

STAT 331 Final Project

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1 Summary

A maximum of 200 words describing the objective of the report, an overview of the statistical analysis, and summary of the main results.

2 Objective

We are looking to investigate the most influential factors that contribute to the average leukocyte telomere length in a person. We would like to especially look for human-adjustable factors such as whether a person smokes or exposure to persistent organic pollutants.

3 Exploratory Data Analysis

The covariates of interest from the provided dataset are

```
names(pollutants)
```

```
## [1] "length"          "POP_PCB1"        "POP_PCB2"        "POP_PCB3"
## [5] "POP_PCB4"        "POP_PCB5"        "POP_PCB6"        "POP_PCB7"
## [9] "POP_PCB8"        "POP_PCB9"        "POP_PCB10"       "POP_PCB11"
## [13] "POP_dioxin1"     "POP_dioxin2"     "POP_dioxin3"     "POP_furan1"
## [17] "POP_furan2"     "POP_furan3"     "POP_furan4"     "whitecell_count"
## [21] "lymphocyte_pct"  "monocyte_pct"    "eosinophils_pct" "basophils_pct"
## [25] "neutrophils_pct" "BMI"             "edu_cat"         "race_cat"
## [29] "male"           "ageyrs"         "yrssmoke"        "smokenow"
## [33] "ln_lbxcot"
```

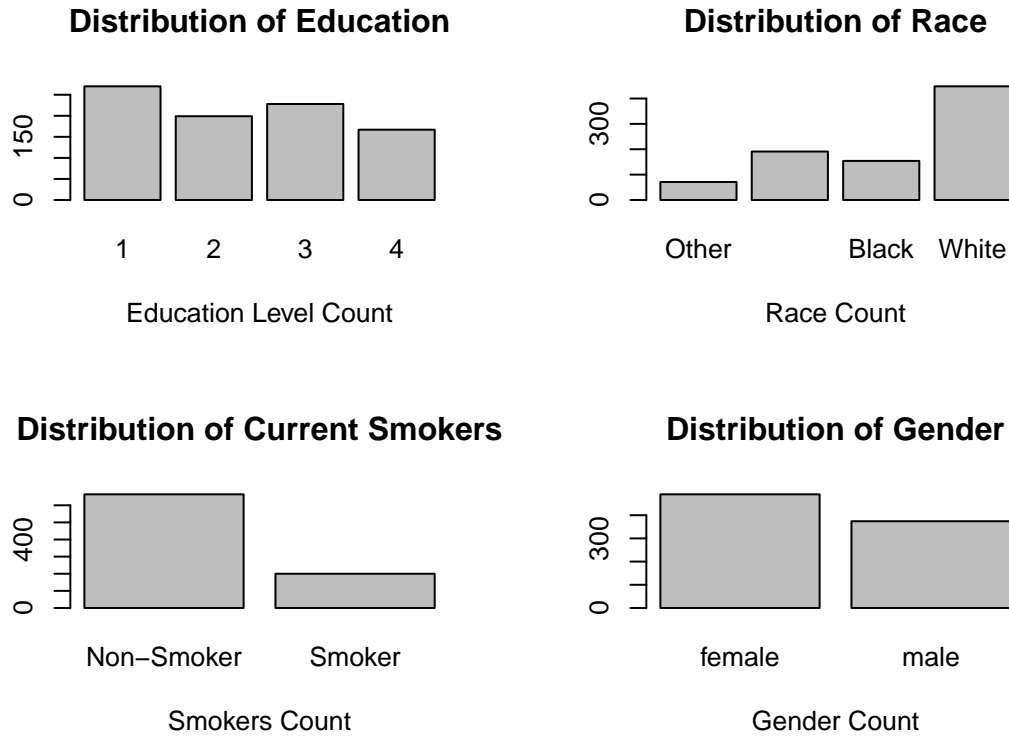
Note that “edu_cat”, “race_cat”, “male”, “smokenow” are categorical values and the rest are continuous.

3.1 Data Distribution

We shall now investigate the distribution of covariates from the supplied data.

From the output of summary statistics on the covariates (see in appendix [7.1](#)), we observed that all values are non-negative and there are more observations with values close to 0 than values with large magnitude across all covariates.

Now we shall have a closer look at the distribution of individual covariate. For categorical data,



We may observe from the bar graphs that there are more data about non-smokers than smokers and white people than other races. There are more entries for lower education than higher, and more female than male. However, the distribution of gender and education is relatively close.

Now for continuous data, we made boxplots to see the distribution of these covariates, the plots can be found in the appendix 7.2. From these plots, we notice some extreme outliers in some concentration values of PCBs, Dioxins, and Furan. The maximum values are sometimes over double the magnitude of the second largest.

However, with a little investigation in the appendix 7.3, we see that the extreme outliers across different types of PCB mostly came from one observation.

```
pollutants[436, 3:12]
```

```
##      POP_PCB2 POP_PCB3 POP_PCB4 POP_PCB5 POP_PCB6 POP_PCB7 POP_PCB8 POP_PCB9
## 436   165000   123000   487000   708000   319000   127000   187000   144000
##      POP_PCB10 POP_PCB11
## 436         131         137
```

This observation contributes to the maximum value for PCB1 to PCB6, as well as PCB8 and PCB9

Similarly, the most extreme outliers from Dioxin and Furan also came from the same entry of data:

- Entry 285 contain the highest value for Dioxin 1 and 3, which are the two extreme outliers as we can see from the boxplots
- Entry 559 contain the highest value for Furan 2 and 4, where Furan 4 has an extreme outlier

Other covariates, as we see from the boxplots, do not have outliers that are as extreme as those from pollutant data. We further observe that they do not have a common entry that contributes to the outliers.

3.2 Multicollinearity

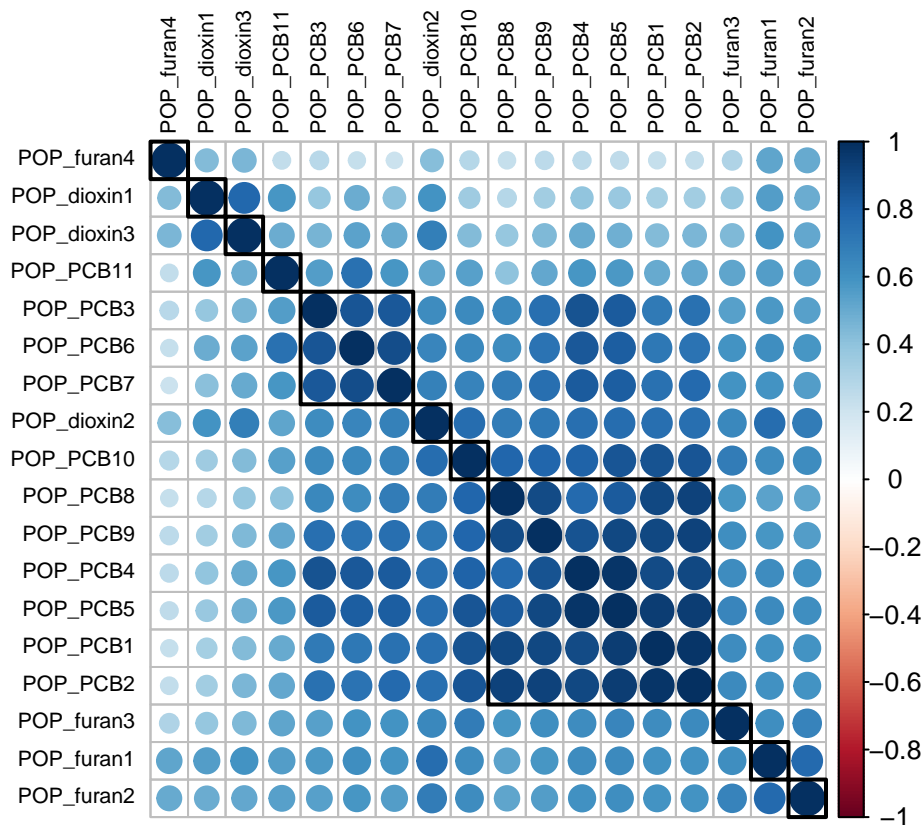
We learned that severe multicollinearity between covariates could result in unstable coefficient estimates and inflated standard errors. Therefore, in this section, we will investigate correlations among values that we may

expect multicollinearity to appear, such as between different types of organic pollutants POP_PCB1–11, POP_dioxin1–3, Pop_furan1–4, as well as white blood cell components.

To obtain the heatmaps that visualize correlations among covariates, we first computed Spearman correlations for each pair of covariates of interest and represented the measured values through gradients of a color scheme. In our example, blue refers to positive correlations and red, negative. Furthermore, the darker colours signify a higher correlation among the covariates. Finally, we clustered variables with higher correlations together such that the covariates within the same rectangles are highly correlated such that they may have dependencies on each other.

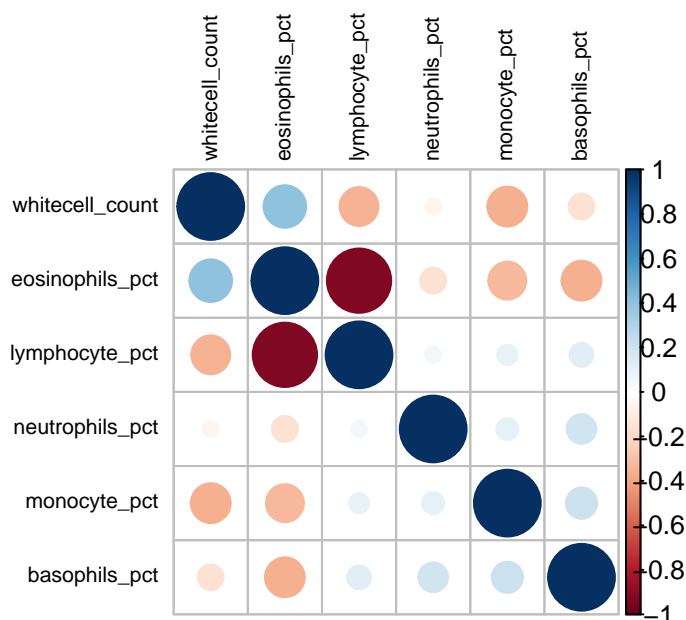
3.2.1 Correlation among Persistent Pollution

```
## corplot 0.84 loaded
```



Based on the above plot, we noticed the correlations mostly exist among the organic pollutants of the same kind. Specifically, the correlations among POP_PCB3,6,7 and POP_PCB8,9,4,5,1,2 are higher than others.

3.2.2 Correlation between White Blood Cells



From the graph above, we see that there is no strong positive correlation among the components of white blood cells, however, there is a strong negative correlation between lymphocytes and eosinophils percentage in the given data.

We shall omit the analysis on correlations between other covariate from this section as we do not expect personal health data such as BMI or years of smoke to have a logical significant correlation with each other, white blood cell data, or exposure to pollutants.

To further investigate how these listed correlations affect the observed data, we may use variance inflation factor (VIF), which we would further discuss in Methods sections.

3.2.3 Possible Interactions among Persistent Pollution and White Blood Cells

Associations between different covariates might affect their relationships with the outcomes. Therefore, it is also necessary to explore the possibility of adding interaction terms. In our data analysis, we are interested in whether the relationship between mean leukocyte telomere length and the white blood cells are influenced by the concentration of persistent pollution; To test our hypothesis, we performed a p-test and check their statistical significance. More details are discussed under the Methods section.

4 Methods

Describe your statistical analysis: What is your model? Did you use any transformations or extensions of the basic multiple linear regression model? How did you select a model? Does the model fit the data well? Are the necessary assumptions met? Be sure to explain and justify your decisions.

4.1 Linear Model Assumptions

Since we have no access to data collection process, we shall proceed by assuming that the independence assumption is satisfied. As for the normality assumption, as the given dataset is relatively large, we may assume the data is approximately Normally distributed due to the Central Limit Theorem.

Now to assess whether any covariate has a nonlinearity relationship with the outcome in the multiple linear regression model, we used added-variable plots(avPlot), as shown in appendix 7.4. The plots isolate the relationship between the outcome and each of the covariates after adjusting for the other covariate. If the

plot of the outcome versus a covariate x has a nonlinear shape, it may indicate a regression model with a higher power of this variable, for example, x^2 . With the given data, we see from the `avPlots` that all plots have a linear shape, thus the outcome is expected to have a linear relationship with all of the covariates. Therefore, the models constructed in this report do not consider non-linear terms.

Finally, we also need to verify the equal variance (homoscedasticity) assumption. As shown in the appendix 7.5, if there are evident patterns in the residuals, we might not be able to simply trust the results. Fortunately, we can see that the random residuals are uncorrelated and uniform.

4.2 Finding the model

We shall first split the data into training and testing set to ensure the final model is well-generalized without problems such as overfitting or underfitting.

```
set.seed(23)
train_idx <- sample(nrow(pollutants), 650, replace = FALSE, prob = NULL)
train_data <- pollutants[train_idx,]
test_data <- pollutants[-train_idx, ]
```

4.2.1 Investigate Interactions

As we have seen in the EDA section, we would like to investigate interactions among pollutants as well as white blood cell-related data. By building a large linear model and filtering the interactions with p values ≤ 0.05 , we have selected the following potential interaction terms that we may consider in the model building process:

```
names(selected)

## [1] "POP_PCB1:POP_PCB9"          "POP_PCB2:POP_PCB4"
## [3] "POP_PCB2:POP_PCB5"          "POP_PCB2:POP_PCB6"
## [5] "POP_PCB2:POP_PCB8"          "POP_PCB2:POP_PCB9"
## [7] "POP_PCB2:POP_PCB10"         "POP_PCB2:POP_furan3"
## [9] "POP_PCB2:POP_furan4"        "POP_PCB2:lymphocyte_pct"
## [11] "POP_PCB2:monocyte_pct"       "POP_PCB2:eosinophils_pct"
## [13] "POP_PCB2:basophils_pct"      "POP_PCB4:POP_PCB10"
## [15] "POP_PCB4:POP_dioxin3"        "POP_PCB5:POP_PCB11"
## [17] "POP_PCB5:POP_dioxin2"        "POP_PCB5:POP_dioxin3"
## [19] "POP_PCB5:POP_furan2"        "POP_PCB6:POP_PCB8"
## [21] "POP_PCB6:POP_PCB10"          "POP_PCB7:POP_PCB9"
## [23] "POP_PCB7:POP_dioxin2"        "POP_PCB8:POP_PCB10"
## [25] "POP_PCB8:POP_PCB11"          "POP_PCB8:POP_furan3"
## [27] "POP_PCB9:POP_dioxin2"        "whitecell_count:lymphocyte_pct"
## [29] "whitecell_count:monocyte_pct" "whitecell_count:eosinophils_pct"
## [31] "whitecell_count:basophils_pct"
```

We now shall select a linear model with all covariate and interaction terms, we can find the summary of the resulting model in the appendix 7.7.1.

```
MAIC_Interaction

##
## Call:
## lm(formula = length ~ POP_PCB1 + POP_PCB10 + POP_furan3 + whitecell_count +
##     eosinophils_pct + race_cat + male + ageyrs + ln_lbxcot, data = train_data)
##
## Coefficients:
##      (Intercept)      POP_PCB1      POP_PCB10      POP_furan3
```

```
##      1.305e+00      -7.505e-07      1.527e-03      3.658e-03
## whitecell_count eosinophils_pct race_catMexican race_catBlack
##      -6.718e-03      2.110e-03      -1.834e-02      5.185e-02
##      race_catWhite      malemale      ageyrs      ln_lbxcot
##      -1.286e-02      -5.164e-02      -6.727e-03      5.046e-03
```

```
AIC_MSPE
```

```
## [1] 0.0471547
```

```
MBIC_Interaction
```

```
##
## Call:
## lm(formula = length ~ POP_PCB10 + male + ageyrs, data = train_data)
##
## Coefficients:
## (Intercept) POP_PCB10      malemale      ageyrs
##      1.399288      0.001788      -0.053197      -0.007457
```

```
BIC_MSPE
```

```
## [1] 0.04679024
```

This result shows that the model selected by BIC is preferred as it has a lower MSPE, is more generalized, and easier to interpret. At the same time, note that the model chosen by AIC has more parameters but a lower prediction score, this implies that the added parameters added too much variability to the model and seems to have overfitted the training data.

We decided to name the model selected by BIC here as our first candidate model (Model 1), which has the formula:

```
model1_f <- formula(MBIC_Interaction)
model1_f
```

```
## length ~ POP_PCB10 + male + ageyrs
```

Furthermore, as we had only selected one interaction term in the AIC model and it did not improve the performance of the model. We decided that none of the interaction terms contribute significantly to the outcome of interest (telomere length). In the next part of the analysis, we have removed these terms for simplicity.

4.2.2 Reduce Multicollinearity

An additional technique we may use to reduce the impact of multicollinearity on our model is checking variance inflation factor (VIF). As interaction terms were eliminated, we shall regress on all non-categorical covariates and identify those with the largest VIF one at a time until there were no more with 'high' multicollinearity. We used a VIF (Variance Inflation Factor) > 10 as an indicator of "high" multicollinearity (general practice). And after the covariate eliminations, The explanatory variables that remained from the selection are:

```
VIFselected
```

```
## [1] "POP_PCB3"      "POP_PCB6"      "POP_PCB7"      "POP_PCB8"
## [5] "POP_PCB9"      "POP_PCB10"     "POP_PCB11"     "POP_dioxin1"
## [9] "POP_dioxin2"   "POP_dioxin3"   "POP_furan1"    "POP_furan2"
## [13] "POP_furan3"   "POP_furan4"   "whitecell_count" "lymphocyte_pct"
## [17] "monocyte_pct"  "basophils_pct" "neutrophils_pct" "BMI"
## [21] "edu_cat"       "race_cat"      "male"          "ageyrs"
## [25] "yrssmoke"      "smokenow"      "ln_lbxcot"
```

To validate our parameter selection steps, we could run stepwise selection again on the reduced model.

4.2.3 Model via Forward-Backward Selection

```
MAIC_reduced
```

```
##
## Call:
## lm(formula = length ~ POP_dioxin3 + POP_furan3 + lymphocyte_pct +
##     race_cat + male + ageyrs + ln_lbxcot, data = train_data)
##
## Coefficients:
##      (Intercept)      POP_dioxin3      POP_furan3  lymphocyte_pct
##      1.436e+00      -3.528e-05      5.877e-03      -1.801e-03
## race_catMexican  race_catBlack  race_catWhite      malemale
##      -1.633e-02      5.850e-02      -1.014e-02      -5.309e-02
##      ageyrs      ln_lbxcot
##      -6.600e-03      3.965e-03
```

```
AIC_MSPE
```

```
## [1] 0.04709662
```

```
MBIC_reduced # model 1
```

```
##
## Call:
## lm(formula = length ~ POP_furan3 + ageyrs, data = train_data)
##
## Coefficients:
## (Intercept)  POP_furan3      ageyrs
##      1.373603      0.005311     -0.007226
```

```
BIC_MSPE
```

```
## [1] 0.04554553
```

We observe that the model selected by AIC is smaller compared to the previous section. The smaller model yields a better MSPE score which further confirms that the previous model selected by AIC has overfitted the training data. The model selected by BIC is still smaller than the one with AIC, and it also outperforms it. This model is different from Model 1 but as interpretable. Therefore, we decided to use the BIC model as our second candidate model, named Model 2. The formula of Model 2 is:

The formula of model 1 is:

```
model2_f <- formula(MBIC_reduced)
model2_f
```

```
## length ~ POP_furan3 + ageyrs
```

4.2.4 Model Selection via Forward-Backward Selection without Outliers

Recall that when we were performing EDA in section 3.1, we have identified 3 entries that contribute to the extreme outliers in the pollutant exposure values, which were entry with index 436,285,and 559. In this section we shall remove these outliers and observe its effect on the model selection process.

```
MAIC_no
```

```
##
## Call:
## lm(formula = length ~ POP_furan3 + ageyrs + ln_lbxcot + male,
##     data = train_data_no)
```

```
##
## Coefficients:
## (Intercept)  POP_furan3      ageyrs    ln_lbxcot    malemale
##      1.372700      0.006585    -0.007083     0.005477    -0.025957
```

```
AIC_MSPE
```

```
## [1] 0.04364918
```

```
MBIC_no
```

```
##
## Call:
## lm(formula = length ~ POP_furan3 + ageyrs, data = train_data_no)
##
## Coefficients:
## (Intercept)  POP_furan3      ageyrs
##      1.369268      0.006571    -0.007345
```

```
BIC_MSPE
```

```
## [1] 0.04374874
```

We observe that without the outliers identified in the EDA section, stepwise algorithm selected the a smaller model with AIC and the same model as Model 2 with BIC. Since the model selected with AIC has a good prediction score and is interpretable, we shall consider this as another candidate model, called Model 3, which has the formula:

```
model3_f <- formula(MAIC_no)
model3_f
```

```
## length ~ POP_furan3 + ageyrs + ln_lbxcot + male
```

4.2.5 Model Tuning via Cross-Validation with Ridge

In order to get accurate prediction evaluations for our models, we used the idea of 75% and 25% train-test split; to ensure the entire training set was covered and each observation was well represented, we divided the training data into 10 folds and repeatedly cross-validated the MSPE.

Besides, we performed shrinkage methods like LASSO and ridge to solve the overfitting problem. For example, we used ridge with cross validation to tune our Model 1, 2, and 3:

```
## Loading required package: Matrix
```

```
## Loaded glmnet 4.1-1
```

```
model1_f
```

```
## length ~ POP_PCB10 + male + ageyrs
```

```
Ridge_MSPE1
```

```
## [1] 0.04661126
```

```
model2_f
```

```
## length ~ POP_furan3 + ageyrs
```

```
Ridge_MSPE2
```

```
## [1] 0.04568024
```

```
model3_f

## length ~ POP_furan3 + ageyrs + ln_lbxcot + male
Ridge_MSPE3

## [1] 0.04605872
```

4.2.6 Model Selection via Cross-Validation with LASSO

With the consideration that lasso could also do parameter selections, we examined sending the remaining covariates in the VIF reduced model alongwith the categorical covariates to 'glmnet' function and let it pick the best model for us. We named it model 2.

```
f_lasso

## length ~ POP_furan3 + lymphocyte_pct + monocyte_pct + edu_cat_1 +
##      race_cat_Black + male_female + male_male + ageyrs + ln_lbxcot
lasso_MSPE

## [1] 0.04653322
```

5 Results

Report on the findings of your analysis

In the end, we looked at the model performance on the remaining test set and computed the MPSE of each model.

```
Ridge_MSPE1

## [1] 0.04661126
Ridge_MSPE2

## [1] 0.04568024
Ridge_MSPE3

## [1] 0.04605872
lasso_MSPE

## [1] 0.04653322
```

Comparing the MSE of the three different candidates we found earlier, model2 with the formula $f = \text{length} \sim \text{POP_furan3} + \text{ageyrs}$ has the best performance. As mentioned earlier, this model is also generalized, easy to interpret, and unlikely to get overfitted. We can now answer the question asked in our objective, that the age of the person, and the concentration of foran 3 contribute greatly to the average leukocyte telomere length in a person.

6 Discussion

Comment on your findings/conclusions; describe any limitations of your analysis.

We have considered the multicollinearity and interactions within the eleven PCB covariates and similarly for the three dioxin covariates and four furan covariates. However, the multicollinearity and interactions between these eighteen exposure covariates and other covariates are not considered. It is expected that there does not exist any causal relationship between exposure covariates and other covariates since the former relates to the

surrounding environment and the latter relates to personal characteristics. For example, it's believed that the concentration of POP_PCB10 is unrelated to the value of ageys and BMI.

Besides, a linear regression model has four assumptions, namely linearity, normality, heteroskedasticity and independence. We have analyzed and confirmed that the first three assumptions hold. Generally, we can make the assumption of independence when constructing the model. To further confirm the assumption, time-series data and a closer look at the data collection process will be helpful.

7 Appendix

7.1 Data Summary

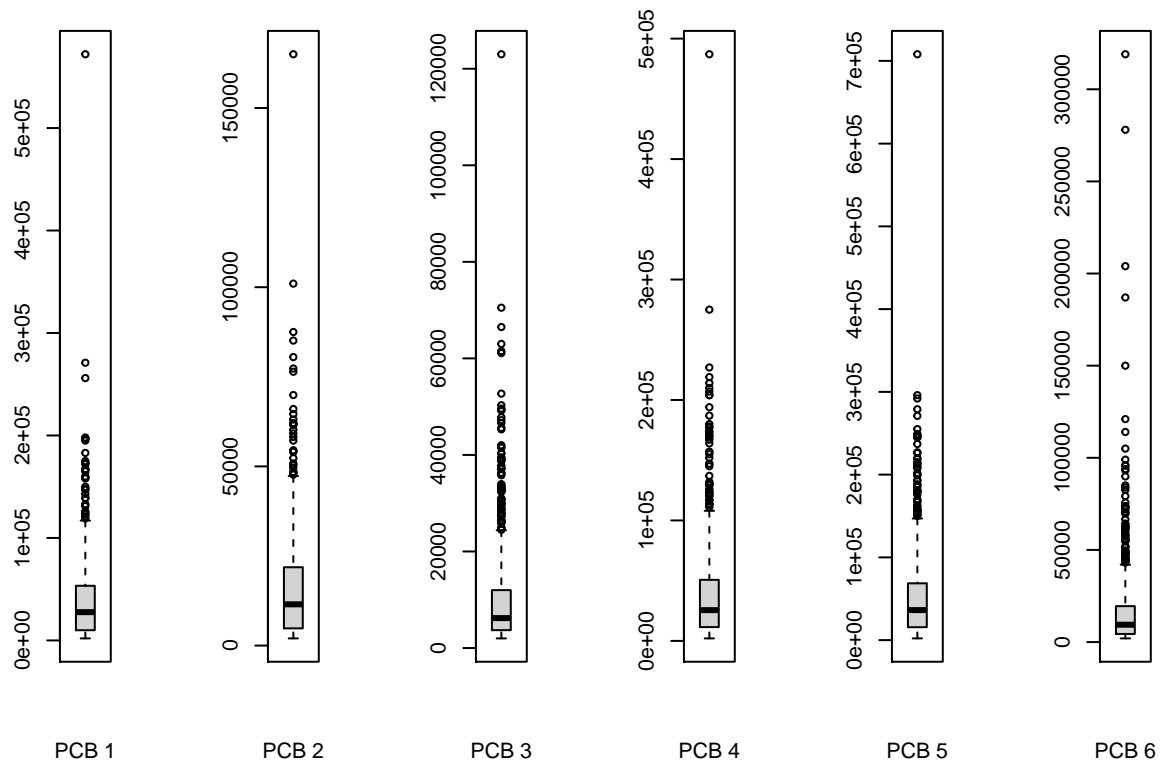
Looking at the useful metrics for the data

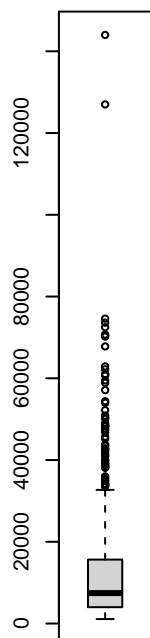
```
summary(pollutants)
```

```
##      length      POP_PCB1      POP_PCB2      POP_PCB3
## Min.   :0.5266   Min.    : 2000   Min.    : 2000   Min.    : 2000
## 1st Qu.:0.8754   1st Qu.: 9975   1st Qu.: 4800   1st Qu.: 3700
## Median :1.0286   Median : 27600   Median : 11500   Median : 6200
## Mean   :1.0543   Mean    : 38082   Mean    : 15637   Mean    : 10158
## 3rd Qu.:1.2095   3rd Qu.: 53325   3rd Qu.: 21825   3rd Qu.: 12000
## Max.   :2.3512   Max.    :572000   Max.    :165000   Max.    :123000
##      POP_PCB4      POP_PCB5      POP_PCB6      POP_PCB7
## Min.    : 2100   Min.    : 2100   Min.    : 2000   Min.    : 1100
## 1st Qu.: 11475   1st Qu.: 15600   1st Qu.: 4400   1st Qu.: 4000
## Median : 25550   Median : 36300   Median : 9400   Median : 7450
## Mean    : 38456   Mean    : 52650   Mean    : 16820   Mean    : 12682
## 3rd Qu.: 50650   3rd Qu.: 68625   3rd Qu.: 19500   3rd Qu.: 15625
## Max.    :487000   Max.    :708000   Max.    :319000   Max.    :144000
##      POP_PCB8      POP_PCB9      POP_PCB10     POP_PCB11
## Min.    : 1100   Min.    : 1100   Min.    : 1.70   Min.    : 1.30
## 1st Qu.: 3800   1st Qu.: 3900   1st Qu.: 9.10   1st Qu.: 14.80
## Median : 6950   Median : 8050   Median : 18.35   Median : 24.50
## Mean    : 10530   Mean    : 12220   Mean    : 24.49   Mean    : 38.15
## 3rd Qu.: 14425   3rd Qu.: 16025   3rd Qu.: 34.90   3rd Qu.: 42.95
## Max.    :187000   Max.    :144000   Max.    :172.00   Max.    :845.00
##      POP_dioxin1    POP_dioxin2    POP_dioxin3    POP_furan1
## Min.    : 1.90   Min.    : 1.40   Min.    : 36.8   Min.    : 1.000
## 1st Qu.: 23.90   1st Qu.: 21.27   1st Qu.: 197.0   1st Qu.: 3.200
## Median : 41.35   Median : 37.80   Median : 342.5   Median : 5.200
## Mean    : 57.65   Mean    : 47.81   Mean    : 494.4   Mean    : 6.371
## 3rd Qu.: 71.62   3rd Qu.: 62.42   3rd Qu.: 603.0   3rd Qu.: 7.700
## Max.    :760.00   Max.    :281.00   Max.    :8190.0   Max.    :44.400
##      POP_furan2    POP_furan3    POP_furan4    whitecell_count
## Min.    : 0.800   Min.    : 0.700   Min.    : 0.90   Min.    : 2.300
## 1st Qu.: 2.600   1st Qu.: 2.200   1st Qu.: 6.40   1st Qu.: 5.600
## Median : 4.200   Median : 5.050   Median : 9.65   Median : 6.900
## Mean    : 5.390   Mean    : 6.669   Mean    : 11.54   Mean    : 7.191
## 3rd Qu.: 6.825   3rd Qu.: 9.300   3rd Qu.: 14.00   3rd Qu.: 8.300
## Max.    :33.500   Max.    :38.300   Max.    :234.00   Max.    :20.100
##      lymphocyte_pct  monocyte_pct  eosinophils_pct  basophils_pct
## Min.    : 5.80   Min.    : 1.600   Min.    :21.60   Min.    : 0.000
## 1st Qu.:24.00   1st Qu.: 6.600   1st Qu.:52.35   1st Qu.: 1.500
## Median :28.95   Median : 7.700   Median :59.30   Median : 2.300
## Mean    :29.92   Mean    : 7.936   Mean    :58.62   Mean    : 2.903
## 3rd Qu.:35.42   3rd Qu.: 9.100   3rd Qu.:65.22   3rd Qu.: 3.700
## Max.    :73.40   Max.    :23.800   Max.    :88.10   Max.    :28.200
##      neutrophils_pct      BMI      edu_cat      race_cat      male
## Min.    :0.0000   Min.    :16.16   1:270   Other   : 71   female:490
## 1st Qu.:0.4000   1st Qu.:23.88   2:199   Mexican:191   male   :374
## Median :0.6000   Median :27.38   3:228   Black   :154
## Mean    :0.6669   Mean    :28.09   4:167   White   :448
```

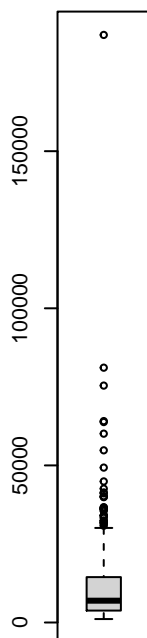
```
## 3rd Qu.:0.8000 3rd Qu.:31.17
## Max. :5.5000 Max. :62.99
## ageyrs yrssmoke smokenow ln_lbxcot
## Min. :20.00 Min. : 0.0 Non-Smoker:664 Min. : -4.5099
## 1st Qu.:34.00 1st Qu.: 0.0 Smoker :200 1st Qu.: -4.0745
## Median :46.00 Median : 0.0 Median : -2.7334
## Mean :48.36 Mean :10.6 Mean : -0.9804
## 3rd Qu.:63.00 3rd Qu.:20.0 3rd Qu.: 2.8000
## Max. :85.00 Max. :69.0 Max. : 6.5848
```

7.2 Boxplots

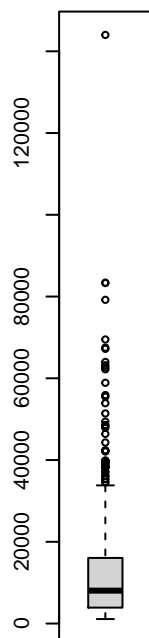




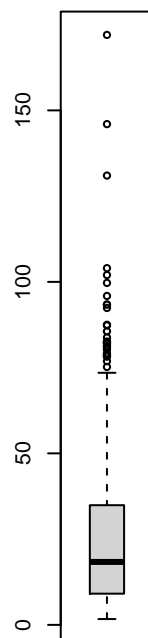
PCB 7



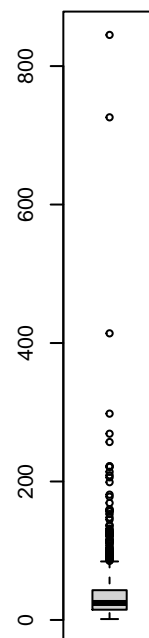
PCB 8



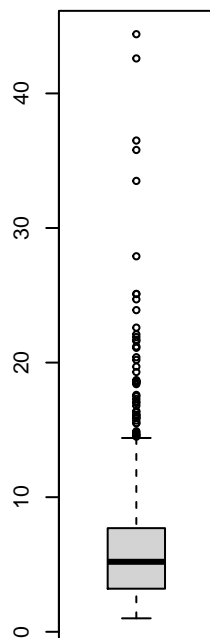
PCB 9



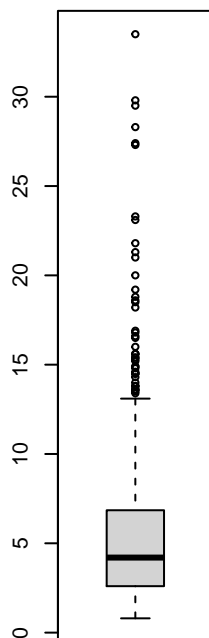
PCB 10



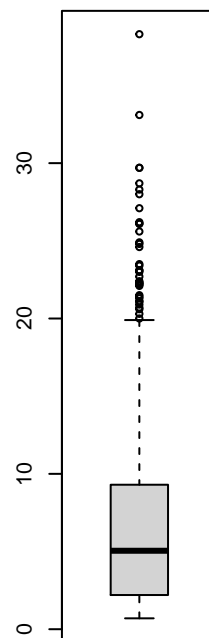
PCB 11



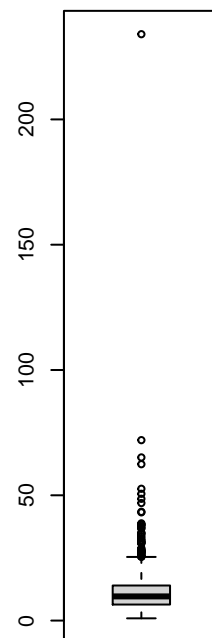
Furan 1



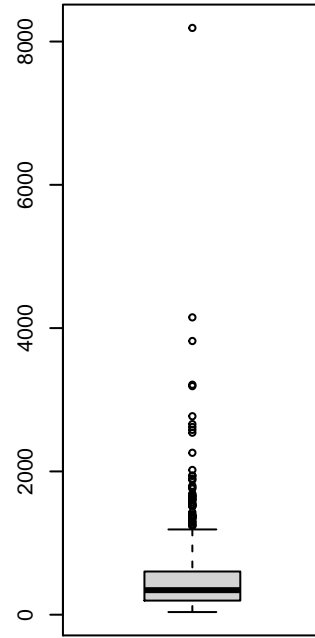
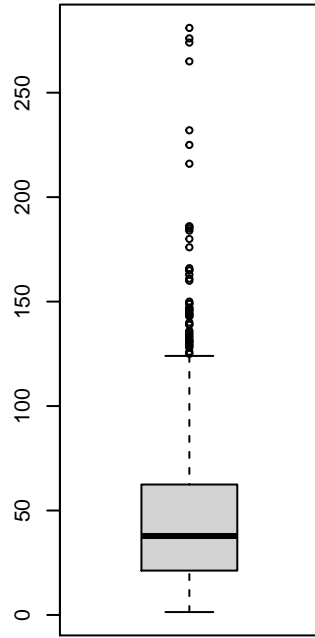
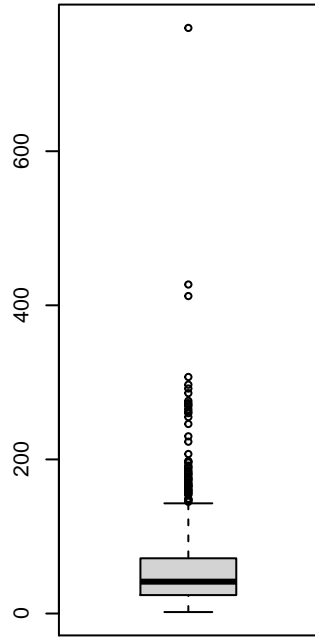
Furan 2



Furan 3



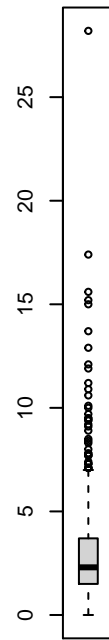
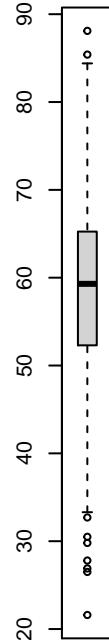
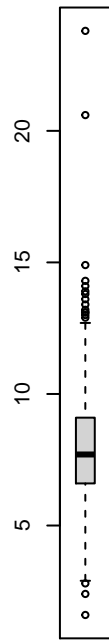
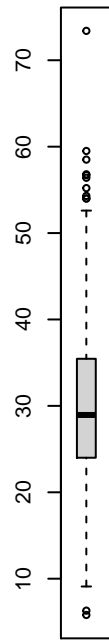
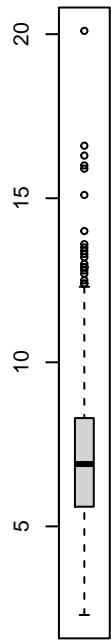
Furan 4



Dioxin 1

Dioxin 2

Dioxin 3



WBC Cnt

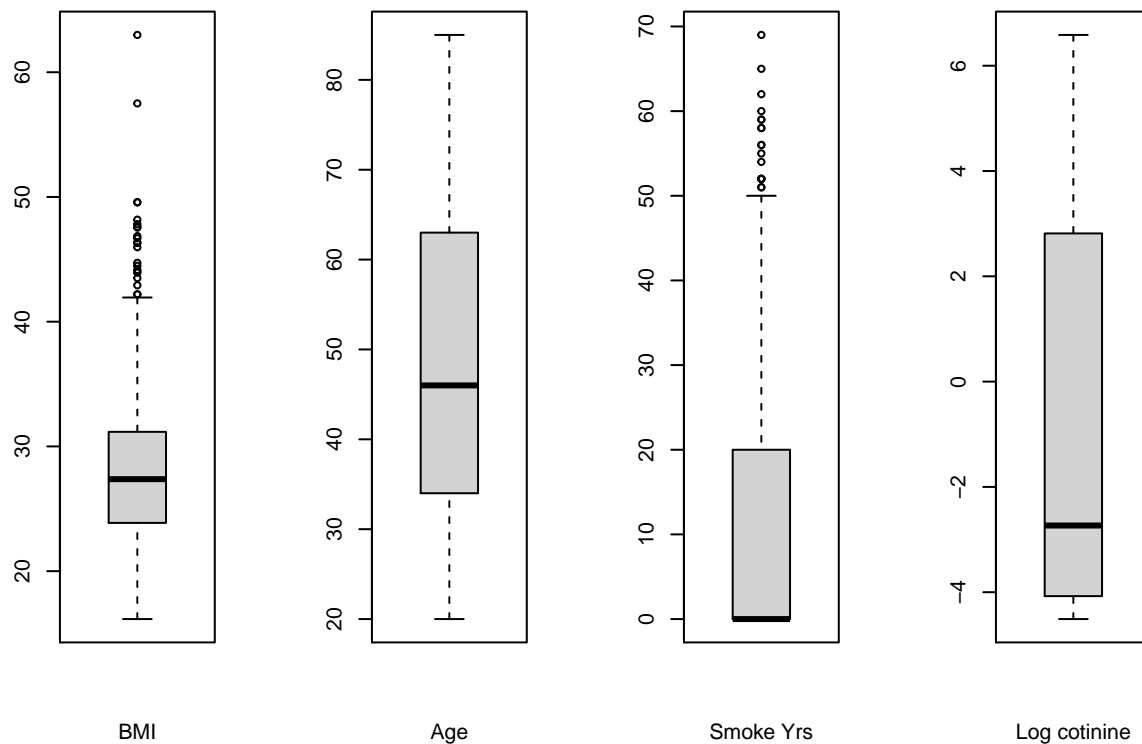
lymph %

mono %

eosin %

baso %

neutro %



7.3 Outlier Entries

Here we will find entries where outliers for different covariate occurred.

```
pollutant_mat = data.matrix(pollutants, rownames.force = NA)
```

```
max_PCB_idx = c()
for (c in 2:12) {
  max_PCB_idx[c-1] = which.max(pollutant_mat[, c])
}
max_PCB_idx
```

```
## [1] 436 436 436 436 436 436 426 436 436 298 272
```

```
max_dioxin_idx = c()
for (c in 13:15) {
  max_dioxin_idx[c-12] = which.max(pollutant_mat[, c])
}
max_dioxin_idx
```

```
## [1] 285 573 285
```

```
max_furan_idx = c()
for (c in 16:19) {
  max_furan_idx[c-15] = which.max(pollutant_mat[, c])
}
max_furan_idx
```

```
## [1] 230 559 590 559
```

```
max_WBC_idx = c()
for (c in 20:25) {
```

```

    max_WBC_idx[c-19] = which.max(pollutant_mat[, c])
  }
  max_WBC_idx

```

```
## [1] 211 766 440 782 739 415
```

7.4 AvPlots

```

# testing non-linearity in SLR
# if for any covariate, residual vs x for M1 has a pattern and
# residual vs x for M2 seems random, then y has a nonlinear
# relationship with with x.
# M1: fitting y to x
# M2: fitting y to x^2

par(mfrow=c(1, 3))
outcome <- pollutants$length
check <- function(x) {
  M1 <- lm(outcome ~ x)
  print(paste("residual for M1: ", sigma(M1)))
  M2 <- lm(outcome ~ x + I(x^2))
  print(paste("residual for M2: ", sigma(M2)))
  plot(x, M1$residual)
  plot(x, M2$residual)
  plot(x, outcome)
}

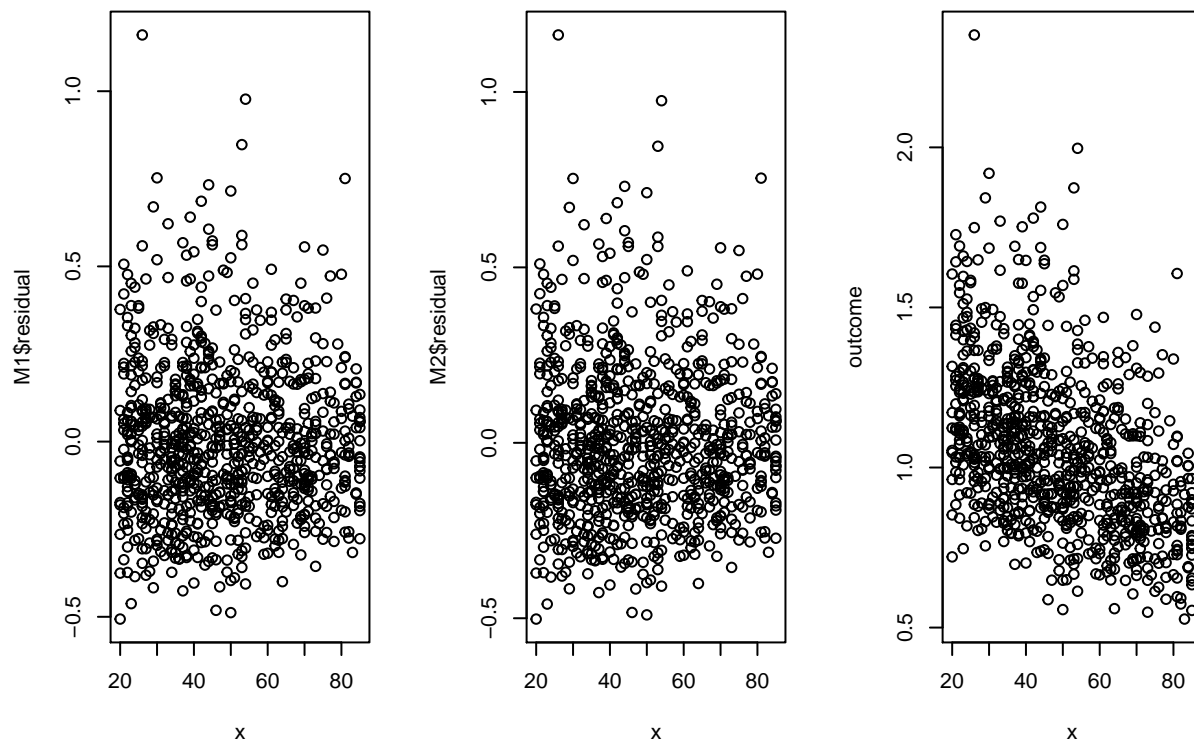
list <- list(pollutants$ageyrs, pollutants$yrssmoke,
             pollutants$BMI, pollutants$ln_lbxcot,
             pollutants$whitecell_count, pollutants$lymphocyte_pct,
             pollutants$monocyte_pct, pollutants$eosinophils_pct,
             pollutants$basophils_pct, pollutants$neutrophils_pct)
for (column in list) {
  check(column)
}

```

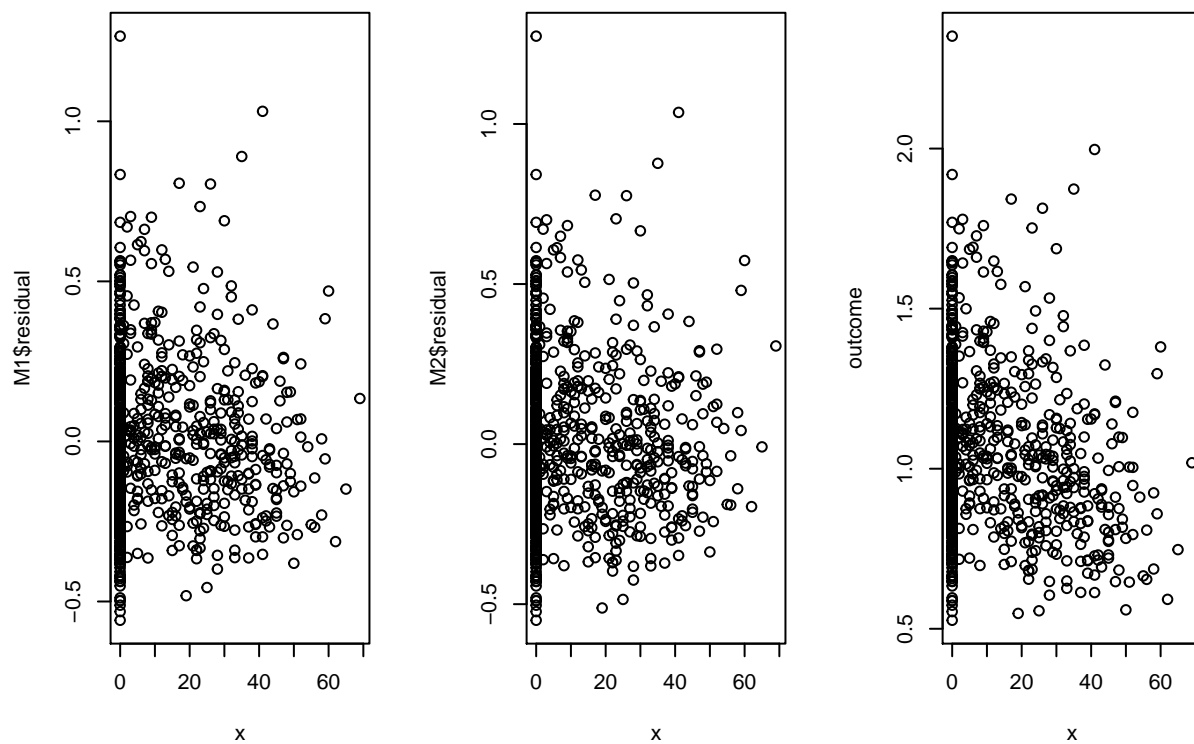
```

## [1] "residual for M1: 0.224172364185412"
## [1] "residual for M2: 0.22429269961392"

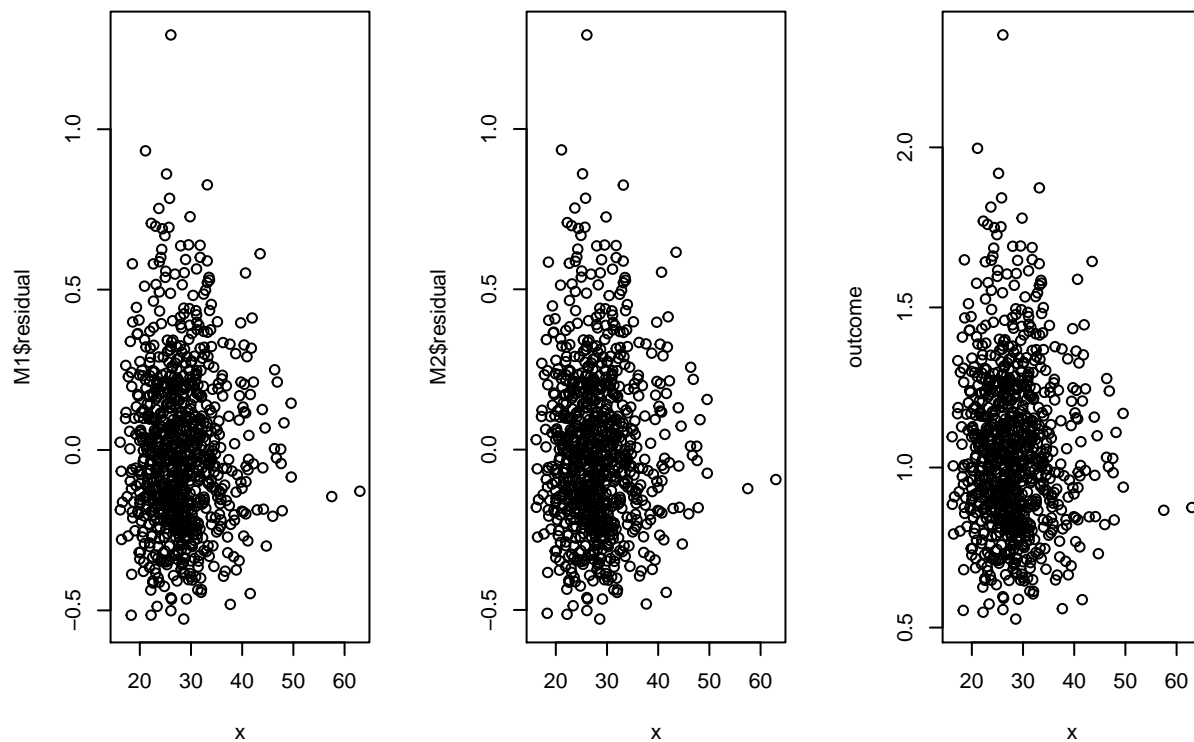
```



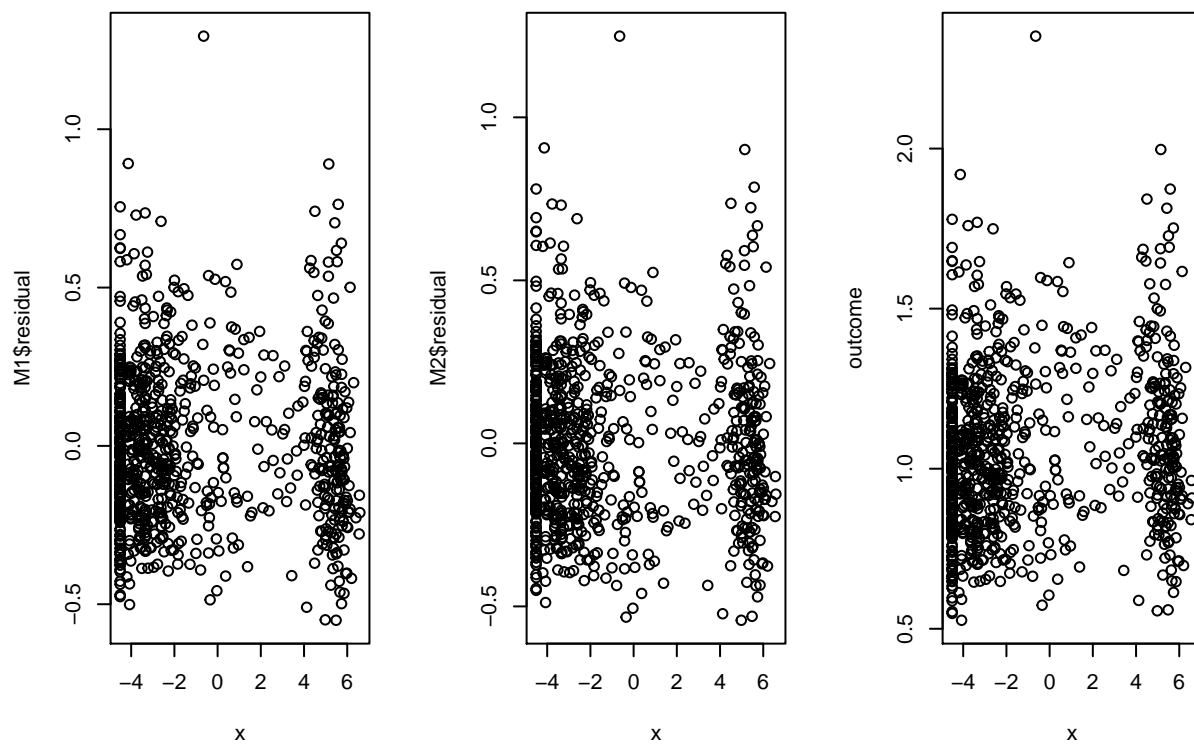
```
## [1] "residual for M1: 0.246320733146214"
## [1] "residual for M2: 0.245622720856213"
```



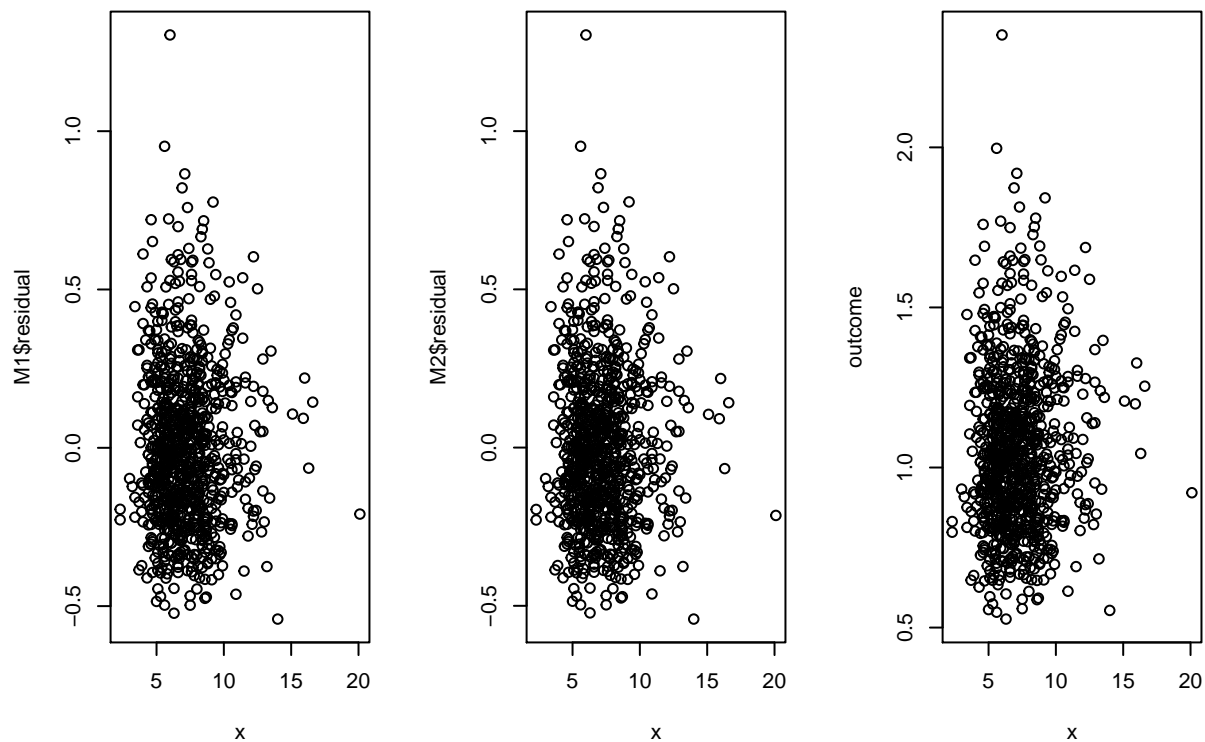
```
## [1] "residual for M1: 0.250228706427173"
## [1] "residual for M2: 0.25036248052387"
```



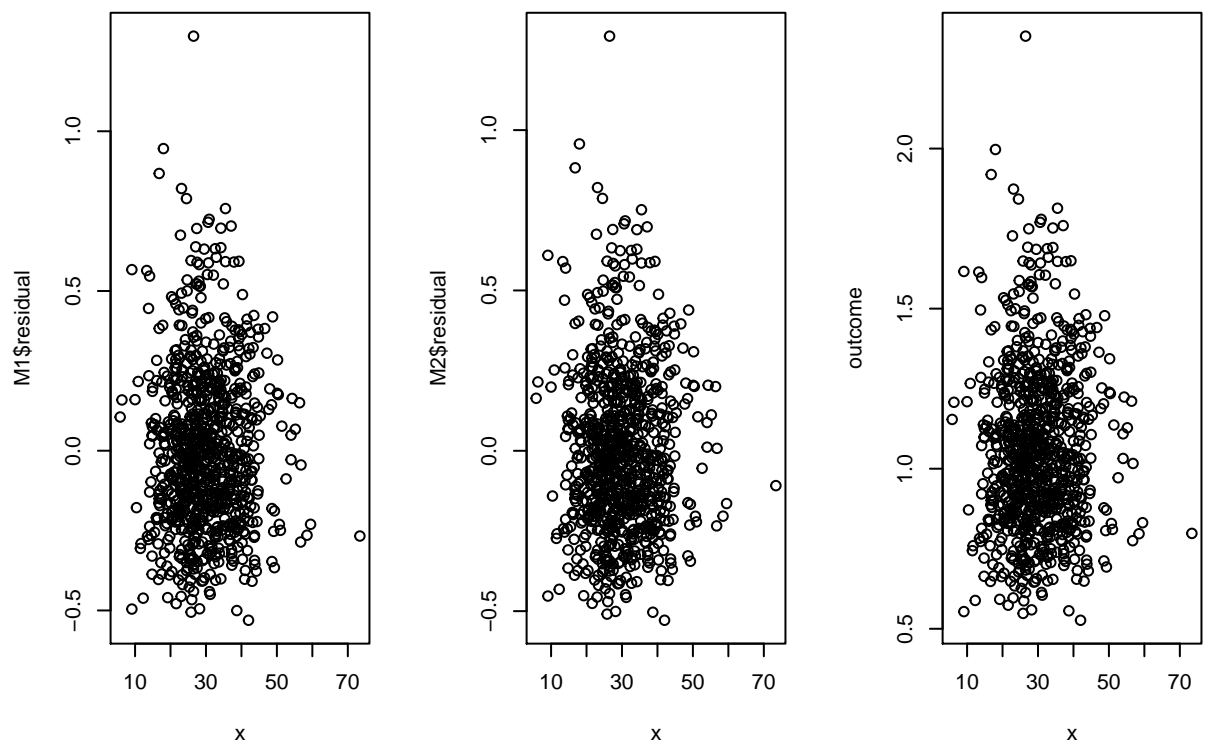
```
## [1] "residual for M1: 0.248212063673837"
## [1] "residual for M2: 0.24710732733351"
```



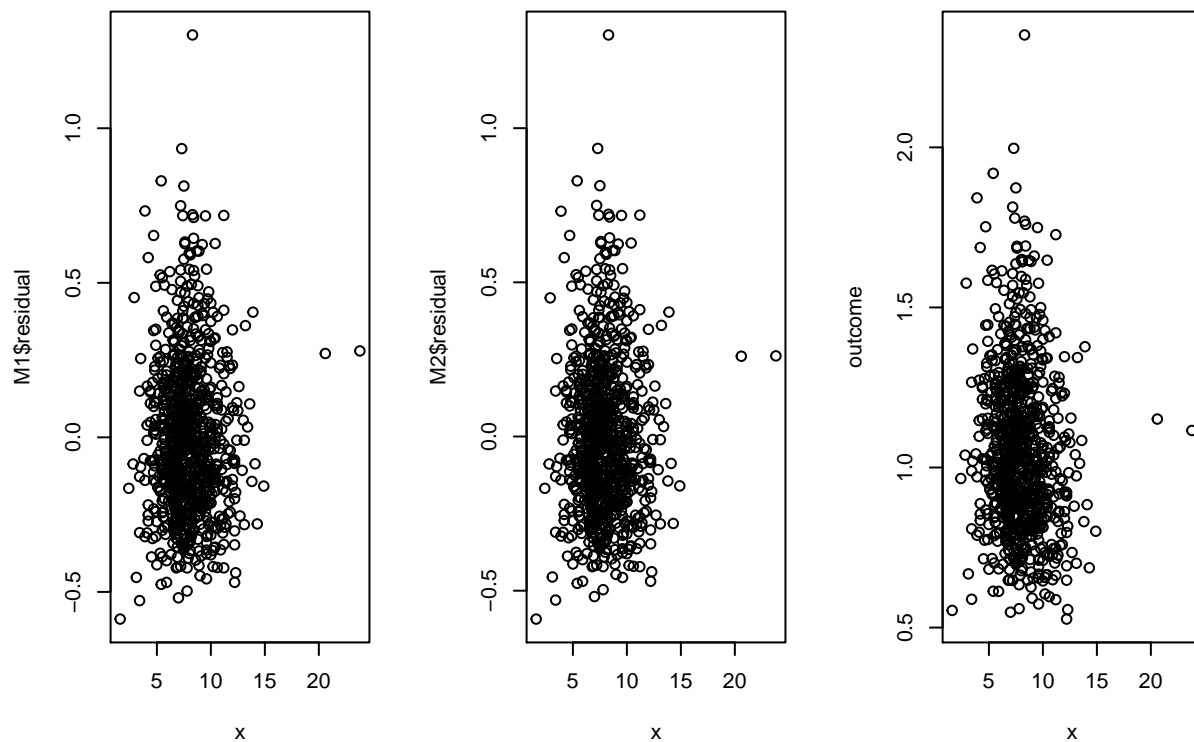
```
## [1] "residual for M1: 0.250065445847753"
## [1] "residual for M2: 0.250210403543218"
```



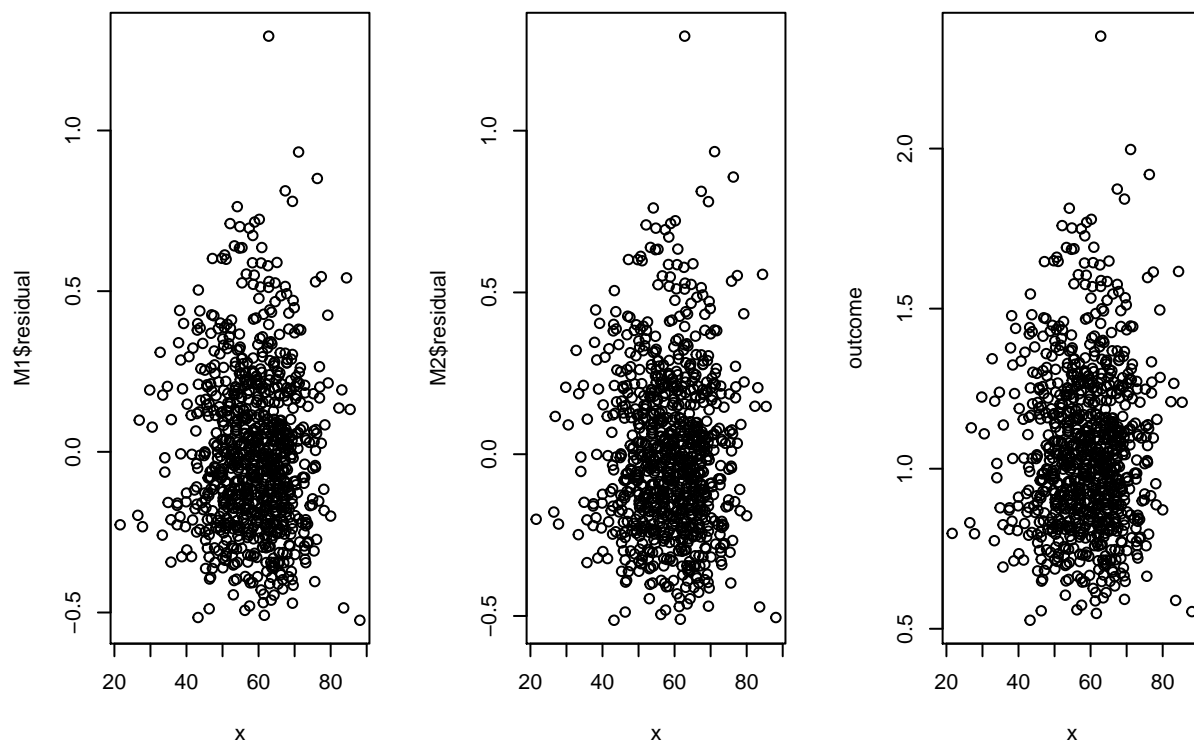
```
## [1] "residual for M1: 0.250373616826691"
## [1] "residual for M2: 0.250255208638358"
```



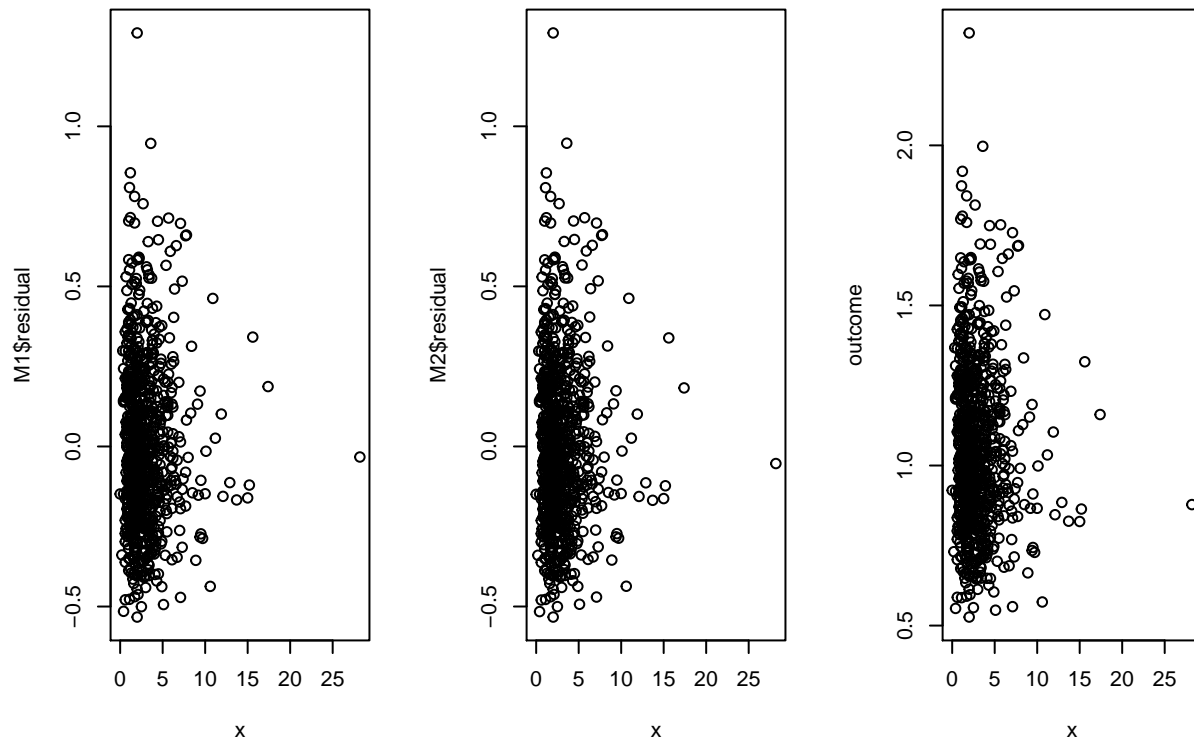
```
## [1] "residual for M1: 0.248704466454944"
## [1] "residual for M2: 0.248847192837983"
```



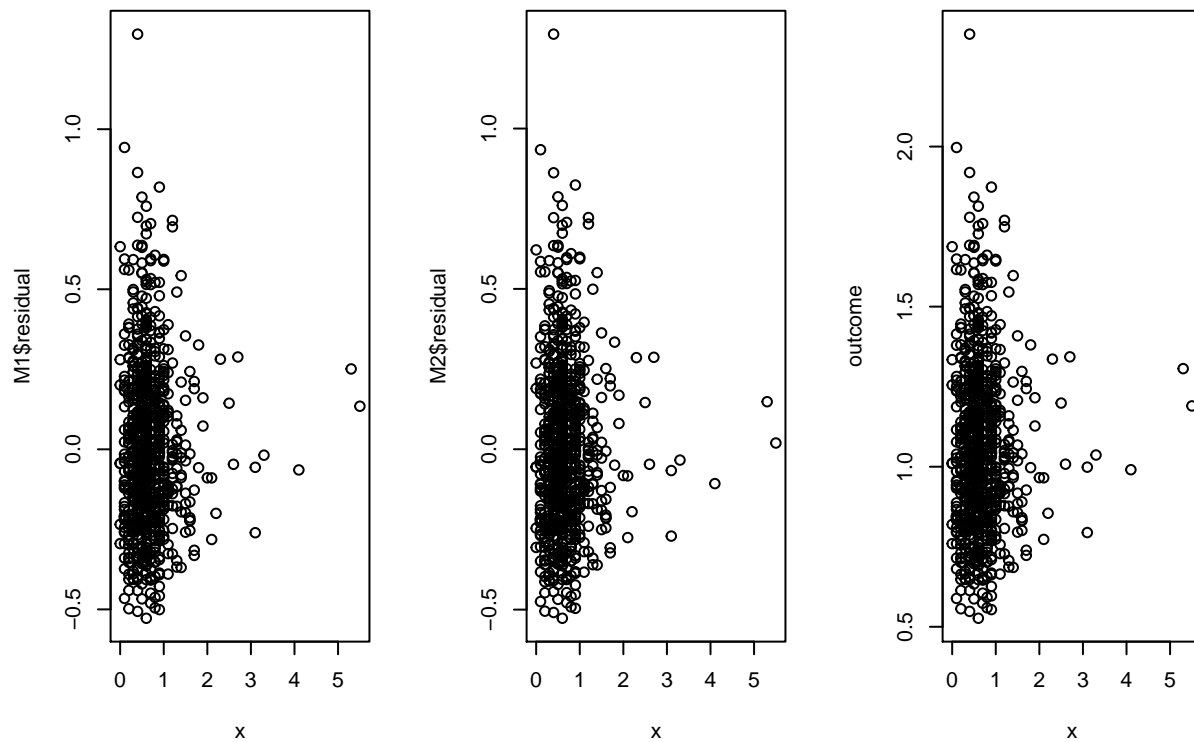
```
## [1] "residual for M1: 0.25026710930793"
## [1] "residual for M2: 0.250393729526099"
```



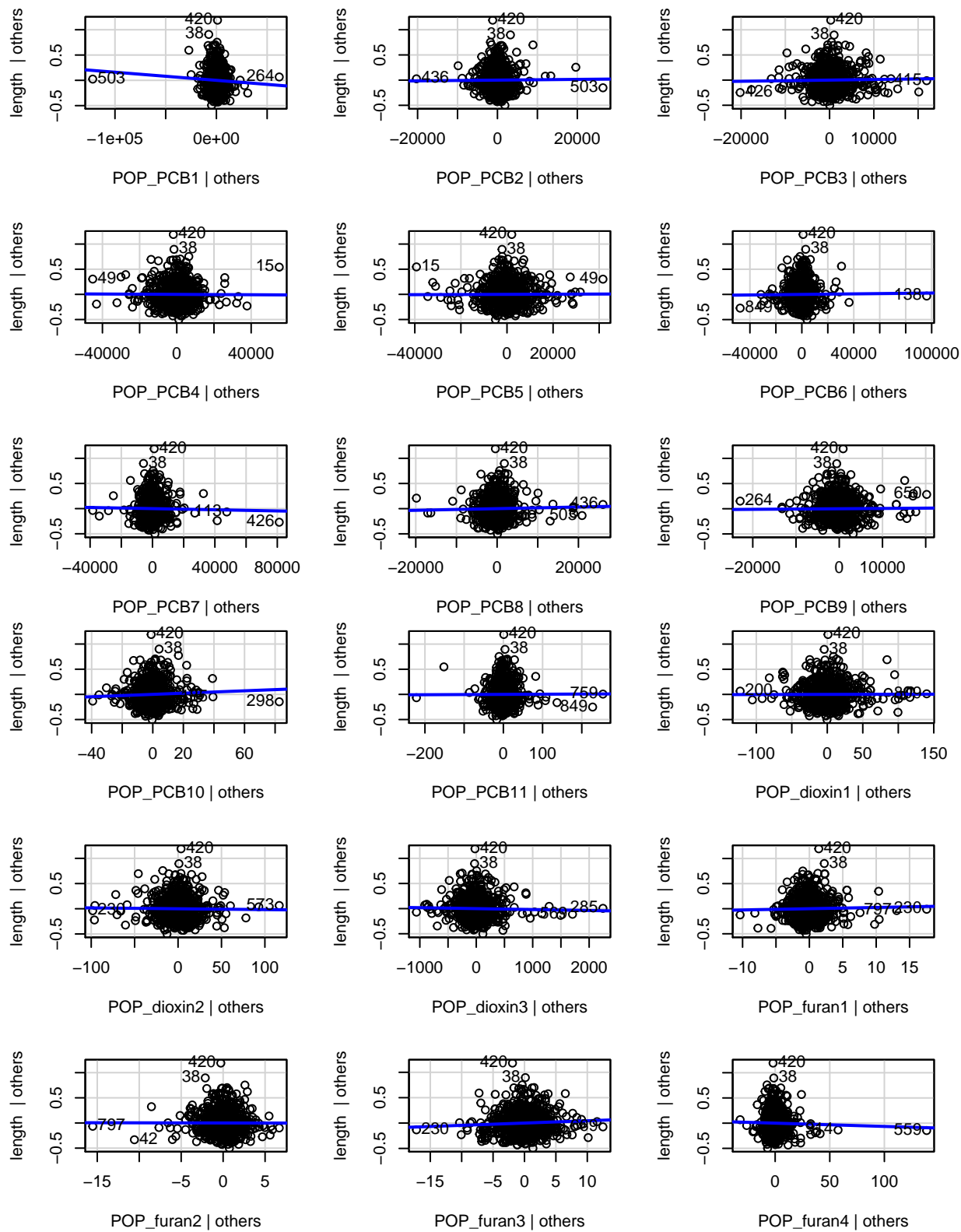
```
## [1] "residual for M1: 0.250043388210667"
## [1] "residual for M2: 0.25018695270193"
```

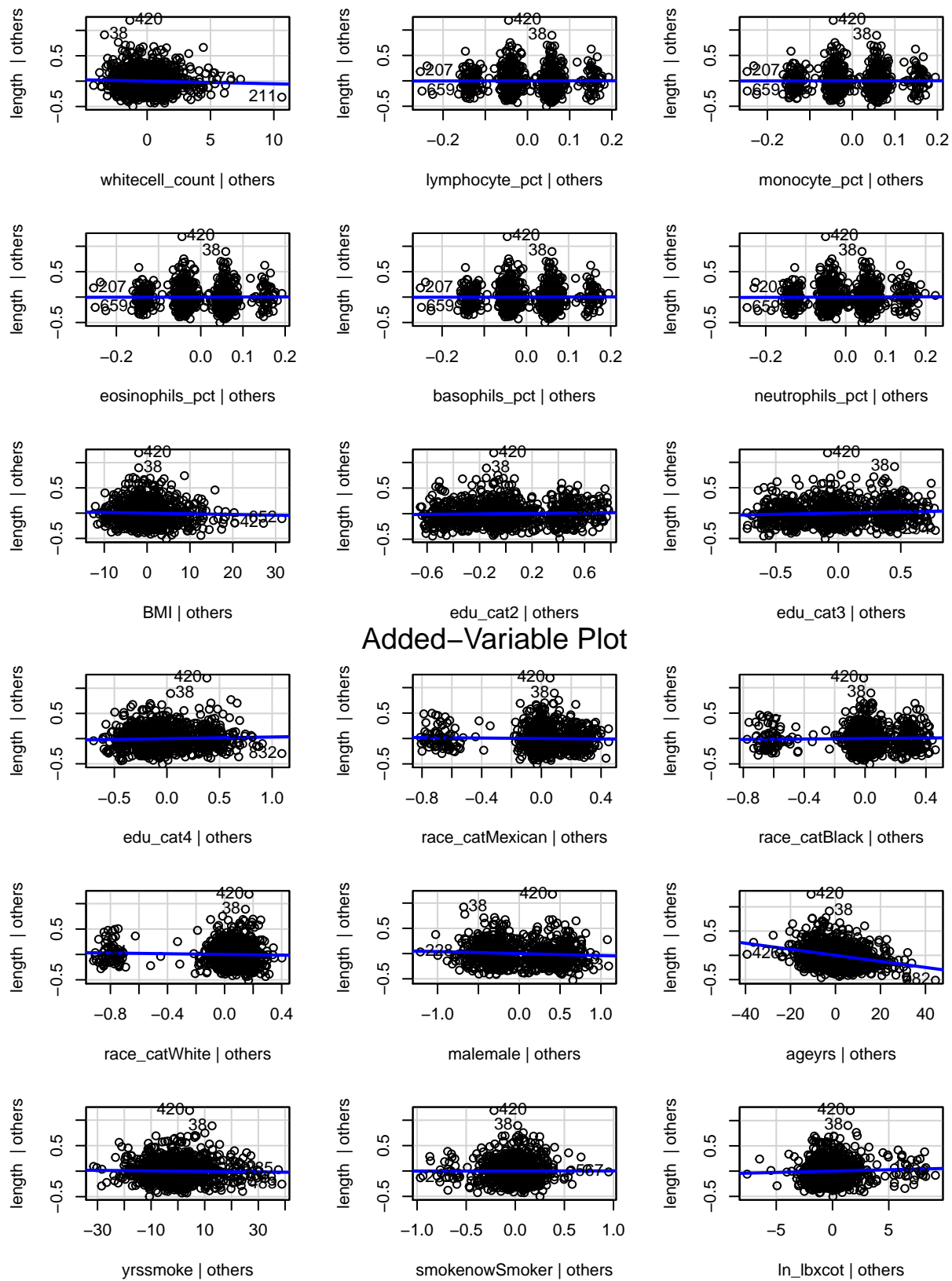


```
## [1] "residual for M1: 0.250382476371691"
## [1] "residual for M2: 0.25042580861039"
```



```
# testing non-linearity in MLR
library(car)
M <- lm(length ~ ., data=pollutants)
avPlots(M, main="Added-Variable Plot")
```



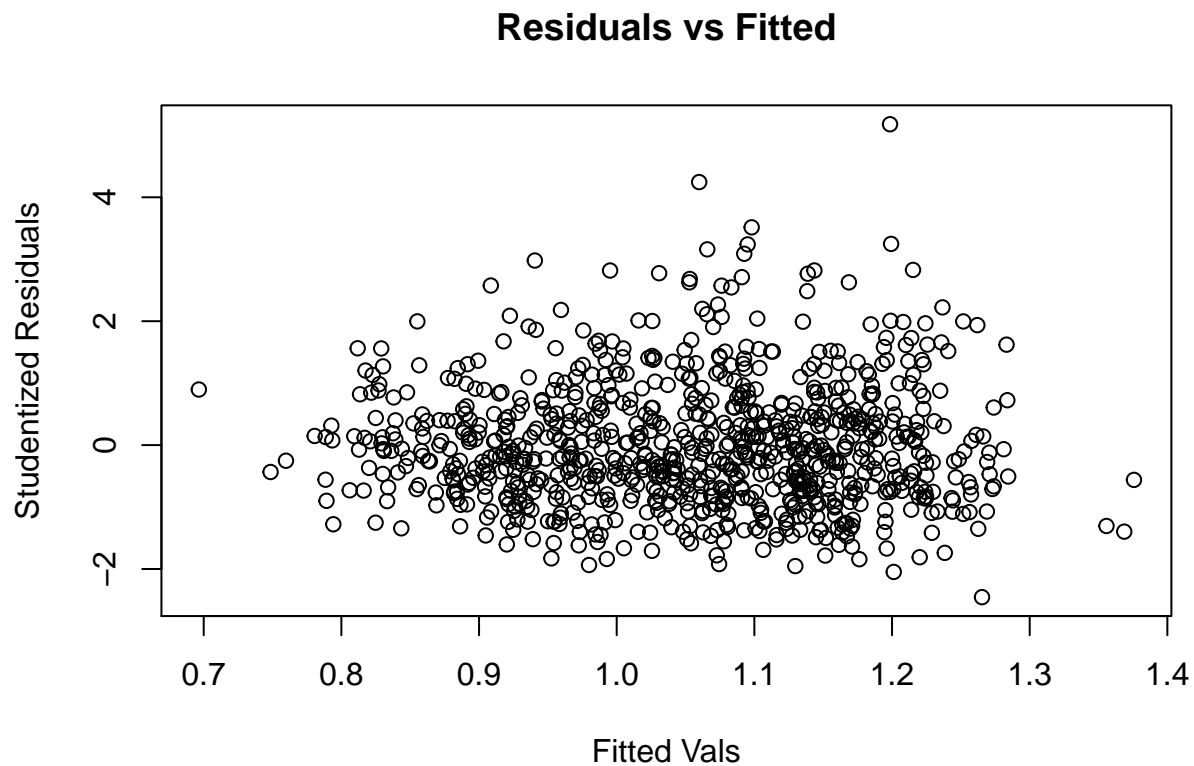


Added-Variable Plot

7.5 Residuals vs Fitted plot

```
# Heteroskedasticity
## fit model
Mh <- lm(length ~ . - smokenow - race_cat
          - edu_cat - male , data = pollutants)
## residuals
res1 <- resid(Mh) # raw residuals
stud1 <- res1/(sigma(Mh)*sqrt(1-hatvalues(Mh))) # studentized residuals

## plot of studentized residuals vs fitted values
plot(stud1~fitted(Mh),
     xlab="Fitted Vals",
     ylab="Studentized Residuals",
     main="Residuals vs Fitted")
```

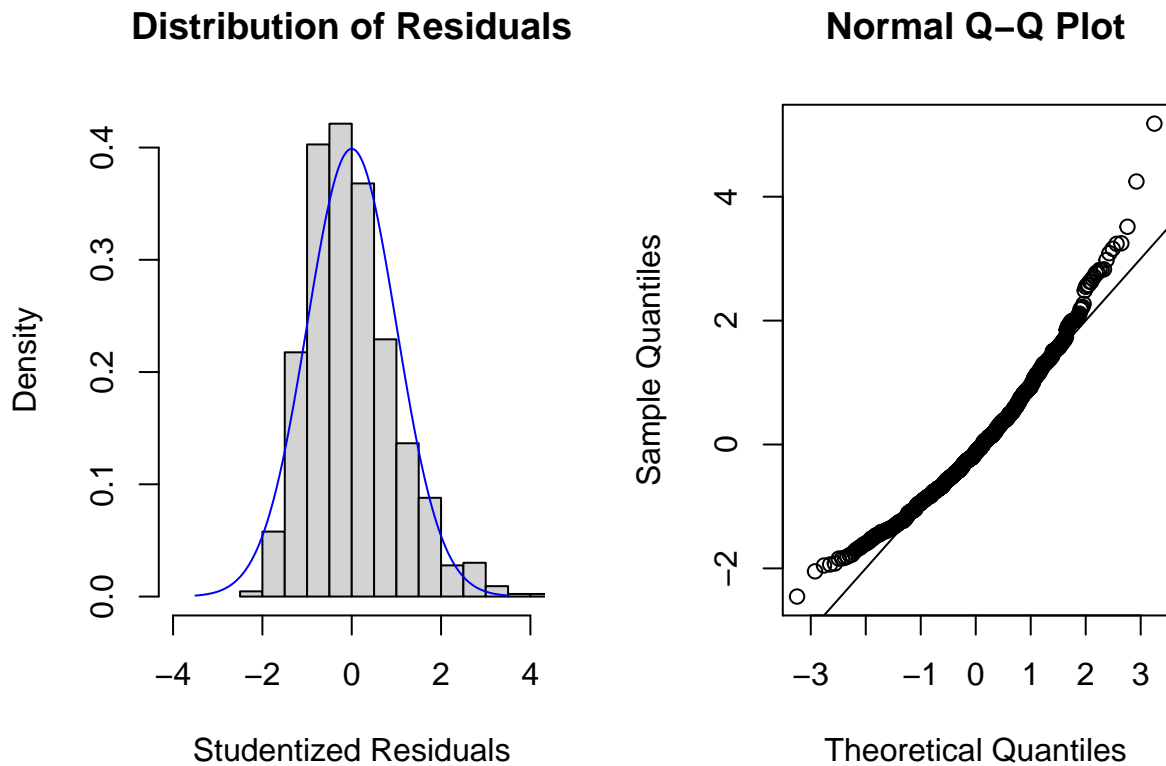


7.6 Histograms and QQ plot

```
par(mfrow = c(1, 2))
## plot distribution of studentized residuals
hist(stud1,breaks=12,
     probability=TRUE,xlim=c(-4,4),
     xlab="Studentized Residuals",
     main="Distribution of Residuals")
grid <- seq(-3.5,3.5,by=0.05)
lines(x=grid,y=dnorm(grid),col="blue") # add N(0,1) pdf

## qqplot of studentized residuals
qqnorm(stud1)
```

```
abline(0,1)
```



7.7 Model Summaries

comments by Estella: !need to revise, now we only have 3 models, see result above for more information

7.7.1 Models Selected with Interactions

```
# stepwiseB_Adjusted R2  
# summary(cv_ridge_model1)  
# summary(MBIC_Interaction)
```

7.7.2 Models after VIF Selection

```
# summary(MAIC_reduced)  
# summary(MBIC_reduced)
```