Morality Analysis

Load the data

```r
## Load the data
library(readxl)

file_path <- "/Users/daryani/Desktop/data.xlsx"
data <- read_excel(file_path)

Sys.setenv(RGL_USE_NULL = "TRUE")
options(rgl.useNULL = TRUE)
# Packages
library(dplyr)
```

```
Attaching package: 'dplyr'
```

```
The following objects are masked from 'package:stats':

    filter, lag
```

```
The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```r
library(car)          # Levene tests, Type-III ANCOVA tables
```

```
Loading required package: carData
```

```
Attaching package: 'car'


The following object is masked from 'package:dplyr':

    recode
```

```r
library(heplots)      # Box's M, multivariate SSPE/HE utilities
```

```
Loading required package: broom
```

```r
library(MVN)          # Multivariate normality + Mahalanobis outliers
library(emmeans)      # Estimated marginal means + contrasts
```

```
Welcome to emmeans.
Caution: You lose important information if you filter this package's results.
See '? untidy'
```

```r
library(effectsize)  # Effect sizes (partial eta^2, CI)
```

Ensure factors are factors

```r
# Robust recode to canonical labels
data <- data %>%
  mutate(
    group_clean = case_when(
      group %in% c(1, "1", "Prolife", "prolife")      ~ "Prolife",
      group %in% c(2, "2", "Prochoice", "prochoice")  ~ "Prochoice",
      TRUE ~ NA_character_
    ),
    condition_clean = case_when(
      condition %in% c(1, "1", "Outgroup", "outgroup", "Actual", "Actual Perception") ~ "Outg
      condition %in% c(2, "2", "Metaperception", "metaperception", "Meta")            ~ "Meta
      condition %in% c(3, "3", "Ingroup", "ingroup")                                  ~ "Ing
      TRUE ~ NA_character_
    ),
    group     = factor(group_clean, levels = c("Prolife", "Prochoice")),
    condition = factor(condition_clean, levels = c("Outgroup", "Metaperception", "Ingroup"))
```

```
  ) %>%
  select(-group_clean, -condition_clean)

# Sanity check: you should now see real levels, not NA
print(with(data, table(group, condition, useNA = "ifany")))
```

```
          condition
group        Outgroup Metaperception Ingroup
  Prolife          89             85      89
  Prochoice        96             97      96
```

Create Composite Scores

```
item_cols <- c(
  "care_1","care_2","equality_1","equality_2","proportionality_1","proportionality_2",
  "loyalty_1","loyalty_2","authority_1","authority_2","purity_1","purity_2"
)
missing <- setdiff(item_cols, names(data))
if (length(missing)) stop("Missing columns: ", paste(missing, collapse = ", "))

data <- data %>%
  mutate(across(all_of(item_cols), ~ suppressWarnings(as.numeric(.)))) %>%
  mutate(
    care_mean            = rowMeans(pick(care_1, care_2), na.rm = TRUE),
    equality_mean        = rowMeans(pick(equality_1, equality_2), na.rm = TRUE),
    proportionality_mean = rowMeans(pick(proportionality_1, proportionality_2), na.rm = TRUE)
    individualizing      = rowMeans(cbind(care_mean, equality_mean), na.rm = TRUE),
    loyalty_mean   = rowMeans(pick(loyalty_1, loyalty_2), na.rm = TRUE),
    authority_mean = rowMeans(pick(authority_1, authority_2), na.rm = TRUE),
    purity_mean    = rowMeans(pick(purity_1, purity_2), na.rm = TRUE),
    binding        = rowMeans(cbind(loyalty_mean, authority_mean, purity_mean,proportionality
  )
```

Simple Descriptives

```
desc <- data %>%
  group_by(group, condition) %>%
  summarise(
```

```
    n         = dplyr::n(),
    mean_ind  = mean(individualizing, na.rm = TRUE),
    sd_ind    = sd(individualizing, na.rm = TRUE),
    mean_bind = mean(binding, na.rm = TRUE),
    sd_bind   = sd(binding, na.rm = TRUE),
    .groups   = "drop"
  )

# Print PDF-friendly
print(as.data.frame(desc), row.names = FALSE)
```

```
    group        condition  n mean_ind    sd_ind mean_bind   sd_bind
   Prolife         Outgroup 89 3.078652 0.9650096  2.029494 1.0121812
   Prolife Metaperception 85 3.064706 0.7371447  3.573529 0.8654440
   Prolife          Ingroup 89 3.508427 0.7644902  3.556180 0.8209809
 Prochoice         Outgroup 96 2.119792 0.7880515  3.334635 0.9404112
 Prochoice Metaperception 97 3.113402 1.0819426  1.472938 0.2773026
 Prochoice          Ingroup 96 3.841146 0.8112043  2.098958 0.8269548
```

```
# Quick wide views
ind_wide <- tidyr::pivot_wider(desc |> select(group, condition, mean_ind),
                               names_from = condition, values_from = mean_ind)
bind_wide <- tidyr::pivot_wider(desc |> select(group, condition, mean_bind),
                                names_from = condition, values_from = mean_bind)
cat("\nIndividualizing (means):\n"); print(as.data.frame(ind_wide), row.names = FALSE)
```

```
Individualizing (means):

    group Outgroup Metaperception  Ingroup
   Prolife 3.078652        3.064706 3.508427
 Prochoice 2.119792        3.113402 3.841146
```

```
cat("\nBinding (means):\n");        print(as.data.frame(bind_wide), row.names = FALSE)
```

```
Binding (means):

    group Outgroup Metaperception  Ingroup
   Prolife 2.029494        3.573529 3.556180
 Prochoice 3.334635        1.472938 2.098958
```

Equality of covariance matrices

```
# Note: Box's M is sensitive to non-normality; interpret alongside Pillai later
boxM(cbind(individualizing, binding) ~ group * condition, data = data)
```
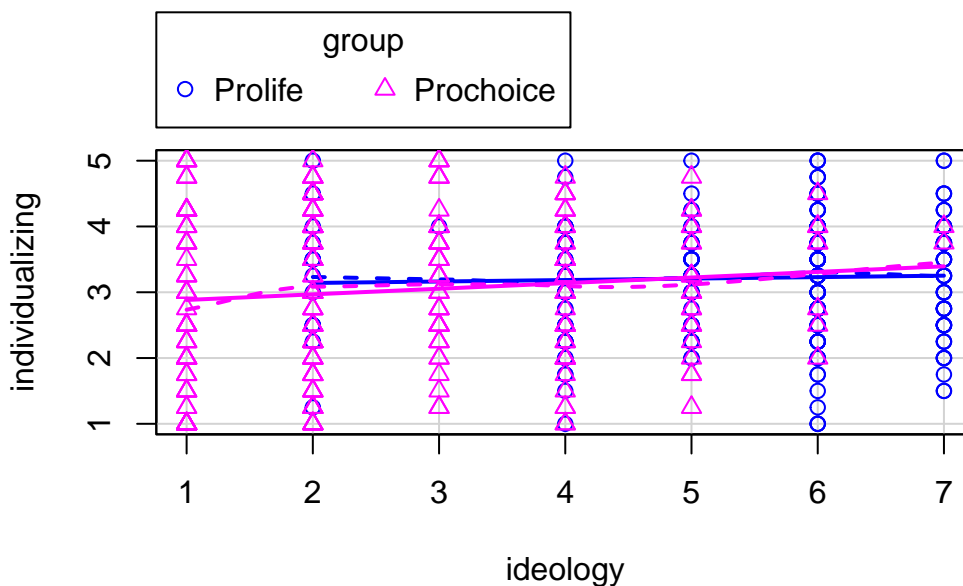
```
    Box's M-test for Homogeneity of Covariance Matrices

data:  Y
Chi-Sq (approx.) = 175.02, df = 15, p-value < 2.2e-16
```
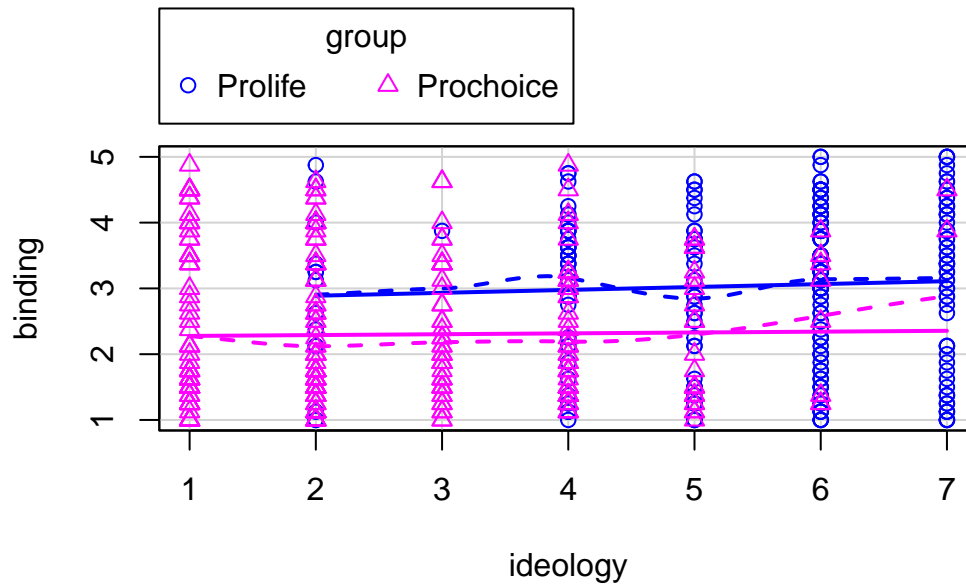
Linearity of DV–covariate relations (quick visual check)

```
# Scatterplots of DV vs ideology, stratified by factors (optional visual check)
car::scatterplot(individualizing ~ ideology | group*condition, data = data)
```



```
car::scatterplot(binding ~ ideology | group*condition, data = data)
```

Homogeneity of regression slopes (covariate × factors)

```r
# For each DV, check whether ideology interacts with group/condition
m_ind <- lm(individualizing ~ ideology * group * condition, data = data)
m_bin <- lm(binding         ~ ideology * group * condition, data = data)

anova(m_ind)  # Look at ideology:group and ideology:condition (and 3-way)
```

```
Analysis of Variance Table

Response: individualizing
                        Df Sum Sq Mean Sq F value    Pr(>F)
ideology                 1   8.64   8.642 11.7160 0.0006666 ***
group                    1   0.05   0.053  0.0720 0.7885106
condition                2 110.72  55.360 75.0555 < 2.2e-16 ***
ideology:group           1   1.77   1.773  2.4031 0.1216785
ideology:condition       2  34.94  17.471 23.6868 1.379e-10 ***
group:condition          2  11.54   5.772  7.8261 0.0004462 ***
ideology:group:condition 2   6.75   3.376  4.5774 0.0106839 *
Residuals              540 398.30   0.738
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m_bin)
```

Analysis of Variance Table

Response: binding
```
                         Df Sum Sq Mean Sq  F value     Pr(>F)
ideology                  1  47.78  47.784  71.1514 3.039e-16 ***
group                     1  29.55  29.546  43.9947 8.010e-11 ***
condition                 2  10.84   5.421   8.0717 0.0003515 ***
ideology:group            1   0.26   0.264   0.3938 0.5305967
ideology:condition        2 183.42  91.710 136.5567 < 2.2e-16 ***
group:condition           2 122.52  61.258  91.2142 < 2.2e-16 ***
ideology:group:condition  2   0.10   0.048   0.0708 0.9316518
Residuals               540 362.66   0.672
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fit the MANCOVA (report both Pillai and Wilks)

```
# Multivariate model
mancova_model <- manova(cbind(individualizing, binding) ~ group * condition + ideology,
                 data = data)

summary(mancova_model, test = "Pillai")  # robust
```

```
                Df  Pillai approx F num Df den Df Pr(>F)
group            1 0.17239   56.658      2    544 <2e-16 ***
condition        2 0.24342   37.762      4   1090 <2e-16 ***
ideology         1 0.00579    1.585      2    544 0.2059
group:condition  2 0.52545   97.104      4   1090 <2e-16 ***
Residuals      545
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mancova_model, test = "Wilks")   # conventional
```

```
                Df   Wilks approx F num Df den Df Pr(>F)
group            1 0.82761   56.658      2    544 <2e-16 ***
```

```
condition          2 0.76243    39.508      4    1088 <2e-16 ***
ideology           1 0.99421     1.585      2     544 0.2059
group:condition    2 0.48066   120.329      4    1088 <2e-16 ***
Residuals        545
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Univariate ANCOVAs with Type-III tests + effect sizes

```r
# Fit per-DV models with Type-III SS
fit_ind <- lm(individualizing ~ group * condition + ideology, data = data)
fit_bin <- lm(binding          ~ group * condition + ideology, data = data)

Anova(fit_ind, type = 3)
```

```
Anova Table (Type III tests)

Response: individualizing
                Sum Sq  Df  F value     Pr(>F)
(Intercept)     197.85   1 262.8672 < 2.2e-16 ***
group            23.12   1  30.7135 4.663e-08 ***
condition        10.77   2   7.1523 0.0008588 ***
ideology          2.72   1   3.6130 0.0578573 .
group:condition  43.11   2  28.6398 1.490e-12 ***
Residuals       410.20 545
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
Anova(fit_bin, type = 3)
```

```
Anova Table (Type III tests)

Response: binding
                Sum Sq  Df  F value Pr(>F)
(Intercept)      99.60   1 147.2381 <2e-16 ***
group            60.79   1  89.8664 <2e-16 ***
condition       138.34   2 102.2486 <2e-16 ***
ideology          0.06   1   0.0931 0.7604
group:condition 300.27   2 221.9296 <2e-16 ***
Residuals       368.69 545
```

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```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Partial eta-squared + 95% CI for key effects
eta_squared(Anova(fit_ind, type = 3), partial = TRUE, ci = 0.95)
```

Type 3 ANOVAs only give sensible and informative results when covariates
  are mean-centered and factors are coded with orthogonal contrasts (such
  as those produced by `contr.sum`, `contr.poly`, or `contr.helmert`, but
  not by the default `contr.treatment`).

Effect Size for ANOVA (Type III)

```
Parameter       | Eta2 (partial) |       95% CI
------------------------------------------------
group           |           0.05 | [0.03, 1.00]
condition       |           0.03 | [0.01, 1.00]
ideology        |       6.59e-03 | [0.00, 1.00]
group:condition |           0.10 | [0.06, 1.00]
```

- One-sided CIs: upper bound fixed at [1.00].

```
eta_squared(Anova(fit_bin, type = 3), partial = TRUE, ci = 0.95)
```

Type 3 ANOVAs only give sensible and informative results when covariates
  are mean-centered and factors are coded with orthogonal contrasts (such
  as those produced by `contr.sum`, `contr.poly`, or `contr.helmert`, but
  not by the default `contr.treatment`).

Effect Size for ANOVA (Type III)

```
Parameter       | Eta2 (partial) |       95% CI
------------------------------------------------
group           |           0.14 | [0.10, 1.00]
condition       |           0.27 | [0.22, 1.00]
ideology        |       1.71e-04 | [0.00, 1.00]
group:condition |           0.45 | [0.40, 1.00]
```

- One-sided CIs: upper bound fixed at [1.00].

Planned Contrasts for Ingroup Perception and Outgroup Perception

```
# EMMs for each DV, adjusted for ideology
emm_ind <- emmeans(fit_ind, ~ group * condition)
emm_bin <- emmeans(fit_bin, ~ group * condition)

# Inspect order (for sanity)
emm_ind
```

group	condition	emmean	SE	df	lower.CL	upper.CL
Prolife	Outgroup	3.01	0.0993	545	2.81	3.20
Prochoice	Outgroup	2.19	0.0958	545	2.00	2.38
Prolife	Metaperception	2.99	0.1020	545	2.79	3.19
Prochoice	Metaperception	3.19	0.0961	545	3.00	3.38
Prolife	Ingroup	3.43	0.1020	545	3.23	3.63
Prochoice	Ingroup	3.91	0.0954	545	3.72	4.10

Confidence level used: 0.95

```
emm_bin
```

group	condition	emmean	SE	df	lower.CL	upper.CL
Prolife	Outgroup	2.02	0.0942	545	1.83	2.20
Prochoice	Outgroup	3.35	0.0908	545	3.17	3.52
Prolife	Metaperception	3.56	0.0970	545	3.37	3.75
Prochoice	Metaperception	1.48	0.0911	545	1.31	1.66
Prolife	Ingroup	3.54	0.0965	545	3.35	3.73
Prochoice	Ingroup	2.11	0.0904	545	1.93	2.29

Confidence level used: 0.95

```
# EMMs (already fit)
emm_ind <- emmeans(fit_ind, ~ group * condition)

# Get the row labels in emm_ind's order (e.g., "Prolife.Ingroup", etc.)
labs <- with(as.data.frame(emm_ind),
             paste(group, condition, sep = "."))

# Helper to create a full-length contrast weight vector safely
make_w <- function(pos_names, neg_names, labels = labs) {
```

```r
  w <- setNames(rep(0, length(labels)), labels)
  w[pos_names] <- w[pos_names] + 1
  w[neg_names] <- w[neg_names] - 1
  w
}

# H1: Ingroup (one group) vs Outgroup (other group)
w1 <- make_w("Prolife.Ingroup",  "Prochoice.Outgroup")
w2 <- make_w("Prochoice.Ingroup","Prolife.Outgroup")

h1_ind <- contrast(
  emm_ind,
  method = list(
    "Prolife Ingroup vs Prochoice Outgroup"  = w1,
    "Prochoice Ingroup vs Prolife Outgroup"  = w2
  ),
  adjust = "none"
)

summary(h1_ind, infer = c(TRUE, TRUE))
```

```
 contrast                               estimate    SE  df lower.CL upper.CL
 Prolife Ingroup vs Prochoice Outgroup     1.236 0.151 545    0.940     1.53
 Prochoice Ingroup vs Prolife Outgroup     0.901 0.147 545    0.612     1.19
 t.ratio p.value
   8.202  <.0001
   6.129  <.0001


Confidence level used: 0.95
```

```r
eff_size(h1_ind, sigma = sigma(fit_ind), edf = df.residual(fit_ind))
```

```
 contrast
 Prolife Ingroup vs Prochoice Outgroup - Prochoice Ingroup vs Prolife Outgroup
 effect.size    SE  df lower.CL upper.CL
       0.386 0.273 545    -0.15    0.923

sigma used for effect sizes: 0.8676
Confidence level used: 0.95
```

```
emm_bin <- emmeans(fit_bin, ~ group * condition)
labs_b  <- with(as.data.frame(emm_bin), paste(group, condition, sep = "."))
make_wb <- function(pos_names, neg_names, labels = labs_b) {
  w <- setNames(rep(0, length(labels)), labels)
  w[pos_names] <- w[pos_names] + 1
  w[neg_names] <- w[neg_names] - 1
  w
}


h1_bin <- contrast(
  emm_bin,
  method = list(
    "Prolife Ingroup vs Prochoice Outgroup"  = make_wb("Prolife.Ingroup",  "Prochoice.Outgrou
    "Prochoice Ingroup vs Prolife Outgroup"  = make_wb("Prochoice.Ingroup","Prolife.Outgroup"
  ),
  adjust = "none"
)
summary(h1_bin, infer = c(TRUE, TRUE))
```

```
 contrast                               estimate    SE  df lower.CL upper.CL
 Prolife Ingroup vs Prochoice Outgroup    0.1984 0.143 545  -0.0823    0.479
 Prochoice Ingroup vs Prolife Outgroup    0.0906 0.139 545  -0.1833    0.364
 t.ratio p.value
   1.388  0.1657
   0.650  0.5162


Confidence level used: 0.95
```

```
eff_size(h1_bin, sigma = sigma(fit_bin), edf = df.residual(fit_bin))
```

```
 contrast
 Prolife Ingroup vs Prochoice Outgroup - Prochoice Ingroup vs Prolife Outgroup
 effect.size    SE  df lower.CL upper.CL
       0.131 0.273 545   -0.405    0.667

sigma used for effect sizes: 0.8225
Confidence level used: 0.95
```

Planned contrast for Outgroup Perception and Metaperception

```
# EMMs for each DV, adjusted for ideology
emm_ind <- emmeans(fit_ind, ~ group * condition)
emm_bin <- emmeans(fit_bin, ~ group * condition)

# Inspect order (sanity check)
emm_ind
```

```
 group     condition      emmean     SE  df lower.CL upper.CL
 Prolife   Outgroup         3.01 0.0993 545     2.81     3.20
 Prochoice Outgroup         2.19 0.0958 545     2.00     2.38
 Prolife   Metaperception   2.99 0.1020 545     2.79     3.19
 Prochoice Metaperception   3.19 0.0961 545     3.00     3.38
 Prolife   Ingroup          3.43 0.1020 545     3.23     3.63
 Prochoice Ingroup          3.91 0.0954 545     3.72     4.10

Confidence level used: 0.95
```

```
emm_bin
```

```
 group     condition      emmean     SE  df lower.CL upper.CL
 Prolife   Outgroup         2.02 0.0942 545     1.83     2.20
 Prochoice Outgroup         3.35 0.0908 545     3.17     3.52
 Prolife   Metaperception   3.56 0.0970 545     3.37     3.75
 Prochoice Metaperception   1.48 0.0911 545     1.31     1.66
 Prolife   Ingroup          3.54 0.0965 545     3.35     3.73
 Prochoice Ingroup          2.11 0.0904 545     1.93     2.29

Confidence level used: 0.95
```

```
# ----- Helper (same as before) -----
labs <- with(as.data.frame(emm_ind), paste(group, condition, sep = "."))
make_w <- function(pos_names, neg_names, labels = labs) {
  w <- setNames(rep(0, length(labels)), labels)
  w[pos_names] <- w[pos_names] + 1
  w[neg_names] <- w[neg_names] - 1
  w
}
```

```
# ==========================
# H2: Outgroup (one group) vs Metaperception (other group)
# ==========================
# Individualizing
w3_ind <- make_w("Prolife.Outgroup",   "Prochoice.Metaperception")
w4_ind <- make_w("Prochoice.Outgroup", "Prolife.Metaperception")

h2_ind <- contrast(
  emm_ind,
  method = list(
    "Prolife Outgroup vs Prochoice Metaperception"   = w3_ind,
    "Prochoice Outgroup vs Prolife Metaperception"   = w4_ind
  ),
  adjust = "none"
)

summary(h2_ind, infer = c(TRUE, TRUE))                  # estimates, SEs, CIs, p
```

```
 contrast                                      estimate    SE  df lower.CL
 Prolife Outgroup vs Prochoice Metaperception    -0.179 0.148 545    -0.47
 Prochoice Outgroup vs Prolife Metaperception    -0.799 0.150 545    -1.09
 upper.CL t.ratio p.value
    0.112  -1.208  0.2276
   -0.504  -5.314  <.0001


Confidence level used: 0.95
```

```
eff_size(h2_ind, sigma = sigma(fit_ind), edf = df.residual(fit_ind))  # standardized effects
```

```
 contrast
 Prolife Outgroup vs Prochoice Metaperception - Prochoice Outgroup vs Prolife Metaperception
 effect.size    SE  df lower.CL upper.CL
       0.714 0.274 545    0.176     1.25

sigma used for effect sizes: 0.8676
Confidence level used: 0.95
```

```
# ----- Binding -----
labs_b <- with(as.data.frame(emm_bin), paste(group, condition, sep = "."))
make_wb <- function(pos_names, neg_names, labels = labs_b) {
```

```r
  w <- setNames(rep(0, length(labels)), labels)
  w[pos_names] <- w[pos_names] + 1
  w[neg_names] <- w[neg_names] - 1
  w
}

w3_bin <- make_wb("Prolife.Outgroup",   "Prochoice.Metaperception")
w4_bin <- make_wb("Prochoice.Outgroup", "Prolife.Metaperception")

h2_bin <- contrast(
  emm_bin,
  method = list(
    "Prolife Outgroup vs Prochoice Metaperception"   = w3_bin,
    "Prochoice Outgroup vs Prolife Metaperception"   = w4_bin
  ),
  adjust = "none"
)

summary(h2_bin, infer = c(TRUE, TRUE))
```

```
 contrast                                     estimate    SE  df lower.CL
 Prolife Outgroup vs Prochoice Metaperception    0.535 0.141 545    0.258
 Prochoice Outgroup vs Prolife Metaperception   -0.217 0.143 545   -0.497
 upper.CL t.ratio p.value
   0.8107   3.803  0.0002
   0.0633  -1.520  0.1291

Confidence level used: 0.95
```

```r
eff_size(h2_bin, sigma = sigma(fit_bin), edf = df.residual(fit_bin))
```

```
 contrast
 Prolife Outgroup vs Prochoice Metaperception - Prochoice Outgroup vs Prolife Metaperception
 effect.size    SE  df lower.CL upper.CL
       0.913 0.274 545    0.376     1.45

sigma used for effect sizes: 0.8225
Confidence level used: 0.95
```

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Graph

```r
# ==========================================
# Ideology-adjusted scores + violin plots
# ==========================================
library(dplyr)
library(tidyr)
library(ggplot2)
library(forcats)

# 0) Ensure ideology is numeric
if (!is.numeric(data$ideology)) {
  data <- data %>% mutate(ideology = suppressWarnings(as.numeric(ideology)))
}

# 1) Fit ANCOVA-style models to get a single slope for ideology (no interactions)
#    This mirrors your main analysis specification.
fit_ind  <- lm(individualizing ~ ideology + group * condition, data = data)
fit_bind <- lm(binding         ~ ideology + group * condition, data = data)

b_ind  <- coef(fit_ind)[["ideology"]]
b_bind <- coef(fit_bind)[["ideology"]]
xbar   <- mean(data$ideology, na.rm = TRUE)

# 2) Compute ideology-adjusted scores (unit-preserving adjustment to the covariate mean)
#    y_adj = y - b_hat * (x - xbar)
data <- data %>%
  mutate(
    individualizing_adj = individualizing - b_ind  * (ideology - xbar),
    binding_adj         = binding          - b_bind * (ideology - xbar)
  )

# 3) Tidy to long format for plotting
plot_df_adj <- data %>%
  filter(!is.na(group), !is.na(condition)) %>%
  mutate(
    # Pretty labels (optional)
    group_label = fct_recode(group, "Pro-life" = "Prolife", "Pro-choice" = "Prochoice"),
    condition_label = fct_recode(
      condition,
      "Outgroup Perception" = "Outgroup",
      "Metaperception"      = "Metaperception",
```

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```
      "Ingroup Perception"  = "Ingroup"
    ),
    condition_label = factor(condition_label,
                             levels = c("Ingroup Perception","Outgroup Perception","Metaperce
  ) %>%
  select(group_label, condition_label, individualizing_adj, binding_adj) %>%
  pivot_longer(
    cols = c(individualizing_adj, binding_adj),
    names_to = "moral_foundation",
    values_to = "value_adj"
  ) %>%
  mutate(
    foundation_label = if_else(
      moral_foundation == "individualizing_adj",
      "Individualizing Foundations",
      "Binding Foundations"
    )
  )

# 4) Summary stats (means and SEs) on adjusted scores
sum_df_adj <- plot_df_adj %>%
  group_by(group_label, condition_label, foundation_label) %>%
  summarise(
    mean = mean(value_adj, na.rm = TRUE),
    sd   = sd(value_adj, na.rm = TRUE),
    n    = sum(!is.na(value_adj)),
    se   = sd / sqrt(n),
    .groups = "drop"
  )

# Optional: inspect adjusted cell means
print(sum_df_adj %>% arrange(foundation_label, group_label, condition_label))
```

```
# A tibble: 12 x 7
   group_label condition_label     foundation_label      mean    sd     n      se
   <fct>       <fct>               <chr>                <dbl> <dbl> <int>   <dbl>
 1 Pro-life    Ingroup Perception  Binding Foundations   3.54 0.819    89 0.0869
 2 Pro-life    Outgroup Perception Binding Foundations   2.02 1.01     89 0.107
 3 Pro-life    Metaperception      Binding Foundations   3.56 0.865    85 0.0939
 4 Pro-choice  Ingroup Perception  Binding Foundations   2.11 0.825    96 0.0842
 5 Pro-choice  Outgroup Perception Binding Foundations   3.35 0.942    96 0.0961
 6 Pro-choice  Metaperception      Binding Foundations   1.48 0.278    97 0.0282
```

```
 7 Pro-life    Ingroup Perception  Individualizing Fou~  3.43 0.761    89 0.0807
 8 Pro-life    Outgroup Perception Individualizing Fou~  3.01 0.968    89 0.103
 9 Pro-life    Metaperception      Individualizing Fou~  2.99 0.742    85 0.0805
10 Pro-choice  Ingroup Perception  Individualizing Fou~  3.91 0.827    96 0.0844
11 Pro-choice  Outgroup Perception Individualizing Fou~  2.19 0.762    96 0.0778
12 Pro-choice  Metaperception      Individualizing Fou~  3.19 1.07     97 0.109
```

```r
# 5) Plot: violins of ideology-adjusted scores
ggplot(plot_df_adj, aes(x = group_label, y = value_adj, fill = condition_label)) +
  geom_violin(position = position_dodge(width = 0.8), alpha = 0.7, width = 0.7, trim = TRUE)

  # mean points (adjusted)
  geom_point(
    data = sum_df_adj,
    aes(x = group_label, y = mean, group = condition_label),
    position = position_dodge(width = 0.8),
    size = 2, color = "black", inherit.aes = FALSE
  ) +

  # mean ± SE error bars (adjusted)
  geom_errorbar(
    data = sum_df_adj,
    aes(x = group_label, ymin = mean - se, ymax = mean + se, group = condition_label),
    width = 0.15,
    position = position_dodge(width = 0.8),
    inherit.aes = FALSE
  ) +

  facet_wrap(~ foundation_label, ncol = 2) +
  scale_fill_manual(
    values = c(
      "Ingroup Perception"  = "#66c2a5",
      "Outgroup Perception" = "#8da0cb",
      "Metaperception"      = "#fc8d62"
    ),
    name = "Condition"
  ) +
  labs(
    title = "Moral Perceptions Across Pro-life and Pro-choice Groups",
    subtitle = "Violins of morality scores with means and mean ± SE",
    x = NULL, y = "Rating (1-5 scale)"
  ) +
```
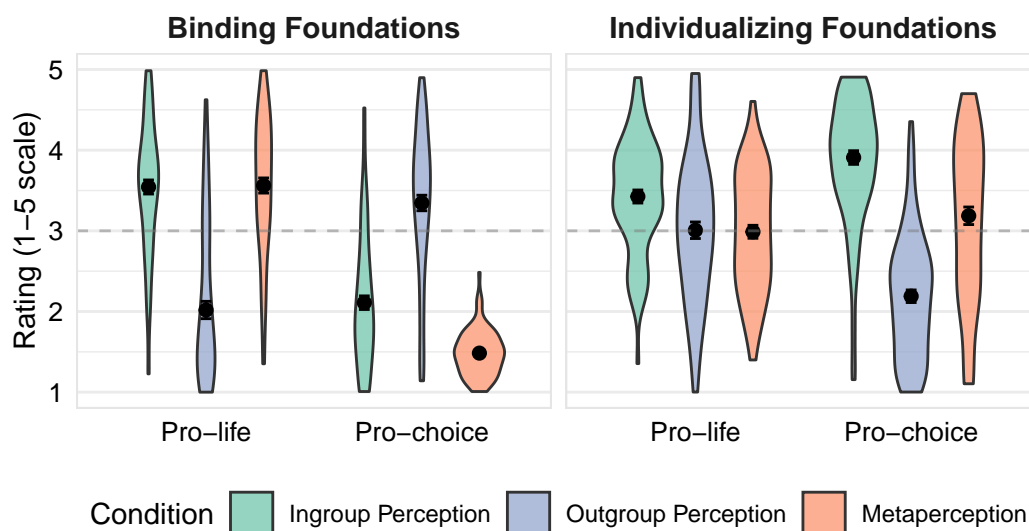
```
  theme_minimal() +
  theme(
    legend.position = "bottom",
    plot.title = element_text(hjust = 0.5, face = "bold", size = 14),
    plot.subtitle = element_text(hjust = 0.5, size = 12),
    strip.text = element_text(face = "bold", size = 11),
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray90"),
    axis.text = element_text(color = "black", size = 10)
  ) +
  geom_hline(yintercept = 3, linetype = "dashed", color = "gray50", alpha = 0.5) +
  scale_y_continuous(limits = c(1, 5), breaks = 1:5)
```

Warning: Removed 26 rows containing non-finite outside the scale range
(`stat_ydensity()`).

Moral Perceptions Across Pro–life and Pro–choice Group
Violins of morality scores with means and mean ± SE

```
# 6) Save
ggsave(
  filename = "/Users/daryani/Desktop//moral_perception_plot_adjusted.jpg",
  width = 8, height = 6, dpi = 300
)
```

```
Warning: Removed 26 rows containing non-finite outside the scale range
(`stat_ydensity()`).
```