## Example R Script code for structural equation modelling

# Install packages

install.packages(“piecewiseSEM”)

install.packages(“lavaan”)

install.packages(“lme4”)

install.packages(“openxlsx”)

install.packages(“MASS”)

# libraries

library(piecewiseSEM)

library(lavaan)

library(lme4)

library(openxlsx)

library(MASS)

## Read in the data

# For SEM analysis

sem\_data <- read.xlsx("Snyder\_Lab\_SEM\_Example\_Data.xlsx")

## Create regression models and test model assumptions based on type of data (*e.g.* normality, overdispersion, homoskedasticity)

nat\_enemies<- glm.nb(nat\_enemies ~ soil\_P\_ppm, data = sem\_data)

summary(nat\_enemies)

herbivores <- glm.nb(herbivores ~ nat\_enemies + soil\_P\_ppm, data = sem\_data)

summary(herbivores)

yield <- lm(yield\_kg ~herbivores + soil\_P\_ppm, data = sem\_data)

summary(yield)

## SEM analysis

# Run SEM model

SEM <- psem(

glm.nb(nat\_enemies ~ soil\_P\_ppm, sem\_data),

glm.nb(herbivores ~ nat\_enemies + soil\_P\_ppm, sem\_data),

lm(yield\_kg ~herbivores + soil\_P\_ppm, sem\_data))

# Get summary of results of model

summary(SEM, conserve = TRUE)

# Model selection – select model with lowest possible AIC value that maintains biological meaning

# First run model with all possible pathways and then slowly remove variables to

optimize AIC

SEM\_testing <- psem(

glm.nb(nat\_enemies ~ soil\_P\_ppm, sem\_data),

glm.nb(herbivores ~ nat\_enemies + soil\_P\_ppm, sem\_data),

lm(yield\_kg ~herbivores + soil\_P\_ppm + nat\_enemies, sem\_data))

# Get summary of results of model

summary(SEM\_testing, conserve = TRUE)