R Minicourse Workshop White River Case Study

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Part 1 - Sept. 2, 2014

Preliminaries

- The R scripts for this lecture are called whiteriver01.r and whiteriver02.r.
- The first script does one reach, distance, and parameter, interactively.
- The second does all combinations of reach, distance, and several parameters and saves the results into files. whiterivertext.txt and whiteriverplot.pdf
- Greg Pelletier provided a spreadsheet
 Q2KW_White_River_observed_and_predicted_data.xlsx
- I saved the two pages of the spreadsheet into two csv files:
 - Q2KW_White_River_observed_data.csv
 - Q2KW_White_River_predicted_data.csv

Loading the Data

Large size of the dataset makes it hard to view interactively.

```
dim(observed)
[1] 47265
dim(predicted)
[1] 48450
names(observed)
[1] "Reach.number"
[2] "Distance..Km."
[3] "Date.time"
[4] "Temperature..degC."
[5] "Conductivity..uS.cm.25C." ...
names(predicted)
[1] "Reach"
[2] "Distance..Km."
[3] "Date.time"
[4] "Temperature..degC."
[5] "Conductivity..uS.cm.25C." ...
```

Observed vs. predicted reaches

- We want to use reach and distance as a site.
- Examining reaches in both observed and predicted shows that the observed reaches are a subset of the predicted reaches.
- So we can use the same reach, e.g. 23, for both files.

```
observed.reaches <- unique(sort(observed$Reach.number))
observed.reaches
[1]  3  8  13  20  21  22  23  25  27  28  31  33
predicted.reaches <- unique(sort(predicted$Reach))
predicted.reaches
[1]  0  1  2  3  4  5  6  7  8  9  10  11  12  13  14  15  16  17  18  19  20  21  22  23  24  25  26  27  2
my.reach <- 23</pre>
```

Observed vs. predicted distances

- Distances are not the same in the two files.
- We will have to find a closest distance in the predicted file to match any distance in the observed file.

```
observed.distances
[1] 0.03574664 2.15476664 5.81305664 7.90000000 9.37570664 12.01200000 13.31981664 1
[9] 24.72141000 31.85200000 39.69900000
predicted.distances
[1] 0.04 1.12 2.15 3.35 4.51 5.81 7.09 8.28 9.38 10.72 11.83 13.32 15.25 16.20 1
[18] 20.75 22.08 23.44 24.72 26.12 27.46 28.73 30.23 31.85 33.58 34.85 36.57 38.21 39.70 my.observed.distance <- observed.distances[6]
min.difference.index <- which.min(abs(predicted.distances - my.observed.distance))
my.predicted.distance <- predicted.distances[min.difference.index]
```

Parameter names and columns

```
observed.parameter.name <- "pH"
observed.parameter.column <- which(names(observed) == observed.parameter.name)
predicted.parameter.name <- "pH"
predicted.parameter.column <- which(names(predicted) == predicted.parameter.name)</pre>
```

- Now we can use any of the following:
 - observed[[observed.parameter.column]]
 - observed[,observed.parameter.column]
 - observed\$pH
 - observed[[observed.parameter.name]]
- And similarly for predicted

Creating an ID for selected parameter, reach, distance

- We have now selected a parameter, a reach, and a distance.
- It will be helpful to print these out here and there, so we make a string with all this information in it.

Selecting the rows

- We want only the data from the selected reach and distance, which also has a valid date and a valid datum.
- So we select just those rows.
- If the number of rows is too small, we can try a different reach and distance.
- Note that reach has different names in the two datasets.

```
observed.rows <- (observed$Reach.number == my.reach) &
  (observed$Distance == my.observed.distance) &
  (!is.na(observed$Date.time)) &
  (!is.na(observed[,observed.parameter.column]))

predicted.rows <- (predicted$Reach == my.reach) &
    (predicted$Distance == my.predicted.distance) &
    (!is.na(predicted$Date.time))&
    (!is.na(predicted[,predicted.parameter.column]))</pre>
```

Subsetting the rows and columns of the data

- We can now select just the rows and columns we want.
- This will be the data we analyze, it has been "cleaned" so that we don't have to worry about missing numbers, etc.

```
date.name <- "Date.time"
observed.date.column <- which(names(observed) == date.name)
predicted.date.column <- which(names(predicted) == date.name)
observed.columns <- c(observed.date.column, observed.parameter.column)
predicted.columns <- c(predicted.date.column, predicted.parameter.column)
observed.subset <- observed[observed.rows, observed.columns]
predicted.subset <- predicted[predicted.rows, predicted.columns]</pre>
```

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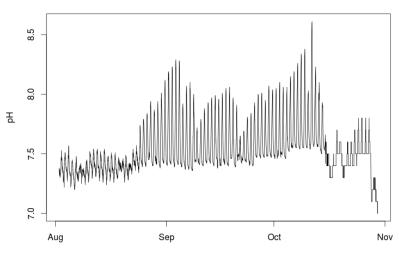
Plotting observed and predicted data

 We want plots of observed and predicted to have the same x and y range, so we find the biggest range needed for each.

Now we can plot the data.

Observed plot

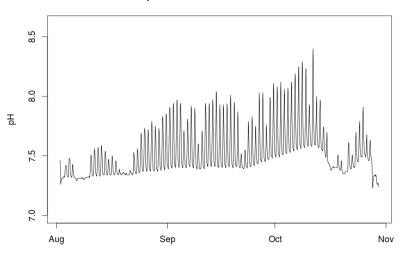
Observed pH reach: 23 distance: 12.012 N= 8539



Predicted plot

Predicted plot

Predicted pH reach: 23 distance: 12.012 N= 1425

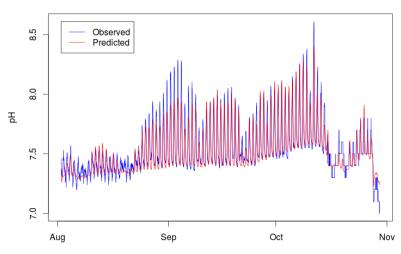


Predicted and observed plot

```
plot(observed.subset,
    type="1",
    xlim=x.range,
    ylim=y.range,
    col="blue",
    main=paste(my.id))
lines(predicted.subset,
    type="1",
    col="red")
legend(x=min(x.range), y=ypos, yjust=yjus,
    lty=1,
    col=c("blue","red"),
    legend=c("Observed","Predicted"))
```

Predicted and observed plot

pH reach: 23 distance: 12.012



Subsample the data

- There are tens of thousands of rows for some of these plots.
- We make analysis more tractable by subsampling.

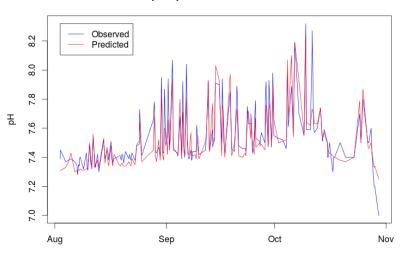
```
n <- min(200, nrow(observed.subset))
sample.rows <- sort(sample(1:nrow(observed.subset), n))
observed.sample <- observed.subset[sample.rows,]
predictions <- rep(0,n)
for (row in 1:n) {
   obs.time <- observed.sample$Date.time[row]
   pred.row <- which.min(abs(predicted.subset$Date.time-obs.time))
   predictions[row] <- predicted.subset[[predicted.parameter.name]][pred.row]
}</pre>
```

Plot the observed and predicted subsample

```
plot(observed.sample,
    type="1",
    xlim=x.range,
    ylim=y.range,
    col="blue",
    main=paste("Subsampled",my.id))
lines(observed.sample$Date.time,predictions,
        type="1",
        col="red")
legend(x=min(x.range), y=ypos, yjust=yjus,
        lty=1,
        col=c("blue","red"),
        legend=c("Observed","Predicted")
    )
}
```

Plot the observed and predicted subsample

Subsampled pH reach: 23 distance: 12.012



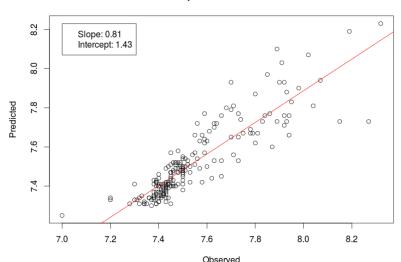
Fit a linear model

```
my.model <- lm(predictions ~ observed.sample[[observed.parameter.name]])</pre>
summarv(mv.model)
Call:
lm(formula = predictions ~ observed.sample[[observed.parameter.name]])
Residuals:
    Min
              10 Median
                                30
                                        Max
-0.25823 -0.03804 -0.00541 0.04324 0.24426
Coefficients:
                                          Estimate Std. Error t value Pr(>|t|)
(Intercept)
                                           1.26902
                                                      0.19073 6.653 2.74e-10 ***
observed.sample[[observed.parameter.name]] 0.82893 0.02526 32.815 < 2e-16 ***
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
Residual standard error: 0.07581 on 198 degrees of freedom
Multiple R-squared: 0.8447, Adjusted R-squared: 0.8439
F-statistic: 1077 on 1 and 198 DF, p-value: < 2.2e-16
```

Plot the observed vs. predicted and the linear fit

Plot the observed vs. predicted and the linear fit

Linear model for pH reach: 23 distance: 12.012



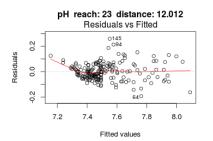
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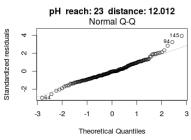
ANOVA on the model

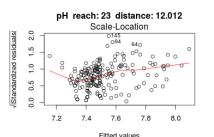
Plot the residuals for the linear model

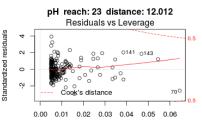
```
par(mfrow=c(2,2))
plot(my.model, main=my.id)
par(mfrow=c(1,1))
```

Plot the residuals for the linear model









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