

# hfg\_noise

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```
Pop_DF <- data.frame(
  site = c("Hudson", "Kenosha", "Platteville", "Madison", "Merrill", "Plymouth", "River Falls", "Sun Prairie",
  pop = c(19680, 122000, 14000, 380000, 10000, 9000, 16000, 34926, 42000, 67000, 42000)
)

MSE <- function(baseVal, meanVal){
  ret <- mean((baseVal - meanVal)^2)
  return(ret)
}
```

```
data("HFGWaste_data", package = "DSIWastewater")
hfgwaste <- HFGWaste_data

hfgwasteavg <- aggregate(hfgwaste[,5:12], list(hfgwaste$site, hfgwaste$date, hfgwaste$Filter), mean)

hfgnoise <- hfgwasteavg %>% rename(site=Group.1) %>%
  group_by(site) %>%
  mutate(rollaveragePMMOV = rollmean(log(as.numeric(PMMOV)), k=7, fill = NA),
         rollaverageN1 = rollmean(log(as.numeric(N1)), k=7, fill = NA)) %>%
  drop_na(rollaveragePMMOV, rollaverageN1)

hfgnoise <- hfgnoise %>%
  group_by(site) %>%
  mutate(rollnoisePMMOV = MSE(log(as.numeric(PMMOV)), rollaveragePMMOV),
         rollnoiseN1 = MSE(log(as.numeric(N1)), rollaverageN1))
hfgnoise <- inner_join(x=hfgnoise, y=Pop_DF, by = "site")
```

```
## Warning in inner_join(x = hfgnoise, y = Pop_DF, by = "site"): Detected an unexpected many-to-many relationship.
## i Row 8 of 'x' matches multiple rows in 'y'.
## i Row 1 of 'y' matches multiple rows in 'x'.
## i If a many-to-many relationship is expected, set 'relationship =
##   "many-to-many"' to silence this warning.
```

```
HFGWaste_data%>%
  pull(site)%>%
  unique()%>%
  length()
```

```
## [1] 10
```

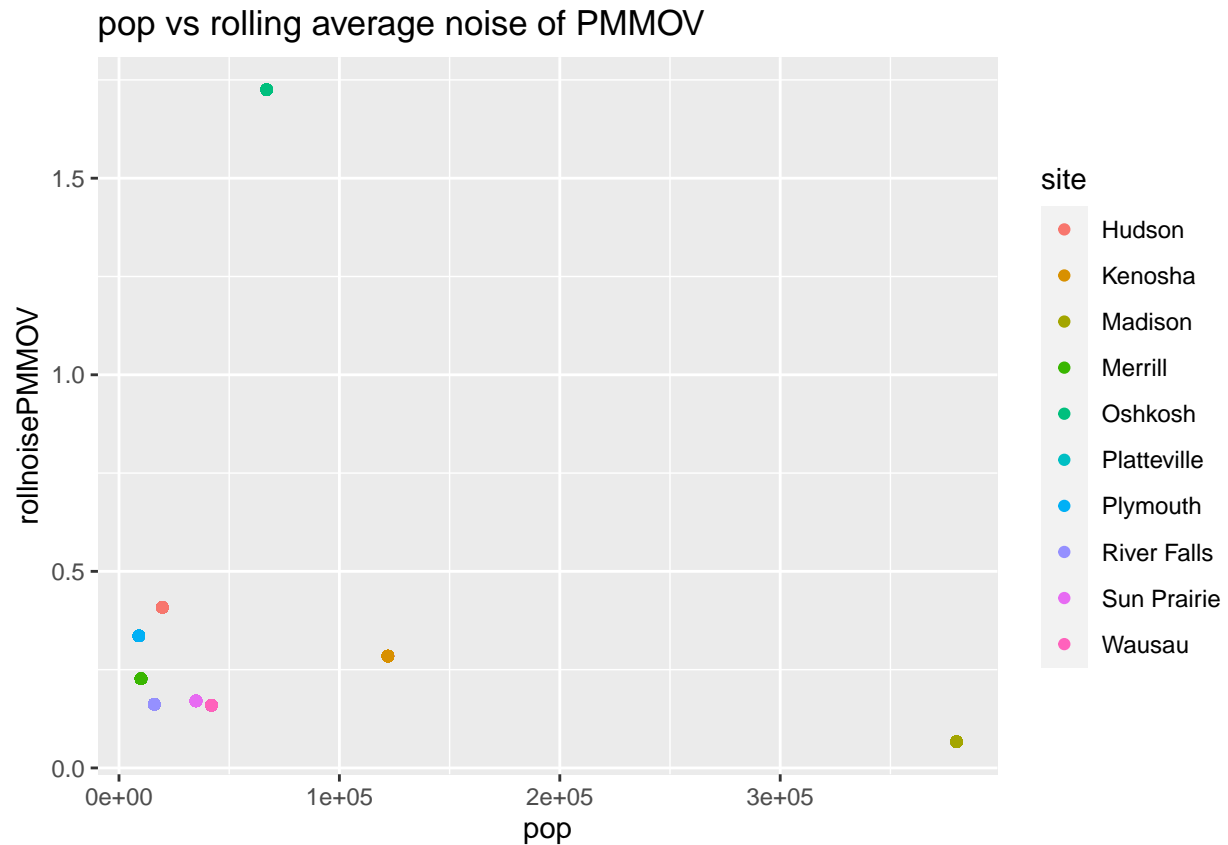
```
max(HFGWaste_data$date) - min(HFGWaste_data$date)
```

```
## Time difference of 42 days
```

```
#hfgnoise <- hfgnoise %>% filter(site != "Platteville")  
#hfgnoise <- hfgnoise %>% filter(site != "Madison")
```

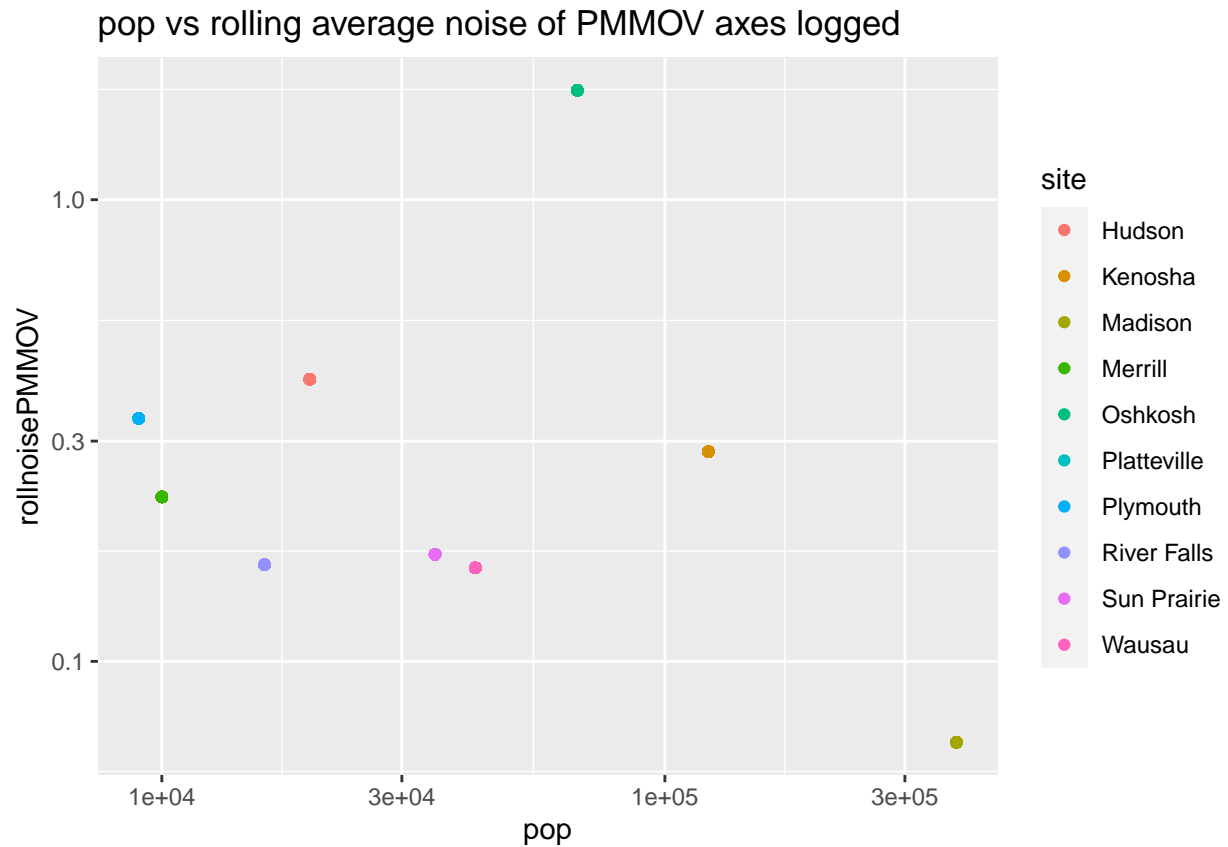
```
ggplot(hfgnoise) +  
  aes(pop,rollnoisePMMOV,color = site)+  
  geom_point() +  
  ggtitle("pop vs rolling average noise of PMMOV")
```

```
## Warning: Removed 6 rows containing missing values ('geom_point()').
```



```
ggplot(hfgnoise) +  
  aes(pop,rollnoisePMMOV,color = site)+  
  geom_point() +  
  scale_x_log10() +  
  scale_y_log10() +  
  ggtitle("pop vs rolling average noise of PMMOV axes logged")
```

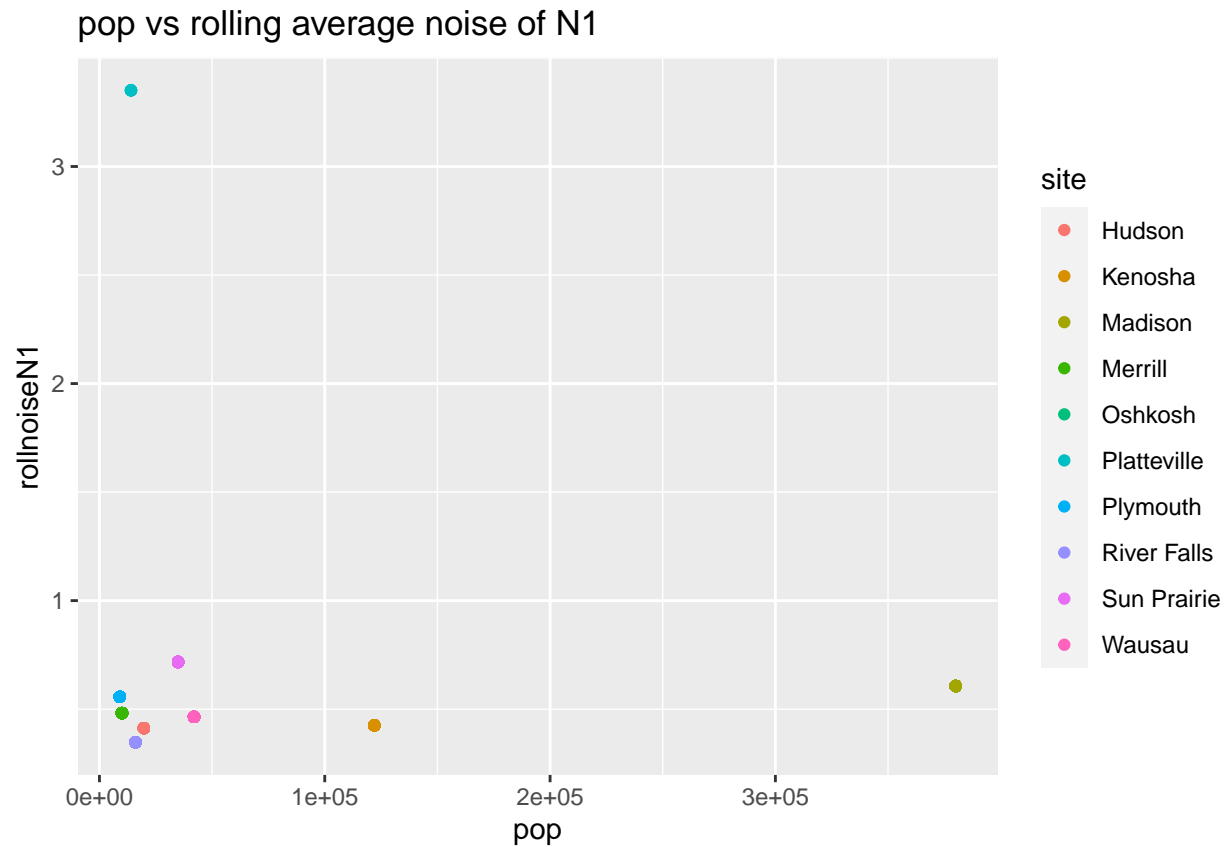
```
## Warning: Removed 6 rows containing missing values ('geom_point()').
```



```
#hfgnoise <- hfgnoise %>% filter(site != "Platteville")
#hfgnoise <- hfgnoise %>% filter(site != "Madison")
```

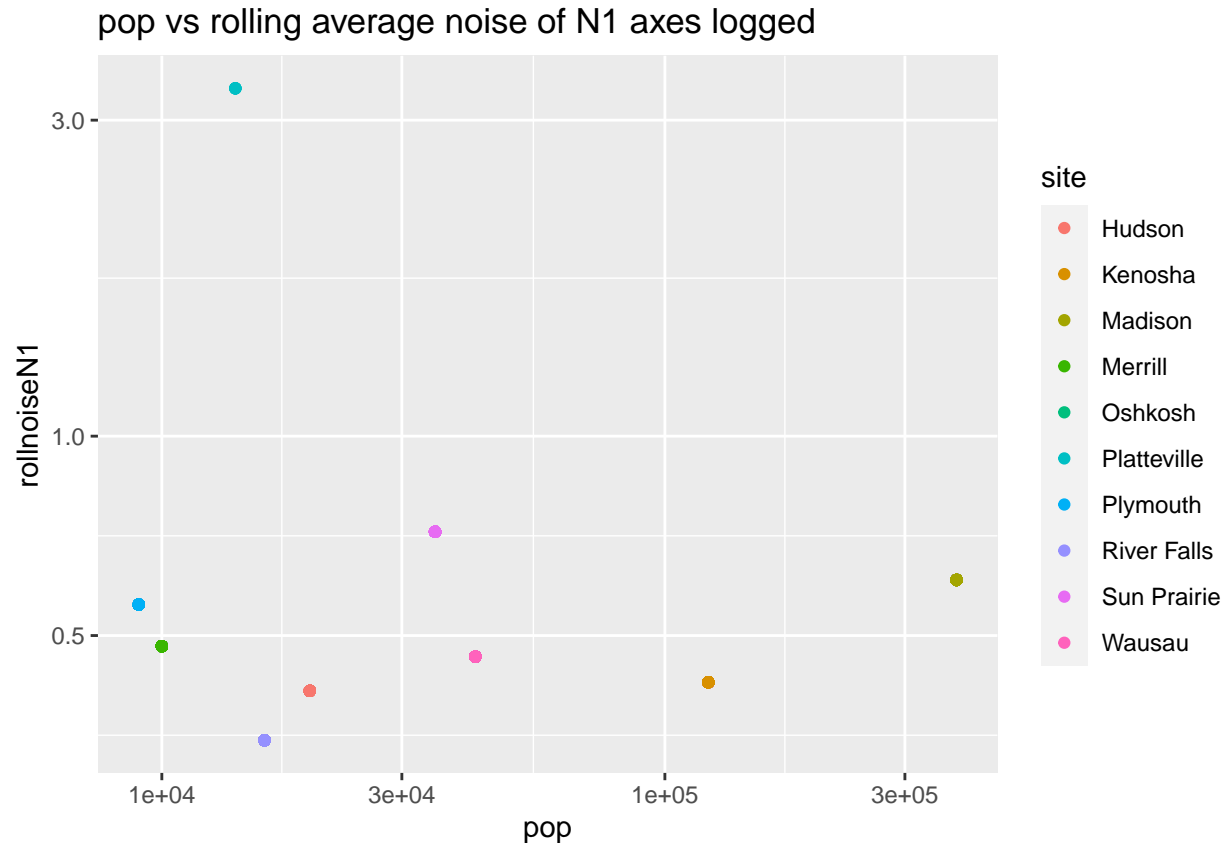
```
ggplot(hfgnoise) +
  aes(pop,rollnoiseN1,color = site)+
  geom_point() +
  ggtitle("pop vs rolling average noise of N1")
```

```
## Warning: Removed 61 rows containing missing values ('geom_point()').
```



```
ggplot(hfgnoise) +  
  aes(pop,rollnoiseN1,color = site)+  
  geom_point() +  
  scale_x_log10() +  
  scale_y_log10() +  
  ggtitle("pop vs rolling average noise of N1 axes logged")
```

```
## Warning: Removed 61 rows containing missing values ('geom_point()').
```

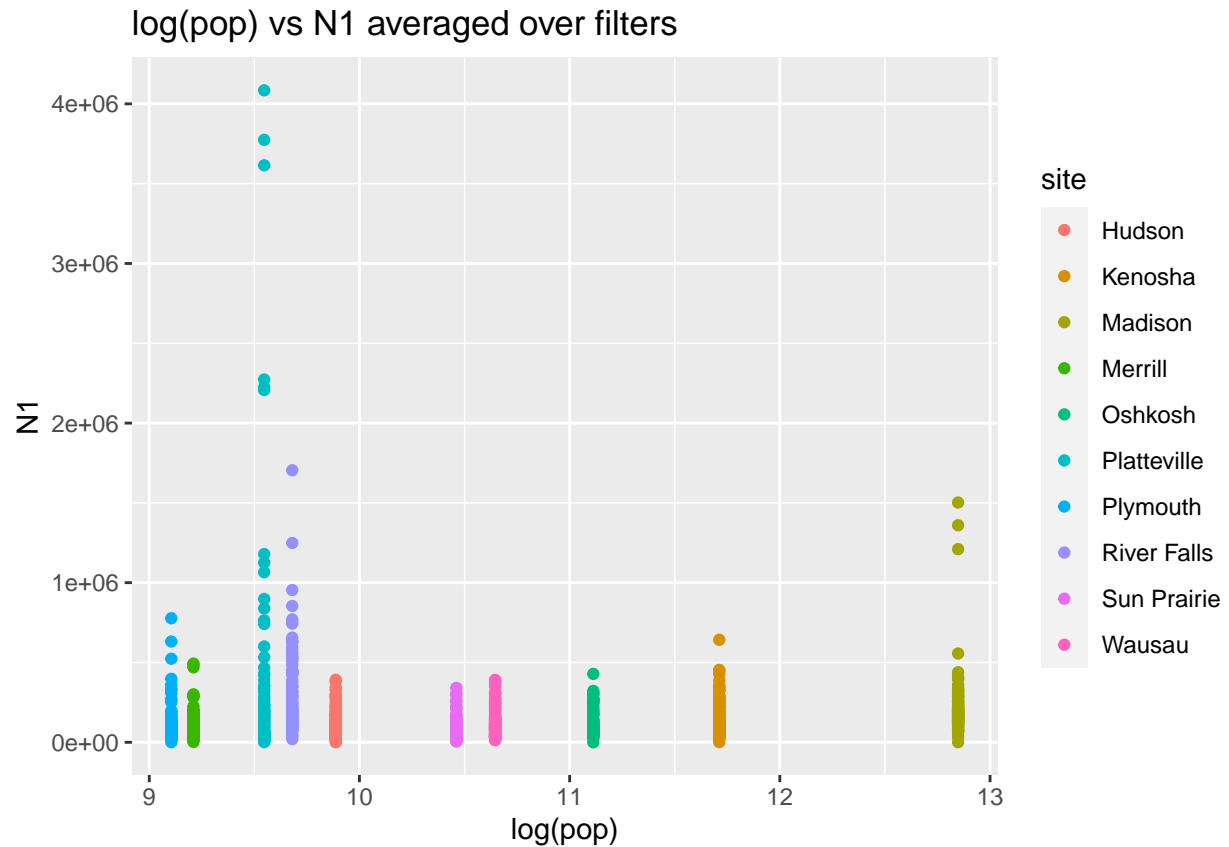


```
hfgwasteavg <- hfgwasteavg %>% rename(site=Group.1)
hfgwasteavg <- inner_join(x=hfgwasteavg, y=Pop_DF, by = "site")
```

```
## Warning in inner_join(x = hfgwasteavg, y = Pop_DF, by = "site"): Detected an unexpected many-to-many
## i Row 8 of 'x' matches multiple rows in 'y'.
## i Row 1 of 'y' matches multiple rows in 'x'.
## i If a many-to-many relationship is expected, set 'relationship =
##   "many-to-many"' to silence this warning.
```

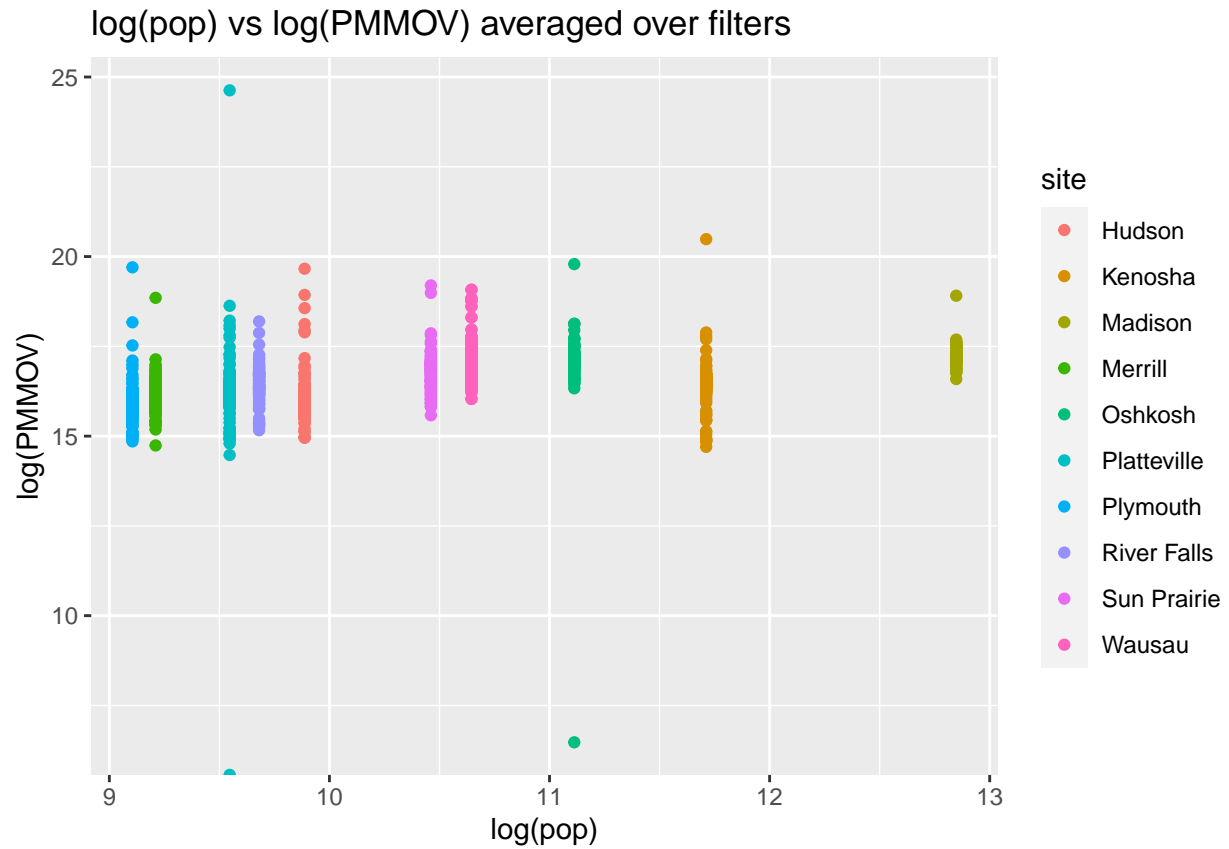
```
ggplot(hfgwasteavg) +
  aes(log(pop), N1, color = site) +
  geom_point() +
  ggtitle("log(pop) vs N1 averaged over filters")
```

```
## Warning: Removed 16 rows containing missing values ('geom_point()').
```



```
ggplot(hfgwasteavg) +
  aes(log(pop),log(PMMOV),color = site)+ #log PMMOV to see better results
  geom_point() +
  ggtitle("log(pop) vs log(PMMOV) averaged over filters")
```

## Warning: Removed 1 rows containing missing values ('geom\_point()').



*#Good result as pmmov concetration should be constant over differernt size populations*