Supplemental Table 1. Basic commands and outputs for fitting the rectangular hyperbola curve (Equation 4) using nls function and nls package in R Statistical Software to determine the parameter I and A and the best model to described crop-weed relationships in additive design.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *R program output* | | | | | | | | | | | | | | | | | | | | | *Commands* |
| ***Step 1. Reading a data file into R*** | | | | | | | | | | | | | | | | | | | | |  |
| Create a R-studio file | | | | | | | | | | | | | | | | | | | | | At the R-studio toolbar, click in file, New Project…, Existing Directory, and choose the folder that contain you data, we recommend to be csv (comma delimited) file. |
| install.packages(nls) | | | | | | | | | | | | | | | | | | | | | This command install the package nls (non-linear sum squares). |
| library(nls) | | | | | | | | | | | | | | | | | | | | | This function loads and activate the package nls in R. |
| dataname=read.csv(“biomass.csv”) | | | | | | | | | | | | | | | | | | | | | Assign the name of your data set (replace “dataname” to a name of your choice). If you use comma (,) for separating decimals places use read.csv2(). If you use a decimal point (.), use read.csv(). In parenthesis, write the name of your data set file. |
| head(dataname) | | | | | | | | | | | | | | | | | | | | | This command prints the first 6 lines of the data set. It is useful for double checking your data set. |
|  | | |  | | | rep | | trt | dweed | | yl | | Weed | | |  | | | | |  |
|  | | | 1 | | | 1 | | 1 | 0 | | -3.52 | | 1 | | |  | | | | |
|  | | | 2 | | | 2 | | 1 | 0 | | 5.89 | | 1 | | |  | | | | |
|  | | | 3 | | | 3 | | 1 | 0 | | 3.18 | | 1 | | |  | | | | |
|  | | | 4 | | | 4 | | 1 | 0 | | -3.73 | | 1 | | |  | | | | |
|  | | | 5 | | | 1 | | 2 | 1 | | 68.04 | | 1 | | |  | | | | |
|  | | | 6 | | | 2 | | 2 | 1 | | 61.63 | | 1 | | |  | | | | |
| ***Step 2. Fitting a full model for two weed species*** | | | | | | | | | | | | | | | | | | | | |  |
| Full=nls(yl ~ (I[weed]\*densityweed)/(1+(I[weed]/A[weed])\*densityweed), data=dataname, start=list(I=c(60,30), A=c(80,60)), trace=T) | | | | | | | | | | | | | | | | | | | | | Full is a user-defined name that will contain all information about the fitted model generated by nls function. Start is used to estimate values of parameter I and A in the model. It can easier be determined from visual inspection of the data set. The bracket [] after each parameter in the equation tell R to estimate a parameter for each weed species. |
| summary(Full) | | | | | | | | | | | | | | | | | | | | | This command provides the estimated parameters I and A for each weed species. |
| ***Step 3. Fitting reduced models and testing hypothesis*** | | | | | | | | | | | | | | | | | | | | |  |
| Red1=nls(yl ~ (I\*densityweed)/(1+(I/A)\*densityweed), data=dataname, start=list(I=40, A=80), trace=T) | | | | | | | | | | | | | | | | | | | | | Red1 is a user-defined name that will contain information about the first reduced model generated by nls function. Notice that we do not include bracket [] after each parameter I and A. In this case we are combining parameter I and A for both weed species. Our hypothesis is that a single parameter I and A for both species is enough to describe the crop-weed relationship. |
| anova(Full, Red1) | | | | | | | | | | | | | | | | | | | | | Testing hypothesis using F-test. We are using the Full model (separated I and A for each species) to compare with Red1 (single I and A for both species). If p>0.05, we should use the Red1 model, which means that the simplest model (Red1) is enough to describe crop-weed relationship. If not we should proceed to the next hypothesis testing. |
| Red2=nls(yl ~ (I\*densityweed)/(1+(I/A[weed])\*densityweed), data=dataname, start=list(I=60, A=c(80,60)), trace=T) | | | | | | | | | | | | | | | | | | | | | Red2 is a user-defined name that will contain information about the second reduced model generated by nls function. Notice that the bracket [] is after the parameter A only, which means that we are testing a hypothesis of single parameter I, but different A for the species. |
| anova(Full, Red2) | | | | | | | | | | | | | | | | | | | | | Testing hypothesis using F-test. We are using the Full model (separated I and A for each species) to compare with Red2 (single I and different A for both species). If p>0.05, we should use the Red2 model, which means that the simplest model (Red2) is enough to describe crop-weed relationship. If not we should proceed to the next hypothesis testing. |
| Red3=nls(yl ~ (I[weed]\*densityweed)/(1+(I[weed]/A)\*densityweed), data=dataname, start=list(I=60, A=c(80,60)), trace=T) | | | | | | | | | | | | | | | | | | | | | Red3 is a user-defined name that will contain information about the third reduced model generated by nls function. Notice that the bracket [] is after the parameter I only, which means that we are testing a hypothesis of different parameter I, but single parameter A for the species. |
| anova(Full, Red3) | | | | | | | | | | | | | | | | | | | | | Testing hypothesis using anova. We are using the Full model (separated I and A for each species) to compare with Red3 (different I and similar A for both species). |
|  |  | | | Res. Df | | | | Res. Sum Sq | | | Df | | Sum Sq | | F-value | | Pr(>F) | | |  | Output of the previous F-test. Notice the P >0.05. Therefore, Full model can be simplified to Red3 model. |
| 1 | | | 37 | | | | 1551.3 | | |  | |  | |  | |  | | |
|  | 2 | | | 36 | | | | 1490.8 | | | 1 | | 20.487 | | 0.4947 | | 0.4864 | | |  |
| summary(Red3) | | | | | | | | | | | | | | | | | | | | | This command provides the estimated parameters I and A of the chosen Red3 model. |
|  | |  | | |  | | Estimate | | | Std. error | | t value | | Pr(>|t|) | |  | |  |  | | Output of *summary*(Red3). Notice that parameter I was estimated and standard errors for weed 1 and 2 (*R. brasiliensis* and *C. benghalensis*), parameter A was estimated for both weed species. |
|  | | 1 | | | I1 | | 159.896 | | | 25.373 | | 6.302 | | 2.45e-07 | | \*\*\* | |  |  | |
|  | | 2 | | | I2 | | 56.432 | | | 4.915 | | 11.482 | | 9.31e-14 | | \*\*\* | |  |  | |
|  | | 3 | | | A | | 109.732 | | | 5.243 | | 20.929 | | <2e-16 | | \*\*\* | |  |  | |
|  | | 4 | | | Signif. Codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 | | | | | | | | | | | | |  |  | |
|  | | 5 | | | Residual standard error: 6.391 on 37 degrees of freedom | | | | | | | | | | | | |  |  | |
| plot(yl~densityweed, data=dataname, subset = weed =="1", pch=16, font.size=2, cex=2, las=1, xlab=expression("Weed Density (plants pot"^-1\*")"), ylim=c(-10,110), ylab = "Biomass Reduction (%)", cex.axis=1.8, cex.lab=2)  lines(yl~densityweed, type="p",data= dataname, subset = weed =="2", col=2, cex=2, pch=1) | | | | | | | | | | | | | | | | | | | | | The command *plot* and *lines* are used to generate the figure and the averaged points of biomass reduction at each density (Figure 4). The *subset* command is adding each weed species separately in the *plot* (weed 1) and *lines* (weed 2). |
| x=seq(0,4,0.25)  *Comm*=(159.896\*x)/(1+(159.896/109.732)\*x)  *Richar*=(56.432\*x)/(1+(56.432/109.732)\*x) | | | | | | | | | | | | | | | | | | | | | The *x* is a user-defined name, it will contain the x-axis sequence of the data set. *Comm* and *Richar* is also a user-defined name, this is the equation with the previous parameter estimates I and A estimated from Red3 model using the *nls* function. |
| lines(x, *Comm*, lty=1, lwd=5, col=1)  lines(x, *Richar*, lty=3, lwd=5, col=2) | | | | | | | | | | | | | | | | | | | | | The command *lines* will insert the previous equation into the plot. Command *lty*, *lwd*, and *col* define the line type, size, and color, respectively. |
| legend("bottomright", legend=c("C. benghalensis", "R. brasiliensis"), text.font = 3, col=c(1,2), pch= c(16,1), lty=c(1,3), lwd= c(5,5), bty="n", cex=2) | | | | | | | | | | | | | | | | | | | | | The command legend will add the legend into the previous created plot. |