# Washington State Drinking Water Fluoridation

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## Introduction

This exploratory data analysis tutorial explores the use of publicly available data to investigate drinking water system fluoride levels in Washington State. Methods for reproducible data cleanup and exploratory analysis using R, RMarkdown, and `knitr`, will be demonstrated, as well as some of the plotting capabilities of R, especially `ggplot2`.

We will compare the various water systems in Washington State relative to the state and federal recommendations for optimum levels of fluoride concentation in drinking water.

According to the US CDC, lower levels of fluoride help prevent tooth decay, but higher levels increase the risk of dental fluorosis.

In April 2015, the US HHS ("Health Department") released a lowering of the recommended fluoride concentration in driking water from the previous range of 0.7 to 1.2 mg/L to the new level of 0.7 mg/L, which falls below Washington State's DOH "optimal" range of 0.8 to 1.3 mg/L.

If Washington State follows this new recommendation, what changes would need to be made to the state's drinking water systems?

## Data Sources

Data files have been prepared using a companion Markdown script to generate text data files. These data and Markdown files are hosted in the wa-water-quality repository on GitHub. (https://github.com/brianhigh/wa-water-quality)

The water system data come from WA DOH Water System Data (2015) and WA DOH Fluoride in Drinking Water (2013). The lat/long coordinates were generated using the ggmap package for R. The federally recommended fluoride levels come from the US HHS ("Health Department") and US EPA.

## Setup

Load the required R packages.

```
for (pkg in c("knitr", "dplyr", "lattice", "ggplot2", "gridExtra", "maps")) {
    if (! suppressWarnings(require(pkg, character.only=TRUE)) ) {
        install.packages(pkg, repos="http://cran.fhcrc.org", dependencies=TRUE)
        if (! suppressWarnings(require(pkg, character.only=TRUE)) ) {
            stop(paste0(c("Can't load package: ", pkg, "!"), collapse = ""))
        }
    }
}
```

Configure `knitr` options.

```
opts_chunk$set(tidy=FALSE, cache=FALSE)
```

Create the data folder, if necessary.

```
datadir <- "data"
dir.create(file.path(datadir), showWarnings=FALSE, recursive=TRUE)
```

Read in the location coordinates from a text file if you have saved one previously.

```
tsv_import <- function(filename) {
    infile <- paste(c(datadir, '/', filename), sep='', collapse='')
    if (file.exists(infile)) {
        read.delim(infile, stringsAsFactors=FALSE, header=TRUE)
    }
    else {
        stop(paste("Can't find", filename, "in folder", datadir, "!", sep=" "))
    }
}

locations <- tsv_import('wa_doh_dw_locations.tsv')
systems <- tsv_import('wa_doh_dw_systems.tsv')
sources <- tsv_import('wa_doh_dw_sources.tsv')
```

```
## Warning in scan(file, what, nmax, sep, dec, quote, skip, nlines,
## na.strings, : EOF within quoted string
```

```
fluoride <- tsv_import('wa_doh_dw_fluoride.tsv')
```

## Join Tables

Join the location and water system data into a new table for use in plotting.

```
systems <- inner_join(locations, systems, by=c("PWSCity", "WSState", "WSZipCode"))
fl <- select(systems, PWSID, PWSCity, WSState, WSZipCode,
                          OwnerTypeDesc, lon, lat)
fl$OwnerTypeDesc <- as.factor(fl$OwnerTypeDesc)

fl <- inner_join(fl, fluoride, by=c("PWSID"))
fl$Treatment <- as.factor(fl$Treatment)

# Add some grouping factors
fl$F.Level <- cut(fl$mgL, c(0, .8, 1.3, Inf),
                  labels=c("Below", "Optimal", "Above"))
fl$Population <- cut(fl$ResPop,
    c(0, 100, 1000, 10000, Inf), labels=c("0-100", "100-1K", "1K-10K", ">10K"))

nat.fl <- filter(fl, Treatment == "NATURAL")
nat.fl <- select(nat.fl, County, PWSID, SystemName, mgL, ResPop, OwnerTypeDesc,
                 lon, lat, Treatment, F.Level, Population)

nat.fl <- nat.fl[complete.cases(nat.fl),]
```

## Exploratory Data Analysis

We'll look at Washington State Drinking Water Systems with natural (non-fluoridated) fluoride levels (concentration in mg/L) using plots and summary tables.

### Scatter Plots

Let's get a first look at the data with some scatter plots. This `pairs` plot of fluoride levels (mg/L), residential population (ResPop), and system owner type descriptions (OwnerTypeDesc) shows some potentially interesting relationships.

```
pairs(nat.fl[4:6], panel = panel.smooth)
```

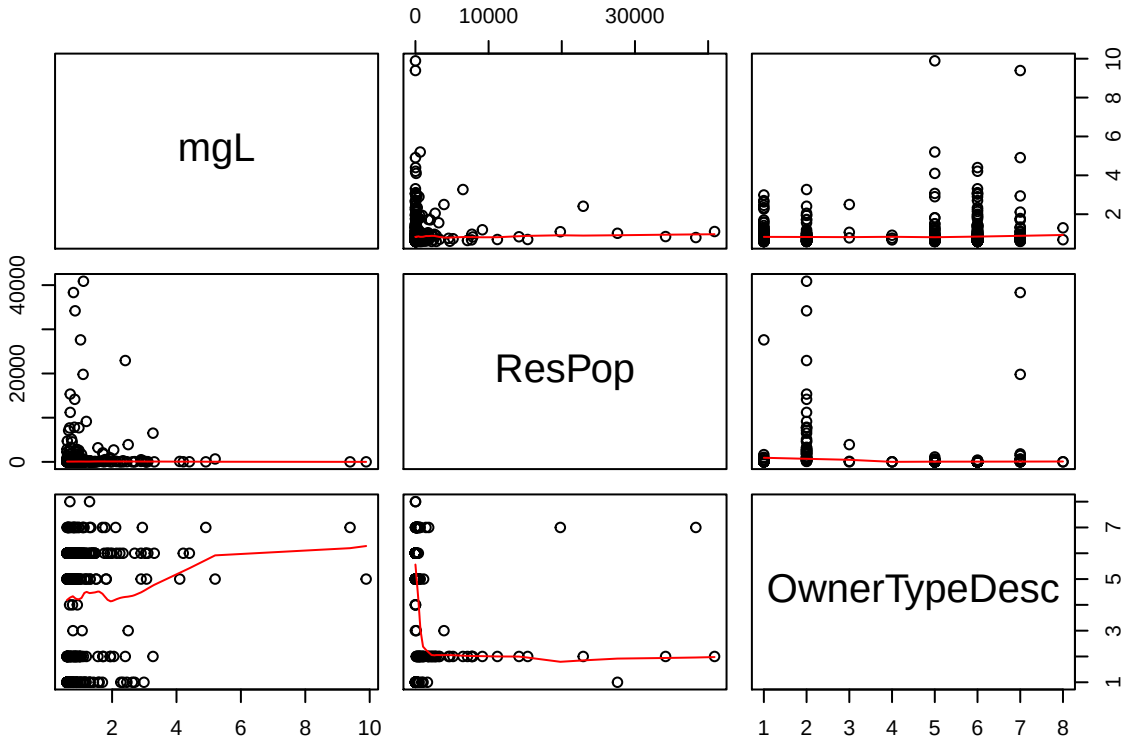



Figure 1: Washington State Untreated Drinking Water Systems Pairs Plot

To spead out the lower values, use a log scale.

```
pairs(nat.fl[4:6], panel = panel.smooth, log="xy")
```

It appears that the untreated water systems serving larger residential populations might have lower natural fluoride levels. Let's look at that a little closer. We'll use `qplot`, which is the simpler interface to the `ggplot2` package.

```
qplot(ResPop, mgL, data=nat.fl, geom=c("point", "smooth"), method="lm",
      facets=~OwnerTypeDesc, log = "xy")
```

The special district owner type seems to be the only one showing at least a marginal trend between natural fluoride levels and residential population.

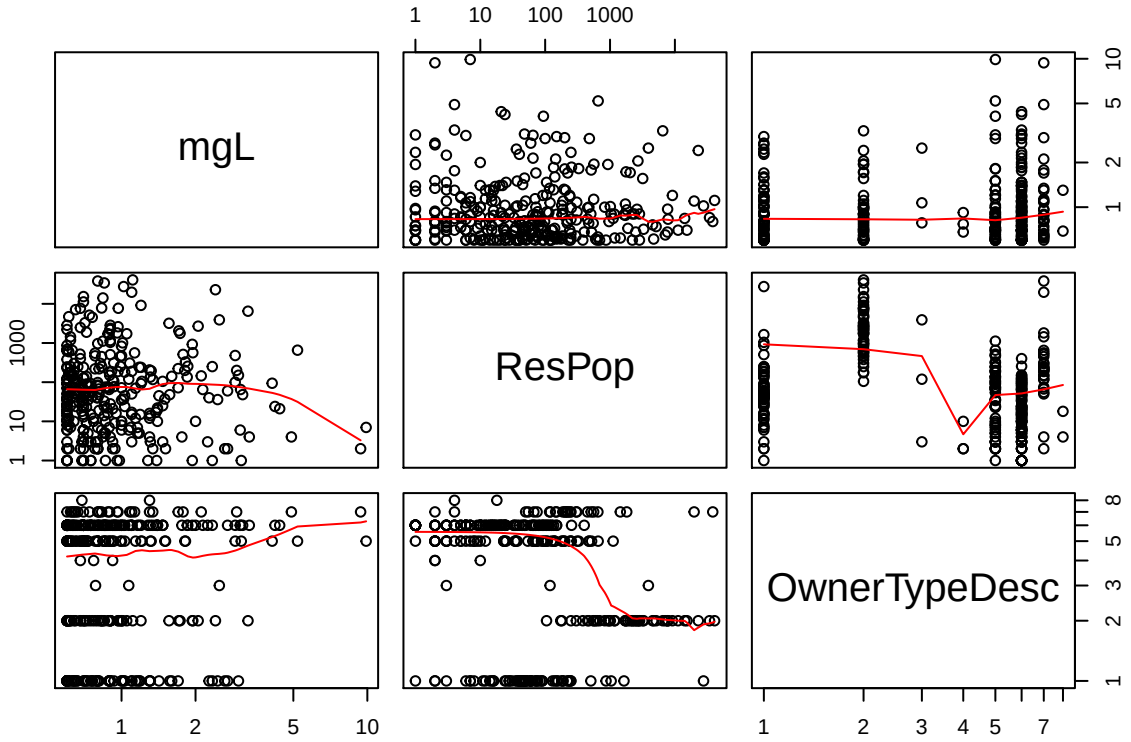



Figure 2: Washington State Drinking Water Systems Fluoride Pairs Plot with Log Scale

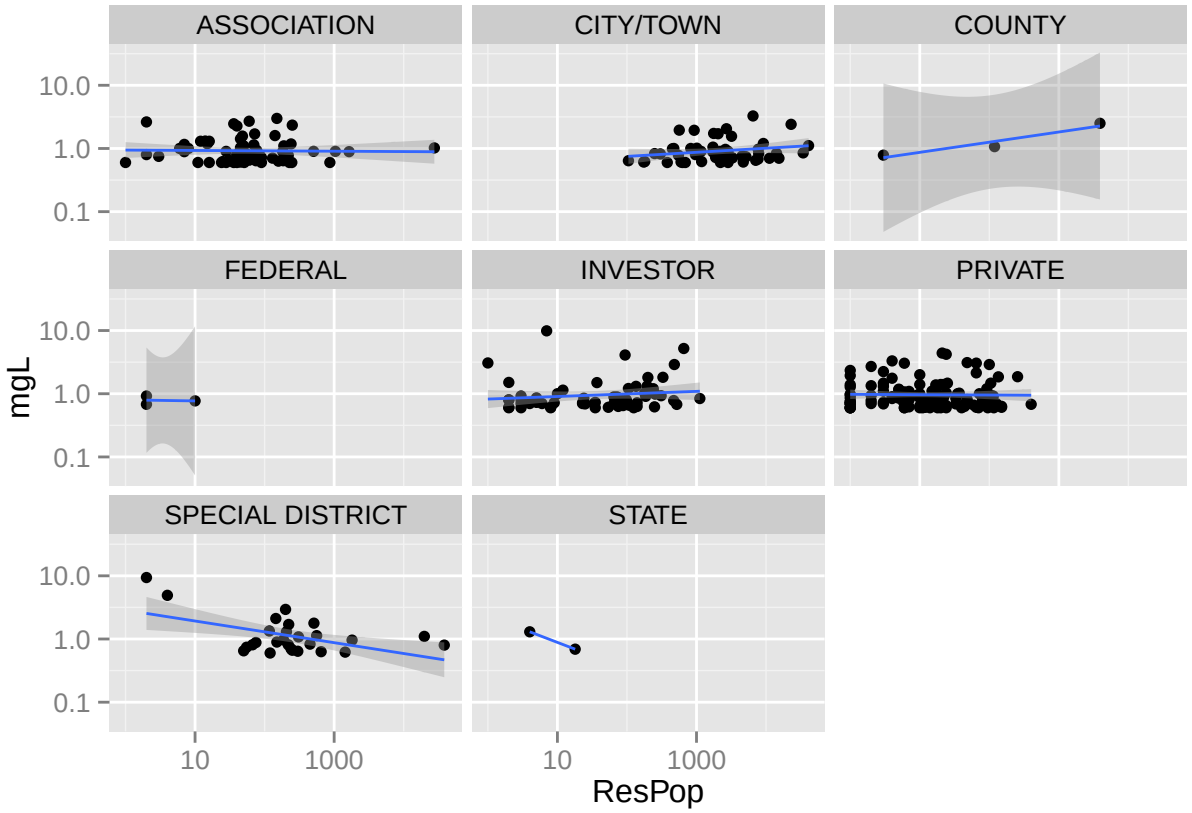



Figure 3: Washington State Drinking Water Systems Fluoride Scatter Plot

```
# Take the log10() of the variables of interest end produce a log-log summary
nat.fl$LmgL <- log10(nat.fl$mgL)
nat.fl$LResPop <- log10(nat.fl$ResPop)
summary(lm(LmgL~LResPop+OwnerTypeDesc, data=nat.fl))
```

```
##
## Call:
## lm(formula = LmgL ~ LResPop + OwnerTypeDesc, data = nat.fl)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.27222 -0.14688 -0.06224  0.07696  1.01417
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   -0.0302415  0.0399915  -0.756   0.4501
## LResPop                       -0.0031847  0.0169949  -0.187   0.8515
## OwnerTypeDescCITY/TOWN        -0.0001291  0.0492157  -0.003   0.9979
## OwnerTypeDescCOUNTY            0.1439772  0.1285041   1.120   0.2634
## OwnerTypeDescFEDERAL          -0.0737953  0.1299786  -0.568   0.5706
## OwnerTypeDescINVESTOR          0.0139625  0.0395117   0.353   0.7240
## OwnerTypeDescPRIVATE           0.0184271  0.0357609   0.515   0.6067
## OwnerTypeDescSPECIAL DISTRICT  0.0872353  0.0510692   1.708   0.0886 .
## OwnerTypeDescSTATE             0.0095953  0.1566532   0.061   0.9512
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2173 on 309 degrees of freedom
## Multiple R-squared:  0.01629,    Adjusted R-squared:  -0.009174
## F-statistic: 0.6398 on 8 and 309 DF,  p-value: 0.7441
```

Let's zoom in on "special district" water systems with `qplot`.

```
# Filter by "special district" water system owner type
nat.fl.special <- filter(nat.fl, OwnerTypeDesc=="SPECIAL DISTRICT")

# Plot points with a linear regression line
qplot(LResPop, LmgL, data=nat.fl.special, geom=c("point", "smooth"), method="lm")
```

Perhaps the smaller systems are less inclined (or less able) to adjust fluoride levels. We see there are two in particular with very high fluoride and very low population.

Incidentally, we can make this same plot with `ggplot`, the more advanced interface to the `ggplot2` package.

```
ggplot(nat.fl.special, aes(LResPop, LmgL)) + geom_point() + geom_smooth(method="lm")
```

Let's take a look at those top-2 highest-fluoride "special district" water systems.

```
nat.fl.special %>% select(SystemName, mgL, ResPop) %>% arrange(desc(mgL)) %>% head(2)
```

```
##                        SystemName  mgL ResPop
## 1      PATERSON ELEMENTARY SCHOOL 9.39      2
## 2 DODD ROAD INDUSTRIAL PARK WATER 4.91      4
```

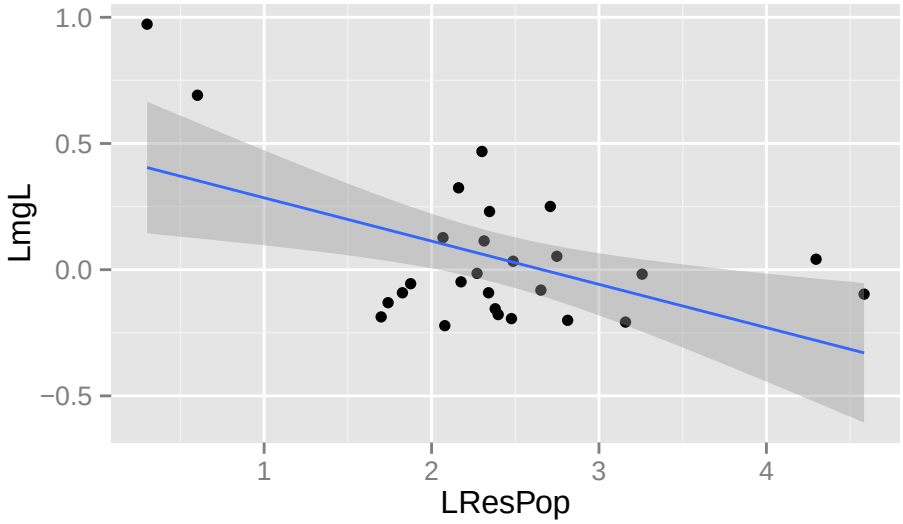



Figure 4: Washington State Drinking Water Systems Fluoride Scatter Plot of Special Districts with qplot

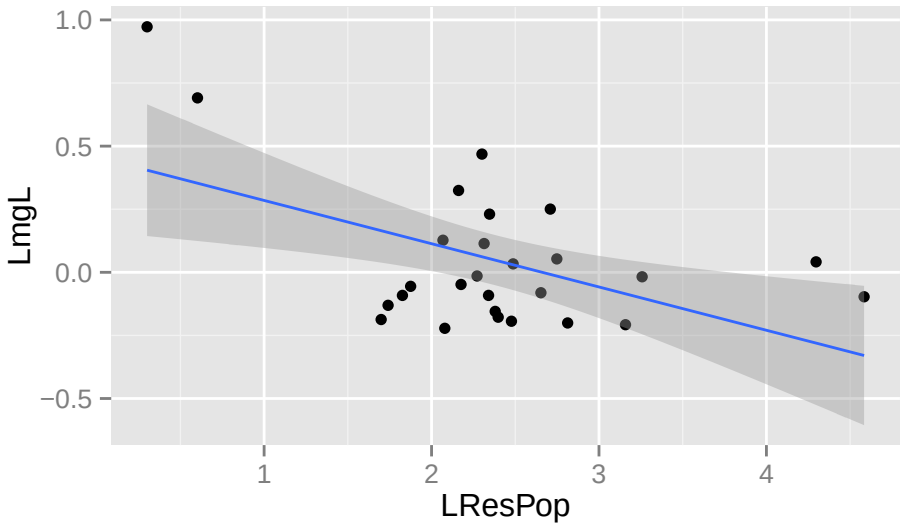



Figure 5: Washington State Drinking Water Systems Fluoride Scatter Plot of Special Districts with ggplot

So, the two "special district" water systems with the highest fluoride concentrations serve just a few residential users. What other systems have high natural fluoride? How high is "too high"?

## Untreated Fluoride Levels over EPA MCL

The US EPA's MCLG (maximum contaminant level goal) of 4 mg/L. This is also the level of the EPA's enforceable MCL (maximum contaminant level).

Which systems are over the EPA MCL of 4 mg/L?

```
nat.fl.over <- filter(nat.fl, mgL > 4)
nat.fl.over[order(nat.fl.over$mgL),
            c("SystemName", "OwnerTypeDesc", "ResPop", "mgL")]
```

```
##                           SystemName    OwnerTypeDesc ResPop  mgL
## 6                  WESTBOURNE ACRES         INVESTOR     94 4.10
## 1                      FROSTY PINES          PRIVATE     24 4.21
## 7          DALLES WATER ASSOCIATION          PRIVATE     21 4.40
## 4   DODD ROAD INDUSTRIAL PARK WATER SPECIAL DISTRICT      4 4.91
## 5 HARRISON-RAY-BURBANK WATER SYSTEM         INVESTOR    656 5.20
## 2        PATERSON ELEMENTARY SCHOOL SPECIAL DISTRICT      2 9.39
## 3       LONG LAKE OPERATORS VILLAGE         INVESTOR      7 9.89
```

One of the highest levels (9.39 mg/L) is at Paterson Elementary School. That's over twice the EPA's regulatory limit of 4 mg/L. Looking at the ResPop column, the table lists the population as 2, yet the school's population of students is over 100 according to Washington OSPI. What are the school's water sources?

```
sources[sources$SystemName=="PATERSON ELEMENTARY SCHOOL",
        c("SystemName", "Src_Name", "TrObjective", "TrProcss")]
```

```
##                       SystemName Src_Name TrObjective TrProcss
## 4935 PATERSON ELEMENTARY SCHOOL  WELL #1
## 4936 PATERSON ELEMENTARY SCHOOL  WELL #2
```

It looks like there is no treatment information available about those two wells.

Let's plot the water systems with fluoride levels over the EPA MCL as a simple bar plot with `ggplot`, using the `theme_light` theme, coloring by system owner type, and flipping the coordinates to accommodate the long water system names.

```
ggplot(nat.fl.over, aes(x=SystemName, y=mgL, fill=OwnerTypeDesc)) + coord_flip() +
    geom_bar(stat="identity", colour="black", binwidth=1) +
    ggtitle(paste("Washington State Drinking Water Systems",
                  "Exceeding EPA MCL of 4 mg/L", sep="\n")) +
    theme(axis.text.y = element_text(hjust = 1, size=10)) + theme_light() +
    labs(y="Fluoride Level (mg/L)", x=NULL)+ scale_fill_brewer(palette="Set2")
```

### Box Plots

Here is a basic boxplot of the fluoride level (concentration in mg/L) by water system owner type description (OwnerTypeDesc).

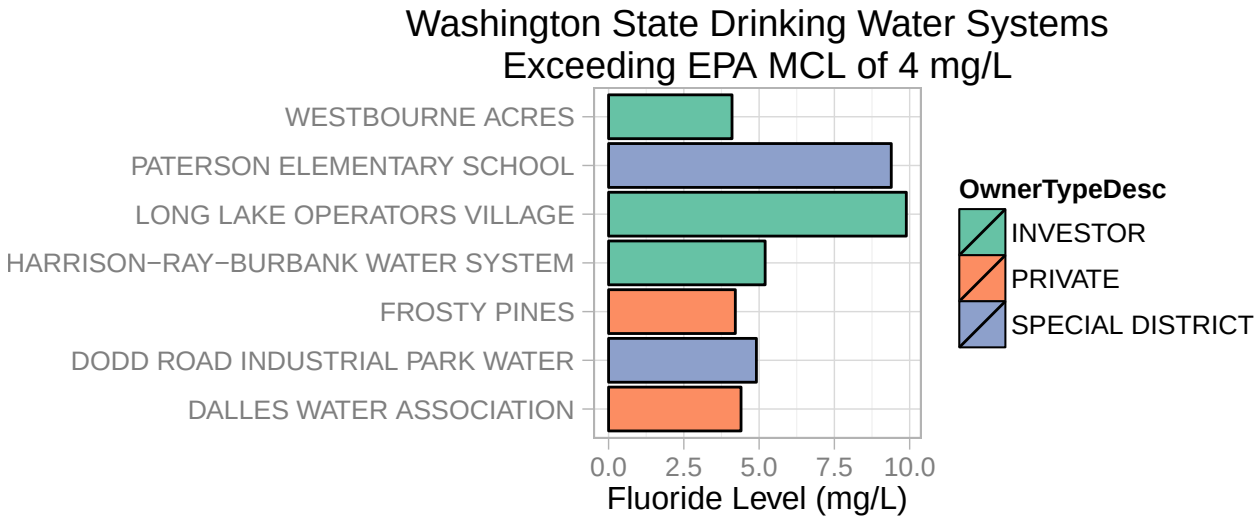



Figure 6: Washington State Drinking Water Systems Exceeding EPA Fluoride MCL of 4 mg/L

```
# Make a basic boxplot of mgL by Water System Owner Type
par(cex.axis=.55)
boxplot(mgL~OwnerTypeDesc, data=nat.fl)
```

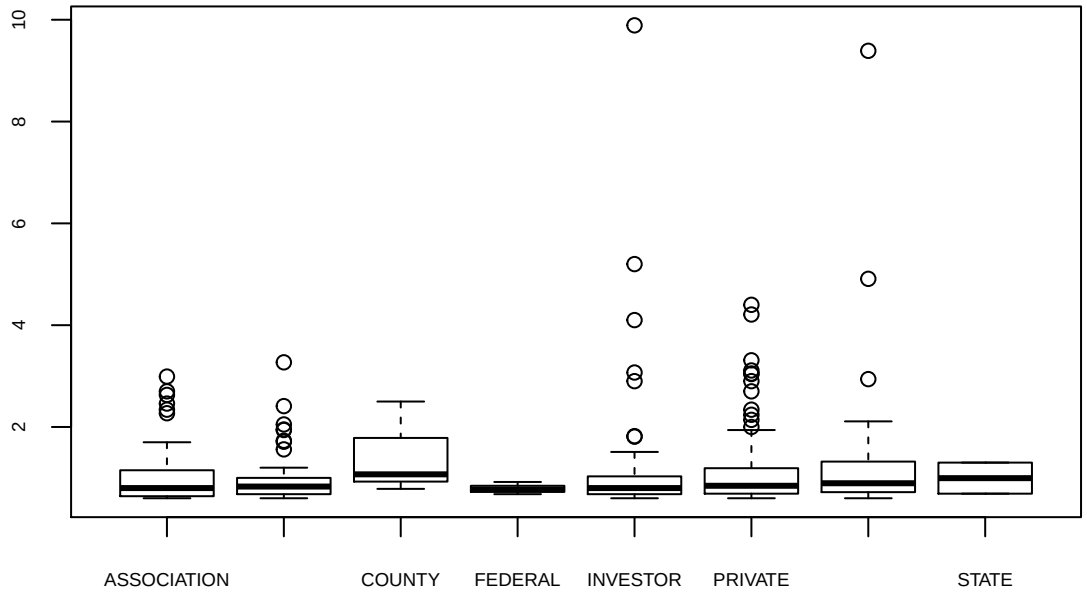



Figure 7: Washington State Drinking Water Systems by Owner Type

As there is a lot of spread at the higher fluoride levels, we'll try again using a log scale for the y-axis.

```
# Make a basic boxplot of mgL by Water System Owner Type
par(cex.axis=.55)
boxplot(LmgL~OwnerTypeDesc, data=nat.fl)
```

As an alternative to the standard "base" plotting in R, we can use the `lattice` plotting system. Here is a boxplot faceted by residental population groups served by the water systems.

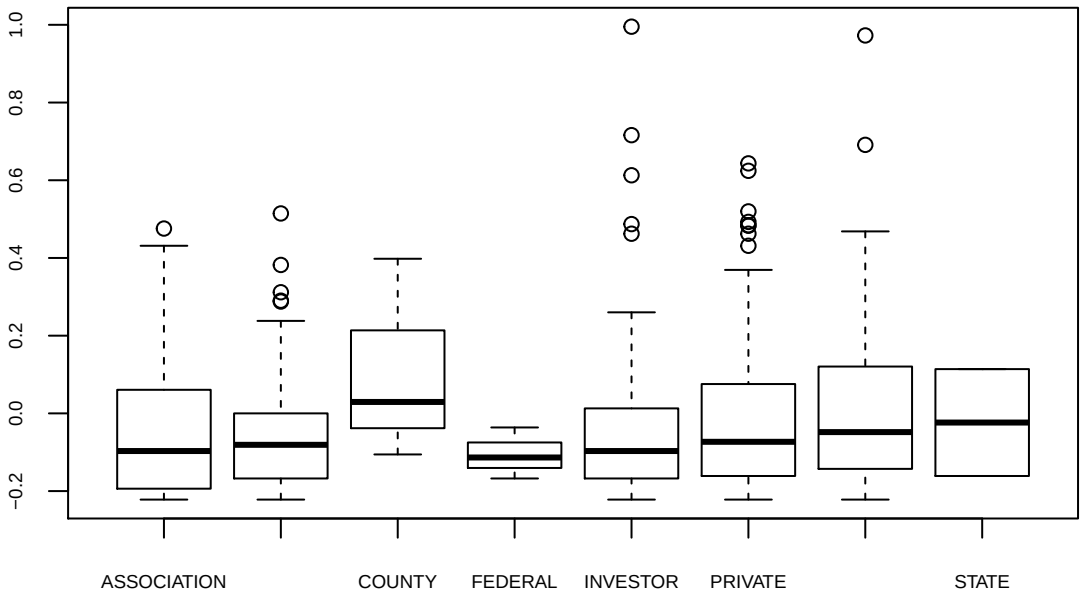



Figure 8: Washington State Drinking Water Systems by Owner Type

```
bwplot(nat.fl$LmgL~nat.fl$OwnerTypeDesc|nat.fl$Population,
        ylab="log(Fluoride Level)", xlab="Water System Owner Type",
        main="Fluoride Level by Water System Owner Type and Population",
        layout=(c(1,4)))
```

Next, let's swap the axes and try a different layout. We'll also use the `with` function so we don't have to keep repeating the name of the data.frame when we refer to column names.

```
with(nat.fl, bwplot(OwnerTypeDesc~LmgL|Population,
        xlab="log(Fluoride Level)", ylab="Water System Owner Type",
        main="Fluoride Level by Water System Owner Type and Population",
        layout=(c(2,2))))
```

One of the most popular plotting systems in R is the versatile `ggplot2` package, which we used earlier with scatter and bar plots. The rest of the plots in this document will be created with `ggplot`.

Here is a faceted plot like the previous one (2x2), without the coordinate swap, and this time made using the `ggplot` function.

```
# Use light theme, 45-degre x-axis lables, smaller outlier dots, and 2x2 facet
ggplot(nat.fl, aes(x=OwnerTypeDesc, y=mgL)) + scale_y_log10() +
    facet_wrap(~Population) +
    labs(title=paste("Natural Fluoride Levels", "in Washington Water Sources",
                     "by Water System Owner Type", sep="\n"),
        x="Water System Owner Type", y = "log(Fluoride Level)") +
        theme_light() +
    theme(axis.text.x = element_text(size=8, angle=45, hjust=1, vjust=1)) +
    geom_boxplot(outlier.size=1)
```

Let's start over again with the basic boxplot. We will store the essential parameters of this next plot to build upon later as we add more features to the plot. For the sake of tidiness, order the boxplots by increasing median levels.

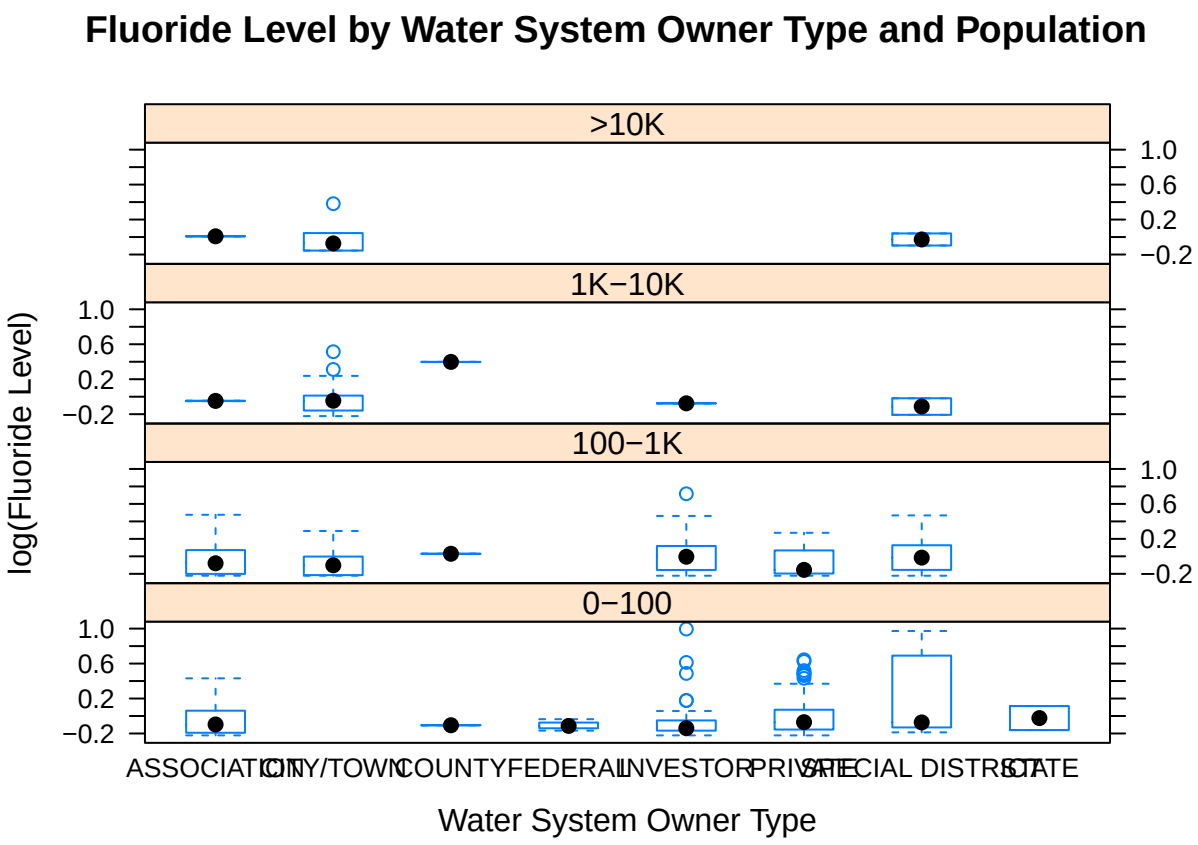



Figure 9: Washington State Drinking Water Systems by Owner Type Lattice Box Plot

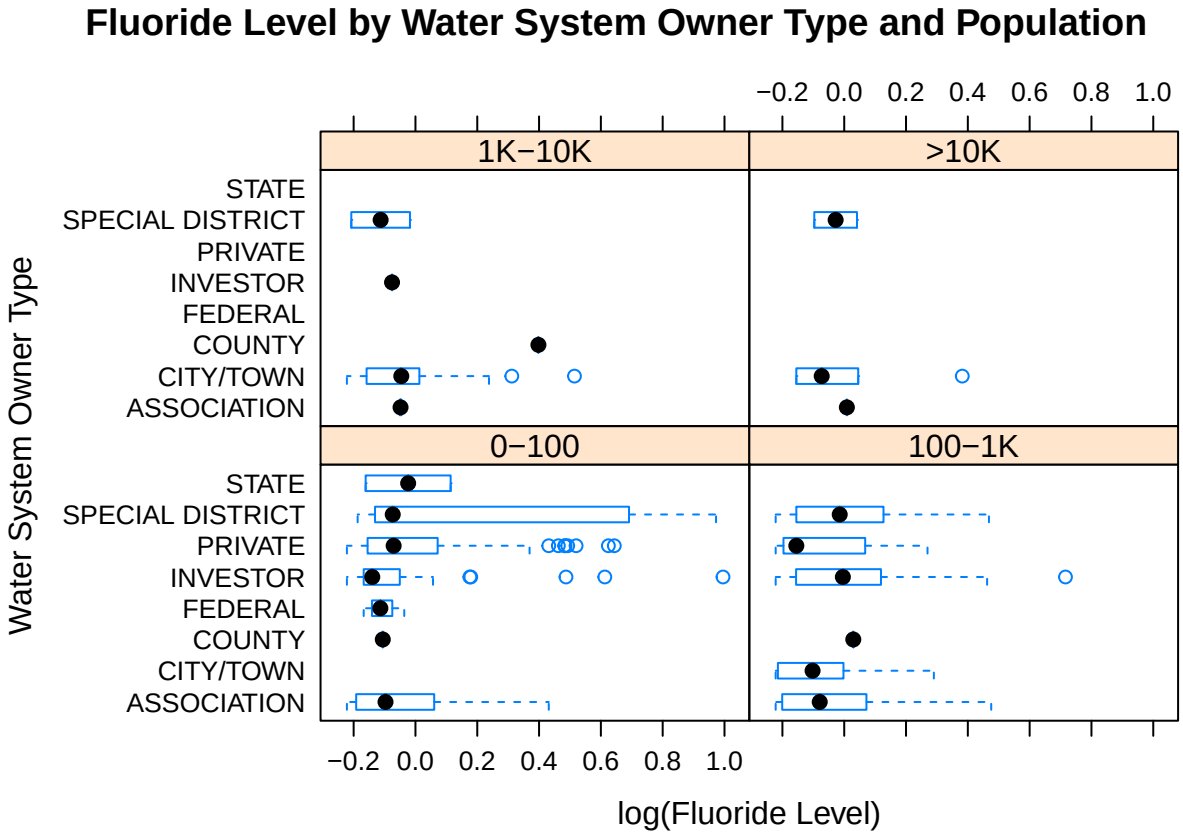



Figure 10: Washington State Drinking Water Systems by Owner Type Lattice Box Plot

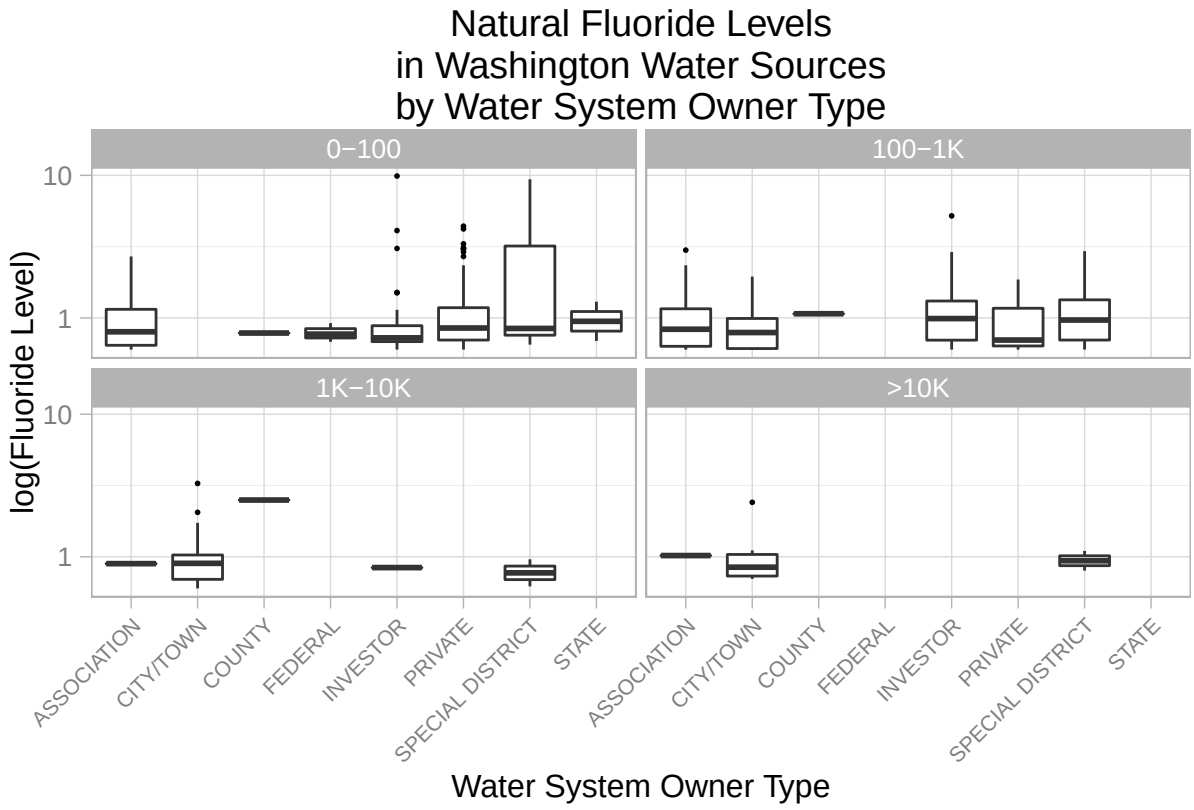



Figure 11: Washington State Drinking Water Systems by Owner Type faceted Box Plot with ggplot

```
# Reorder by median fluoride level (boxplot center)
nat.fl <- group_by(nat.fl, OwnerTypeDesc)
owner.levels <- summarise(nat.fl, median.mgL.by.owner=median(mgL)) %>%
    arrange(median.mgL.by.owner) %>% select(OwnerTypeDesc)
nat.fl$OwnerTypeDesc <- factor(nat.fl$OwnerTypeDesc, levels=owner.levels$OwnerTypeDesc)

# Use light theme, smaller x-asis lables, and use smaller outlier dots
plot <- ggplot(nat.fl, aes(x=OwnerTypeDesc, y=mgL)) + scale_y_log10() +
    labs(title=paste("Natural Fluoride Levels", "in Washington Water Sources",
                     "by Water System Owner Type", sep="\n"),
        x="Water System Owner Type", y = "log(Fluoride Level)") +
        theme_light() + theme(axis.text.x = element_text(size=10,
                                                         angle=20, vjust=.6))

plot + geom_boxplot(outlier.size=1)
```

We can use color instead of faceting to represent the population groups.

We'll also add data points with jitter and remove the (now redundant) black outlier dots.

```
# Add jittered and population-colored points
plot <- plot + geom_jitter(size=3, alpha=0.4,
    position = position_jitter(width = 0.05), aes(color=Population)) +
    scale_color_manual(values=c("darkblue", "darkgreen", "darkorange", "darkred"))
```

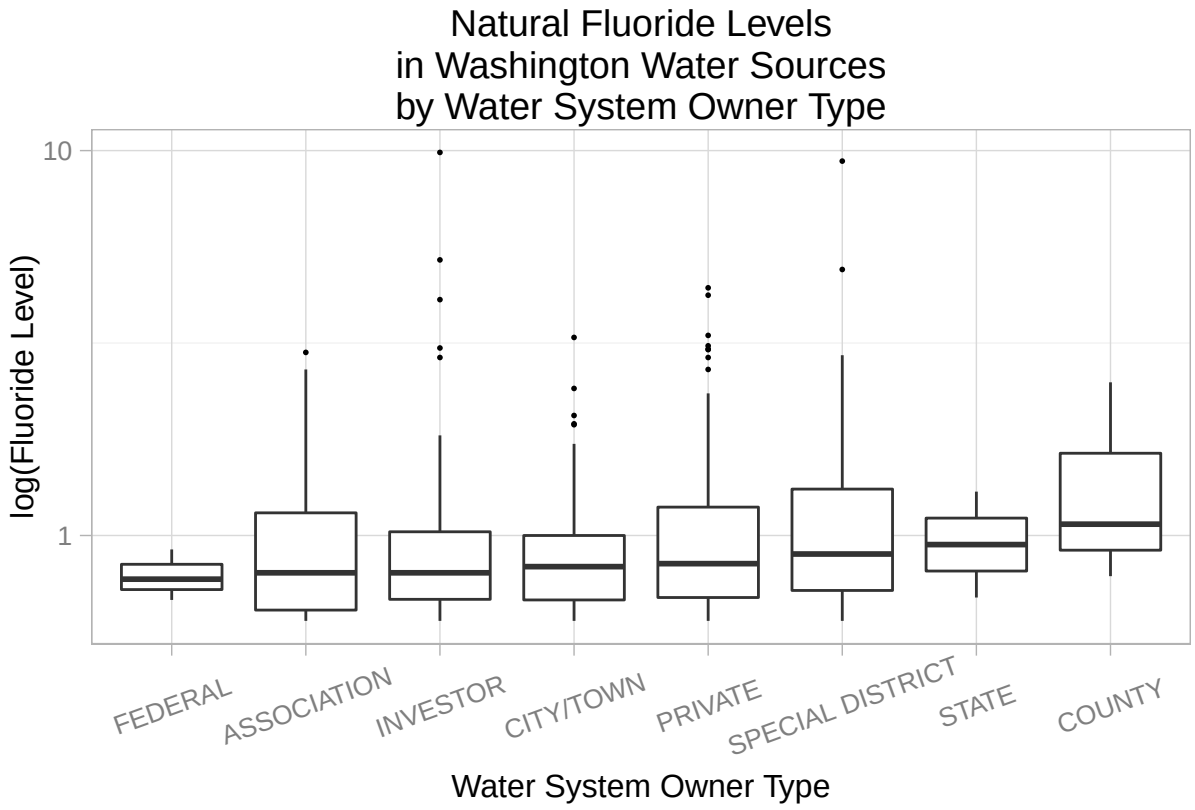



Figure 12: Washington State Drinking Water Systems by Owner Type Basic Box Plot with ggplot

```
plot + geom_boxplot(alpha=0, outlier.size=0)
```

Add a light-green horizontal band to show the optimal fluoride level range and add a label for it.

```
# Add a rectangle for the optimal fluoride level range and a label for it
plot <- plot + geom_rect(data=nat.fl[1,],
              aes(ymin=.8, ymax=1.3, xmin=0, xmax=Inf),
              fill="green", alpha=.2, label="Optimal Fluoridation") +
    annotate("text", x=.74, y=1.15, label="WA Optimal", size = 4, color = "darkgreen")

plot + geom_boxplot(alpha=0, outlier.size=0)
```

Add lines (and labels) for the various US HHS and EPA levels.

```
# Add lines (and labels) for the various US HHS and EPA levels
plot <- plot + geom_hline(aes(yintercept=0.7, alpha=.5), color = "darkgreen") +
    annotate("text", x=.65, y=.6, label="HHS 2015", size = 4, color = "darkgreen") +
    geom_hline(aes(yintercept=2, alpha=.5), color = "darkorange") +
    annotate("text", x=.73, y=1.8, label="EPA SMCL", size = 4, color = "darkorange") +
    geom_hline(aes(yintercept=4, alpha=.5), color = "darkred") +
    annotate("text", x=.65, y=3.6, label="EPA MCL", size = 4, color = "darkred")

plot + geom_boxplot(alpha=0, outlier.size=0)
```

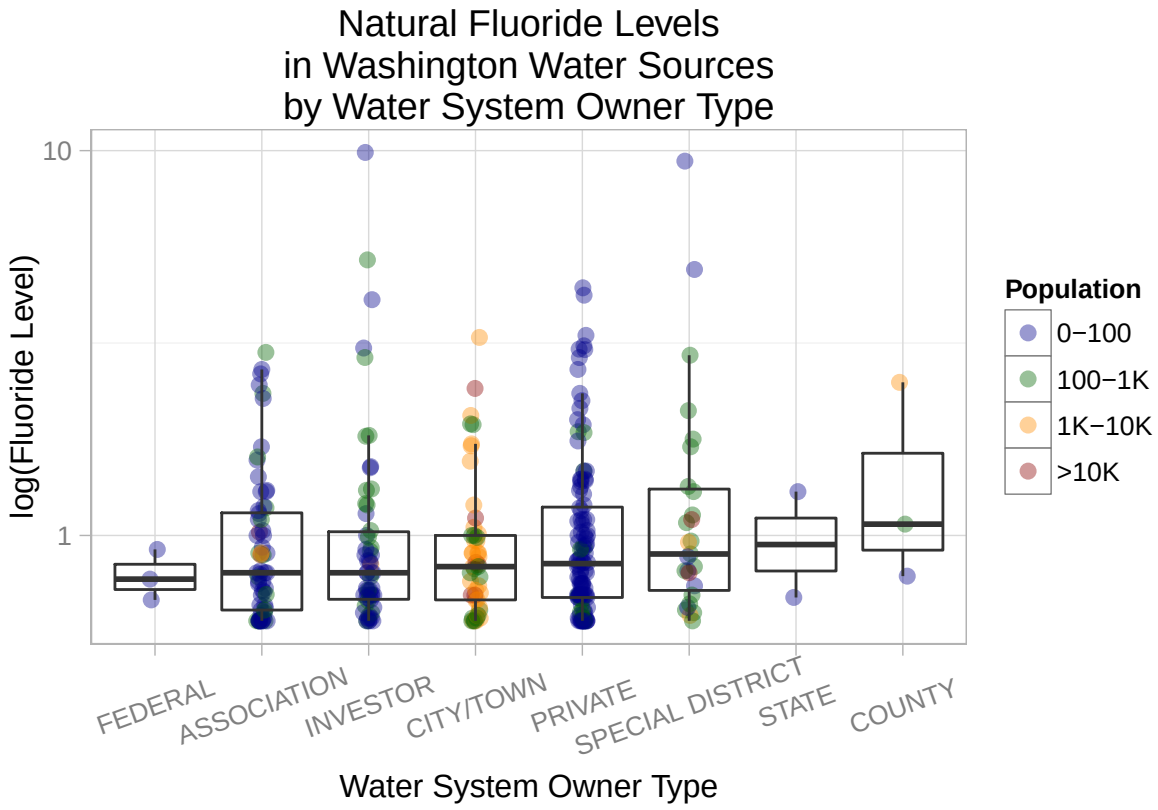



Figure 13: Washington State Drinking Water Systems by Owner Type

## Violin Plot of Natural Fluoride Levels

Make a violin plot of fluoride levels by system owner type. A violin plot is something like a box plot, except the width of the "violin" shape varies with the density of observations at each point along the y-axis. This will help us see density differences where the dots overlap.

```
# Make the violin plot
plot + geom_violin(alpha=0)
```

The colors indicate the size of the population served by the water system. The width of the shapes vary according to the density of points plotted at a given fluoride level.

The light green band shows Washington's range of "optimal" fluoride levels (0.8 to 1.3 mg/L). The green line marks the new (April, 2015) US HHS recommended level of 0.7 mg/L.

The red line marks the level of the US EPA's MCLG (maximum contaminant level goal) of 4 mg/L. This is also the level of the EPA's enforceable MCL (maximum contaminant level). The orange line marks the level of the US EPA's SMCL (secondary standard) of 2 mg/L, a non-enforceable guideline.

For completeness, we'll add a footnote referencing the data sources.

```
# Make the violin plot with data source attribution

plot <- plot + geom_violin(alpha=0)

data.src <- paste0(collapse = ' ', c('Data sources:',
```

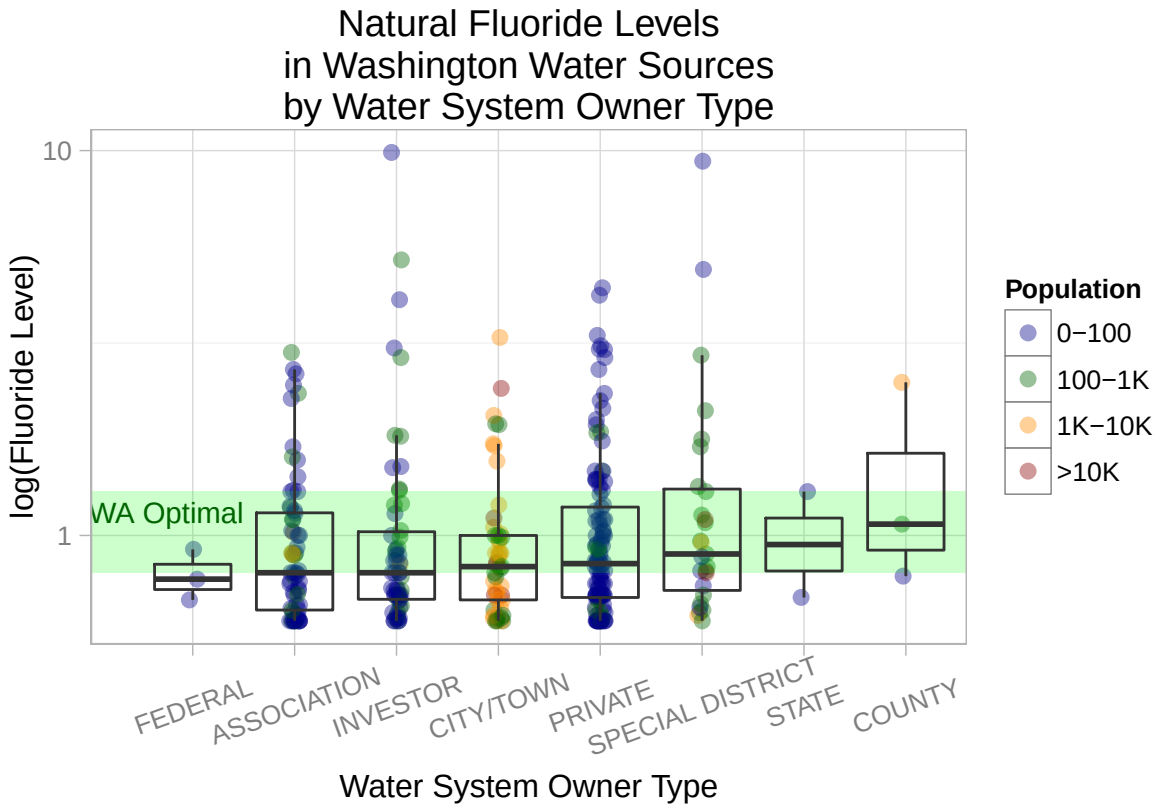



Figure 14: Washington State Drinking Water Systems by Owner Type

```
                    'WA DOH (www.doh.wa.gov),',
                    'US EPA (water.epa.gov)',
                    'and HHS (www.hhs.gov)'))
gplot <- arrangeGrob(plot, sub = textGrob(data.src, x=0, hjust=-0.1, vjust=0.1,
                  gp = gpar(fontface="italic", fontsize=10)))
gplot
```

## Prepare Map Data

Before we plot the water systems on a map, we will need to get a state map with county names and boundaries.

Prepare the map `data.frame` using the `map_data` function from the `ggplot2` package.

```
# Capitalize first letter of word - for use with proper nouns
# From documentation for `tolower` in package _base_ 3.1.3
capwords <- function(s, strict = FALSE) {
    cap <- function(s) paste(toupper(substring(s, 1, 1)),
                  {s <- substring(s, 2); if(strict) tolower(s) else s},
                             sep = "", collapse = " " )
    sapply(strsplit(s, split = " "), cap, USE.NAMES = !is.null(names(s)))
}

# Mappings of counties by state
county_df <- map_data('county')
```

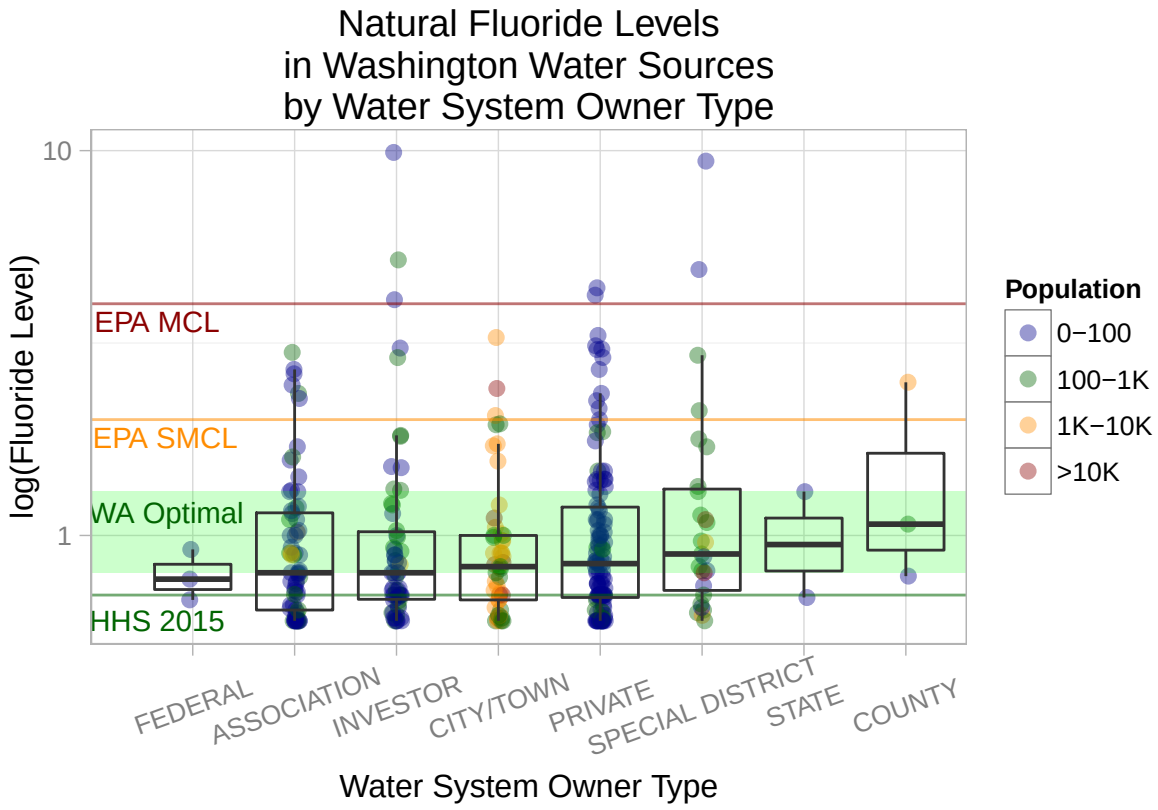



Figure 15: Washington State Drinking Water Systems by Owner Type

```
# Subset just for WA
wa <- subset(county_df, region=="washington")
wa$subregion <- sapply(wa$subregion, function(x) capwords(x))
wa$county <- wa$subregion
cnames <- aggregate(cbind(long, lat) ~ subregion, data=wa,
                    FUN=function(x)mean(range(x)))
write.csv(cnames, file='data/cnames.csv', row.names=FALSE)
```

This allows us to create a base state map with county border in grey that we will build upon later. We'll use the `theme_classic()` theme.

```
# Create the base state map with counties outlined in grey
wamap <- ggplot(wa, aes(long, lat)) +
    geom_polygon(aes(group=group), color='darkgrey', fill=NA) +
    geom_text(data=cnames, aes(long, lat, label = subregion), size=3) +
    theme_classic()  +
    theme(axis.line=element_blank(),
      axis.text.x=element_blank(),
      axis.text.y=element_blank(),
      axis.ticks=element_blank(),
      axis.title.x=element_blank(),
      axis.title.y=element_blank())
wamap
```

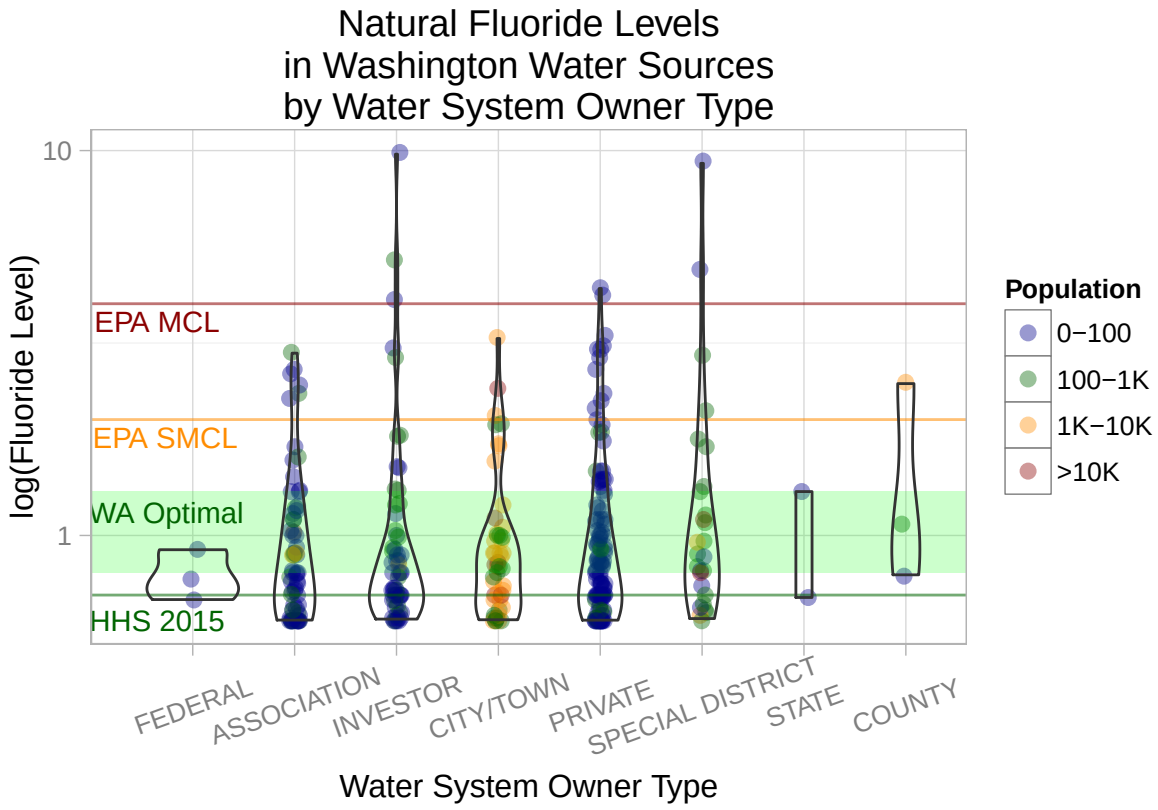



Figure 16: Washington State Drinking Water Systems by Owner Type

## Untreated Systems Exceeding Optimal Fluoride Levels

Make a map of populations Served by Drinking Water Systems with natural fluoride levels above Washington State's "optimal" range of 0.8 - 1.3 mg/L.

```
# Subset the data
nat.fl.high <- nat.fl[nat.fl$mgL>1.3,]
nat.fl.high <- nat.fl.high[complete.cases(nat.fl.high),]

# Make the map
wamap + geom_point(data=nat.fl.high, inherit.aes=FALSE,
               aes(x=lon, y=lat, size=Population), colour="darkred", alpha=.3) +
        scale_size_manual(values = seq(3, 12, by=2)) +
    guides(colour = guide_legend(override.aes = list(size=5))) +
    ggtitle(label = paste("Washington Populations Served by Drinking Water Systems",
                          "with Natural (Untreated) Fluoride Levels",
                          "Above Washington State's",
                          "\"Optimal\" Range (0.8 - 1.3 mg/L)", sep="\n"))
```

## Untreated Natural Fluoride Levels

Make a map of populations served by non-fluoridated water systems with natural fluoride levels.

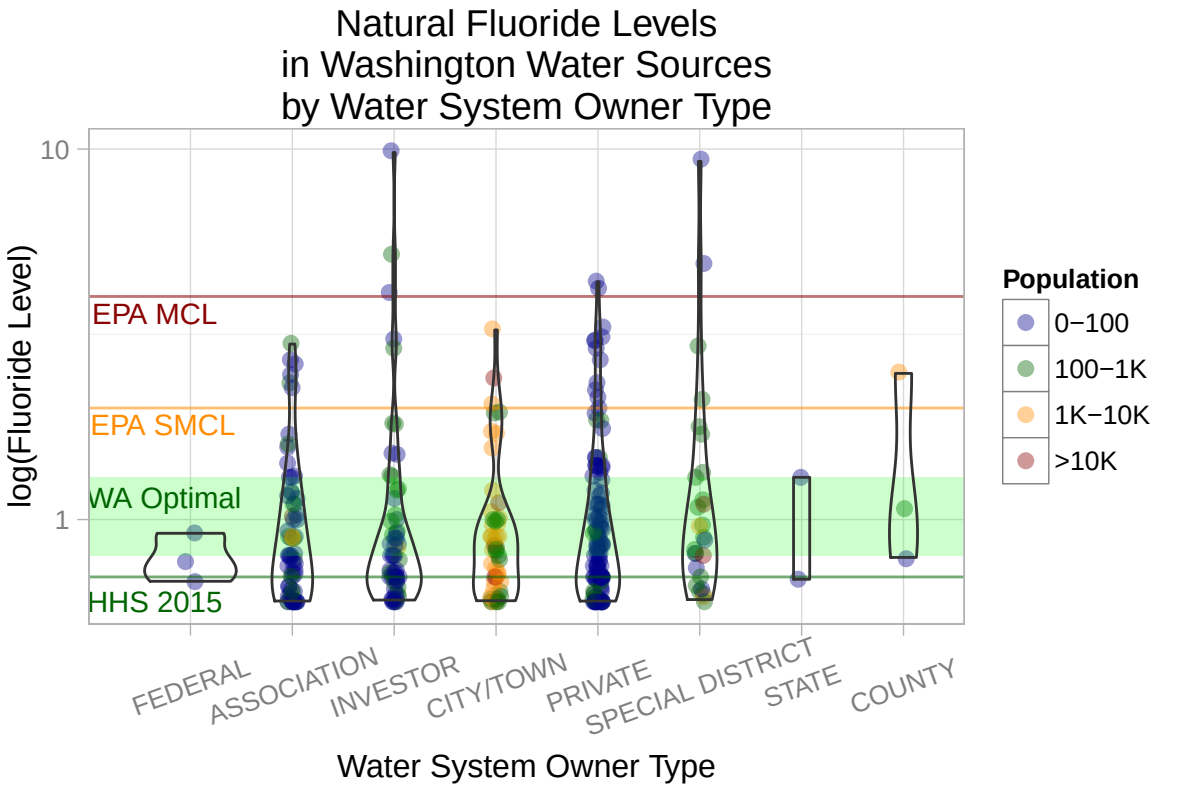



Figure 17: Washington State Drinking Water Systems by Owner Type


Figure 18: Washington State Counties

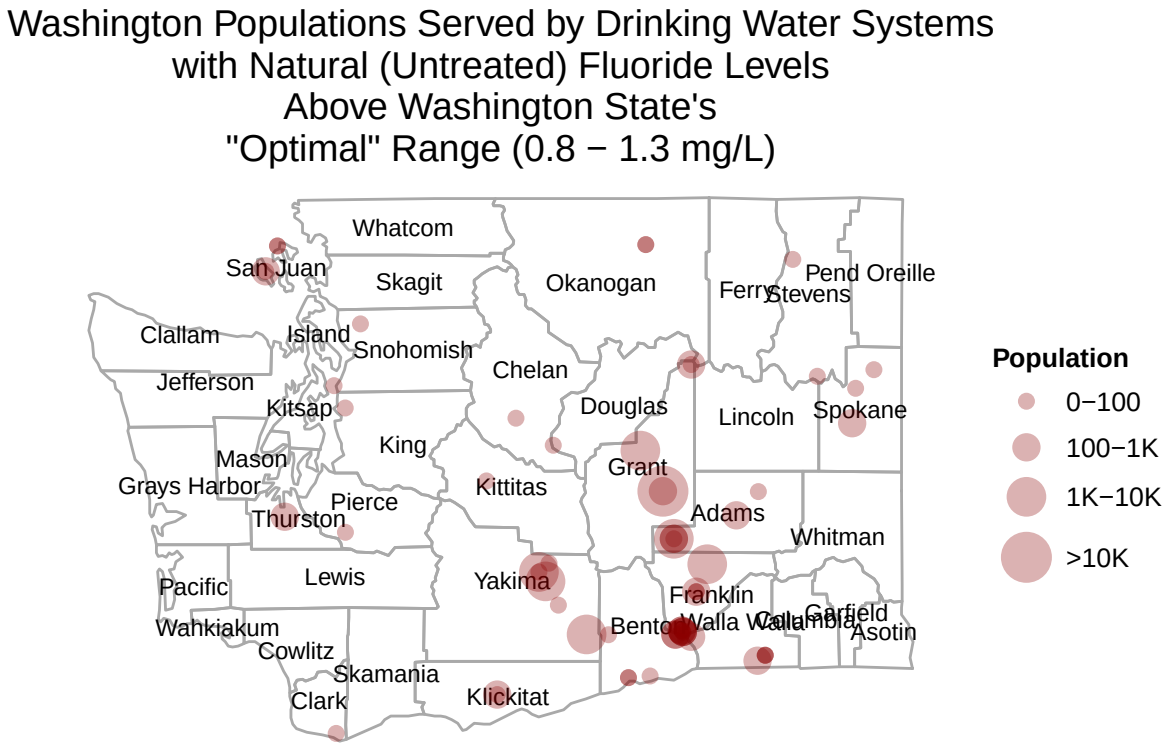



Figure 19: Washington State Natural Fluoride Levels Over Optimal Range

```
# Make the map
wamap + geom_point(data=nat.fl, inherit.aes=FALSE,
            aes(x=lon, y=lat, group=F.Level, color=F.Level, size=Population,
                fill=F.Level),
        position=position_jitterdodge(jitter.width=0.1, dodge.width=0.1),
        alpha=.3) + scale_shape_discrete(solid=T) +
    scale_size_manual(values = seq(3, 12, by=2)) +
    scale_color_manual(values=c("darkblue", "darkgreen", "darkred")) +
    guides(colour = guide_legend(override.aes = list(size=5))) +
    ggtitle(label = paste("Washington Populations Served by Drinking Water Systems",
                          "with Natural (Untreated) Fluoride Levels",
                          "Colored Relative to Washington State's",
                          "\"Optimal\" Range (0.8 - 1.3 mg/L)", sep="\n"))
```

## All Systems: Optimal and Nonoptimal Fluoride Levels

Make a map of populations Served by Drinking Water Systems with natural or treated fluoride levels falling inside or outside of Washington State's "optimal" range of 0.8 - 1.3 mg/L.

```
# Assign Optimal as T/F based on fluoride concentrations (mgL) and system type
fl$Optimal <- with(fl, Treatment=="TREATED" | Treatment=="INTERTIED" | F.Level=="Optimal")

# Convert T/F to Yes/No
fl$Optimal <- factor(c('No', 'Yes')[fl$Optimal + 1])
```

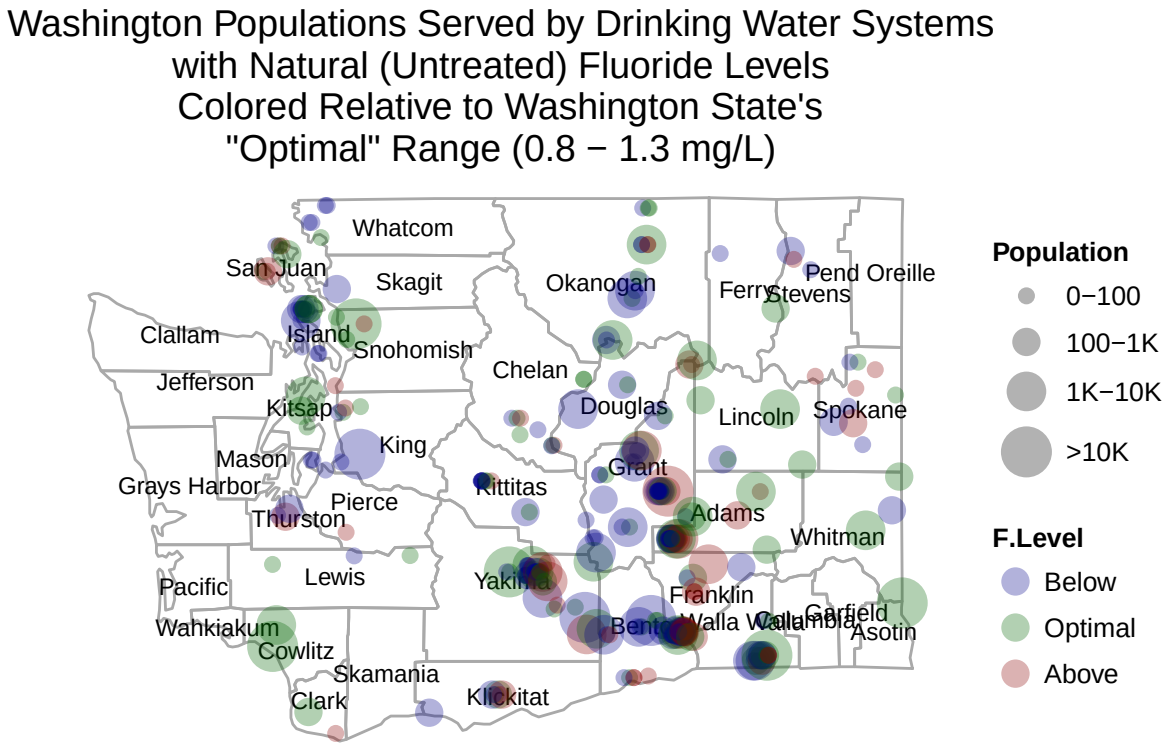



Figure 20: Washington State Untreated Fluoride Water Systems

```
# Subset the columns we want and remove incomplete observations
fl.opt <- select(fl, County, PWSID, SystemName, ResPop, OwnerTypeDesc,
                 lon, lat, Treatment, Population, Optimal)
fl.opt <- fl[complete.cases(fl.opt),]

# Make the map
wamap + geom_point(data=fl.opt, inherit.aes=F,
               aes(x=lon, y=lat, size=Population, color=Optimal), alpha=.3) +
    scale_size_manual(values = seq(3, 12, by=2)) +
    scale_color_manual(values=c("darkred", "darkgreen")) +
    guides(colour = guide_legend(override.aes = list(size=5))) +
    ggtitle(label = paste("Washington Populations Served by Drinking Water Systems",
                          "with Fluoride Levels Colored Relative to Washington State's",
                          "\"Optimal\" Range (0.8 - 1.3 mg/L)", sep="\n"))
```

## All Systems: US Recommended Fluoride Levels

Make a map of populations Served by Drinking Water Systems with natural or treated fluoride levels relative to US HHS ("Health Department") and US EPA guidelines.

```
# Assign US.F.Level based on fluoride concentrations (mgL)
fl$US.F.Level <- cut(fl$mgL, c(-Inf, 0, .7, 2, 4, Inf),
            labels=c("Unknown", "< HHS .7", "< EPA 2", "< EPA 4", "> EPA 4"))

# Assign remaining US.F.Levels for water systems without concentrations (mgL)
```

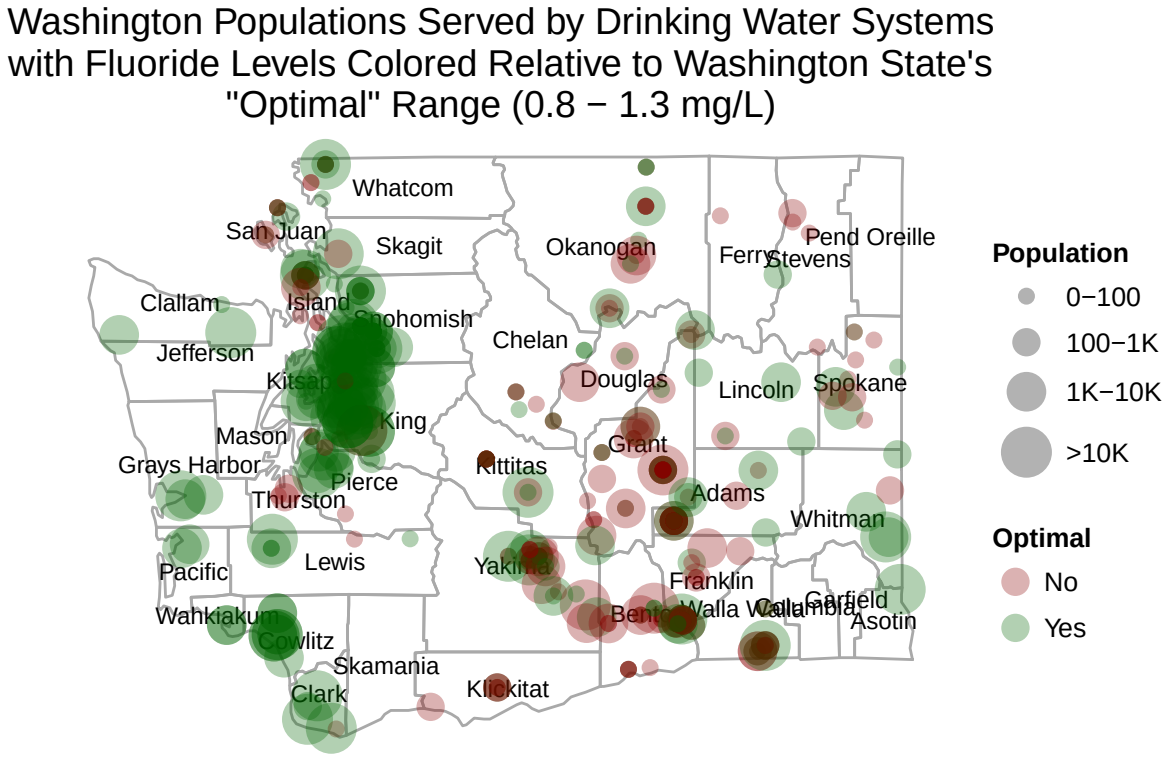
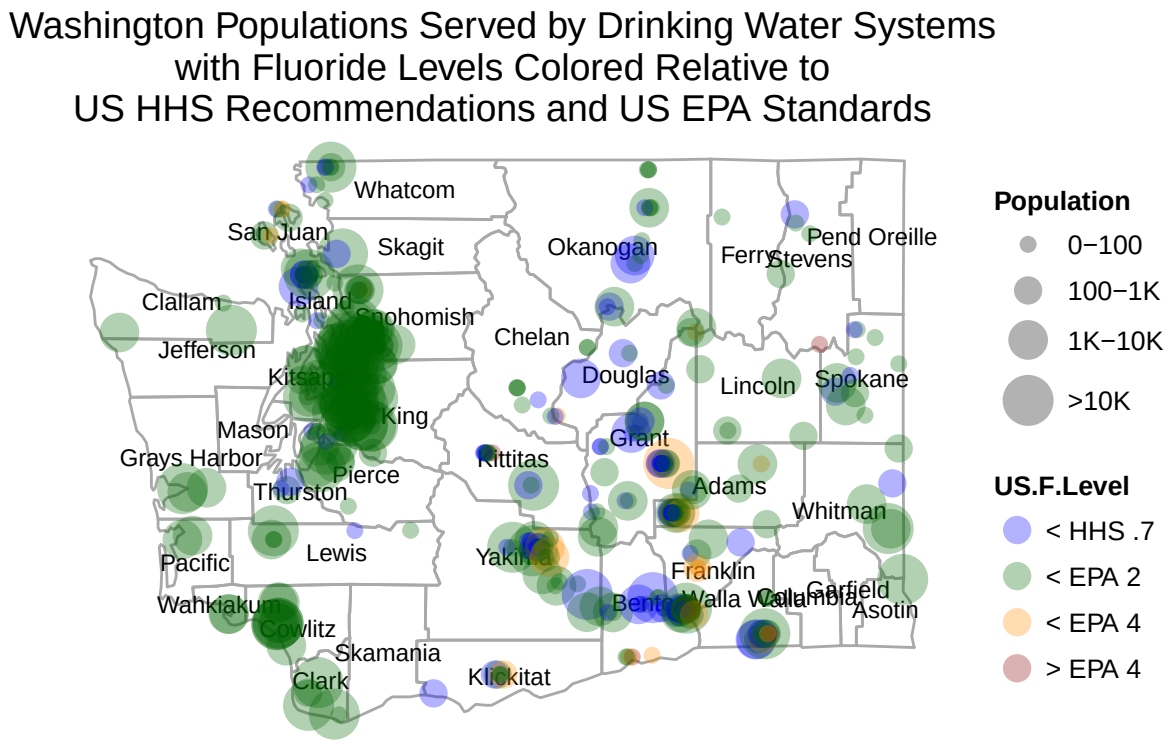



Figure 21: Washington State Optimal and Nonoptimal Fluoride Levels

```
fl$US.F.Level[with(fl, Treatment=="TREATED" | Treatment=="INTERTIED")] <- "< EPA 2"
fl$US.F.Level[with(fl, Treatment=="MIXED")] <- "Unknown"

# Subset the columns we want and remove incomplete observations
fl.us <- select(fl, County, PWSID, SystemName, ResPop, OwnerTypeDesc,
                lon, lat, Treatment, Population, US.F.Level)
fl.us <- fl[complete.cases(fl.us),] # This removes the "Unknown" group

# Make the map
wamap <- wamap + geom_point(data=fl.us, inherit.aes=FALSE,
               aes(x=lon, y=lat, group=US.F.Level, color=US.F.Level,
                   size=Population, fill=US.F.Level),
               position=position_jitterdodge(jitter.width=0.1, dodge.width=0.1),
       alpha=.3) + scale_shape_discrete(solid=TRUE) +
    scale_size_manual(values = seq(3, 12, by=2)) +
    scale_color_manual(values=c("blue", "darkgreen", "darkorange", "darkred")) +
    guides(colour = guide_legend(override.aes = list(size=5))) +
    ggtitle(label = paste("Washington Populations Served by Drinking Water Systems",
                          "with Fluoride Levels Colored Relative to",
                          "US HHS Recommendations and US EPA Standards",
                          sep="\n"))
gmap <- arrangeGrob(wamap, sub = textGrob(data.src, x=0, hjust=-0.1, vjust=0.1,
                  gp = gpar(fontface="italic", fontsize=10)))
gmap
```




*Data sources: WA DOH (www.doh.wa.gov), US EPA (water.epa.gov) and HHS (www.hhs.gov)*

Figure 22: Washington State Fluoride Levels Colored Relative to US Recommendations and Regulations