

Urbanization influences communities of milkweed-specialist herbivorous insects

ON_herb pSEM Checking

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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 (Fig. 1).

We asked the following five questions: **CHECK THESE**

(Q1) Is insect herbivore species diversity, total abundance, and leaf herbivory lower in urban compared to rural habitats? (Q2) Does arthropod community composition vary between urban and rural habitats? (Q3) Does the response of the herbivore community vary with city size? (Q4) Does dispersal ability of insect species influence individual species' responses to urbanization? (Q5) How does urbanization influence interactions among herbivore species?

Here, **PROVIDE SHORT DESCRIPTION ABOUT PSEM MODEL CHECKING**

Data Management

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

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

Abundance Data

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

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

## 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_spp, 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_spp, 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

UPDATE

Prior to fitting the pSEMs, each individual model was fitted and assumptions were visually inspected using the DHARMA package. Models were fitted for both abundance and presence-absence data. Abundance models were fitted using GLMs with a Poisson distribution and log-link function or negative binomial GLMs to account for overdispersion, while presence-absence models were fitted using GLMs with a binomial distribution and logit-link function.

Urbanization (Hypothesized pSEM 1) | Abundance

```
## 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

```
## 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
)

## 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
)
```

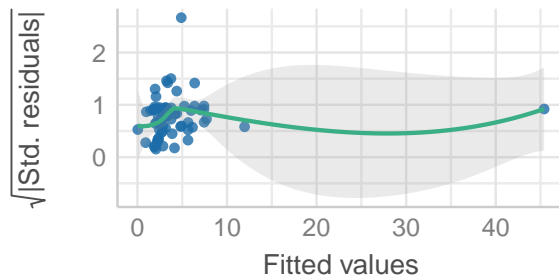
```
## Check model assumptions
```

```
# Danaus abundance GLMs
```

```
check_model(danaus.abundance.early.urb_herb.toronto) # Good fit
```

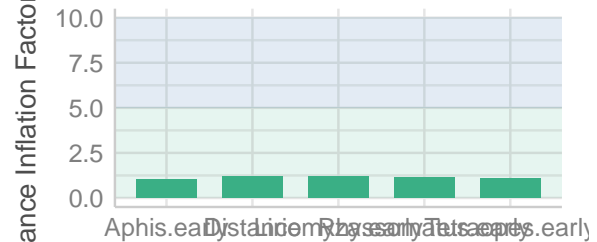
Homogeneity of Variance

Reference line should be flat and horizontal



Collinearity

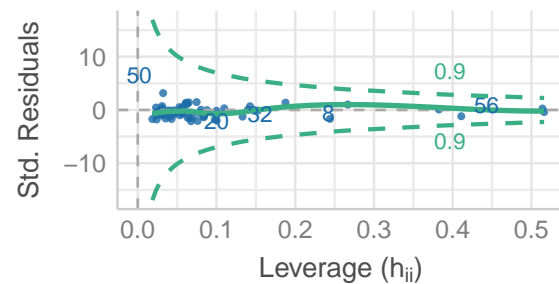
Higher bars (>5) indicate potential collinearity issue:



low (< 5) moderate (< 10) high (>= 10)

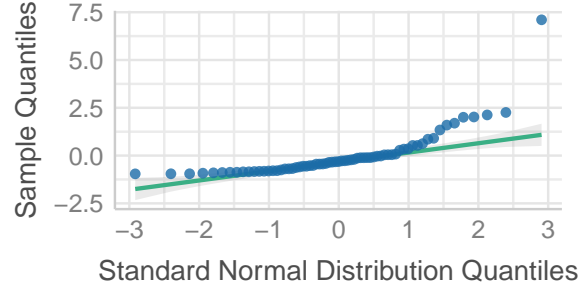
Influential Observations

Points should be inside the contour lines



Normality of Residuals

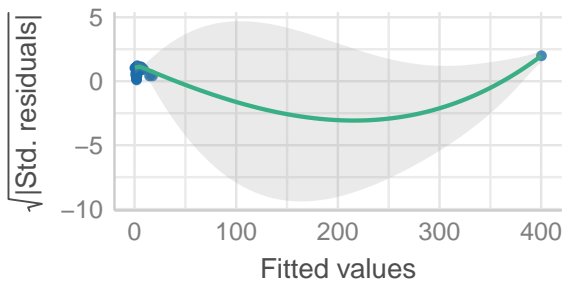
Dots should fall along the line



```
check_model(danaus.abundance.late.urb_herb.toronto) # Good fit
```

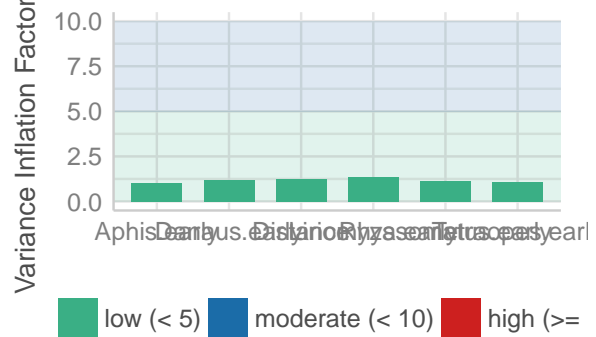
Homogeneity of Variance

Reference line should be flat and horizontal



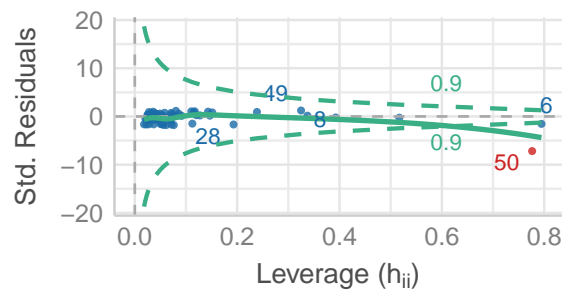
Collinearity

Higher bars (>5) indicate potential collinearity issue:



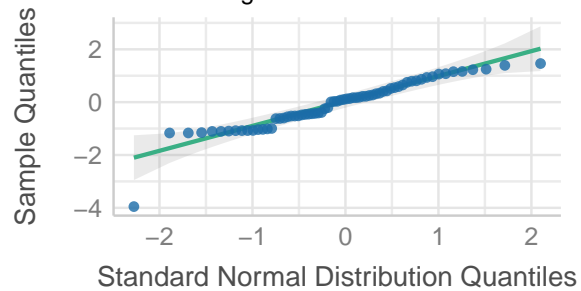
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line

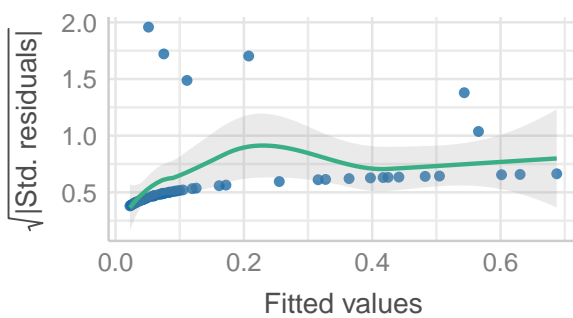


```
# Rhyssomatus abundance GLMs
```

```
check_model(rhyssomatus.abundance.early.urb_herb.toronto) # Good fit
```

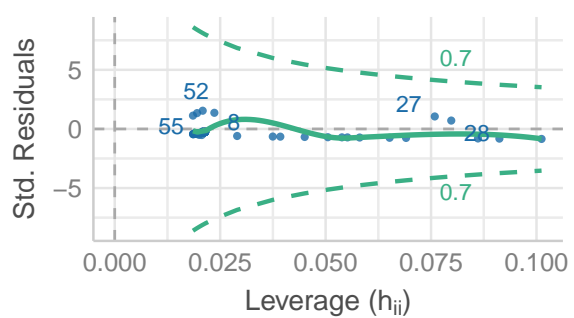
Homogeneity of Variance

Reference line should be flat and horizontal



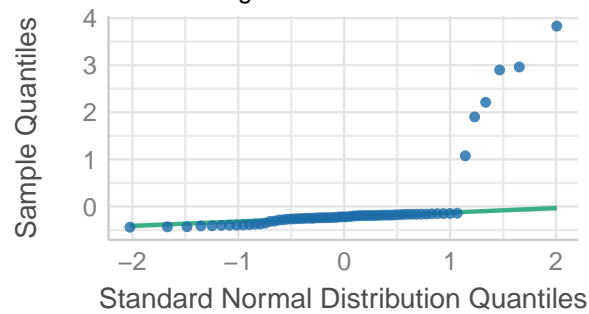
Influential Observations

Points should be inside the contour lines



Normality of Residuals

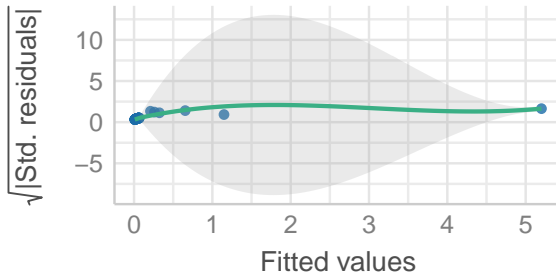
Dots should fall along the line



```
check_model(rhyssomatus.abundance.late.urb_herb.toronto) # Good fit
```

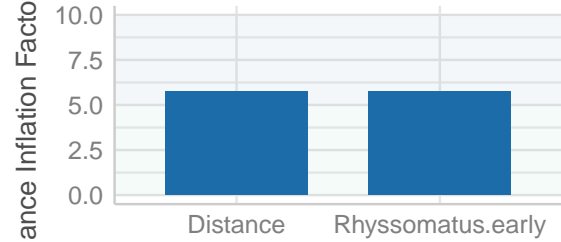
Homogeneity of Variance

Reference line should be flat and horizontal



Collinearity

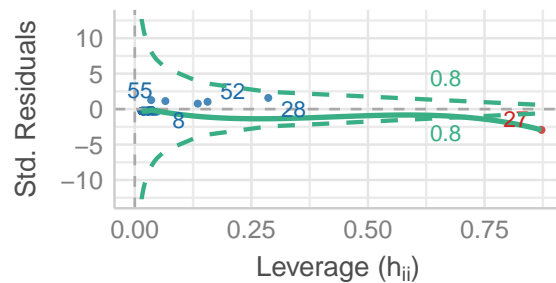
Higher bars (>5) indicate potential collinearity issue:



low (< 5) moderate (< 10) high (>= 10)

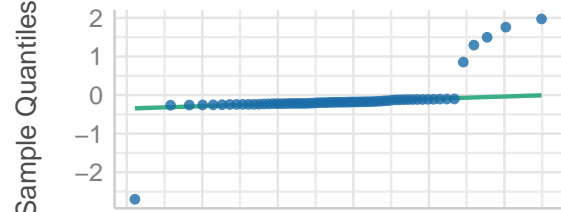
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line



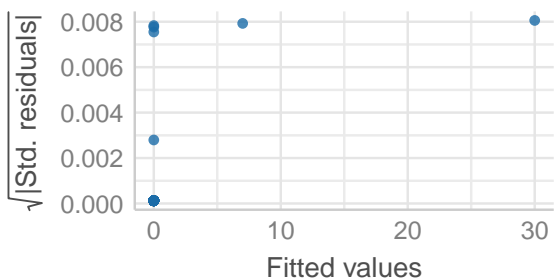
Standard Normal Distribution Quantiles

```
# Aphid abundance GLMs
```

```
check_model(aphis.abundance.early.urb_herb.toronto) # Good fit
```

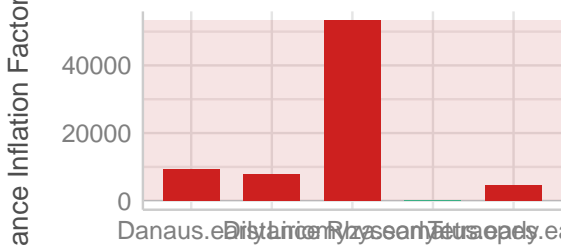
Homogeneity of Variance

Reference line should be flat and horizontal



Collinearity

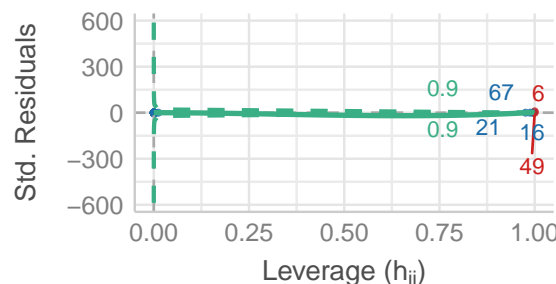
Higher bars (>5) indicate potential collinearity issues



low (< 5) moderate (< 10) high (>= 10)

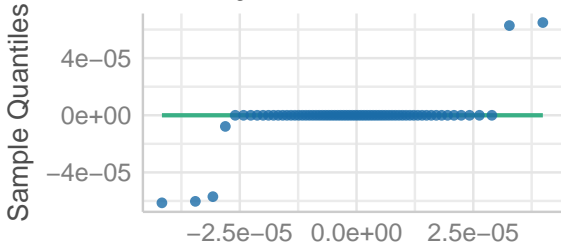
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line



Standard Normal Distribution Quantiles

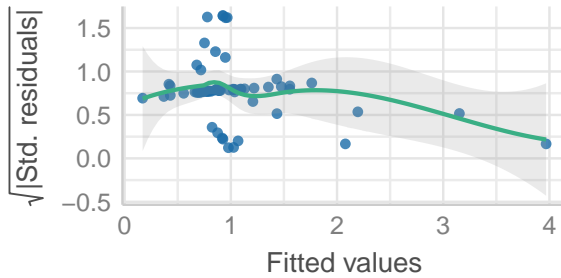
```
#check_model(aphis.abundance.late.urb_herb.toronto) # Good fit
```

```
# Tetraopes abundance GLMs
```

```
check_model(tetraopes.abundance.early.urb_herb.toronto) # Poor fit
```

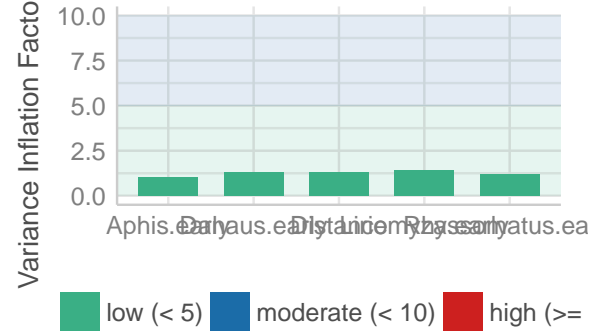
Homogeneity of Variance

Reference line should be flat and horizontal



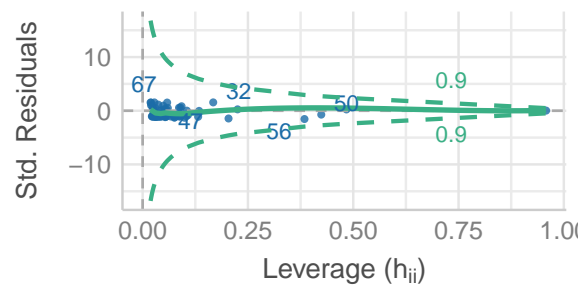
Collinearity

Higher bars (>5) indicate potential collinearity issue



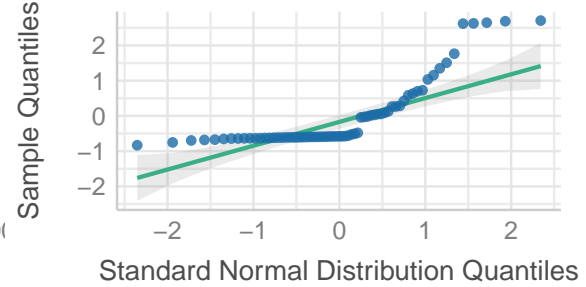
Influential Observations

Points should be inside the contour lines



Normality of Residuals

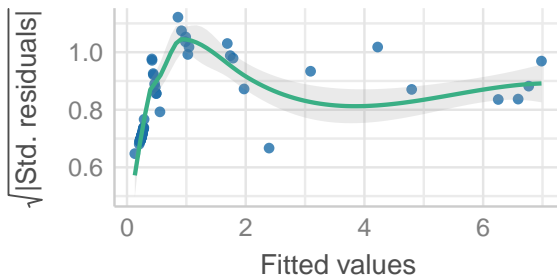
Dots should fall along the line



```
check_model(tetraopes.abundance.late.urb_herb.toronto) # Poor fit
```

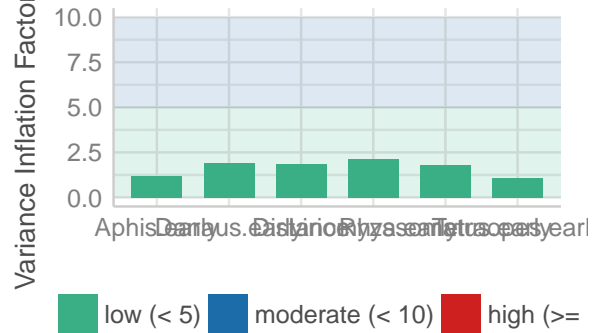

Homogeneity of Variance

Reference line should be flat and horizontal



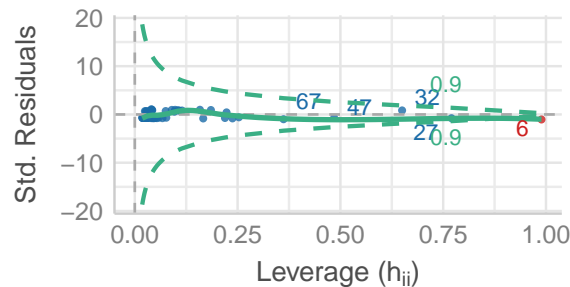
Collinearity

Higher bars (>5) indicate potential collinearity issue:



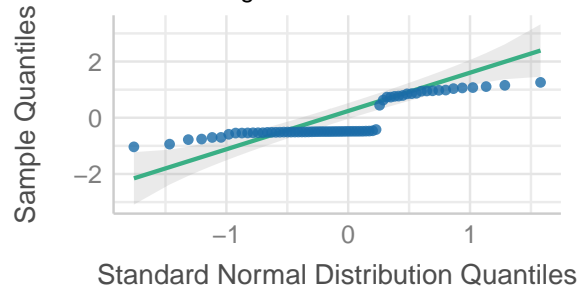
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line

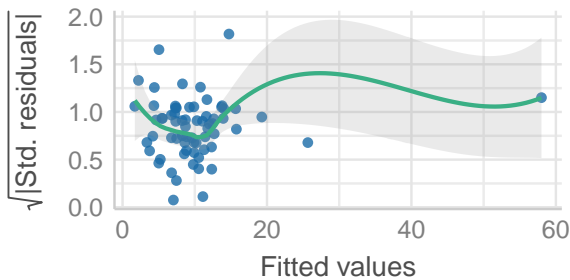


```
# Liriomyza abundance GLMs
```

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

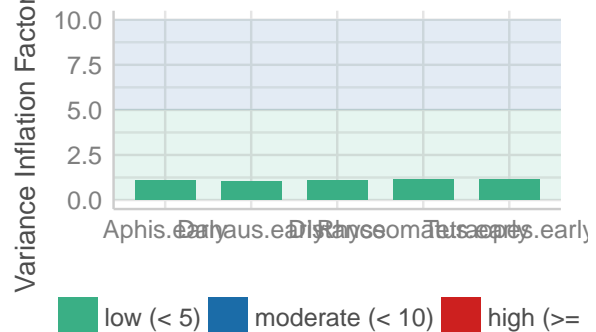
Homogeneity of Variance

Reference line should be flat and horizontal



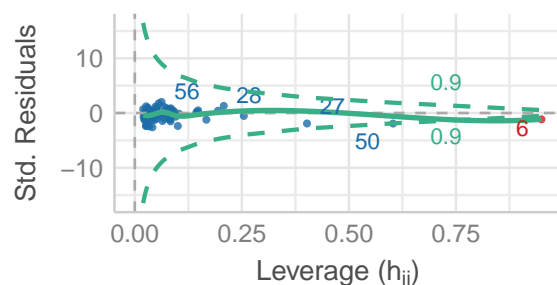
Collinearity

Higher bars (>5) indicate potential collinearity issue:



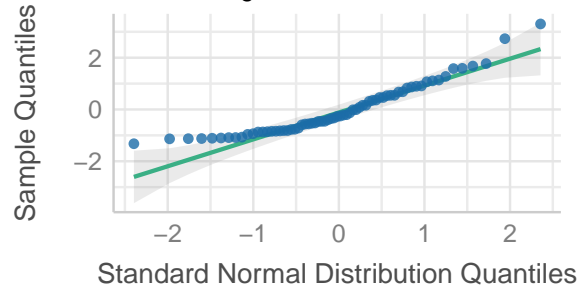
Influential Observations

Points should be inside the contour lines



Normality of Residuals

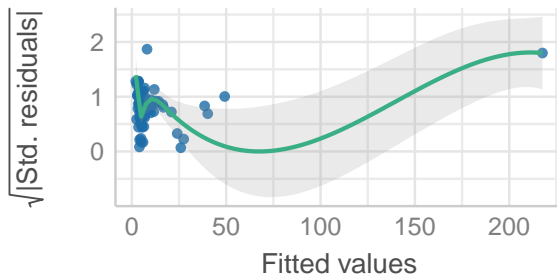
Dots should fall along the line



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

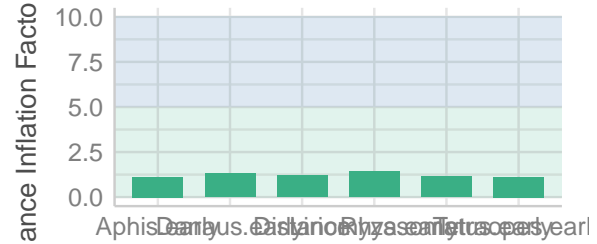
Homogeneity of Variance

Reference line should be flat and horizontal



Collinearity

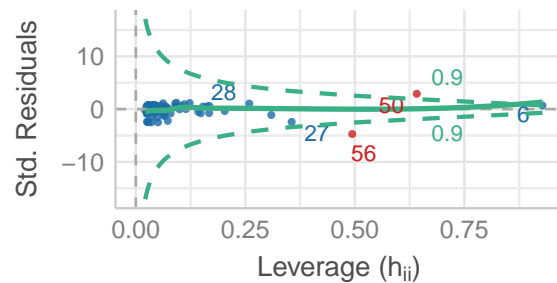
Higher bars (>5) indicate potential collinearity issue:



low (< 5) moderate (< 10) high (\geq)

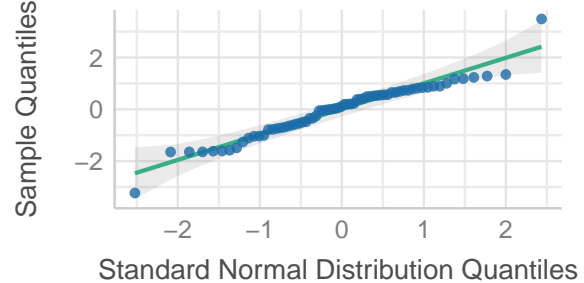
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line



Urbanization (Hypothesized pSEM 1) | Presence-Absence

```
## 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")
)

```

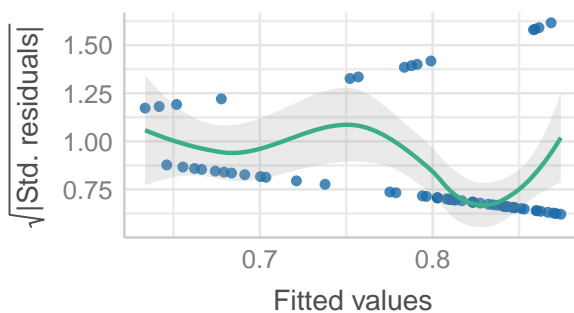
Check model assumptions

Danaus presence-absence GLMs

check_model(danaus.presence.absence.early.urb.toronto) # *Decent fit*

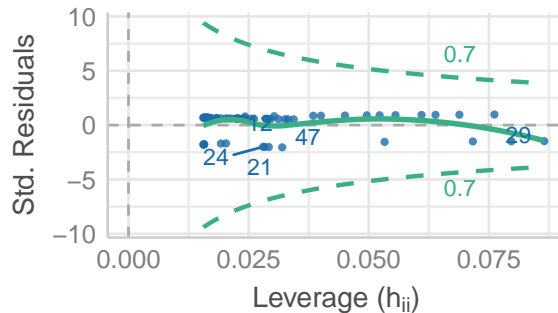
Homogeneity of Variance

Reference line should be flat and horizontal



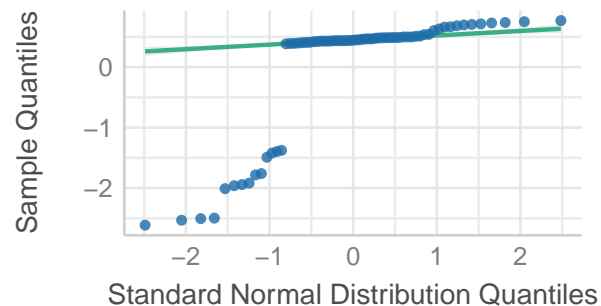
Influential Observations

Points should be inside the contour lines



Normality of Residuals

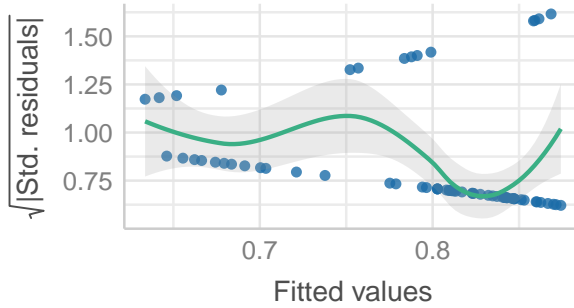
Dots should fall along the line



check_model(danaus.presence.absence.late.urb.toronto) # *Decent fit*

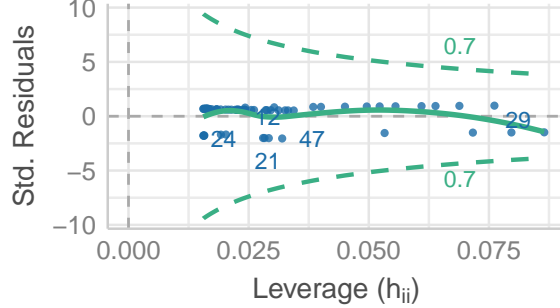
Homogeneity of Variance

Reference line should be flat and horizontal



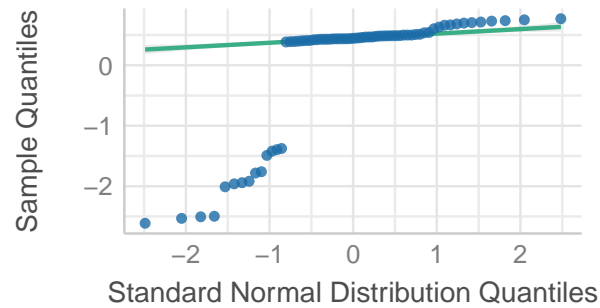
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line

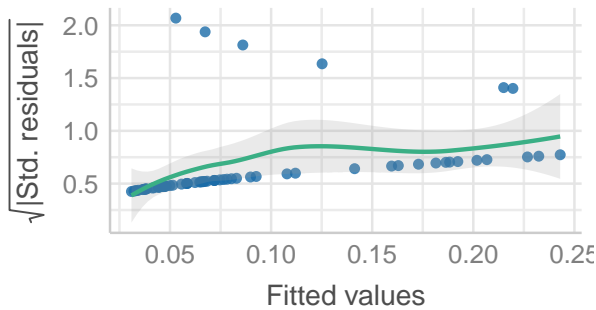


Rhyssomatus presence-absence GLMs

`check_model(rhyssomatus.presence.absence.early.urb.toronto)` *# Good fit*

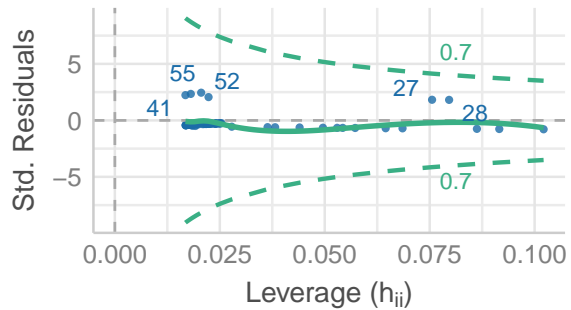
Homogeneity of Variance

Reference line should be flat and horizontal



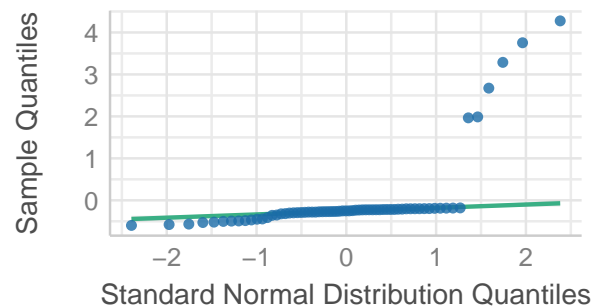
Influential Observations

Points should be inside the contour lines



Normality of Residuals

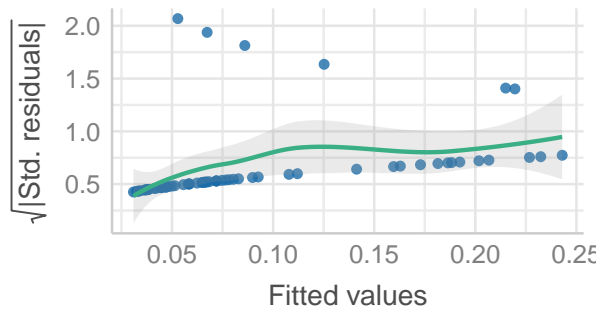
Dots should fall along the line



```
check_model(rhyssomatus.presence.absence.late.urb.toronto) # Good fit
```

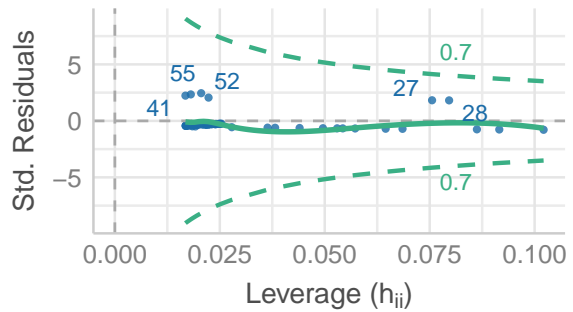
Homogeneity of Variance

Reference line should be flat and horizontal



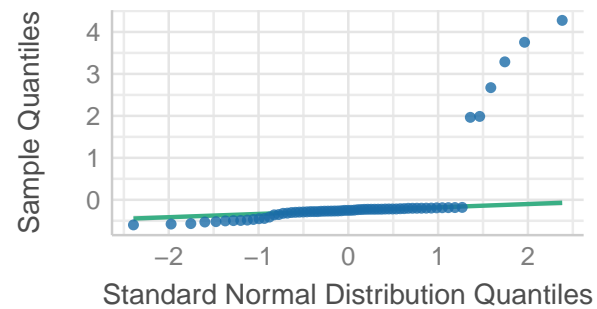
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line

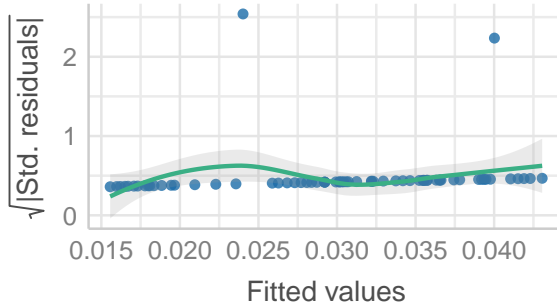


```
# Aphis presence-absence GLMs
```

```
check_model(aphis.presence.absence.early.urb.toronto) # Good fit
```

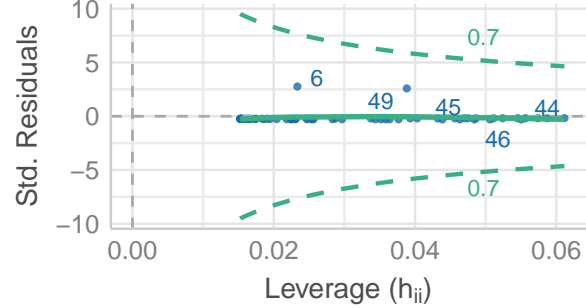
Homogeneity of Variance

Reference line should be flat and horizontal



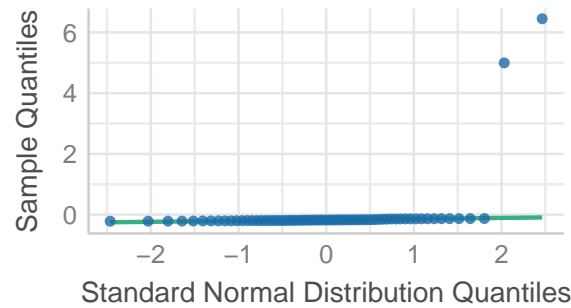
Influential Observations

Points should be inside the contour lines



Normality of Residuals

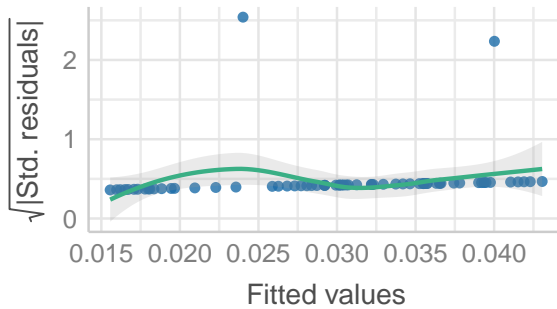
Dots should fall along the line



```
check_model(aphis.presence.absence.late.urb.toronto) # Good fit
```

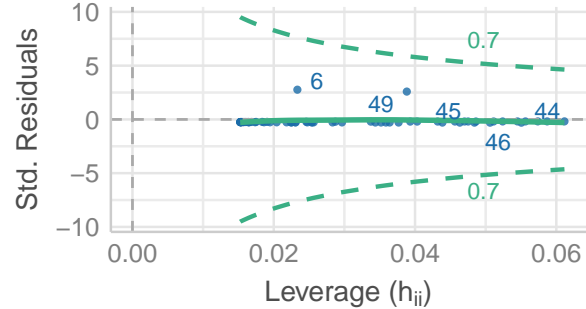
Homogeneity of Variance

Reference line should be flat and horizontal



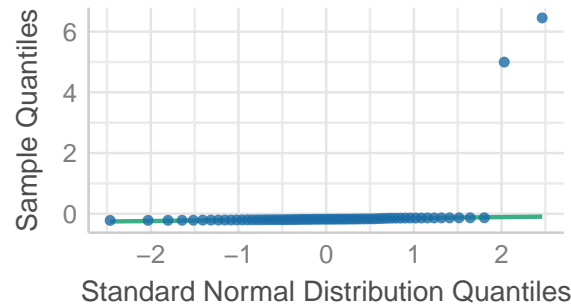
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line

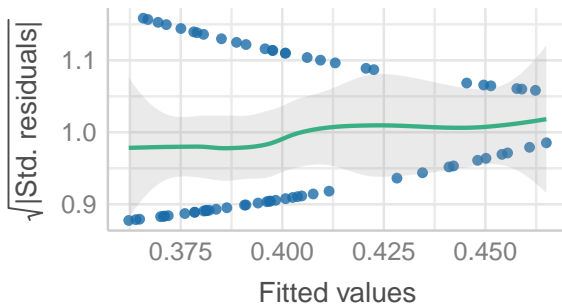


```
# Tetraopes presence-absence GLMs
```

```
check_model(tetraopes.presence.absence.early.urb.toronto) # Poor fit
```

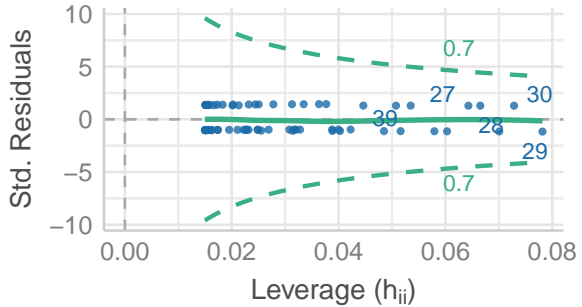
Homogeneity of Variance

Reference line should be flat and horizontal



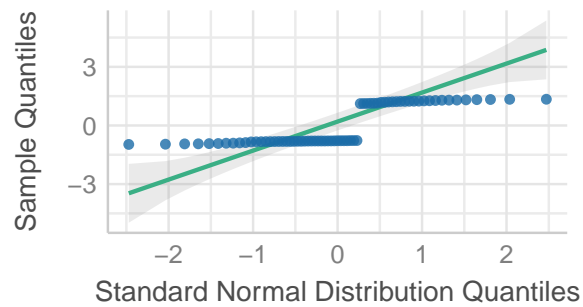
Influential Observations

Points should be inside the contour lines



Normality of Residuals

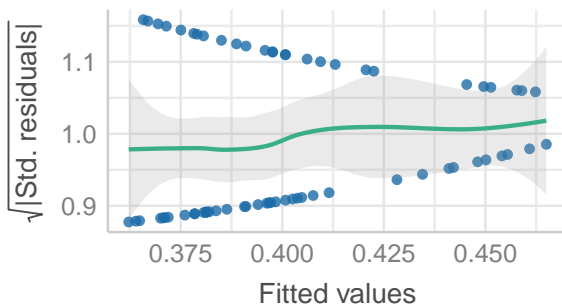
Dots should fall along the line



```
check_model(tetraopes.presence.absence.late.urb.toronto) # Poor fit
```

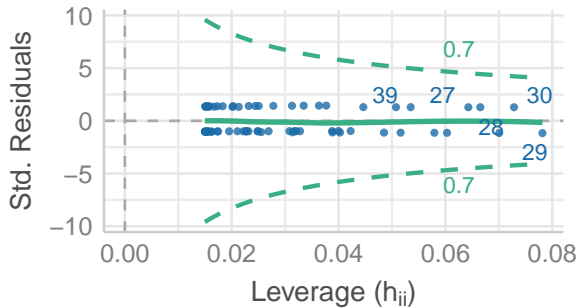
Homogeneity of Variance

Reference line should be flat and horizontal



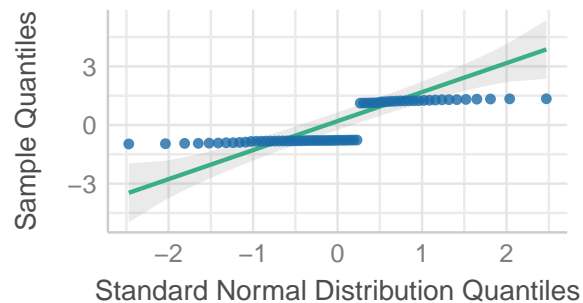
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line

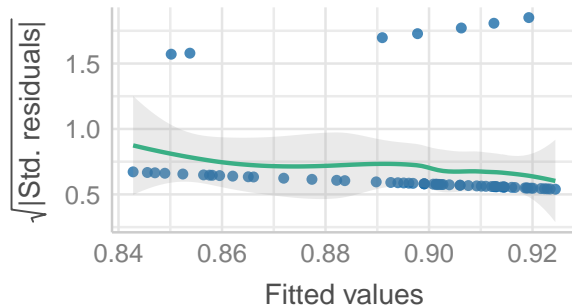



```
# Liriomyza presence-absence GLMs
```

```
check_model(liriomyza.presence.absence.early.urb.toronto) # Good fit
```

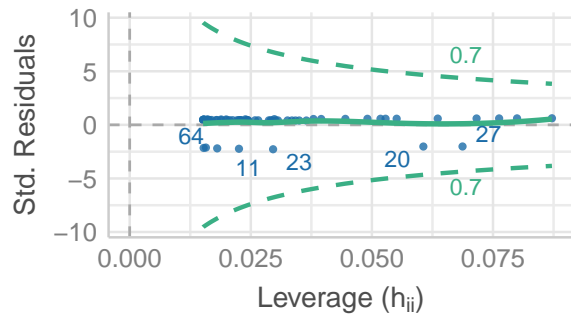
Homogeneity of Variance

Reference line should be flat and horizontal



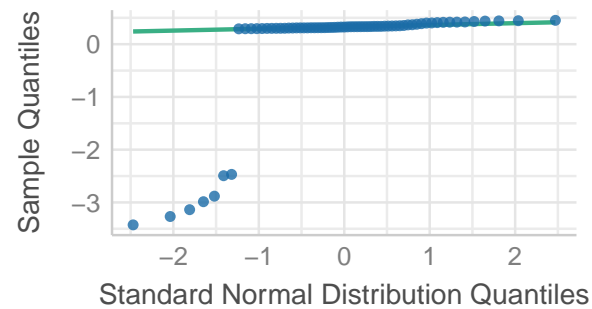
Influential Observations

Points should be inside the contour lines



Normality of Residuals

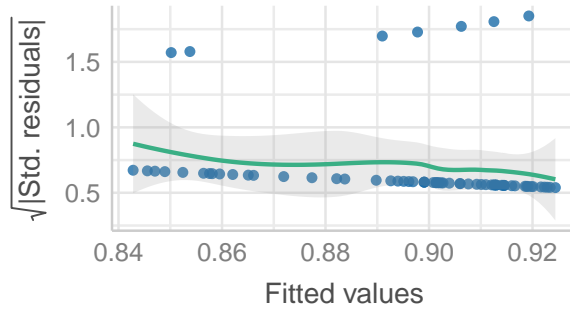
Dots should fall along the line



```
check_model(liriomyza.presence.absence.late.urb.toronto) # Good fit
```

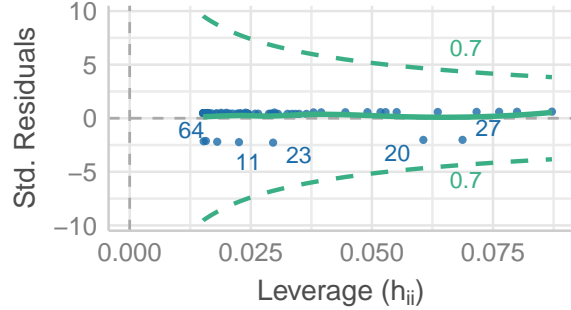
Homogeneity of Variance

Reference line should be flat and horizontal



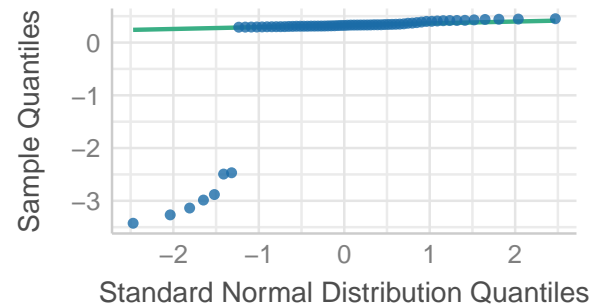
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line



Herbivore Interactions (Hypothesized pSEM 2) | Presence-Absence

```
## 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")
)
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")
)
```

```
## 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

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,  
  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 + Liri
data = final.presence.absence.data,
family = binomial(link = "logit")
)

```

```

## 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

```

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 | 0.16.0 | 2022-01-12 |
| 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 |