

Supplementary material 4 – Scripts used for the analyses of studies 1 and 2

Figure S6. Scripts used for the analyses of Study 1.

```
library(lavaan)

####Model for purchase attitudes and willingness to buy
modella<-'
Hed=~Hed3+Hed2+Hed1
Bio=~Bio4+Bio3+Bio2+Bio1
Alt=~Alt5+Alt4+Alt3+Alt2+Alt1
Ego=~Ego5+Ego4+Ego3+Ego2+Ego1
PA=~PA5+PA4+PA3+PA2+PA1
WTB=~WTB3+WTB2+WTB1 '

fit1a<-cfa(modella, data=base_para_analises, ordered=TRUE)

res1a<-summary(fit1a, rsquare=TRUE, fit.measures=TRUE, standardized=TRUE)
res1a

modellb<-'
Hed=~Hed3+Hed2+Hed1
Bio=~Bio4+Bio3+Bio2+Bio1
Alt=~Alt5+Alt4+Alt3+Alt2+Alt1
Ego=~Ego5+Ego4+Ego3+Ego2+Ego1
PA=~PA5+PA4+PA3+PA2+PA1
WTB=~WTB3+WTB2+WTB1
WTB~PA
WTB~Hed+Bio+Alt+Ego
PA~Hed+Bio+Alt+Ego
'

fit1b<-sem(modellb, data=base_para_analises, ordered=TRUE)
res1b<-summary(fit1b, rsquare=TRUE, fit.measures=TRUE, standardized=TRUE)
res1b
```

```
####Model for consumption attitudes and willingness to consume

model2a<- '
Hed=~Hed3+Hed2+Hed1
Bio=~Bio4+Bio3+Bio2+Bio1
Alt=~Alt5+Alt4+Alt3+Alt2+Alt1
Ego=~Ego5+Ego4+Ego3+Ego2+Ego1
CA=~CA5+CA4+CA3+CA2+CA1
WTC=~WTC3+WTC2+WTC1 '

fit2a<-cfa(model2a, data=base_para_analises, ordered=TRUE)

res2a<-summary(fit2a, rsquare=TRUE, fit.measures=TRUE, standardized=TRUE)
res2a

model2b<- '
Hed=~Hed3+Hed2+Hed1
Bio=~Bio4+Bio3+Bio2+Bio1
Alt=~Alt5+Alt4+Alt3+Alt2+Alt1
Ego=~Ego5+Ego4+Ego3+Ego2+Ego1
CA=~CA5+CA4+CA3+CA2+CA1
WTC=~WTC3+WTC2+WTC1
WTC~CA
WTC~Hed+Bio+Alt+Ego
CA~Hed+Bio+Alt+Ego
'

fit2b<-sem(model2b, data=base_para_analises, ordered=TRUE)

res2b<-summary(fit2b, rsquare=TRUE, fit.measures=TRUE, standardized=TRUE)
res2b
```

```
###Needs to run the SEM in the other script first

library(semPlot)

#####Model for Purchase attitudes and willingness to buy
# Manually specify labels for latent and observed variables
nodeLabels <- c(Hed3 = "Hed3", Hed2 = "Hed2", Hed1 = "Hed1",
               Bio4 = "Bio4", Bio3 = "Bio3", Bio2 = "Bio2", Bio1 = "Bio1",
               Alt5 = "Alt5", Alt4 = "Alt4", Alt3 = "Alt3", Alt2 = "Alt2", Alt1 = "Alt1",
               Ego5 = "Ego5", Ego4 = "Ego4", Ego3 = "Ego3", Ego2 = "Ego2", Ego1 = "Ego1",
               PA5 = "PA5", PA4 = "PA4", PA3 = "PA3", PA2 = "PA2", PA1 = "PA1",
               WTB3 = "WTB3", WTB2 = "WTB2", WTB1 = "WTB1",
               Hed = "Hed", Bio = "Bio", Alt = "Alt", Ego = "Ego",
               PA = "PA", WTB = "WTB")

#color lists
colorVector <- c(
  "Hed3" = "lightpink2", "Hed2" = "lightpink2", "Hed1" = "lightpink2",
  "Bio4" = "palegreen", "Bio3" = "palegreen", "Bio2" = "palegreen", "Bio1" = "palegreen",
  "Alt5" = "wheat1", "Alt4" = "wheat1", "Alt3" = "wheat1", "Alt2" = "wheat1", "Alt1" =
  "wheat1",
  "Ego1" = "skyblue", "Ego2" = "skyblue", "Ego3" = "skyblue", "Ego4" = "skyblue", "Ego5"
  = "skyblue",
  "PA5" = "khaki1", "PA4" = "khaki1", "PA3" = "khaki1", "PA2" = "khaki1", "PA1" = "khaki1",
  "WTB3" = "thistle1", "WTB2" = "thistle1", "WTB1" = "thistle1",
  # Latent variables
  "Hed" = "lightpink2", "Bio" = "palegreen", "Alt" = "wheat1", "Ego" = "skyblue",
  "PA" = "khaki1", "WTB" = "thistle1")

# Create the path diagram with manually specified node labels
semPaths(fit1b, whatLabels="std", edge.label.cex = 0.75, # Emphasize path labels
        layout = "tree", title = FALSE,
        sizeMan = 4, sizeLat = 8, # Adjust size of nodes
        edge.color = "black", # Change edge color if needed
        nodeLabels = nodeLabels, # Use manually specified labels
        nodeWidth = 0.5, nodeHeight = 0.5, # Make nodes thinner
        rotation = 2,
```

```
residuals = FALSE, covariances = TRUE, intercepts=FALSE, thresholds = FALSE,

    nCharNodes=0, nCharEdges=0, mar = c(5,5,5,5),

    color=colorVector,

    text.cex = 0.5) # Adjust text size globally; specific adjustments may require
post-hoc editing

####For Consumption attitudes and willingness to consume
# Manually specify labels for latent and observed variables
nodeLabels2 <- c(Hed3 = "Hed3", Hed2 = "Hed2", Hed1 = "Hed1",

    Bio4 = "Bio4", Bio3 = "Bio3", Bio2 = "Bio2", Bio1 = "Bio1",

    Alt5 = "Alt5", Alt4 = "Alt4", Alt3 = "Alt3", Alt2 = "Alt2", Alt1 =
"Alt1",

    Ego5 = "Ego5", Ego4 = "Ego4", Ego3 = "Ego3", Ego2 = "Ego2", Ego1 =
"Ego1",

    CA5 = "CA5", CA4 = "CA4", CA3 = "CA3", CA2 = "CA2", CA1 = "CA1",

    WTC3 = "WTC3", WTC2 = "WTC2", WTC1 = "WTC1",

    Hed = "Hed", Bio = "Bio", Alt = "Alt", Ego = "Ego",

    CA = "CA", WTC = "WTC")

#color lists
colorVector2 <- c(

    "Hed3" = "lightpink2", "Hed2" = "lightpink2", "Hed1" = "lightpink2",

    "Bio4" = "palegreen", "Bio3" = "palegreen", "Bio2" = "palegreen", "Bio1" = "palegreen",

    "Alt5" = "wheat1", "Alt4" = "wheat1", "Alt3" = "wheat1", "Alt2" = "wheat1", "Alt1" =
"wheat1",

    "Ego5" = "skyblue", "Ego4" = "skyblue", "Ego3" = "skyblue", "Ego2" = "skyblue", "Ego1"
= "skyblue",

    "CA5" = "khaki1", "CA4" = "khaki1", "CA3" = "khaki1", "CA2" = "khaki1", "CA1" = "khaki1",

    "WTC3" = "thistle1", "WTC2" = "thistle1", "WTC1" = "thistle1",

    # Latent variables

    "Hed" = "lightpink2", "Bio" = "palegreen", "Alt" = "wheat1", "Ego" = "skyblue",

    "CA" = "khaki1", "WTC" = "thistle1")

# Create the path diagram with manually specified node labels
semPaths(fit2b, whatLabels="std", edge.label.cex = 0.75, # Emphasize path labels

    layout = "tree", title = FALSE,

    sizeMan = 4, sizeLat = 8, # Adjust size of nodes

    edge.color = "black", # Change edge color if needed
```

```
nodeLabels = nodeLabels2, # Use manually specified labels
nodeWidth = 0.5, nodeHeight = 0.5, # Make nodes thinner
rotation = 2,
residuals = FALSE, covariances = TRUE, intercepts=FALSE, thresholds = FALSE,
nCharNodes=0, nCharEdges=0, mar = c(5,5,5,5),
color=colorVector2,
text.cex = 0.5) # Adjust text size globally; specific adjustments may require
post-hoc editing
```

Figure S7. Scripts used for the analyses of Study 2.

```
# Load necessary libraries

library(dunn.test) # For Dunn's Test

library(dplyr)

library(stats)

library(psych) # For PCA

#### Purchasing attitudes and willingness to buy

# Standardizing and performing PCA

data_standardized_attitudes <- scale(data[,c('AtC1', 'AtC2', 'AtC3', 'AtC4', 'AtC5')])
data_standardized_willingness <- scale(data[,c('WTB1', 'WTB2', 'WTB3')])

pca_attitudes <- principal(data_standardized_attitudes, nfactors=1, scores=TRUE)
pca_willingness <- principal(data_standardized_willingness, nfactors=1, scores=TRUE)

pca_attitudes
pca_willingness

data$PC_Attitudes <- pca_attitudes$scores
data$PC_willingness <- pca_willingness$scores
data$PCAt <- as.numeric(data$PC_Attitudes)
data$PCwill <- as.numeric(data$PC_willingness)

# Kruskal-Wallis Test

kw_test_attitudes <- kruskal.test(PCAt ~ Pub, data = data)
kw_test_willingness <- kruskal.test(PCwill ~ Pub, data = data)

# Convert Pub to a factor if it's not already

data$Pub <- as.factor(data$Pub)

# Dunn's test for attitudes

dunn_test_attitudes <- dunn.test(x = data$PCAt, g = data$Pub, method = "bonferroni")
```

```
# Dunn's test for willingness
dunn_test_willingness <- dunn.test(x = data$PCwill, g = data$Pub, method = "bonferroni")

# Print the results
print(dunn_test_attitudes)
print(dunn_test_willingness)

#### Consumption attitudes and willingness to consume
# Standardizing and performing PCA
data_standardized_attitudes2 <- scale(data[,c('AtA1', 'AtA2', 'AtA3', 'AtA4', 'AtA5')])
data_standardized_willingness2 <- scale(data[,c('WTC1', 'WTC2', 'WTC3')])

pca_attitudes2 <- principal(data_standardized_attitudes2, nfactors=1, scores=TRUE)
pca_willingness2 <- principal(data_standardized_willingness2, nfactors=1, scores=TRUE)

pca_attitudes2
pca_willingness2

data$PC_Attitudes2 <- pca_attitudes2$scores
data$PC_willingness2 <- pca_willingness2$scores
data$PCAt2 <- as.numeric(data$PC_Attitudes2)
data$PCwill2 <- as.numeric(data$PC_willingness2)

# Kruskal-Wallis Test
kw_test_attitudes2 <- kruskal.test(PCAt2 ~ Pub, data = data)
kw_test_willingness2 <- kruskal.test(PCwill2 ~ Pub, data = data)

kw_test_attitudes2
kw_test_willingness2
```

```
###Needs the other script with analysis

# Load necessary libraries

library(ggplot2)

library(dplyr)

library(tidyr)

# Assuming 'data' is your data frame and you've already performed PCA and added the scores
to 'data'

# First, rename the columns to reflect the new names you want

data <- data %>%

  rename(

    `Purchase Attitudes` = PCAt,

    `Willingness to Buy` = PCwill1,

    `Consumption Attitudes` = PCAt2,

    `Willingness to Consume` = PCwill2

  )

# Convert data to long format

data_long <- data %>%

  pivot_longer(cols = c(`Purchase Attitudes`, `Willingness to Buy`, `Consumption
Attitudes`, `Willingness to Consume`),

               names_to = "Measure", values_to = "Score")

# Plot

ggplot(data_long, aes(x = Pub, y = Score, fill = Pub)) +

  geom_boxplot() +

  facet_wrap(~ Measure, scales = "free") +

  theme_bw() +

  theme(legend.position = "none") +

  labs(y = "Score", x = "Advertisement Type") +

  theme(strip.text.x = element_text(size = 12, face = "bold"))

# Save the plot to a file

ggsave("advertisement_comparison_plots.png", width = 16, height = 8)
```