Urbanization influences communities of milkweed-specialist herbivorous insects

ON_herb pSEM Checking

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Contents

Background & Questions

We examined how urbanization could disrupt specialized plant-herbivores species interactions, comparing responses by different cities and by traits of the herbivore species. We surveyed arthropod communities in the early and late growing season of the common milkweed (*Asclepias syriaca*) across six cities in southern Ontario.

We asked the following five questions:

(Q1) Is insect herbivore species abundance, richness, and diversity lower in urban compared to rural habitats?

(Q2) Does leaf herbivory vary with urbanization?

(Q3) Does the response of the herbivore community vary with urbanization?

(Q4) Is dispersal ability related to urbanization?

(Q5) How does urbanization influence herbivore species interactions?

Here, we fit and evaluate individual structural equations that will go into the piecewise structural equation model.

Data Management

```
## Read in data
raw.SEM.data <- read_csv(
    "data/toronto_herbivores.csv",
    col_types = c("ffffnfiiiiiiiiii"),
    show_col_types = FALSE
    ) %>%
    unique()

## Extract site info from the raw data
site.info <- raw.SEM.data %>%
  select(Population, Season, Distance) %>%
    unique()
```

Abundance Data

```r
## Select site info and focal herbivores
abundance.data <- raw.SEM.data %>%
    select(Population, Season, Distance, Danaus, Rhyssomatus, Aphis, Tetraopes, Liriomyza)

## Subset early data
early.abundances <- abundance.data %>%
  filter(Season == "Early") %>%
  rename(
    Danaus.early = Danaus, Rhyssomatus.early = Rhyssomatus, Aphis.early = Aphis,
    Tetraopes.early = Tetraopes, Liriomyza.early = Liriomyza
  )

## Remove season column
early.abundances <- early.abundances[, -2]

## Subset late data
late.abundances <- abundance.data %>%
  filter(Season == "Late") %>%
  rename(
    Danaus.late = Danaus, Rhyssomatus.late = Rhyssomatus, Aphis.late = Aphis,
    Tetraopes.late = Tetraopes, Liriomyza.late = Liriomyza
  )

## Remove season column
late.abundances <- late.abundances[, -2]

## Merge early and late info final abundance dataframe
final.abundance.data <- early.abundances %>%
  left_join(late.abundances) %>%
  na.omit()
```

Presence-Absence Data

```
## Convert abundance matrices to presence-absence matrices
# Danaus
danaus.presabs <- danaus.abundances
danaus.presabs[danaus.presabs > 0] <- 1
danaus.presabs.binary <- cbind(site.info, danaus.presabs)

# Rhyssomatus
rhyssomatus.presabs <- rhyssomatus.abundances
rhyssomatus.presabs[rhyssomatus.presabs > 0] <- 1
rhyssomatus.presabs.binary <- cbind(site.info, rhyssomatus.presabs)

# Aphis
aphis.presabs <- aphis.abundances
aphis.presabs[aphis.presabs > 0] <- 1
aphis.presabs.binary <- cbind(site.info, aphis.presabs)

# Tetraopes
tetraopes.presabs <- tetraopes.abundances
tetraopes.presabs[tetraopes.presabs > 0] <- 1
tetraopes.presabs.binary <- cbind(site.info, tetraopes.presabs)

# Liriomyza
liriomyza.presabs <- liriomyza.abundances
liriomyza.presabs[liriomyza.presabs > 0] <- 1
liriomyza.presabs.binary <- cbind(site.info, liriomyza.presabs)
```

```r
## Bind herbivore presence-absence together
herbivore.presabs <- danaus.presabs.binary %>%
  left_join(rhyssomatus.presabs.binary) %>%
  left_join(aphis.presabs.binary) %>%
  left_join(tetraopes.presabs.binary) %>%
  left_join(liriomyza.presabs.binary)

## Merge site info with presence-absence data
presence.absence.data <- site.info %>%
  full_join(herbivore.presabs)

## Subset early data
early.presence.absence <- presence.absence.data %>%
  filter(Season == "Early") %>%
  rename(
    Danaus.early = Danaus, Rhyssomatus.early = Rhyssomatus,
    Aphis.early = Aphis, Tetraopes.early = Tetraopes,
    Liriomyza.early = Liriomyza
  )

## Remove season column
early.presence.absence <- early.presence.absence[, -2]

## Subset late data
late.presence.absence <- presence.absence.data %>%
  filter(Season == "Late") %>%
  rename(
    Danaus.late = Danaus, Rhyssomatus.late = Rhyssomatus,
    Aphis.late = Aphis, Tetraopes.late = Tetraopes,
    Liriomyza.late = Liriomyza
  )

## Remove season column
late.presence.absence <- late.presence.absence[, -2]

## Merge early and late info final presence-absence dataframe
final.presence.absence.data <- early.presence.absence %>%
  left_join(late.presence.absence) %>%
  na.omit()
```

Model Fitting & Diagnostics

Briefly, pSEM structures were as follows: (1) the urbanization pSEM only fitted distance from the city center as a predictor on each herbivore; (2) the species interaction pSEM only fitted relationships between herbivores without any accounting for effects of urbanization; and (3) the urbanization and species interactions pSEM integrated distance from the city center with species interactions. Prior to fitting the pSEMs, each individual model was fitted and assumptions were visually inspected using `check_model()`. Models were fitted for both abundance and presence-absence data. Abundance models were fitted using GLMs with a negative binomial distribution to account for overdispersion, while presence-absence models were fitted using GLMs with a binomial distribution and logit-link function.

Note: Piecewise SEMs fitted with abundance data either had poor model fit or failed to converge; therefore, presence-absence models were reported and interpreted by default.

Urbanization (Hypothesized pSEM 1) | Abundance

```r
## Danaus
danaus.abundance.early.urb.toronto <- glm.nb(
    Danaus.early ~ Distance,
    data = final.abundance.data
    )
danaus.abundance.late.urb.toronto <- glm.nb(
    Danaus.late ~ Distance,
  data = final.abundance.data
    )


## Rhyssomatus
rhyssomatus.abundance.early.urb.toronto <- glm.nb(
    Rhyssomatus.early ~ Distance,
  data = final.abundance.data
    )
rhyssomatus.abundance.late.urb.toronto <- glm.nb(
    Rhyssomatus.late ~ Distance,
  data = final.abundance.data
    )


## Aphis
aphis.abundance.early.urb.toronto <- glm.nb(
    Aphis.early ~ Distance,
  data = final.abundance.data
    )
aphis.abundance.late.urb.toronto <- glm.nb(
    Aphis.late ~ Distance,
  data = final.abundance.data
    )


## Tetraopes
tetraopes.abundance.early.urb.toronto <- glm.nb(
    Tetraopes.early ~ Distance,
  data = final.abundance.data
    )
tetraopes.abundance.late.urb.toronto <- glm.nb(
    Tetraopes.late ~ Distance,
  data = final.abundance.data
    )


## Liriomyza
liriomyza.abundance.early.urb.toronto <- glm.nb(
    Liriomyza.early ~ Distance,
  data = final.abundance.data
    )
liriomyza.abundance.late.urb.toronto <- glm.nb(
    Liriomyza.late ~ Distance,
  data = final.abundance.data
    )
```

```
## Check model assumptions
# Danaus abundance GLMs
check_model(danaus.abundance.early.urb.toronto) # Decent fit
check_model(danaus.abundance.late.urb.toronto) # Decent fit

# Rhyssomatus abundance GLMs
check_model(rhyssomatus.abundance.early.urb.toronto) # Good fit
check_model(rhyssomatus.abundance.late.urb.toronto) # Good fit

# Aphis abundance GLMs
check_model(aphis.abundance.early.urb.toronto) # Good fit
check_model(aphis.abundance.late.urb.toronto) # Good fit

# Tetraopes abundance GLMs
check_model(tetraopes.abundance.early.urb.toronto) # Decent fit
check_model(tetraopes.abundance.late.urb.toronto) # Poor fit

# Liriomyza abundance GLMs
check_model(liriomyza.abundance.early.urb.toronto) # Good fit
check_model(liriomyza.abundance.late.urb.toronto) # Good fit
```

Herbivore Interactions (Hypothesized pSEM 2) | Abundance

```r
## Danaus
danaus.abundance.early.herb.toronto <- glm.nb(
    Danaus.early ~ Rhyssomatus.early + Aphis.early + Tetraopes.early + Liriomyza.early,
    data = final.abundance.data
    )
danaus.abundance.late.herb.toronto <- glm.nb(
    Danaus.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                  + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )


## Rhyssomatus
rhyssomatus.abundance.late.herb.toronto <- glm.nb(
    Rhyssomatus.late ~ Rhyssomatus.early,
  data = final.abundance.data
    )


## Aphis
aphis.abundance.early.herb.toronto <- glm.nb(
    Aphis.early ~ Danaus.early + Rhyssomatus.early + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )
aphis.abundance.late.herb.toronto <- glm.nb(
    Aphis.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                 + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )


## Tetraopes
tetraopes.abundance.early.herb.toronto <- glm.nb(
    Tetraopes.early ~ Danaus.early + Rhyssomatus.early + Aphis.early + Liriomyza.early,
  data = final.abundance.data
    )
tetraopes.abundance.late.herb.toronto <- glm.nb(
    Tetraopes.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                     + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )


## Liriomyza
liriomyza.abundance.early.herb.toronto <- glm.nb(
    Liriomyza.early ~ Danaus.early + Rhyssomatus.early + Aphis.early + Tetraopes.early,
  data = final.abundance.data
    )
liriomyza.abundance.late.herb.toronto <- glm.nb(
    Liriomyza.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                     + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )
```

```r
## Check model assumptions
# Danaus abundance GLMs
check_model(danaus.abundance.early.herb.toronto) # Good fit
check_model(danaus.abundance.late.herb.toronto) # Good fit

# Rhyssomatus abundance GLMs
check_model(rhyssomatus.abundance.late.herb.toronto) # Good fit

# Aphis abundance GLMs
check_model(aphis.abundance.early.herb.toronto) # Good fit
check_model(aphis.abundance.late.herb.toronto) # Good fit

# Tetraopes abundance GLMs
check_model(tetraopes.abundance.early.herb.toronto) # Decent fit
check_model(tetraopes.abundance.late.herb.toronto) # Poor fit

# Liriomyza abundance GLMs
check_model(liriomyza.abundance.early.herb.toronto) # Good fit
check_model(liriomyza.abundance.late.herb.toronto) # Good fit
```

Urbanization & Herbivore Interactions (Hypothesized pSEM 3) | Abundance

```
## Danaus
danaus.abundance.early.urb_herb.toronto <- glm.nb(
    Danaus.early ~ Distance + Rhyssomatus.early + Aphis.early
                   + Tetraopes.early + Liriomyza.early,
    data = final.abundance.data
    )
danaus.abundance.late.urb_herb.toronto <- glm.nb(
    Danaus.late ~ Distance + Danaus.early + Rhyssomatus.early
                  + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )


## Rhyssomatus
rhyssomatus.abundance.early.urb_herb.toronto <- glm.nb(
    Rhyssomatus.early ~ Distance,
  data = final.abundance.data
    )
rhyssomatus.abundance.late.urb_herb.toronto <- glm.nb(
    Rhyssomatus.late ~ Distance + Rhyssomatus.early,
  data = final.abundance.data
    )


## Aphis
aphis.abundance.early.urb_herb.toronto <- glm.nb(
    Aphis.early ~ Distance + Danaus.early + Rhyssomatus.early
                  + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )
aphis.abundance.late.urb_herb.toronto <- glm.nb(
    Aphis.late ~ Distance + Danaus.early + Rhyssomatus.early
                  + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )


## Tetraopes
tetraopes.abundance.early.urb_herb.toronto <- glm.nb(
    Tetraopes.early ~ Distance + Danaus.early + Rhyssomatus.early
                      + Aphis.early + Liriomyza.early,
  data = final.abundance.data
    )
tetraopes.abundance.late.urb_herb.toronto <- glm.nb(
    Tetraopes.late ~ Distance + Danaus.early + Rhyssomatus.early
                      + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )


## Liriomyza
liriomyza.abundance.early.urb_herb.toronto <- glm.nb(
    Liriomyza.early ~ Distance + Danaus.early + Rhyssomatus.early
                      + Aphis.early + Tetraopes.early,
  data = final.abundance.data
    )
```

```
liriomyza.abundance.late.urb_herb.toronto <- glm.nb(
    Liriomyza.late ~ Distance + Danaus.early + Rhyssomatus.early
                    + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.abundance.data
    )
```

```
## Check model assumptions
# Danaus abundance GLMs
check_model(danaus.abundance.early.urb_herb.toronto) # Good fit
check_model(danaus.abundance.late.urb_herb.toronto) # Good fit

# Rhyssomatus abundance GLMs
check_model(rhyssomatus.abundance.early.urb_herb.toronto) # Good fit
check_model(rhyssomatus.abundance.late.urb_herb.toronto) # Good fit

# Aphis abundance GLMs
check_model(aphis.abundance.early.urb_herb.toronto) # Good fit
#check_model(aphis.abundance.late.urb_herb.toronto) # Good fit

# Tetraopes abundance GLMs
check_model(tetraopes.abundance.early.urb_herb.toronto) # Poor fit
check_model(tetraopes.abundance.late.urb_herb.toronto) # Poor fit

# Liriomyza abundance GLMs
check_model(liriomyza.abundance.early.urb_herb.toronto) # Good fit
check_model(liriomyza.abundance.late.urb_herb.toronto) # Good fit
```

Urbanization (Hypothesized pSEM 1) | Presence-Absence

```r
## Danaus
danaus.presence.absence.early.urb.toronto <- glm(
    Danaus.early ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
danaus.presence.absence.late.urb.toronto <- glm(
    Danaus.late ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Rhyssomatus
rhyssomatus.presence.absence.early.urb.toronto <- glm(
    Rhyssomatus.early ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
rhyssomatus.presence.absence.late.urb.toronto <- glm(
    Rhyssomatus.late ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Aphis
aphis.presence.absence.early.urb.toronto <- glm(
    Aphis.early ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
aphis.presence.absence.late.urb.toronto <- glm(
    Aphis.late ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Tetraopes
tetraopes.presence.absence.early.urb.toronto <- glm(
    Tetraopes.early ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
tetraopes.presence.absence.late.urb.toronto <- glm(
    Tetraopes.late ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Liriomyza
liriomyza.presence.absence.early.urb.toronto <- glm(
    Liriomyza.early ~ Distance,
  data = final.presence.absence.data,
```

```
    family = binomial(link = "logit")
    )
liriomyza.presence.absence.late.urb.toronto <- glm(
    Liriomyza.late ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
```

```
## Check model assumptions
# Danaus presence-absence GLMs
check_model(danaus.presence.absence.early.urb.toronto) # Decent fit
check_model(danaus.presence.absence.late.urb.toronto) # Decent fit

# Rhyssomatus presence-absence GLMs
check_model(rhyssomatus.presence.absence.early.urb.toronto) # Good fit
check_model(rhyssomatus.presence.absence.late.urb.toronto) # Good fit

# Aphis presence-absence GLMs
check_model(aphis.presence.absence.early.urb.toronto) # Good fit
check_model(aphis.presence.absence.late.urb.toronto) # Good fit

# Tetraopes presence-absence GLMs
check_model(tetraopes.presence.absence.early.urb.toronto) # Poor fit
check_model(tetraopes.presence.absence.late.urb.toronto) # Poor fit

# Liriomyza presence-absence GLMs
check_model(liriomyza.presence.absence.early.urb.toronto) # Good fit
check_model(liriomyza.presence.absence.late.urb.toronto) # Good fit
```

Herbivore Interactions (Hypothesized pSEM 2) | Presence-Absence

```r
## Danaus
danaus.presence.absence.early.herb.toronto <- glm(
    Danaus.early ~ Rhyssomatus.early + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
danaus.presence.absence.late.herb.toronto <- glm(
    Danaus.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                 + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Rhyssomatus
rhyssomatus.presence.absence.late.herb.toronto <- glm(
    Rhyssomatus.late ~ Rhyssomatus.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Aphis
aphis.presence.absence.early.herb.toronto <- glm(
    Aphis.early ~ Danaus.early + Rhyssomatus.early + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
aphis.presence.absence.late.herb.toronto <- glm(
    Aphis.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                 + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Tetraopes
tetraopes.presence.absence.early.herb.toronto <- glm(
    Tetraopes.early ~ Danaus.early + Rhyssomatus.early + Aphis.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
tetraopes.presence.absence.late.herb.toronto <- glm(
    Tetraopes.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                     + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Liriomyza
liriomyza.presence.absence.early.herb.toronto <- glm(
    Liriomyza.early ~ Danaus.early + Rhyssomatus.early + Aphis.early + Tetraopes.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
```

```r
liriomyza.presence.absence.late.herb.toronto <- glm(
    Liriomyza.late ~ Danaus.early + Rhyssomatus.early + Aphis.early
                    + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
```

```r
## Check model assumptions
# Danaus presence-absence GLMs
check_model(danaus.presence.absence.early.herb.toronto) # Decent fit
check_model(danaus.presence.absence.late.herb.toronto) # Good fit

# Rhyssomatus presence-absence GLMs
check_model(rhyssomatus.presence.absence.late.herb.toronto) # Good fit

# Aphis presence-absence GLMs
check_model(aphis.presence.absence.early.herb.toronto) # Good fit
check_model(aphis.presence.absence.late.herb.toronto) # Good fit

# Tetraopes presence-absence GLMs
check_model(tetraopes.presence.absence.early.herb.toronto) # Poor fit
check_model(tetraopes.presence.absence.late.herb.toronto) # Poor fit

# Liriomyza presence-absence GLMs
check_model(liriomyza.presence.absence.early.herb.toronto) # Good fit
check_model(liriomyza.presence.absence.late.herb.toronto) # Good fit
```

Urbanization & Herbivore Interactions (Hypothesized pSEM3) | Presence-Absence

```r
## Danaus
danaus.presence.absence.early.urb_herb.toronto <- glm(
    Danaus.early ~ Distance + Rhyssomatus.early + Aphis.early
                    + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
danaus.presence.absence.late.urb_herb.toronto <- glm(
    Danaus.late ~ Distance + Danaus.early + Rhyssomatus.early
                + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Rhyssomatus
rhyssomatus.presence.absence.early.urb_herb.toronto <- glm(
    Rhyssomatus.early ~ Distance,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
rhyssomatus.presence.absence.late.urb_herb.toronto <- glm(
    Rhyssomatus.late ~ Distance + Rhyssomatus.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Aphis
aphis.presence.absence.early.urb_herb.toronto <- glm(
    Aphis.early ~ Distance + Danaus.early + Rhyssomatus.early
                + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
aphis.presence.absence.late.urb_herb.toronto <- glm(
    Aphis.late ~ Distance + Danaus.early + Rhyssomatus.early
                + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )


## Tetraopes
tetraopes.presence.absence.early.urb_herb.toronto <- glm(
    Tetraopes.early ~ Distance + Danaus.early + Rhyssomatus.early
                        + Aphis.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
tetraopes.presence.absence.late.urb_herb.toronto <- glm(
    Tetraopes.late ~ Distance + Danaus.early + Rhyssomatus.early
                        + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
```

```r
    family = binomial(link = "logit")
    )


## Liriomyza
liriomyza.presence.absence.early.urb_herb.toronto <- glm(
    Liriomyza.early ~ Distance + Danaus.early + Rhyssomatus.early
                    + Aphis.early + Tetraopes.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
liriomyza.presence.absence.late.urb_herb.toronto <- glm(
    Liriomyza.late ~ Distance + Danaus.early + Rhyssomatus.early
                    + Aphis.early + Tetraopes.early + Liriomyza.early,
  data = final.presence.absence.data,
  family = binomial(link = "logit")
    )
```

```r
## Check model assumptions
# Danaus presence-absence GLMs
check_model(danaus.presence.absence.early.urb_herb.toronto) # Good fit
check_model(danaus.presence.absence.late.urb_herb.toronto) # Good fit

# Rhyssomatus presence-absence GLMs
check_model(rhyssomatus.presence.absence.early.urb_herb.toronto) # Good fit
check_model(rhyssomatus.presence.absence.late.urb_herb.toronto) # Good fit

# Aphis presence-absence GLMs
check_model(aphis.presence.absence.early.urb_herb.toronto) # Good fit
check_model(aphis.presence.absence.late.urb_herb.toronto) # Good fit

# Tetraopes presence-absence GLMs
check_model(tetraopes.presence.absence.early.urb_herb.toronto) # Decent fit
check_model(tetraopes.presence.absence.late.urb_herb.toronto) # Poor fit

# Liriomyza presence-absence GLMs
check_model(liriomyza.presence.absence.early.urb_herb.toronto) # Good fit
check_model(liriomyza.presence.absence.late.urb_herb.toronto) # Good fit
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R Session Information

Table 1: Packages for data management and analyses.

Package	Loaded Version	Date
bayestestR	0.11.5	2021-10-30
broom	0.7.12	2022-01-28
correlation	0.8.0	2022-02-14
datawizard	0.3.0	2022-03-03
dplyr	1.0.8	2022-02-08
easystats	0.4.3	2021-11-07
effectsize	0.6.0.1	2022-01-26
forcats	0.5.1	2021-01-27
ggplot2	3.3.5	2021-06-25
insight	0.16.0	2022-02-17
kableExtra	1.3.4	2021-02-20
knitr	1.37	2021-12-16
MASS	7.3-55	2022-01-13
modelbased	0.7.2	2022-02-28
parameters	0.17.0	2022-03-10
performance	0.8.0	2021-10-01
purrr	0.3.4	2020-04-17
readr	2.1.2	2022-01-30
report	0.5.1	2022-02-22
see	0.6.9	2022-02-15
stringr	1.4.0	2019-02-10
tibble	3.1.6	2021-11-07
tidyr	1.2.0	2022-02-01
tidyverse	1.3.1	2021-04-15