Supplemental Material for Structural Equation Model, Total Phosphorus Loads, Red River of the North Basin - Code and Results

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options(width = 90)

This document provides the R code (R Core Team, 2016) used to produce the results presented in the paper for which this is part of the supporting material. The first code section presents functions written to perform tasks later in the process.

Note: the code was not optimized for the best figure presentation in this html file. Instead, the code is used to generate figures for the paper and because of the device size used when generating them, the figures may look better in the paper and supporting information. In addition, many of the figures were for exploratory analysis only and were not intended to be print or presentation quality.

knitr::opts_chunk$set(echo = TRUE, warning = FALSE, fig.width = 16, fig.height = 10)

JoinDFs <- function(basinnum) {
  require(plyr)
  pptcol <- paste("b", basinnum, "ppt", sep = "")
  precipS1 <- basinPrecipS1[, c("wy", pptcol)]
  dimnames(precipS1)[[2]] <- c("year", "s1precip")
  precipS2 <- basinPrecipS2[, c("year", pptcol)]
  dimnames(precipS2)[[2]] <- c("year", "s2precip")
  fert <- subset(fertilizer, basin == basinnum)[, c("year", "PfromFert", "PfromManure")]
  crop <- subset(crops, basin == basinnum)[, c("year", "wheat", "soy", "corn")]
  wwt <- subset(wwtp, basin == basinnum)[, c("year", "TPFlux_kg")]
  dimnames(wwt)[[2]] <- c("year", "wwtpTPLoad")
  tp <- subset(TP, basin == basinnum)[, c("year", "FluxKgPerYr")]
  dimnames(tp)[[2]] <- c("year", "LoadKgPerYr")
  dfs <- list(precipS1, precipS2, wwt, fert, crop, tp)
  bdat <- join_all(dfs, by = c("year"))
  bdat <- subset(bdat, !is.na(TotalKgPerYr))
  bdat
}

DescriptiveStats <- function(dataset, varnom, basinnum) {
  n <- length(dataset[, varnom])
  pck <- is.na(dataset[, varnom])
  missing <- sum(pck)
  my.sum <- fivenum(dataset[, varnom],na.rm = TRUE)
  my.min <- round(my.sum[1], digits = 3)
  my.25 <- round(my.sum[2], digits = 3)
  my.med <- round(my.sum[3], digits = 3)
  qmean <- round(mean(dataset[, varnom],na.rm = TRUE), digits = 3)
  my.75 <- round(my.sum[4], digits = 3)
  my.max <- round(my.sum[5], digits = 3)
  my.sd <- round(sd(dataset[, varnom], na.rm = TRUE), digits = 3)
}
my.dfnums <- cbind(missing, my.min, my.25, my.med, qmean, my.75, my.max, my.sd)
n <- format(n, digits = 1, big.mark = ",", scientific = FALSE)
my.df <- as.data.frame(cbind(basinnum, varnom, n, my.dfnums), stringsAsFactors = FALSE)
dimnames(my.df)[[2]] <- c("basin", "variable", "n", "NA", "Min", "Q1", "Med", "Mean", "Q3", "Max", "StdDev")

my.df

BasinDescriptiveStats <- function(dataset, basinnum) {
  vars <- dimnames(dataset)[[2]][-1]
  summary <- data.frame(basin = numeric(0), variable = character(0), n = numeric(0),
                        Missing = numeric(0), Min = numeric(0), Q1 = numeric(0),
                        Med = numeric(0), Mean = numeric(0), Q3 = numeric(0),
                        Max = numeric(0), StdDev = numeric(0), stringsAsFactors = FALSE)
  for (i in 1:length(vars)) {
    summary[i, ] <- DescriptiveStats(dataset, vars[i], basinnum = basinnum)
  }
  summary
}

panel.cor <- function(x, y, digits = 2, prefix = "", cex.cor) {
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r <- cor(x, y, use = "complete.obs")
  txt <- format(c(r, 0.123456789), digits = digits)[1]
  txt <- paste(prefix, txt, sep = "")
  if (missing(cex.cor)) cex <- 0.75/strwidth(txt)
  test <- cor.test(x, y, na.action = "na.omit", method = "kendall")
  Signif <- symnum(test$p.value, corr = FALSE, na = FALSE,
                    cutpoints = c(0, 0.001, 0.01, 0.05, 0.1, 1),
                    symbols = c("***", "**", ",", ",", ",", ","))
  text(0.5, 0.5, txt, cex = max(cex * abs(r),.9))
  text(0.8, 0.8, Signif, cex = cex, col = 2)
}

NormTestVars <- function(var2test, mtitle) {
  par(mar = c(3, 3, 3, 2) + 0.1, las = 1, tck = 0.02, mfrow = c(2, 1))
  hist(var2test, main = paste("Histogram of ", mtitle))
  qqnorm(y = var2test, cex.main = 0.8)
  mtext(mtitle, side = 3, line = 0.5, cex = 0.8)
  qqline(var2test)
  legend("bottomright", legend = round(shapiro.test(var2test)$p.value, digits = 4),
         title = "p-value for Shapiro-Wilk Normality test", cex = 0.75, bty = "n")
}

NormTestVarsTransformationComparison <- function(var2test, mtitle, var2test.t, mtitle.t) {
  par(mar = c(3, 3, 3, 2) + 0.1, las = 1, tck = 0.02, mfrow = c(2, 2))
  hist(var2test, main = paste("Histogram of untransformed ", mtitle))
qqnorm(y = var2test, cex.main = 0.8)
mtext(mtitle, side = 3, line = 0.5, cex = 0.8)
qqline(var2test)
legend("bottomright", legend = round(shapiro.test(var2test)$p.value, digits = 4),
title = "p-value for \nShapiro-Wilk Normality test", cex = 0.75, bty = "n")

hist(var2test.t, main = paste("Histogram of transformed ", mtitle))
qqnorm(y = var2test.t, cex.main = 0.8)
mtext(mtitle, side = 3, line = 0.5, cex = 0.8)
qqline(var2test.t)
legend("bottomright", legend = round(shapiro.test(var2test.t)$p.value, digits = 4),
title = "p-value for \nShapiro-Wilk Normality test", cex = 0.75, bty = "n")
}

DataSetScaleTransformStandardize <- function(dataset) {
  row.names(dataset) <- dataset$year
  dataset <- dataset[, -1]
  dataset.s <- 1 + 99*scale(dataset[, 4:dim(dataset)[2]],
    center = sapply(dataset[, 4:dim(dataset)[2]], min, na.rm = TRUE),
    scale = sapply(dataset[, 4:dim(dataset)[2]], function(x)
      diff(range(x, na.rm = TRUE)))

  require(car)
  trans1 <- powerTransform(dataset.s ~ 1)
  print(summary(trans1))
  dataset.t <- bcPower(dataset.s, lambda = coef(trans1, round = TRUE))
  colnames(dataset.t) <- names(dataset[4:dim(dataset)[2]])
  require("MVN")
  cat("\n", "\n")
  print(mardiaTest(dataset.t))

  dataset.t <- cbind.data.frame(dataset[,1:3], scale(dataset.t))
  dataset.t
}

FitMeasuresBootstrap <- function(mymod, nboot = 100, mytype = "yuan", origT) {
  FM.boot <- bootstrapLavaan(mymod, R = nboot, type = mytype, FUN = fitMeasures,
    fit.measures = c("chisq", "df", "pvalue", "cfi", "tli", "srmr", "rmsea"),
    parallel = "multicore", ncpus = 2)
  T.boot <- FM.boot[, "chisq"]
  #summary(FM.boot)[4,]
  pvalue.boot <- length(which(T.boot > origT))/length(T.boot)
  list(summary(FM.boot[,c("cfi", "tli", "srmr", "rmsea")]), pvalue.boot)
}

Data Import

The data import assumes that the code resides in the same working directory as the data files. The data are available in a U.S. Geological Survey Data Release (Ryberg et al., 2016) as comma-separated values (csv) files.

monthlyprecip <- read.csv("Basin_Monthly_Mean_Precipitation.csv", stringsAsFactors = FALSE)
Monthly precipitation by year:

```r
monthlyprecip$year <- apply(monthlyprecip, 1,
  function(x) if ( x[2] > 9 ) { x[1] + 1 } else { x[1] })
```

Basin precipitation:

```r
basinPrecipS1 <- aggregate(subset(monthlyprecip, month > 10 | month < 3),
  by = list(subset(monthlyprecip, month > 10 | month < 3)$year),
  FUN = sum)
```

```r
dimnames(basinPrecipS1)[[2]][1] <- "wy"
```

```r
basinPrecipS2 <- aggregate(subset(monthlyprecip, month > 2 & month < 7),
  by = list(subset(monthlyprecip, month > 2 & month < 7)$year), FUN = sum)
```

```r
dimnames(basinPrecipS2)[[2]][1] <- "year"
```

Fertilizer data:

```r
fertilizer <- read.csv("fertilizerEstimates.csv", stringsAsFactors = FALSE)
crops <- read.csv("wheatCornSoyEstimates.csv", stringsAsFactors = FALSE)
wwtp <- read.csv("WWTPFluxEstimates.csv", stringsAsFactors = FALSE)
TP <- read.csv("TPFluxEstimates.csv", stringsAsFactors = FALSE)
```

Summary Statistics:

Next, summary statistics are calculated for the observed variables used in the structural equation model (SEM).

```r
b1dat <- JoinDFs(1)
b1sum <- BasinDescriptiveStats(b1dat, 1)
b2sum <- BasinDescriptiveStats(b2dat, 2)
b3sum <- BasinDescriptiveStats(b3dat, 3)
b4sum <- BasinDescriptiveStats(b4dat, 4)
b5sum <- BasinDescriptiveStats(b5dat, 5)
b8sum <- BasinDescriptiveStats(b8dat, 8)
```

Summary statistics:

```r
summaryStats <- rbind.data.frame(b1sum, b2sum, b3sum, b4sum, b5sum, b8sum)
```

```r
summaryStats
```

```r
## basin variable n Missing Min Q1 Med Mean Q3
## 1 1 s1precip 42 0 24.58 49.71 67.465 72.303 92.4
## 2 1 s2precip 42 0 134.67 205.15 252.025 248.512 283.1
## 3 1 wwtpTPLoad 42 7 7074.16 7842.785 8234.485 8624.827 9348.484
## 4 1 PfromFert 42 0 471.499 593.1 658.55 686.097 754.5
## 5 1 PfromManure 42 0 172.813 186.196 196.516 198.363 214.145
## 6 1 wheat 42 0 0.059 0.134 0.163 0.155 0.179
## 7 1 soy 42 0 0.039 0.088 0.156 0.15 0.209
## 8 1 corn 42 0 0.056 0.105 0.127 0.136 0.162
```
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Max  StdDev
---  ---
1  148.87  30.309
2  386.56  64.935
3  10212.26  995.436
4  916.3  120.431
5  229.2  16.285
6  0.214  0.035
7  0.262  0.068
## 8  0.25   0.047
## 9 1156677  322721.675
##11 134.96  25.733
##21 324.33   55.12
##31 7118.862 1020.329
##41  517.9 107.969
##51   85.003  8
##61   0.129  0.009
##71   0.095  0.027
##81   0.021  0.003
##91 805146 179147.937
##12 120.11  22.619
##22  316.92  46.38
##32  4156.39 396.768
##42   639.1  90.255
##52   155    4.236
##62   0.29   0.039
##72   0.233  0.061
##82   0.129  0.028
##92  576438 113702.83
##13  122.8  24.563
##23  361.67  55.148
##33  75728.83 11586.532
##43   828   125.155
##53  186.381  17.917
##63   0.282  0.041
##73   0.268  0.075
##83   0.183  0.036
##93 3515682  842952.981
##14  108.61  25.38
##24   328.2  49.361
##34  1177.64  87.516
##44  1070.7  169.432
##54   39.552  2.828
##64   0.378  0.017
##74   0.078  0.016
##84   0.012  0.003
##94 1139693 330578.806
##15  120.36  23.282
##25   339.9  48.846
##35 118967.45 15525.541
##45   985.379  176.665
##55  133.74  13.753
##65   0.266  0.047
##75   0.242  0.066
##85   0.138  0.029
##95 4654889 1224421.072

# results written to a csv file, but task not performed in this illustration
# write.csv(summaryStats, file = "SummaryStats.csv", row.names = FALSE)
Correlation

The following plots use pairs plots to provide graphical analysis of correlation between variables, as well as a statistical test of Kendall’s tau correlation. The scatterplots represent bivariate plots of the data. The pairs plots with numbers in the center indicates Kendall’s tau correlation. The larger the font, the larger the absolute value of the correlation. A statistical significance test was also done on the correlation. If there is one red dot, the correlation is significant at the 0.10 significance level, one red asterisk indicates the correlation is significant at the 0.05 significance level, two asterisks represent a 0.01 significance level, and three asterisks represent a 0.001 significance level.

```r
pairs(b1dat, lower.panel = panel.smooth, upper.panel = panel.cor)
```

```r
pairs(b2dat, lower.panel = panel.smooth, upper.panel = panel.cor)
```
pairs(b3dat, lower.panel = panel.smooth, upper.panel = panel.cor)

pairs(b4dat, lower.panel = panel.smooth, upper.panel = panel.cor)
pairs(b5dat, lower.panel = panel.smooth, upper.panel = panel.cor)

pairs(b8dat, lower.panel = panel.smooth, upper.panel = panel.cor)
Tests of Normality

Next the variables were tested for univariate normality; scaled, transformed, and standardized; and tested for multivariate normality. Some variables violated these assumptions; however, robust methods (described in the associated paper) were used to overcome these issues.

```r
basins <- list(b1dat, b2dat, b3dat, b4dat, b5dat, b8dat)
bnum <- c(1, 2, 3, 4, 5, 8)
vars <- dimnames(b1dat)[[2]][-1]

par(mfrow = c(2,1))
for (i in 1:length(basins)) {
  for (j in 1:length(vars)) {
    mtitle <- vars[j]
    NormTestVars(basins[[i]][, vars[j]], paste("Basin ", bnum[i], ", ", vars[j], sep = ""))
  }
}
```
Histogram of Basin 1, Load Kg Per Year

Frequency

Normal Q-Q Plot
Sample Quantiles
Basin 1, Load Kg Per Year

p-value for Shapiro-Wilk Normality test: 0.0016

Histogram of Basin 2, s1precip

Frequency

Normal Q-Q Plot
Sample Quantiles
Basin 2, s1precip

p-value for Shapiro-Wilk Normality test: 0.0795
Histogram of Basin 4, s2precip

Normal Q-Q Plot

Histogram of Basin 4, wwtpTPLoad

Normal Q-Q Plot

p-value for
Shapiro-Wilk Normality test

0.8272

5e−04
Histogram of Basin 8, s2precip

Normal Q-Q Plot
Sample Quantiles
Basin 8, s2precip
p-value for Shapiro-Wilk Normality test
0.9896

Histogram of Basin 8, wwtpTPLoad

Normal Q-Q Plot
Sample Quantiles
Basin 8, wwtpTPLoad
p-value for Shapiro-Wilk Normality test
5e-04
# Not all variables are univariate normal and will therefore require transformations

```r
b1dat.t <- DataSetScaleTransformStandardize(b1dat)
```

## Loading required package: car

## bcPower Transformations to Multinormality

##
## |          | Est.Power | Std.Err. | Wald Lower Bound | Wald Upper Bound |
## |----------|-----------|----------|------------------|------------------|
## PfromFert | 0.6537    | 0.1267   | 0.4054          | 0.9020           |
## PfromManure | 0.7338   | 0.0466   | 0.6425          | 0.8251           |
## wheat     | 1.0671    | 0.0773   | 0.9155          | 1.2186           |
## soy       | 1.1068    | 0.0673   | 0.9750          | 1.2387           |
## corn      | 0.8555    | 0.0552   | 0.7473          | 0.9637           |
## LoadKgPerYr | 0.3803   | 0.1371   | 0.1116          | 0.6491           |

## Likelihood ratio tests about transformation parameters

##
## |          | LRT       | df | pval         |
## |----------|-----------|----|--------------|
## LR test, lambda = (0 0 0 0 0 0) | 428.547022 | 6  | 0.0000000e+00 |
## LR test, lambda = (1 1 1 1 1 1) | 48.949901  | 6  | 7.630086e-09  |
## LR test, lambda = (0.5 0.73 1 1 0.86 0.5) | 7.053448  | 6  | 3.159326e-01  |

## Loading required package: MVN

## sROC 0.1-2 loaded
## Mardia's Multivariate Normality Test

### data : dataset.t

```r
## g1p     : 16.18661
## chi.skew : 113.3063
## p.value.skew : 9.231927e-06
##
## g2p     : 65.98069
## z.kurtosis : 5.946556
## p.value.kurt : 2.73843e-09
##
## chi.small.skew : 123.8687
## p.value.small : 4.868598e-07

## Result : Data are not multivariate normal.
```

### bcPower Transformations to Multinormality

```r
b2dat.t <- DataSetScaleTransformStandardize(b2dat)
```

### bcPower Transformations

<table>
<thead>
<tr>
<th></th>
<th>Est.</th>
<th>Std.Err.</th>
<th>Wald Lower Bound</th>
<th>Wald Upper Bound</th>
</tr>
</thead>
<tbody>
<tr>
<td>PfromFert</td>
<td>0.5225</td>
<td>0.1297</td>
<td>0.2683</td>
<td>0.7767</td>
</tr>
<tr>
<td>PfromManure</td>
<td>1.0630</td>
<td>0.1180</td>
<td>0.8318</td>
<td>1.2942</td>
</tr>
<tr>
<td>wheat</td>
<td>0.7576</td>
<td>0.1540</td>
<td>0.4558</td>
<td>1.0594</td>
</tr>
<tr>
<td>soy</td>
<td>0.6753</td>
<td>0.0858</td>
<td>0.5072</td>
<td>0.8434</td>
</tr>
<tr>
<td>corn</td>
<td>0.7593</td>
<td>0.1504</td>
<td>0.4644</td>
<td>1.0541</td>
</tr>
</tbody>
</table>
## LoadKgPerYr

0.3471 0.1439 0.0651 0.6290

## Likelihood ratio tests about transformation parameters

<table>
<thead>
<tr>
<th>LRT</th>
<th>df</th>
<th>pval</th>
</tr>
</thead>
<tbody>
<tr>
<td>LR test, lambda = (0 0 0 0 0 0)</td>
<td>197.685920</td>
<td>6 0.000000e+00</td>
</tr>
<tr>
<td>LR test, lambda = (1 1 1 1 1 1)</td>
<td>51.605338</td>
<td>6 2.238584e-09</td>
</tr>
<tr>
<td>LR test, lambda = (0.5 1 1 0.68 1 0.5)</td>
<td>6.379593</td>
<td>6 3.820373e-01</td>
</tr>
</tbody>
</table>

## Mardia's Multivariate Normality Test

---------------------------------------
data : dataset.t

<table>
<thead>
<tr>
<th>g1p</th>
<th>chi.skew</th>
<th>p.value.skew</th>
</tr>
</thead>
<tbody>
<tr>
<td>29.32733</td>
<td>200.4034</td>
<td>4.01646e-18</td>
</tr>
<tr>
<td>g2p</td>
<td>z.kurtosis</td>
<td>p.value.kurt</td>
</tr>
<tr>
<td>77.88381</td>
<td>9.764777</td>
<td>0</td>
</tr>
<tr>
<td>chi.small.skew</td>
<td>p.value.small</td>
<td></td>
</tr>
<tr>
<td>219.5477</td>
<td>3.186161e-21</td>
<td></td>
</tr>
</tbody>
</table>

Result: Data are not multivariate normal.

---------------------------------------

b3dat.t <- DataSetScaleTransformStandardize(b3dat)

## bcPower Transformations to Multinormality

<table>
<thead>
<tr>
<th>Est.Power</th>
<th>Std.Err.</th>
<th>Wald Lower Bound</th>
<th>Wald Upper Bound</th>
</tr>
</thead>
<tbody>
<tr>
<td>PfromFert</td>
<td>0.5865</td>
<td>0.1463</td>
<td>0.2998</td>
</tr>
<tr>
<td>PfromManure</td>
<td>0.5941</td>
<td>0.1234</td>
<td>0.3523</td>
</tr>
<tr>
<td>wheat</td>
<td>0.7684</td>
<td>0.1110</td>
<td>0.5509</td>
</tr>
<tr>
<td>soy</td>
<td>0.9188</td>
<td>0.0878</td>
<td>0.7466</td>
</tr>
<tr>
<td>corn</td>
<td>0.8760</td>
<td>0.0993</td>
<td>0.6814</td>
</tr>
<tr>
<td>LoadKgPerYr</td>
<td>0.1996</td>
<td>0.1380</td>
<td>-0.0709</td>
</tr>
</tbody>
</table>

## Likelihood ratio tests about transformation parameters

<table>
<thead>
<tr>
<th>LRT</th>
<th>df</th>
<th>pval</th>
</tr>
</thead>
<tbody>
<tr>
<td>LR test, lambda = (0 0 0 0 0 0)</td>
<td>226.118767</td>
<td>6 0.0000000e+00</td>
</tr>
<tr>
<td>LR test, lambda = (1 1 1 1 1 1)</td>
<td>61.672509</td>
<td>6 2.056966e-11</td>
</tr>
<tr>
<td>LR test, lambda = (0.5 0.5 0.77 1 1 0)</td>
<td>4.626364</td>
<td>6 5.925462e-01</td>
</tr>
</tbody>
</table>

## Mardia's Multivariate Normality Test

---------------------------------------
data : dataset.t

<table>
<thead>
<tr>
<th>g1p</th>
<th>chi.skew</th>
<th>p.value.skew</th>
</tr>
</thead>
<tbody>
<tr>
<td>35.841</td>
<td>221.0195</td>
<td>1.824292e-21</td>
</tr>
<tr>
<td>g2p</td>
<td>77.32558</td>
<td></td>
</tr>
</tbody>
</table>
## z.kurtosis  : 9.102945
## p.value.kurt  : 0
##
## chi.small.skew  : 244.454
## p.value.small  : 2.193653e-25
##
## Result  : Data are not multivariate normal.
## ---------------------------------------------------------------

b4dat.t <- DataSetScaleTransformStandardize(b4dat)

## bcPower Transformations to Multinormality
##
## Est.Power Std.Err. Wald Lower Bound Wald Upper Bound
## PfromFert 1.0667 0.0958 0.8789 1.2544
## PfromManure 0.7642 0.0747 0.6178 0.9106
## wheat 1.2221 0.1441 0.9398 1.5045
## soy 0.8085 0.0659 0.6793 0.9377
## corn 1.0165 0.0775 0.8646 1.1683
## LoadKgPerYr 0.4878 0.1395 0.2144 0.7612
##
## Likelihood ratio tests about transformation parameters
##
## LRT df pval
## LR test, lambda = (0 0 0 0 0 0) 426.734226 6 0.000000e+00
## LR test, lambda = (1 1 1 1 1 1) 40.898123 6 3.032598e-07
## LR test, lambda = (1 0.76 1 0.81 1 0.5) 4.982353 6 5.460785e-01
##
## Mardia's Multivariate Normality Test
## ---------------------------------------------------------------

b5dat.t <- DataSetScaleTransformStandardize(b5dat)

## bcPower Transformations to Multinormality
##
## Est.Power Std.Err. Wald Lower Bound Wald Upper Bound
## PfromFert 0.7333 0.2194 0.3032 1.1634
## PfromManure 0.4115 0.1562 0.1053 0.7177
## wheat 0.6798 0.2853 0.1205 1.2390
## soy 0.5856 0.1437 0.3039 0.8672
## corn 0.9671 0.1796 0.6151 1.3191
## LoadKgPerYr 0.3506 0.1972 -0.0358 0.7371
##
## Likelihood ratio tests about transformation parameters
LRT df pval
## LR test, lambda = (0 0 0 0 0 0) 91.17314 6 0.0000000e+00
## LR test, lambda = (1 1 1 1 1 1) 34.91760 6 4.470835e-06
## LR test, lambda = (1 0.5 1 0.5 1 0) 10.26340 6 1.139889e-01
##
## Mardia's Multivariate Normality Test
---------------------------------------
data : dataset.t
g1p : 27.36332
chi.skew : 86.65052
p.value.skew : 0.005362801

g2p : 52.48891
z.kurtosis : 0.998509
p.value.kurt : 0.3180326

chi.small.skew : 104.8247
p.value.small : 8.397043e-05

Result : Data are not multivariate normal.
---------------------------------------
b8dat.t <- DataSetScaleTransformStandardize(b8dat)

## bcPower Transformations to Multinormality
##
## Est.Power Std.Err. Wald Lower Bound Wald Upper Bound
PfromFert 1.0697 0.1263 0.8222 1.3171
PfromManure 0.6744 0.0844 0.5089 0.8398
wheat 1.7932 0.2704 1.2631 2.3233
soy 0.4733 0.1015 0.2744 0.6722
corn 0.7873 0.0979 0.5953 0.9793
LoadKgPerYr 0.5829 0.1542 0.2806 0.8851

## Likelihood ratio tests about transformation parameters
LRT df pval
## LR test, lambda = (0 0 0 0 0 0) 375.967399 6 0.0000000e+00
## LR test, lambda = (1 1 1 1 1 1) 56.730537 6 2.071389e-10
## LR test, lambda = (1 0.67 2 0.5 0.79 0.5) 1.752151 6 9.410245e-01

## Mardia's Multivariate Normality Test
---------------------------------------
data : dataset.t
g1p : 9.271619
chi.skew : 66.44661
p.value.skew : 0.1601663

g2p : 44.8206
## z.kurtosis : -1.06393
## p.value.kurt : 0.2873603
##
## chi.small.skew : 72.49465
## p.value.small : 0.06823222
##
## Result : Data are multivariate normal.
#
# basins.t <- list(b1dat.t, b2dat.t, b3dat.t, b4dat.t, b5dat.t, b8dat.t)
bnum.t <- c(1, 2, 3, 4, 5, 8)
vars.t <- dimnames(b1dat.t)[[2]]

for (i in 1:length(basins.t)) {
  for (j in 1:length(vars.t)) {
    mtitle <- vars.t[j]
    NormTestVars(basins.t[[i]][, vars.t[j]], paste("Basin ", bnum.t[i], ", ", vars.t[j], sep = ""))
  }
}
Histogram of Basin 2, s1precip

Normal Q-Q Plot
Basin 2, s1precip

p-value for Shapiro-Wilk Normality test: 0.0795

Histogram of Basin 2, s2precip

Normal Q-Q Plot
Basin 2, s2precip

p-value for Shapiro-Wilk Normality test: 0.5995

47
Histogram of Basin 2, PfromManure

Normal Q-Q Plot
Sample Quantiles
Basin 2, PfromManure

p-value for Shapiro-Wilk Normality test
0.1119

Histogram of Basin 2, wheat

Normal Q-Q Plot
Sample Quantiles
Basin 2, wheat

p-value for Shapiro-Wilk Normality test
0.0289
Histogram of Basin 2, LoadKgPerYr

Normal Q-Q Plot
Basin 2, LoadKgPerYr

p-value for Shapiro-Wilk Normality test
0.3388

Histogram of Basin 3, s1precip

Normal Q-Q Plot
Basin 3, s1precip

p-value for Shapiro-Wilk Normality test
0.3012
Histogram of Basin 3, s2precip

Normal Q-Q Plot
Basin 3, s2precip

p-value for Shapiro-Wilk Normality test
0.3286

Histogram of Basin 3, wwtpTPLoad

Normal Q-Q Plot
Basin 3, wwtpTPLoad

p-value for Shapiro-Wilk Normality test
0
Histogram of Basin 3, wheat

Histogram of Basin 3, soy

Normal Q-Q Plot
Basin 3, wheat

Normal Q-Q Plot
Basin 3, soy

p-value for Shapiro-Wilk Normality test
0.2221

p-value for Shapiro-Wilk Normality test
0.0066
Histogram of Basin 3, corn

Normal Q-Q Plot
Basin 3, corn

Histogram of Basin 3, LoadKgPerYr

Normal Q-Q Plot
Basin 3, LoadKgPerYr

p-value for Shapiro-Wilk Normality test: 0.0353

p-value for Shapiro-Wilk Normality test: 0.2937
Histogram of Basin 4, s1precip

Normal Q-Q Plot
Sample Quantiles
Basin 4, s1precip
p-value for Shapiro-Wilk Normality test
0.1343

Histogram of Basin 4, s2precip
Normal Q-Q Plot
Sample Quantiles
Basin 4, s2precip
p-value for Shapiro-Wilk Normality test
0.8272
Histogram of Basin 5, wheat

Normal Q-Q Plot
Basin 5, wheat

p-value for Shapiro-Wilk Normality test
0.259

Histogram of Basin 5, soy

Normal Q-Q Plot
Basin 5, soy

p-value for Shapiro-Wilk Normality test
0.4767
Histogram of Basin 5, corn

Normal Q-Q Plot
Sample Quantiles
Basin 5, corn
p-value for Shapiro-Wilk Normality test 0.9028

Histogram of Basin 5, LoadKgPerYr

Normal Q-Q Plot
Sample Quantiles
Basin 5, LoadKgPerYr
p-value for Shapiro-Wilk Normality test 0.0237

64
Histogram of Basin 8, s1precip

Normal Q-Q Plot

Sample Quantiles

Basin 8, s1precip

p-value for Shapiro-Wilk Normality test
0.1062

Histogram of Basin 8, s2precip

Normal Q-Q Plot

Sample Quantiles

Basin 8, s2precip

p-value for Shapiro-Wilk Normality test
0.9896
Histogram of Basin 8, wetpTPLoad

Histogram of Basin 8, PtromFert

Normal Q-Q Plot
Basin 8, wetpTPLoad

Normal Q-Q Plot
Basin 8, PtromFert

p-value for Shapiro-Wilk Normality test
5e−04

p-value for Shapiro-Wilk Normality test
0.0012
for (i in 1:length(basins)) {
  for (j in 1:length(vars)) {
    NormTestVarsTransformationComparison(var2test = basins[[i]], vars[j]),
    mtitle = paste("Basin ", bnum[i],
      " ", vars[j], sep = ""),
    var2test.t = basins.t[[i]], vars.t[j]],
    mtitle.t = paste("Basin ", bnum.t[i],
      " ", vars.t[j], sep = ""))
  }
}
Histogram of untransformed Basin 1, s1precip

Histogram of transformed Basin 1, s1precip

Normal Q-Q Plot
Sample Quantiles
Basin 1, s1precip

p-value for Shapiro-Wilk Normality test
0.2118

Histogram of untransformed Basin 1, s2precip

Histogram of transformed Basin 1, s2precip

Normal Q-Q Plot
Sample Quantiles
Basin 1, s2precip

p-value for Shapiro-Wilk Normality test
0.4627

Histogram of untransformed Basin 1, s3precip

Histogram of transformed Basin 1, s3precip

Normal Q-Q Plot
Sample Quantiles
Basin 1, s3precip

p-value for Shapiro-Wilk Normality test
0.4627
Histogram of untransformed Basin 1, wwtpTPLoad

Histogram of transformed Basin 1, wwtpTPLoad

Histogram of untransformed Basin 1, PfromFert

Histogram of transformed Basin 1, PfromFert

Normal Q-Q Plot

Theoretical Quantiles

Sample Quantiles

p−value for Shapiro−Wilk Normality test

0.0042

0.039

0.174
Histogram of untransformed Basin 1, soy

Histogram of transformed Basin 1, soy

Histogram of untransformed Basin 1, corn

Histogram of transformed Basin 1, corn

Normal Q-Q Plot
Theoretical Quantiles
Sample Quantiles

p-value for Shapiro-Wilk Normality test
0.0834

p-value for Shapiro-Wilk Normality test
0.3196
Histogram of untransformed Basin 2, s2precip

Histogram of transformed Basin 2, s2precip

Histogram of untransformed Basin 2, wwtpTPLoad

Histogram of transformed Basin 2, wwtpTPLoad

Normal Q-Q Plot

Theoretical Quantiles

Sample Quantiles

Basin 2, s2precip

p-value for Shapiro-Wilk Normality test

0.5995
Histogram of untransformed Basin 3, soy

Histogram of transformed Basin 3, soy

Histogram of untransformed Basin 3, corn

Histogram of transformed Basin 3, corn

Normal Q-Q Plot

Sample Quantiles

Basin 3, soy

p-value for Shapiro-Wilk Normality test

0.0066

Normal Q-Q Plot

Sample Quantiles

Basin 3, corn

p-value for Shapiro-Wilk Normality test

0.0353
Histogram of untransformed Basin 4, s2precip

Histogram of transformed Basin 4, s2precip

Histogram of untransformed Basin 4, wwtpTPLoad

Histogram of transformed Basin 4, wwtpTPLoad
Histogram of untransformed Basin 4, PfromFert

Histogram of transformed Basin 4, PfromFert

Histogram of untransformed Basin 4, PfromManure

Histogram of transformed Basin 4, PfromManure

Normal Q−Q Plot
Theoretical Quantiles
Sample Quantiles

p−value for Shapiro−Wilk Normality test
0.1624

p−value for Shapiro−Wilk Normality test
0.0025

p−value for Shapiro−Wilk Normality test
0.0032
Histogram of untransformed Basin 4, wheat

Histogram of transformed Basin 4, wheat

Histogram of untransformed Basin 4, soy

Histogram of transformed Basin 4, soy

Normal Q-Q Plot
Sample Quantiles
Basin 4, wheat
p-value for Shapiro-Wilk Normality test
4e−04

Normal Q-Q Plot
Sample Quantiles
Basin 4, soy
p-value for Shapiro-Wilk Normality test
0.0487

Normal Q-Q Plot
Sample Quantiles
Basin 4, soy
p-value for Shapiro-Wilk Normality test
0.1381
Histogram of untransformed Basin 4, corn

Histogram of transformed Basin 4, corn

Histogram of untransformed Basin 4, LoadKgPerYr

Histogram of transformed Basin 4, LoadKgPerYr

Normal Q-Q Plot
Theoretical Quantiles
Sample Quantiles
Basin 4, corn
p-value for Shapiro-Wilk Normality test
0.0394

Normal Q-Q Plot
Theoretical Quantiles
Sample Quantiles
Basin 4, LoadKgPerYr
p-value for Shapiro-Wilk Normality test
0.0077

Normal Q-Q Plot
Theoretical Quantiles
Sample Quantiles
Basin 4, LoadKgPerYr
p-value for Shapiro-Wilk Normality test
0.7777
Histogram of untransformed Basin 8, s2precip

Histogram of transformed Basin 8, s2precip

Histogram of untransformed Basin 8, wwtpTPLoad

Histogram of transformed Basin 8, wwtpTPLoad

Normal Q-Q Plot
Theoretical Quantiles
Sample Quantiles

p-value for Shapiro-Wilk Normality test
0.9896

p-value for Shapiro-Wilk Normality test
5e-04
Combination of Water-Quality Sites

Once the data were scaled, transformed, and standardized, the load estimates at six sites were examined for the possibility of combining the six sites into a single analysis.
```r
par(las = 1, tck = 0.02, mfrow = c(1, 1))
plot(row.names(b8dat.t), b8dat.t$LoadKgPerYr, col = "red", pch = 16,
     xlab = "", ylab = "Transformed and standardized flux", ylim = c(-3, 3),
     yaxs = "i", xlim = c(1970, 2012))
lines(row.names(b8dat.t), predict(loess(LoadKgPerYr ~ row.names(b8dat.t), b8dat.t)),
     col = "red", lwd = 2)
p points(row.names(b1dat.t), b1dat.t$LoadKgPerYr, col = "blue", pch = 16)
lines(row.names(b1dat.t), predict(loess(LoadKgPerYr ~ row.names(b1dat.t), b1dat.t)),
     col = "blue", lwd = 2)
points(row.names(b2dat.t), b2dat.t$LoadKgPerYr, col = "green", pch = 17)
lines(row.names(b2dat.t), predict(loess(LoadKgPerYr ~ row.names(b2dat.t), b2dat.t)),
     col = "green", lwd = 1.5)
points(row.names(b3dat.t), b3dat.t$LoadKgPerYr, col = "pink", pch = 15)
lines(row.names(b3dat.t), predict(loess(LoadKgPerYr ~ row.names(b3dat.t), b3dat.t)),
     col = "pink", lwd = 1.5)
points(row.names(b4dat.t), b4dat.t$LoadKgPerYr, col = "black", pch = 16)
lines(row.names(b4dat.t), predict(loess(LoadKgPerYr ~ row.names(b4dat.t), b4dat.t)),
     col = "black", lwd = 2)
points(row.names(b5dat.t), b5dat.t$LoadKgPerYr, col = "orange", pch = 18, cex = 1.25)
lines(row.names(b5dat.t),
     predict(loess(LoadKgPerYr ~ row.names(b5dat.t), b5dat.t)),
     col = "orange", lwd = 1.5)
leg.txt <- c("Red River basin downstream of Emerson, Manitoba",
             "Red River upstream of Fargo, ND",
             "Red River upstream of Halstad, MN (includes area upstream of Fargo)",
             "Sheyenne River upstream of Kindred, ND",
             "Red Lake River upstream of Crookston, MN",
             "Pembina River upstream of Neche, ND")
legend("topleft", leg.txt, col = c("red", "blue", "black", "pink", "green", "orange"),
       pch = c(rep(16, 3), 15, 17, 18), lty = 1, bty = "n",
       lwd = c(rep(2, 3), rep(1.5, 3)), pt.cex = c(rep(1, 5), 1.25),
       title = "Annual flux with loess curves")
```
par(las = 1, tck = 0.02, mar = c(3, 5, 2, 2) + 0.1, mgp = c(4, 1, 0))

plot(subset(wwtp, basin == 8)$year, subset(wwtp, basin == 8)$TPFlux_kg,
ylim = c(100, 500000), pch = 16, xlim = c(1975, 2015),
xaxs = "i", yaxs = "i", xlab = "", col = "red", log = "y", yaxt = "n",
ylab = "Annual total phosphorus flux from wastewater treatment plants, in kilograms per year")


axis(2, at = c(100, 200, 500, 1000, 2000, 5000, 10000, 20000, 50000, 100000, 200000, 500000),
labels = c("100", "200", "500", "1,000", "2,000", "5,000", "10,000", "20,000",
"50,000", "100,000", "200,000", "500,000"))

points(subset(wwtp, basin == 1)$year, subset(wwtp, basin == 1)$TPFlux_kg, col = "blue",
pch = 16)

points(subset(wwtp, basin == 2)$year, subset(wwtp, basin == 2)$TPFlux_kg, col = "green",
pch = 17)

points(subset(wwtp, basin == 3)$year, subset(wwtp, basin == 3)$TPFlux_kg, col = "pink",
pch = 15)

points(subset(wwtp, basin == 4)$year, subset(wwtp, basin == 4)$TPFlux_kg, col = "black",
pch = 16)

points(subset(wwtp, basin == 5)$year, subset(wwtp, basin == 5)$TPFlux_kg, col = "orange",
pch = 18)

leg.txt <- c("Red River basin downstream of Emerson, Manitoba",
"Red River upstream of Halstad, Minnesota",
"Red River upstream of Fargo, North Dakota",
"Red Lake River upstream of Crookston, Minnesota",
"Sheyenne River upstream of Kindred, North Dakota",
"Pembina River upstream of Neche, North Dakota")

legend("topleft", leg.txt, col = c("red", "black", "blue", "green", "pink", "orange"),
pch = c(rep(16, 3), 17, 15, 18), bty = "n")
Structural Equation Modeling

The data for the six sites was combined and analyzed in a structural equation model.

```r
b1b2b3b4b5b8 <- rbind.data.frame(b1dat.t, b2dat.t, b3dat.t, b4dat.t, b5dat.t, b8dat.t)
library(lavaan)
## This is lavaan 0.5-20
## lavaan is BETA software! Please report any bugs.
mod.TPflux <- ' # regressions
LoadKgPerYr ~ s1precip + s2precip + AgPract + wwpTPLoad
AgPract ~ s2precip
AgPract =~ PfromFert + PfromManure + wheat + soy
'
modFit <- sem(mod.TPflux, data = b1b2b3b4b5b8, missing = "fiml", estimator = "MLR",
               verbose = FALSE, std.lv = FALSE, std.ov = FALSE, fixed.x = TRUE,
               test = "Satorra.Bentler", warn = TRUE)
summary(modFit, stand = TRUE, rsq = TRUE, fit.measures = TRUE)
```

## lavaan (0.5-20) converged normally after 63 iterations
##
## Number of observations: 192
##
## Estimator: ML Robust
## Minimum Function Test Statistic: 30.466
## Degrees of freedom: 16
## P-value (Chi-square)  0.016  0.028
## Scaling correction factor  1.070
## for the Yuan-Bentler correction
## Model test baseline model:
## Minimum Function Test Statistic  733.192  541.503
## Degrees of freedom  25  25
## P-value  0.000  0.000
## User model versus baseline model:
## Comparative Fit Index (CFI)  0.980  0.976
## Tucker-Lewis Index (TLI)  0.968  0.962
## Loglikelihood and Information Criteria:
## Loglikelihood user model (H0)  -5185.664  -5185.664
## Scaling correction factor  1.390
## for the MLR correction
## Loglikelihood unrestricted model (H1)  -5170.431  -5170.431
## Scaling correction factor  1.243
## for the MLR correction
## Number of free parameters  19  19
## Akaike (AIC)  10409.328  10409.328
## Bayesian (BIC)  10471.221  10471.221
## Sample-size adjusted Bayesian (BIC)  10411.035  10411.035
## Root Mean Square Error of Approximation:
## RMSEA  0.069  0.064
## 90 Percent Confidence Interval  0.029  0.105  0.023  0.100
## P-value RMSEA <= 0.05  0.186  0.245
## Standardized Root Mean Square Residual:
## SRMR  0.056  0.056
## Parameter Estimates:
## Information Observed
## Standard Errors Robust.huber.white
## Latent Variables:
## Estimate Std.Err Z-value P(|z|) Std.lv Std.all
## AgPract =~
## PfromFert  1.000
## PfromManure  -3.679  1.147  -3.208  0.001  -0.878  -0.933
## wheat  -3.136  0.960  -3.265  0.001  -0.749  -0.766
## soy  3.678  1.110  3.313  0.001   0.878   0.977
## Regressions:
## Estimate Std.Err Z-value P(|z|) Std.lv Std.all
## LoadKgPerYr ~

|            | Estimate | Std.Err | Z-value |  P(>|z|) | Std.lv | Std.all |
|------------|----------|---------|---------|---------|-------|---------|
| s1precip   | 0.024    | 0.002   | 13.495  | 0.000   | 0.024 | 0.661   |
| s2precip   | 0.005    | 0.001   | 5.432   | 0.000   | 0.005 | 0.268   |
| AgPract    | 0.886    | 0.330   | 2.687   | 0.007   | 0.212 | 0.215   |
| wwtTPLoad  | 0.000    | 0.000   | 1.021   | 0.307   | 0.000 | 0.047   |

## s2precip ~

|            | Estimate | Std.Err | Z-value |  P(>|z|) | Std.lv | Std.all |
|------------|----------|---------|---------|---------|-------|---------|
|            | 0.001    | 0.001   | 2.749   | 0.006   | 0.006 | 0.323   |

## Intercepts:

|            | Estimate | Std.Err | Z-value |  P(>|z|) | Std.lv | Std.all |
|------------|----------|---------|---------|---------|-------|---------|
| PfromFert | -0.165   | 0.121   | -1.363  | 0.173   | -0.165| -0.196  |
| PfromManure| 0.989   | 0.234   | 4.230   | 0.000   | 0.989 | 1.051   |
| wheat      | 0.908    | 0.206   | 4.414   | 0.000   | 0.908 | 0.929   |
| soy        | -0.963   | 0.234   | -4.109  | 0.000   | -0.963| -1.072  |
| LoadKgPerYr| -2.915  | 0.229   | -12.746 | 0.000   | -2.915| -2.969  |
| AgPract    | 0.000    |         |         |         |       |         |

## Variances:

|            | Estimate | Std.Err | Z-value |  P(>|z|) | Std.lv | Std.all |
|------------|----------|---------|---------|---------|-------|---------|
| PfromFert | 0.649    | 0.079   | 8.188   | 0.000   | 0.649 | 0.919   |
| PfromManure| 0.115   | 0.033   | 3.471   | 0.001   | 0.115 | 0.130   |
| wheat      | 0.395    | 0.076   | 5.196   | 0.000   | 0.395 | 0.414   |
| soy        | 0.037    | 0.020   | 1.857   | 0.063   | 0.037 | 0.046   |
| LoadKgPerYr| 0.411   | 0.040   | 10.221  | 0.000   | 0.411 | 0.427   |
| AgPract    | 0.051    | 0.031   | 1.621   | 0.105   | 0.896 | 0.896   |

## R-Square:

<table>
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<th>Estimate</th>
</tr>
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<tbody>
<tr>
<td>PfromFert</td>
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</tr>
<tr>
<td>PfromManure</td>
<td>0.870</td>
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<tr>
<td>wheat</td>
<td>0.586</td>
</tr>
<tr>
<td>soy</td>
<td>0.954</td>
</tr>
<tr>
<td>LoadKgPerYr</td>
<td>0.573</td>
</tr>
<tr>
<td>AgPract</td>
<td>0.104</td>
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</table>

modindices(modFit, power = TRUE)

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<th>op</th>
<th>rhs</th>
<th>mi</th>
<th>mi.scaled</th>
<th>epc</th>
<th>sepc.all</th>
<th>delta</th>
<th>ncp</th>
<th>power</th>
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</thead>
<tbody>
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<td>=~</td>
<td>PfromFert</td>
<td>0.000</td>
<td>-0.399</td>
<td>-0.096</td>
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<td>0.050</td>
<td>0.050</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>s1precip</td>
<td>=~</td>
<td>s1precip</td>
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<td>0.000</td>
<td>0.000</td>
<td>0.1</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>s1precip</td>
<td>=~</td>
<td>s2precip</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.1</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>s2precip</td>
<td>=~</td>
<td>s2precip</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.1</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
</tr>
<tr>
<td>27</td>
<td>s1precip</td>
<td>=~</td>
<td>-1</td>
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<td>0.000</td>
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<td>0.1</td>
<td>0.050</td>
<td>0.050</td>
<td></td>
</tr>
<tr>
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<td>=~</td>
<td>-1</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.1</td>
<td>1.000</td>
<td>1.000</td>
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</tr>
<tr>
<td>32</td>
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<td>PfromManure</td>
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<td>0.472</td>
<td>0.016</td>
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<tr>
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<td>0.389</td>
<td>0.014</td>
<td>0.1</td>
<td>0.996</td>
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</tr>
<tr>
<td>35</td>
<td>PfromFert</td>
<td>=~</td>
<td>LoadKgPerYr</td>
<td>0.004</td>
<td>0.003</td>
<td>0.002</td>
<td>0.1</td>
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</tr>
<tr>
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<td>PfromManure</td>
<td>=~</td>
<td>wheat</td>
<td>0.240</td>
<td>0.224</td>
<td>0.020</td>
<td>0.1</td>
<td>0.707</td>
<td>0.707</td>
<td></td>
</tr>
<tr>
<td>37</td>
<td>PfromManure</td>
<td>=~</td>
<td>soy</td>
<td>0.671</td>
<td>0.627</td>
<td>0.068</td>
<td>0.1</td>
<td>0.224</td>
<td>0.224</td>
<td></td>
</tr>
<tr>
<td>38</td>
<td>PfromManure</td>
<td>=~</td>
<td>LoadKgPerYr</td>
<td>0.537</td>
<td>0.502</td>
<td>-0.013</td>
<td>0.1</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
</tr>
<tr>
<td>39</td>
<td>wheat</td>
<td>=~</td>
<td>soy</td>
<td>0.047</td>
<td>0.044</td>
<td>0.009</td>
<td>0.1</td>
<td>0.675</td>
<td>0.675</td>
<td></td>
</tr>
<tr>
<td>40</td>
<td>wheat</td>
<td>=~</td>
<td>LoadKgPerYr</td>
<td>2.701</td>
<td>2.525</td>
<td>0.049</td>
<td>0.1</td>
<td>0.919</td>
<td>0.919</td>
<td></td>
</tr>
<tr>
<td>41</td>
<td>soy</td>
<td>=~</td>
<td>LoadKgPerYr</td>
<td>3.311</td>
<td>3.095</td>
<td>0.029</td>
<td>0.1</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
</tr>
<tr>
<td>42</td>
<td>AgPract</td>
<td>=~</td>
<td>LoadKgPerYr</td>
<td>12.489</td>
<td>11.674</td>
<td>0.064</td>
<td>0.1</td>
<td>1.000</td>
<td>1.000</td>
<td></td>
</tr>
</tbody>
</table>
library(semPlot)
par(mfrow = c(1, 1))

semPaths(modFit, what = "stand", edge.label.cex = 0.6, sizeMan = 8, sizeLat = 8,
nCharNodes = 0, nCharEdges = 0, exoVar = FALSE, exoCov = FALSE,
nDigits = 3, fixed.x = TRUE, intercepts = FALSE, label.scale = FALSE,
label.cex = 0.75)
parmEstTable <- standardizedSolution(modFit)
parmEstTable

```
##  lhs   op   rhs  est.std  se  z  pvalue
## 1 LoadKgPerYr ~ s1precip  0.661  0.032 20.524  0.000
## 2 LoadKgPerYr ~ s2precip  0.268  0.049  5.475  0.000
## 3 LoadKgPerYr ~  AgPract  0.215  0.049  4.356  0.000
## 4 LoadKgPerYr ~  wwtpTPLoad 0.047  0.046  1.015  0.310
## 5  AgPract ~ s2precip  0.323  0.059  5.433  0.000
## 6  AgPract ~  PfromFert  0.284  0.089  3.181  0.001
## 7  AgPract ~  PfromManure -0.933  0.019 -48.101  0.000
## 8  AgPract ~ wheat  -0.766  0.038 -19.970  0.000
## 9   AgPract ~   soy  0.977  0.013  77.874  0.000
##10  PfromFert ~~ PfromFert 0.919  0.051 18.132  0.000
##11 PfromManure ~~ PfromManure 0.130  0.036  3.584  0.000
##12   wheat ~~ wheat  0.414  0.059  7.045  0.000
##13    soy ~~   soy  0.046  0.025  1.863  0.062
##14 LoadKgPerYr ~~ LoadKgPerYr 0.427  0.038 11.158  0.000
##15   AgPract ~~ AgPract  0.896  0.038 23.384  0.000
##16   s1precip ~~ s1precip  1.000  0.000  NA  NA
##17   s1precip ~~ s2precip -0.053  0.000  NA  NA
##18   s1precip ~~  wwtpTPLoad 0.021  0.000  NA  NA
##19   s2precip ~~ s2precip  1.000  0.000  NA  NA
```
Bootstrapping

Because of inherent non-normalities in water-quality data and associated ancillary data, bootstrapping was performed to check the consistency of model results. See associated paper for more details. Note, because of the nature of bootstrapping, the estimates may vary slightly when this code is rerun; however, with 2,000 bootstrap replicates, the estimates are fairly stable.

Hardware, Software, Additional Packages, and Versions Used to Generate Results

```r
cat("\n", format(Sys.time(), "%a %d %b %Y %X"))
```

```r
print(sessionInfo(), locale = TRUE)
```

```r
# R version 3.3.2 (2016-10-31)
# Platform: x86_64-apple-darwin13.4.0 (64-bit)
# Running under: macOS Sierra 10.12.3
```

```r
# locale:
```
References
