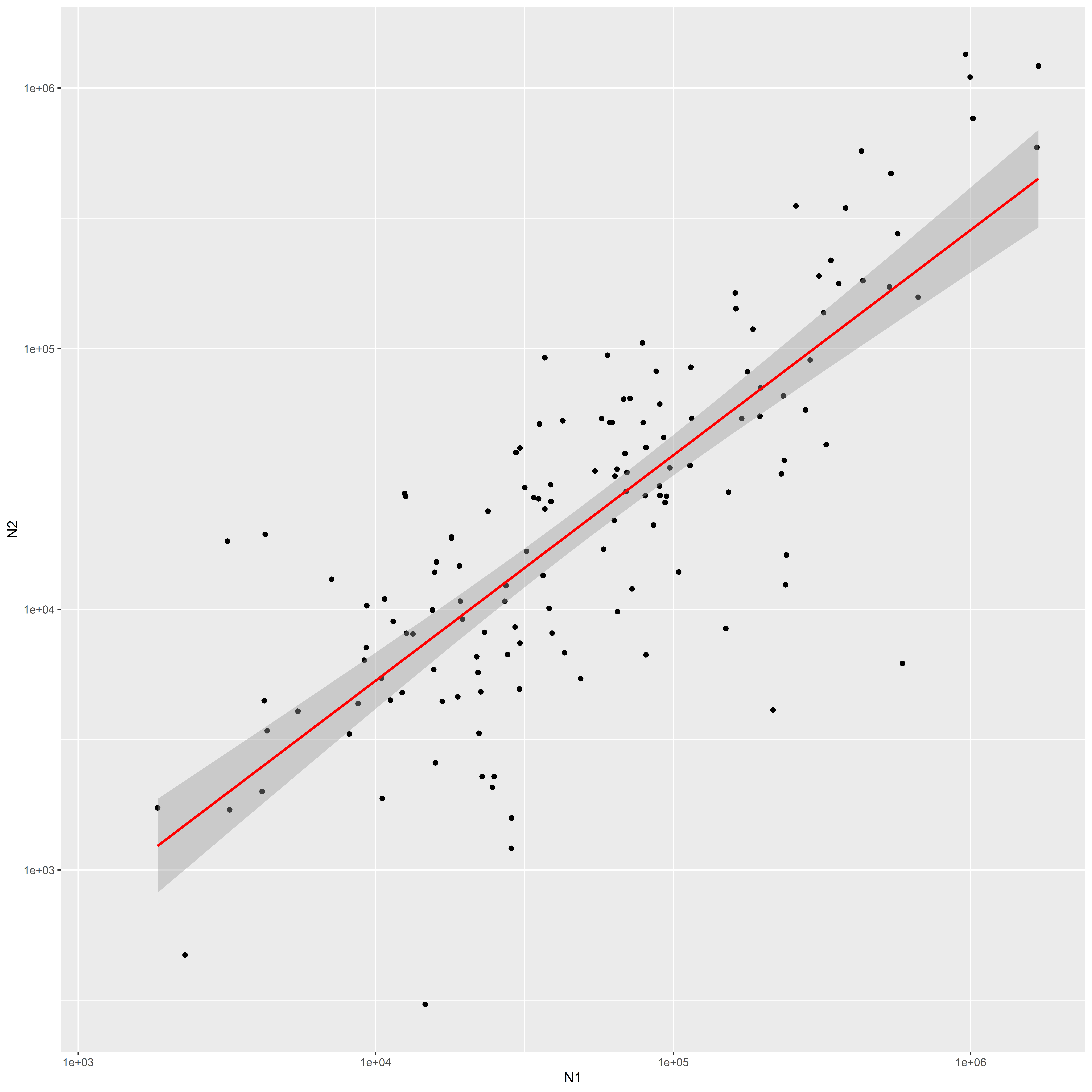
N1 predict N2

`Marlin derived from work by Brian Yandell

The code was derived from work by the DSI. This analysis seeks to model % of tests positive using wastewater Data. This model has logical reasons to be predictive but only finds moderate success when broken down by collection site. Particularly it consistently underpredicts the % positive rate in the P2 district.  
The Original R code file can be found in the [pandemic github repository](https://github.com/UW-Madison-DataScience/pandemic/blob/master/wastewater.Rmd).  
The Code for this R File can be found in the [Marlin Lee waste Water Work](https://github.com/MarlinRLee/Covid-Waste-Water-Exploration/blob/main/general%20model%20finding.Rmd)

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## [1] "Out of the 186 Data points in the data base, 42 N2 points are missing. This means the dataframe is missing 23 Percent of the N2 data"



##   
## Call:  
## lm(formula = N2 ~ N1, data = water)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -495528 -14262 5098 14907 724151   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -1.048e+04 1.027e+04 -1.02 0.309   
## N1 6.586e-01 3.474e-02 18.96 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 107500 on 140 degrees of freedom  
## (44 observations deleted due to missingness)  
## Multiple R-squared: 0.7197, Adjusted R-squared: 0.7177   
## F-statistic: 359.5 on 1 and 140 DF, p-value: < 2.2e-16

