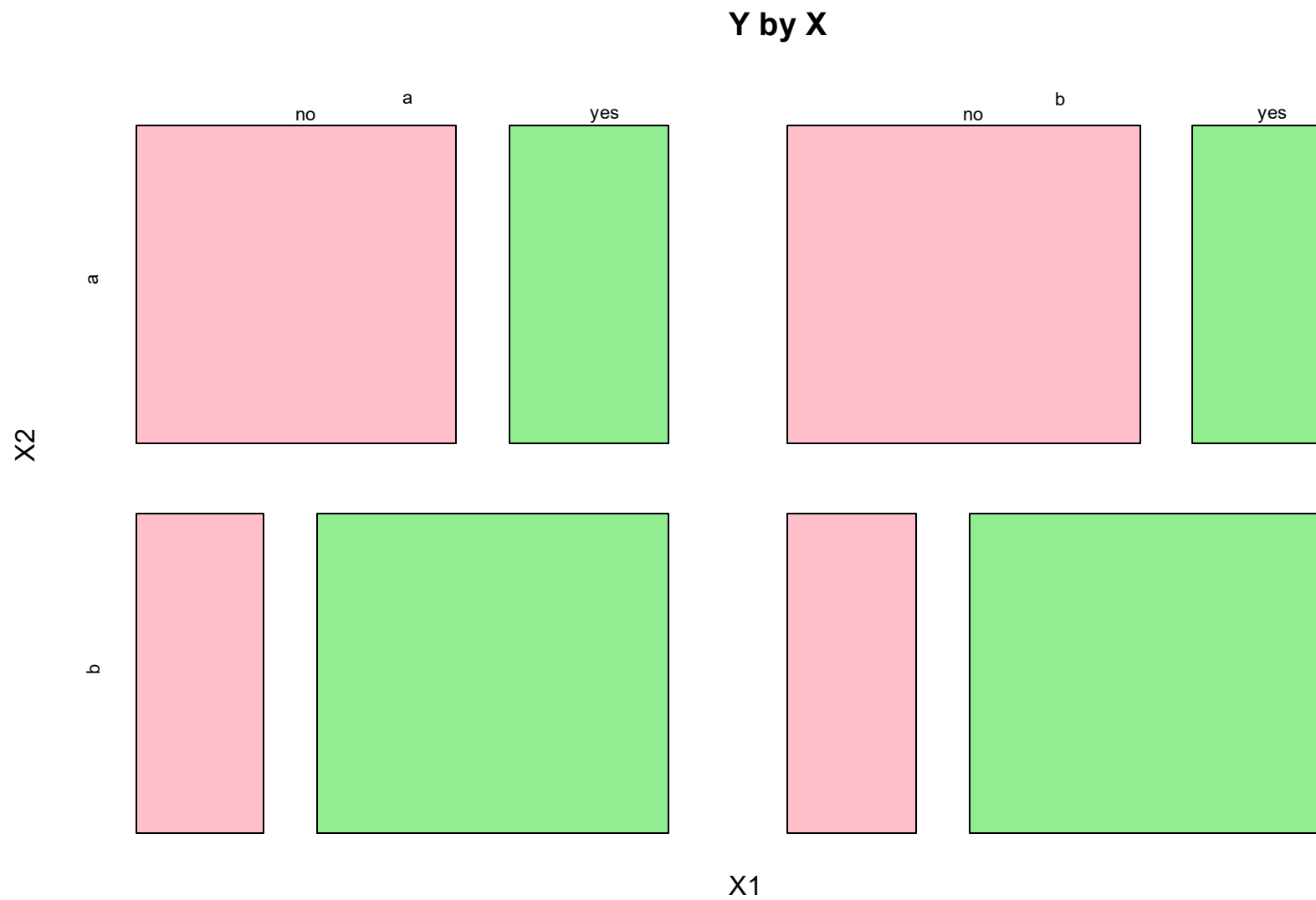| Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Binomial	logit	*Logistic regression:* Dichotomous responses (i.e., nominal responses with two categories)	"Figure 14 shows the number of 'no' and 'yes' responses for each X1×X2 condition. An analysis of variance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

Figure 14

Y by X

Figure 15

Y by X

GLM / GLMM

Distributions and canonical links

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

Ordinal	cumulative logit	*Ordinal logistic regression:* Ordinal responses (e.g., Likert-type scales)	```library(MASS) # for polr```
			```library(car) # for Anova```
			```df$PId = factor(df$PId)```
			```df$X1 = factor(df$X1)```
			```df$X2 = factor(df$X2)```
			```df$Y = ordered(df$Y) # ordinal response```
			```contrasts(df$X1) <- "contr.sum"```
			```contrasts(df$X2) <- "contr.sum"```
			```m = polr(Y ~ X1*X2, data=df, Hess=TRUE)```
			```Anova(m, type=3)```
				```library(ordinal) # for clmm```
				```library(RVAideMemoire) # for Anova.clmm```
				```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)```

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

GLM / GLMM

Distributions and canonical links

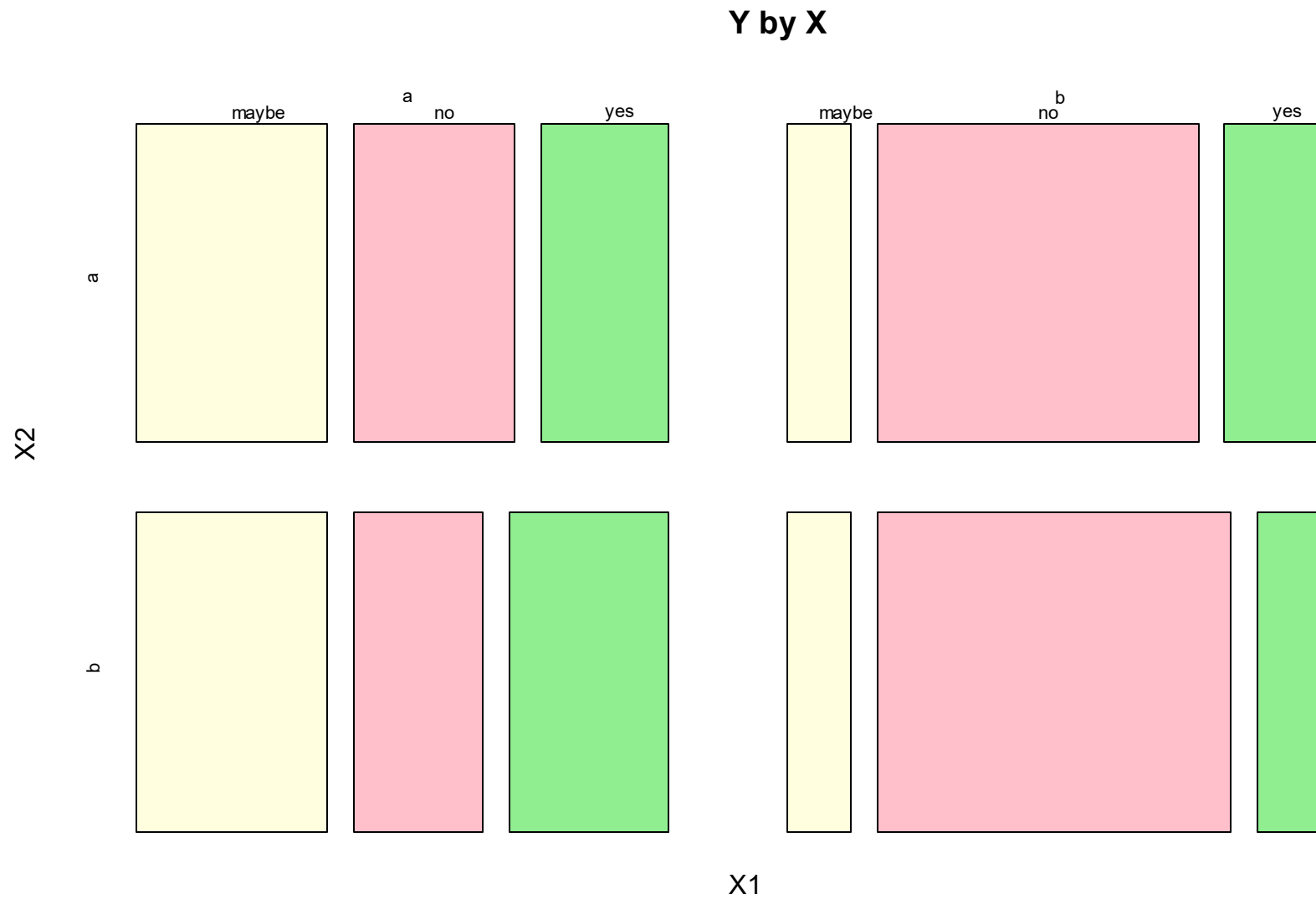| Distribution	Link	Typical Uses	Report for GLM (between-Ss)	Report for GLMM (within-Ss)
Ordinal	cumulative logit	*Ordinal logistic regression:* Ordinal responses (e.g., Likert-type scales)	"Figure 16 shows the distribution of Likert responses (1-7) for each X1×X2 condition. An analysis of variance based 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

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

Poisson	log	*Poisson regression:*
		Count responses
			```library(car) # for Anova```
			```library(performance) # for check_overdispersion```
			```df$PId = factor(df$PId)```
			```df$X1 = factor(df$X1)```
			```df$X2 = factor(df$X2)```
			```contrasts(df$X1) <- "contr.sum"```
			```contrasts(df$X2) <- "contr.sum"```
			```m = glm(Y ~ X1*X2, data=df, family=poisson)```
			```print(check_overdispersion(m))```
			```# use family=quasipoisson or negative binomial```
			```# regression if overdispersed```
			```Anova(m, type=3)```
				```library(lme4) # for glmer```
				```library(lmerTest)```
				```library(car) # for Anova```
				```library(performance) # for check_overdispersion```
				```df$PId = factor(df$PId)```
				```df$X1 = factor(df$X1)```
				```df$X2 = factor(df$X2)```
				```contrasts(df$X1) <- "contr.sum"```
				```contrasts(df$X2) <- "contr.sum"```
				```m = glmer(Y ~ X1*X2 + (1|PId), data=df, family=poisson)```
				```print(check_overdispersion(m))```
				```# use mixed negative binomial regression if overdispersed```
				```Anova(m, type=3)```

Zero-Inflated Poisson	log	*Zero-inflated Poisson regression:*
		Zero-inflated count responses
			```library(glmmTMB) # for glmmTMB```
			```library(car) # for Anova```
			```library(performance) # for check_zeroinflation```
			```df$PId = factor(df$PId)```
			```df$X1 = factor(df$X1)```
			```df$X2 = factor(df$X2)```
			```contrasts(df$X1) <- "contr.sum"```
			```contrasts(df$X2) <- "contr.sum"```
			```m0 = glm(Y ~ X1*X2, data=df, family=poisson)```
			```print(check_zeroinflation(m0))```
			```m = glmmTMB(Y ~ X1*X2, data=df,```
			``` family=poisson, ziformula=~1)```
			```Anova(m, type=3)```
				```library(lme4) # for glmer```
				```library(lmerTest)```
				```library(glmmTMB) # for glmmTMB```
				```library(car) # for Anova```
				```library(performance) # for check_zeroinflation```
				```df$PId = factor(df$PId)```
				```df$X1 = factor(df$X1)```
				```df$X2 = factor(df$X2)```
				```contrasts(df$X1) <- "contr.sum"```
				```contrasts(df$X2) <- "contr.sum"```
				```m0 = glmer(Y ~ X1*X2 + (1|PId), data=df, family=poisson)```
				```print(check_zeroinflation(m0))```
				```m = glmmTMB(Y ~ X1*X2 + (1|PId), data=df, REML=TRUE,```
				``` family=poisson, ziformula=~1)```
				```Anova(m, type=3)```

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

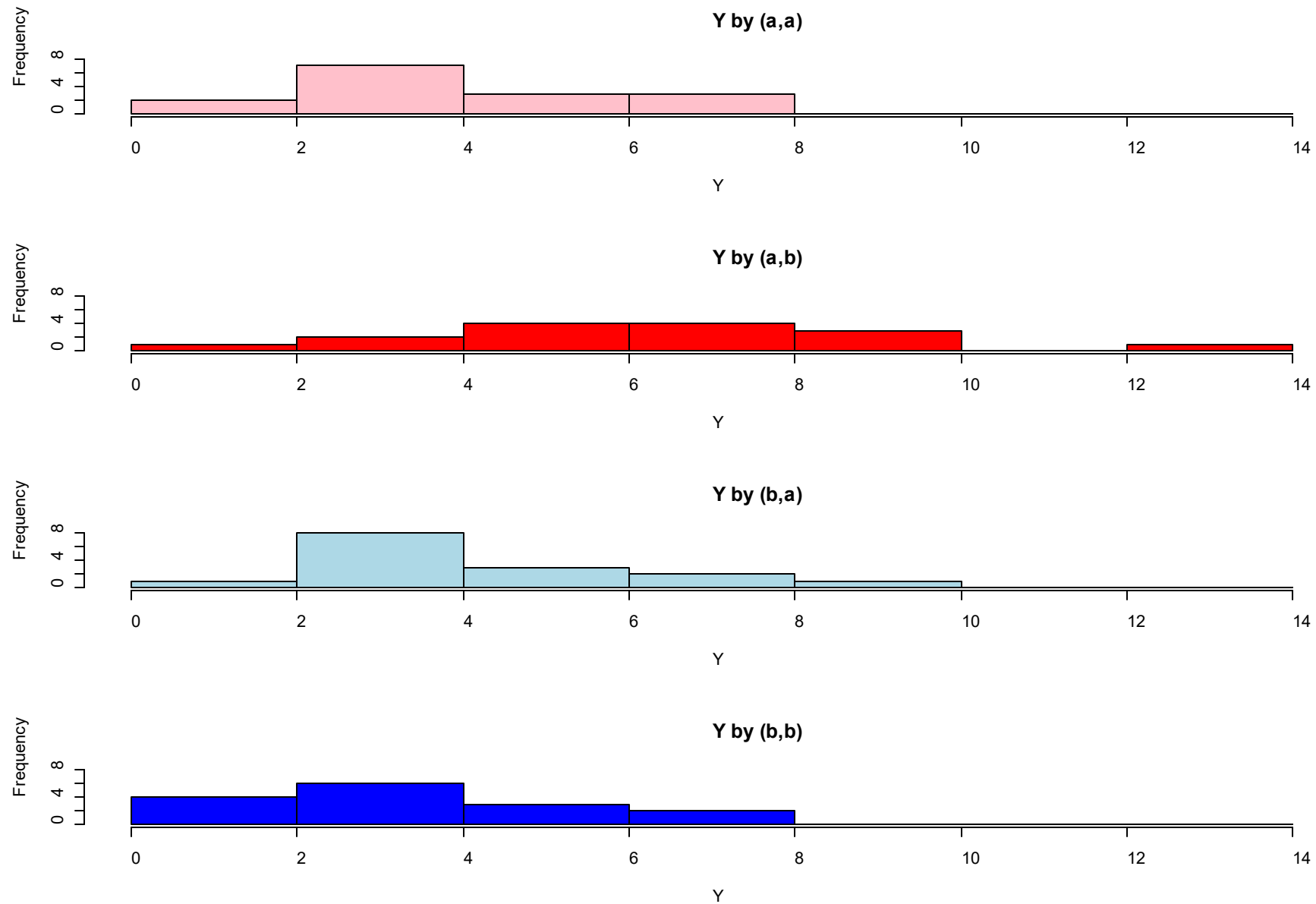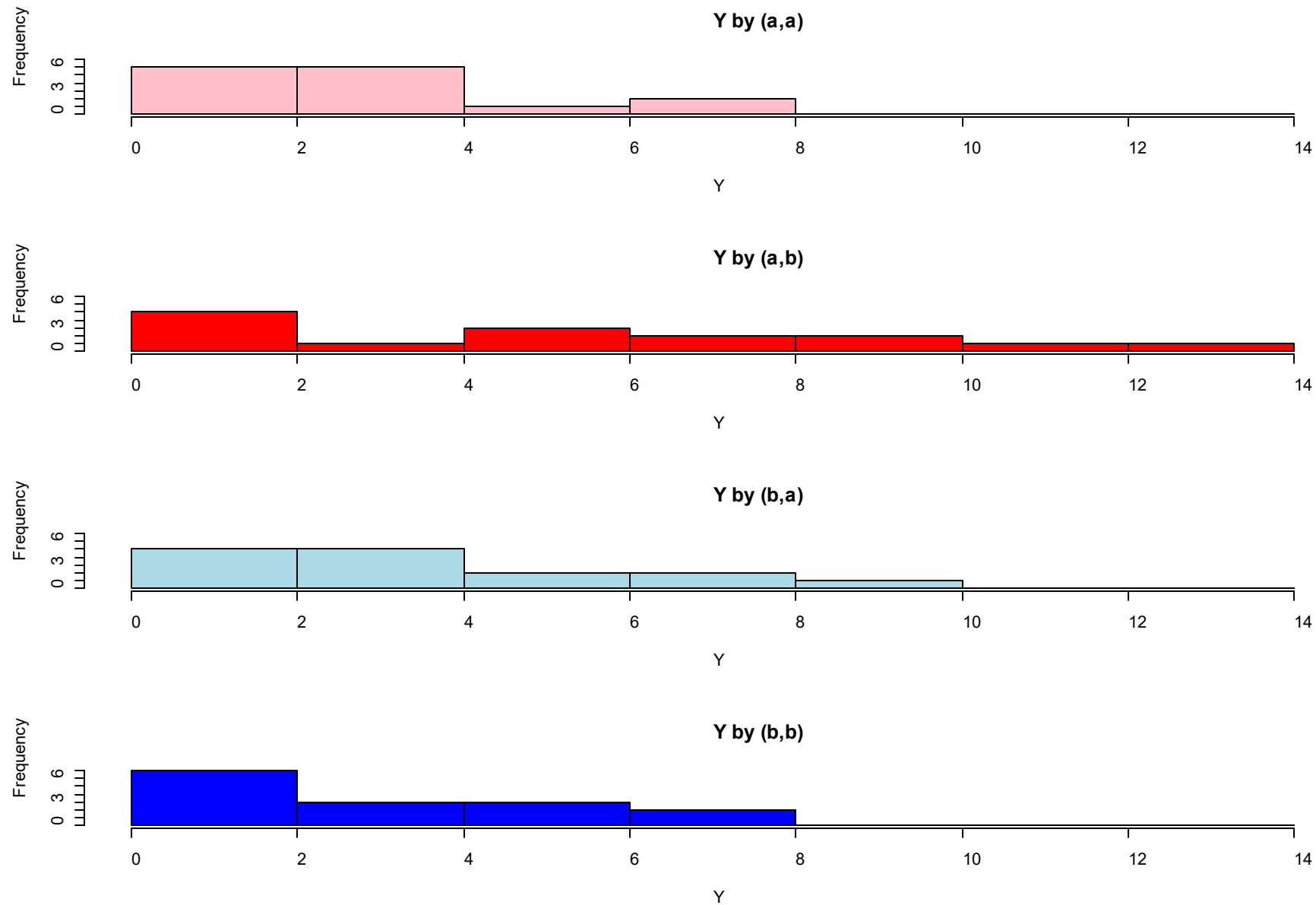| Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Poisson	log	*Poisson regression:* Count responses	"Figure 17 shows histograms of count responses in each X1×X2 condition. An analysis of variance based on Poisson regression indicated a statistically significant 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

Figure 18

GLM / GLMM

Distributions and canonical links

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

Negative Binomial	log	*Negative binomial regression:* Overdispersed count responses	```library(MASS) # for glm.nb```
			```library(car) # for Anova```
			```df$PId = factor(df$PId)```
			```df$X1 = factor(df$X1)```
			```df$X2 = factor(df$X2)```
			```contrasts(df$X1) <- "contr.sum"```
			```contrasts(df$X2) <- "contr.sum"```
			```m = glm.nb(Y ~ X1*X2, data=df)```
			```Anova(m, type=3)```
				```library(lme4) # for glmer.nb```
				```library(lmerTest)```
				```library(car) # for Anova```
				```df$PId = factor(df$PId)```
				```df$X1 = factor(df$X1)```
				```df$X2 = factor(df$X2)```
				```contrasts(df$X1) <- "contr.sum"```
				```contrasts(df$X2) <- "contr.sum"```
				```m = glmer.nb(Y ~ X1*X2 + (1|PId), data=df)```
				```Anova(m, type=3)```

Zero-Inflated Negative Binomial	log	*Zero-inflated negative binomial regression:* Overdispersed zero-inflated count responses	```library(MASS) # for glm.nb```
			```library(glmmTMB) # for glmmTMB```
			```library(car) # for Anova```
			```library(performance) # for check_zeroinflation```
			```df$PId = factor(df$PId)```
			```df$X1 = factor(df$X1)```
			```df$X2 = factor(df$X2)```
			```contrasts(df$X1) <- "contr.sum"```
			```contrasts(df$X2) <- "contr.sum"```
			```m0 = glm.nb(Y ~ X1*X2, data=df)```
			```print(check_zeroinflation(m0))```
			```m = glmmTMB(Y ~ X1*X2, data=df,```
			``` family=nbinom2, ziformula=~1)```
			```Anova(m, type=3)```
				```library(lme4) # for glmer.nb```
				```library(lmerTest)```
				```library(glmmTMB) # for glmmTMB```
				```library(car) # for Anova```
				```library(performance) # for check_zeroinflation```
				```df$PId = factor(df$PId)```
				```df$X1 = factor(df$X1)```
				```df$X2 = factor(df$X2)```
				```contrasts(df$X1) <- "contr.sum"```
				```contrasts(df$X2) <- "contr.sum"```
				```m0 = glmer.nb(Y ~ X1*X2 + (1|PId), data=df)```
				```print(check_zeroinflation(m0))```
				```m = glmmTMB(Y ~ X1*X2 + (1|PId), data=df, REML=TRUE,```
				``` family=nbinom2, ziformula=~1)```
				```Anova(m, type=3)```

GLM / GLMM

Distributions and canonical links

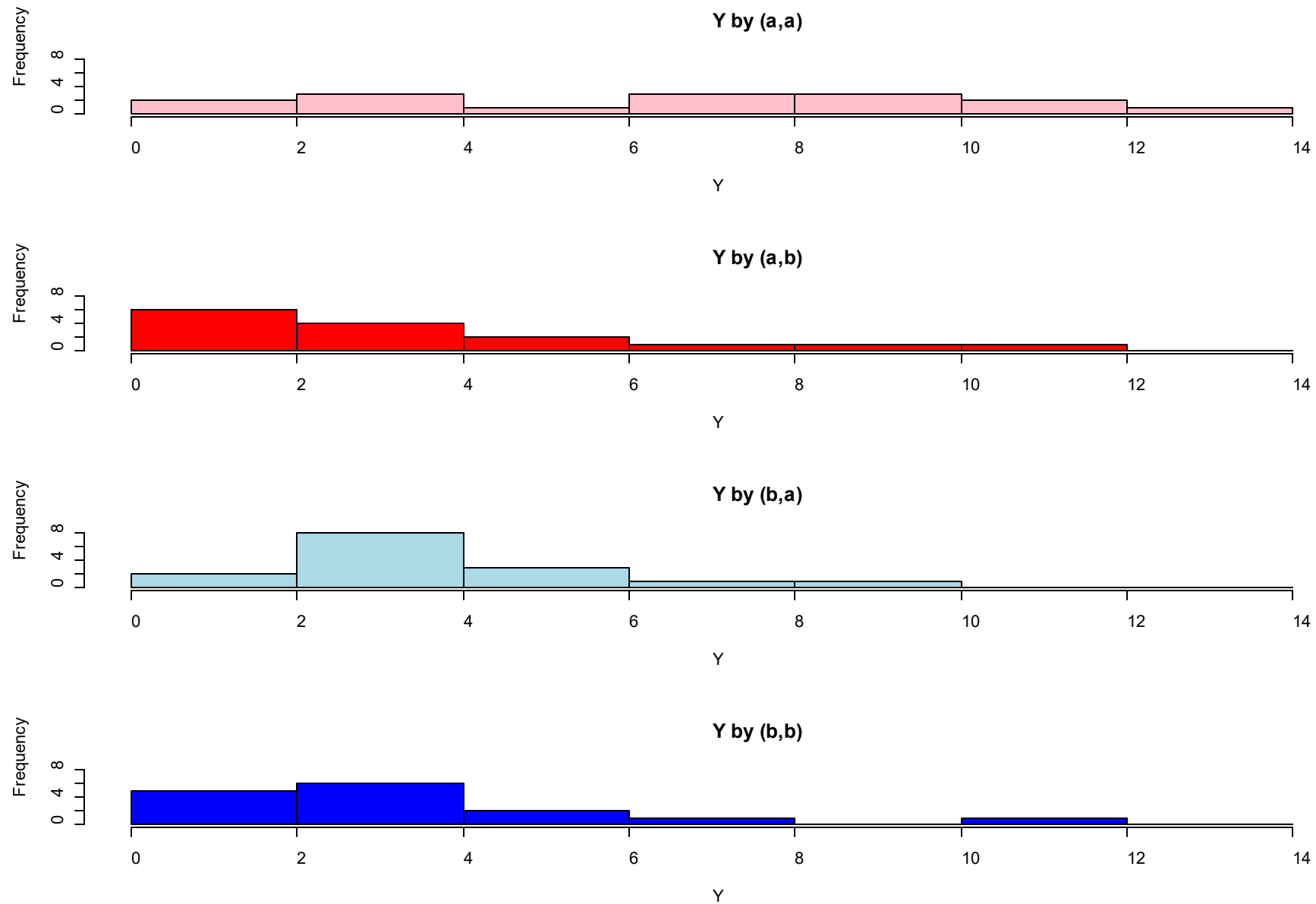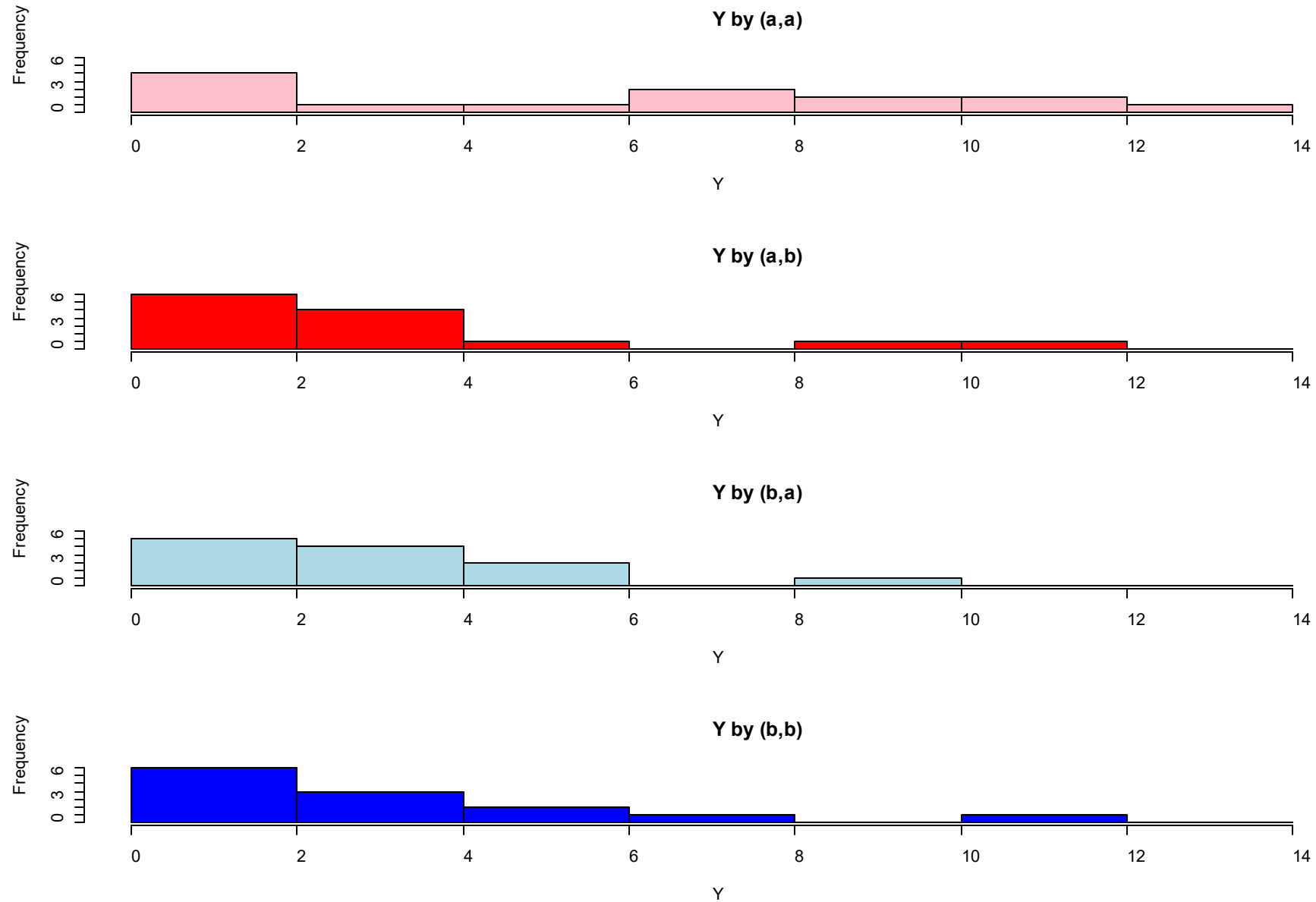| Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Negative Binomial	log	*Negative binomial regression:* Overdispersed count responses	"Figure 19 shows histograms of count responses in each X1×X2 condition. An analysis of variance based on negative binomial regression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

Figure 20

GLM / GLMM

Distributions and canonical links

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

Exponential	log	*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

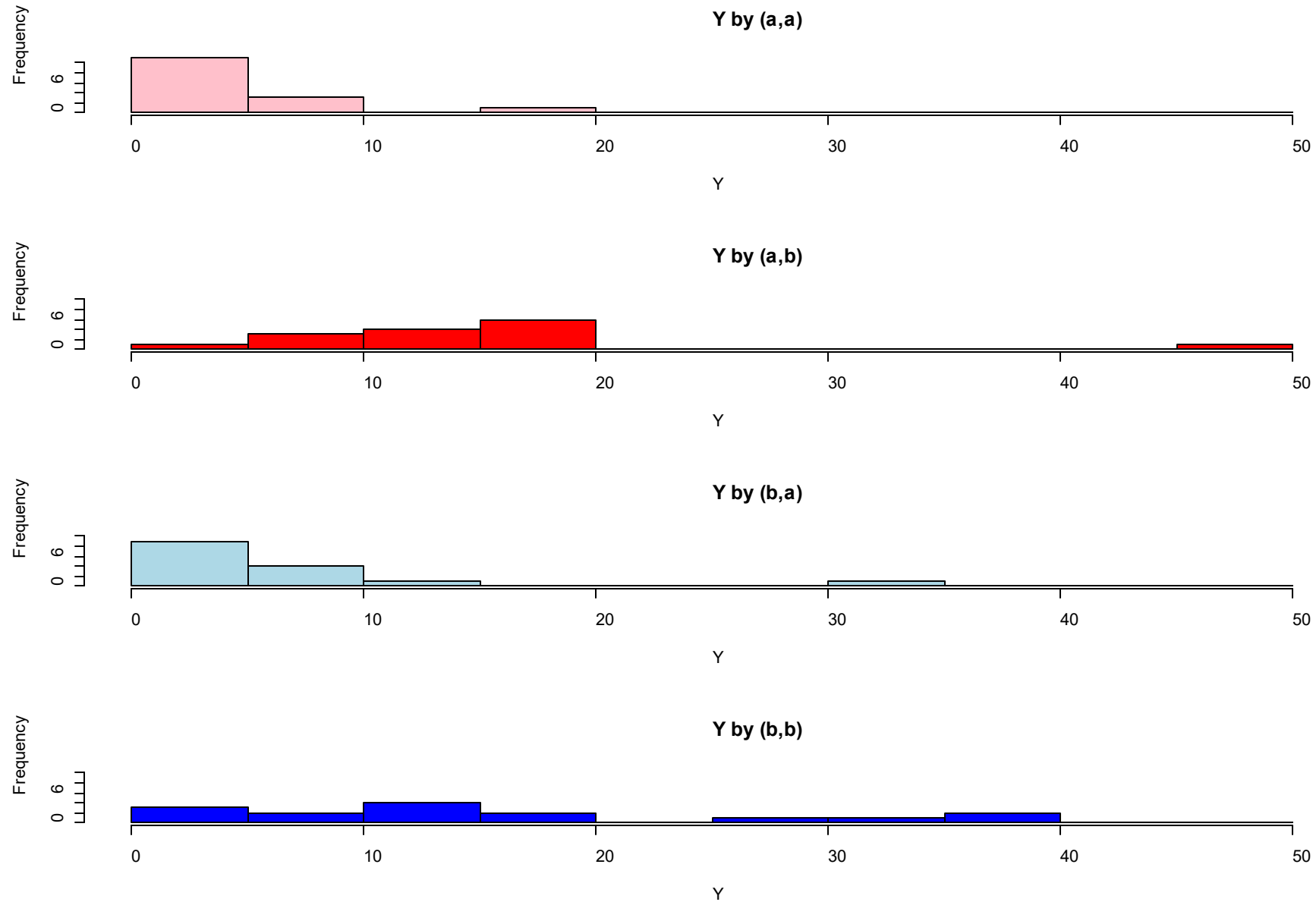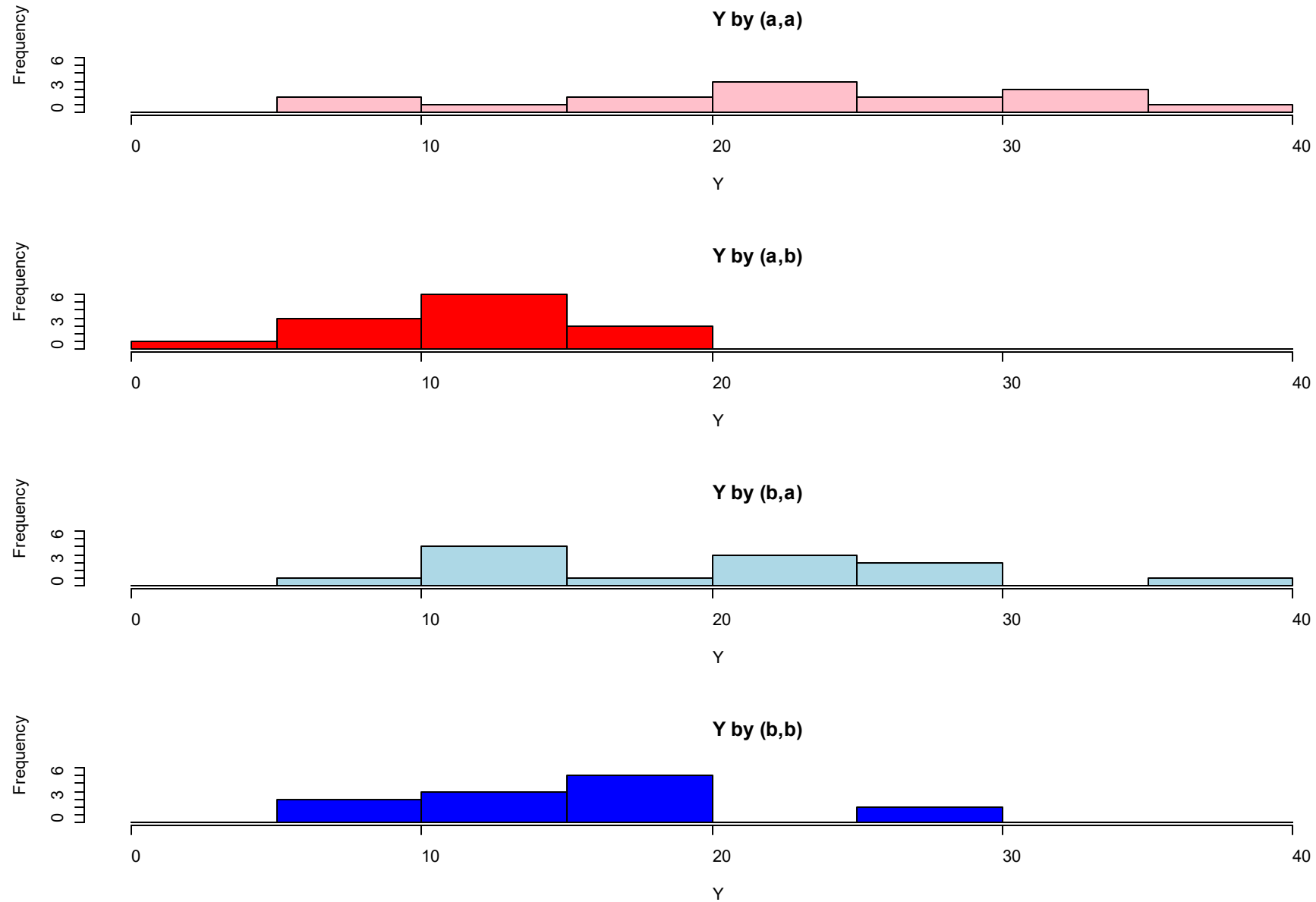| Distribution	Link	Typical Uses	Report for GLM (between-Ss.)	Report for GLMM (within-Ss.)
Exponential	log	*Exponential regression:* Exponentially distributed responses (e.g., income)	"Figure 21 shows exponential histograms for each X1×X2 condition. An analysis of variance based on exponential regression 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)

Y by (a,b)

Y by (b,a)

Y by (b,b)

Figure 22

Generalized Linear (Mixed) Models

Post hoc pairwise comparisons

GLM / GLMM

Post hoc pairwise comparisons – One factor

Factors	Levels	Omnibus Model	Test	B/W	R Code

1	≥2	Linear regression	*t*-test	Btwn, Within	``# 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 detectably 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 no two levels were detectably different."
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 comparison was 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 comparison was 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."

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