STAT 331 Final Project

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Contents

1 Summary

In this report, we would like to investigate the effect of the persistent pollutants on peoples' cellular aging, particularly, telomere lengths. With the given data, to explore the most influential covariates that contribute to the average leukocyte telomere length, we first look at the distribution of different covariates and then use several different tools such as t-test stepwise-algorithm, LASSO, and Ridge to select models.

After confirming the fundamental assumptions of the linear regression model, we first use AIC and BIC in stepwise selection to get our first potential model, Model 1, with minimum mean prediction squared error (MPSE). Then as we noticed there are no significant interactions, we eliminated covariates with high variance inflation factor (VIF) to reduce multicollinearity and used the stepwise function to get Model 2. Finally, with cross-validation and shrinkage methods like LASSO and ridge, Model 3 and 4 are selected.

By comparing different models, we found Model 2 has the lowest MPSE while maintaining interpretability and parsimony. This model considers one type of furan pollutant (POP_furan3) and people's age (ageyrs) and finds that age has a negative linear effect on average leukocyte telomere length while the pollutant has a small positive influence.

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"
```

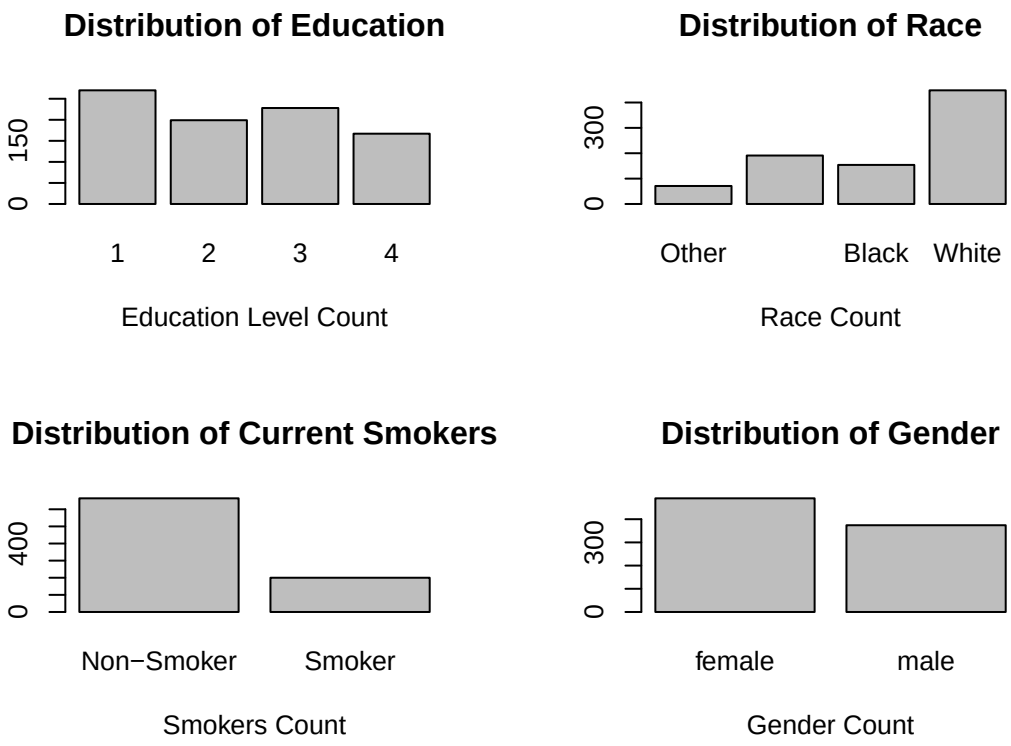
Note that "edu_cat", "race_cat", "male", "smokenow" are categorical values and the rest are continuous.

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 Multicolinearity

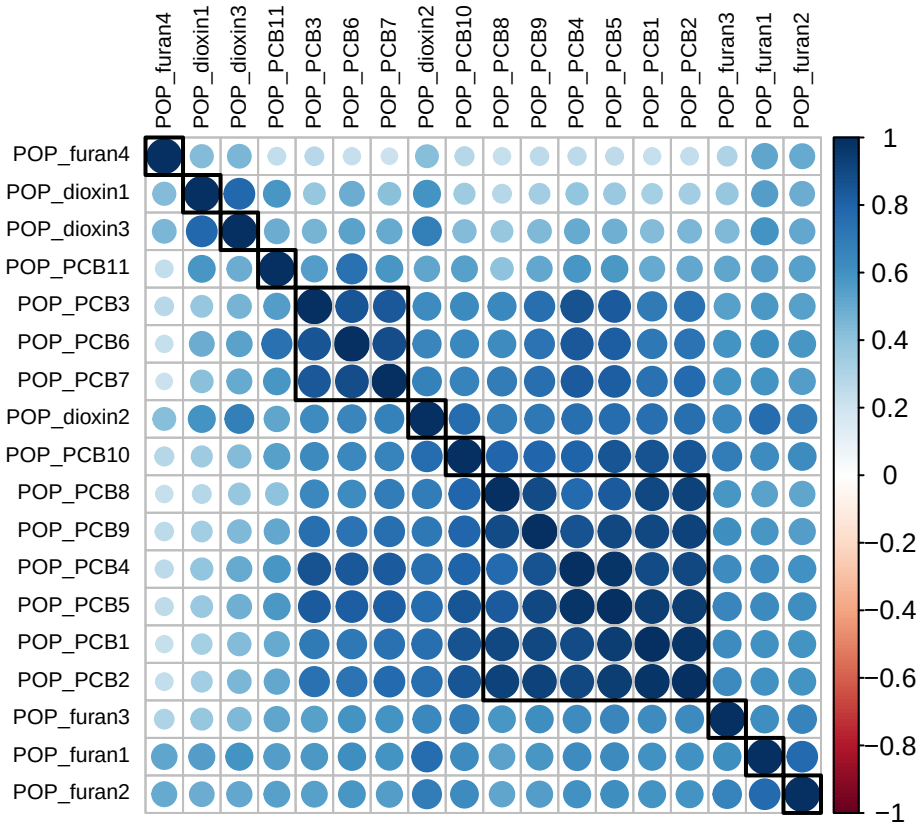
We learned that severe multicollinearity between covariates could result in unstable coefficient estimates and inflated standard errors. Therefore, in this section, we will investigate correlations among values that we may

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.

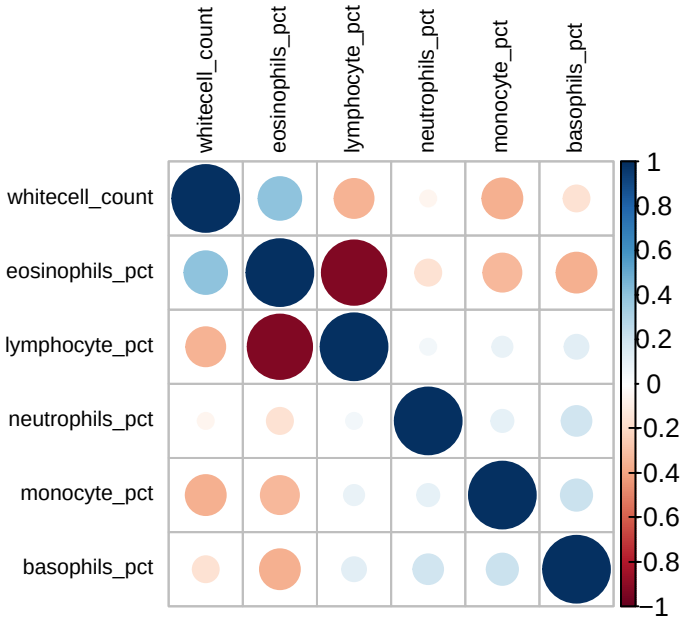
3.2.1 Correlation among Persistent Pollution

```
## corrplot 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 covariates from this section as we do not expect personal health data such as BMI or years of smoke to have a logically 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 the Methods sections below.

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 would like to investigate whether the relationship between average leukocyte telomere length and white blood cells is 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

4.1 Linear Model Assumptions

Since we have no access to the 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 # model 1
```

```
##
## 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 have 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 Multicolinearity

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 2
```

```
##
## 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 detailed model summaries can be found in the appendix 7.7.2.

The model selected by BIC is still smaller than the one with AIC, and it also outperforms it. This model has different from Model 1 but is very parsimonious. Therefore, we decided to use the BIC model as our second candidate model, named Model 2.

The formula of Model 2 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 entries with index 436,285, and 559. In this

section, we shall remove these outliers and observe their 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, the stepwise algorithm selected 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

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.

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

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

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:

```
# Model 1 Test Score
Ridge_MSPE1
```

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

```
# Model 2 Test Score
Ridge_MSPE2
```

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

```
# Model 3 Test Score
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 along with the categorical covariates to the 'glmnet' function and let it pick the best model for us. We named it Model 4.

```
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
```

By comparing the performance on the testset, we observed that the model with the formula

```
model2_f
```

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

This model is also the most parsimonious and interpretable. Thus we shall further analyse this model and draw conclusion from it.

5 Results

In the end, we looked at the model performance on the remaining test set and computed the MPSE of each model. The MPSE of the four models we have considered are as follows:

```
Ridge_MSPE1
```

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

```
Ridge_MSPE2
```

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

```
Ridge_MSPE3
```

```
## [1] 0.04605872
```

```
lasso_MSPE
```

```
## [1] 0.04653322
```

By comparing different models, we found that Model 2 has the best prediction performance on new data. It is also the most interpretable and parsimonious. We shall now take a closer look at the parameters and coefficients of this model.

```
coef(cv_ridge_model2)
```

```
## 4 x 1 sparse Matrix of class "dgCMatrix"
##                            1
## (Intercept)  1.195259310
```

```
## (Intercept)  .
## POP_furan3  -0.001241580
## ageyrs      -0.002664294
```

The output shows that Model 2 considers POP_furan3 and ageyrs and the coefficient values suggest that age has a negative linear effect on average leukocyte telomere length while the pollutant has a small positive influence. This implies that telomere length decreases with increasing age (result 1) and increases with increasing exposure to furan3 (result 2).

The first result is intuitive while the second one is not. Further investigating the other three models (in appendix 7.8), we noticed that with all models, when age is present as a covariate, other covariates generally have a positive influence on the telomere length. We shall further discuss this in the Discussion section below.

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

We have considered the multicollinearity and interactions within the eleven PCB covariates and similarly for the three dioxin covariates and four furan covariates with white blood cell components. It is expected that there is no causal relationship between exposure covariates and other personal characteristics variables. For example, it is reasonable to assume that the concentration of POP_PCB10 is unrelated to the value of ageyrs and BMI. However, it may still be useful to confirm this hypothesis by p-tests.

In addition, a linear regression model has four assumptions, namely linearity, normality, homoscedasticity, and independence. We have analyzed and confirmed that the first three assumptions hold. Generally, we can assume 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.

We have mentioned in the previous section that when age is present as a covariate, the coefficients for other variables are generally negative, which can be counter-intuitive. Since in all four models we have considered, age has always been a covariate, it may be interesting to investigate linear models with age being the only covariate. We may also analyse the data again while placing our focus on non-age variables and building models with covariates other than age.

7 Appendix

7.1 Data Summary

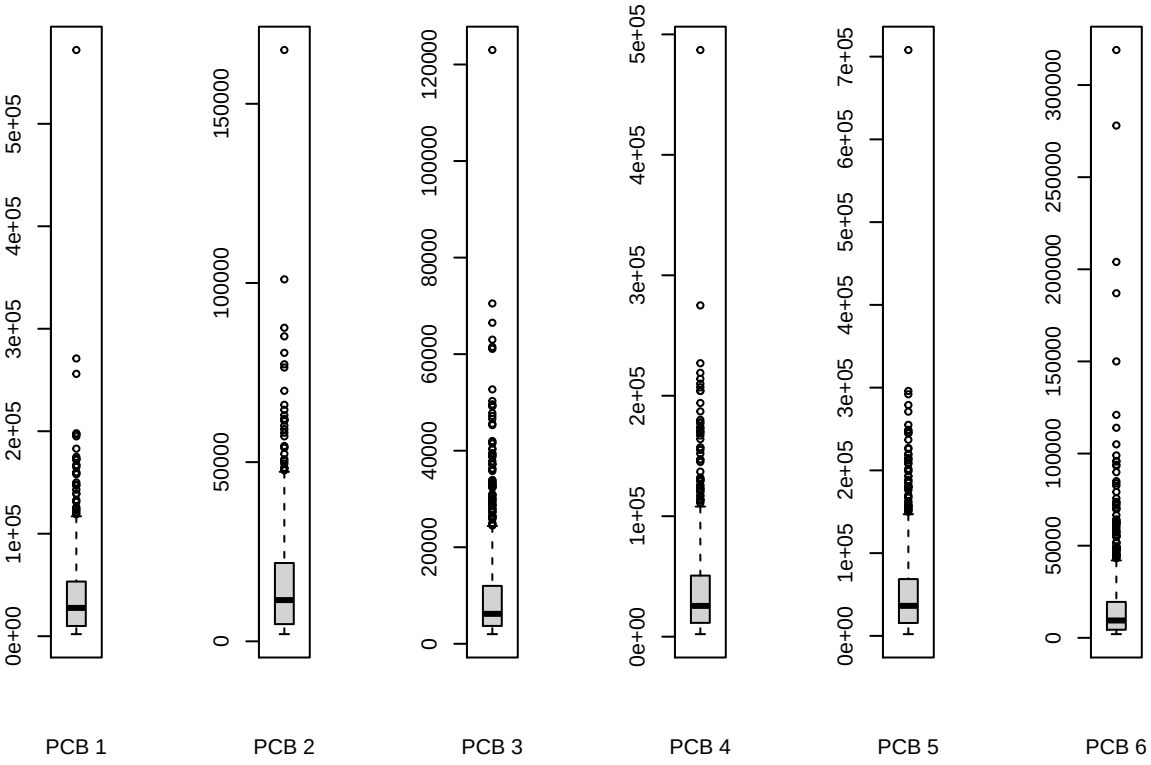
Looking at the useful metrics for the data

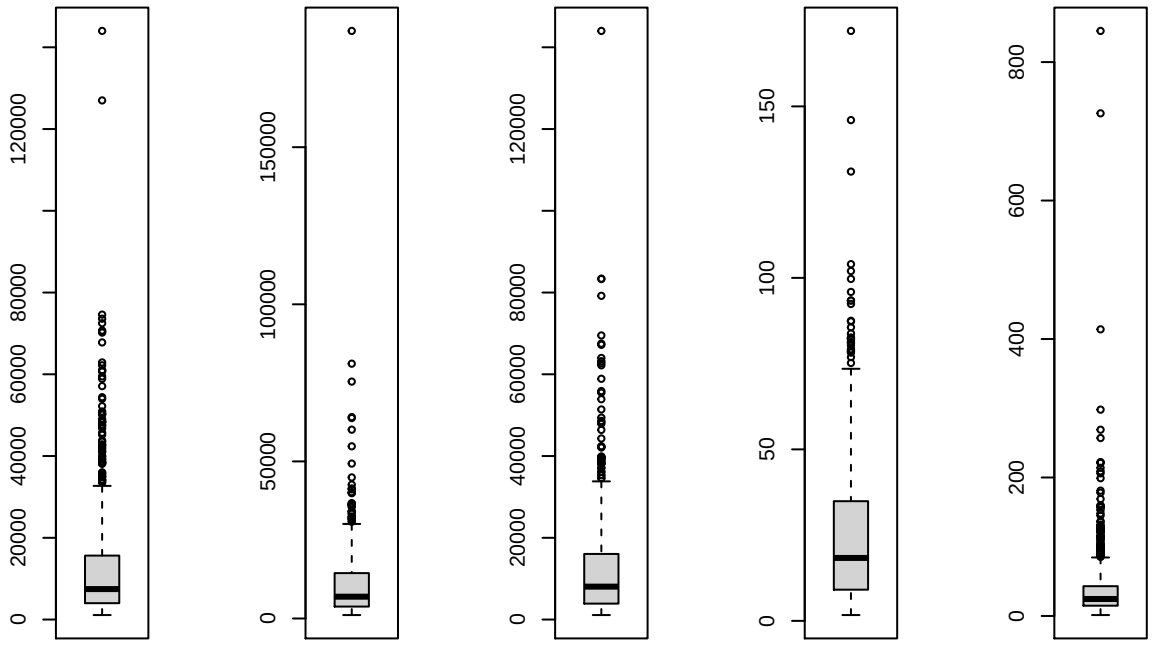
```
summary(pollutants)
```

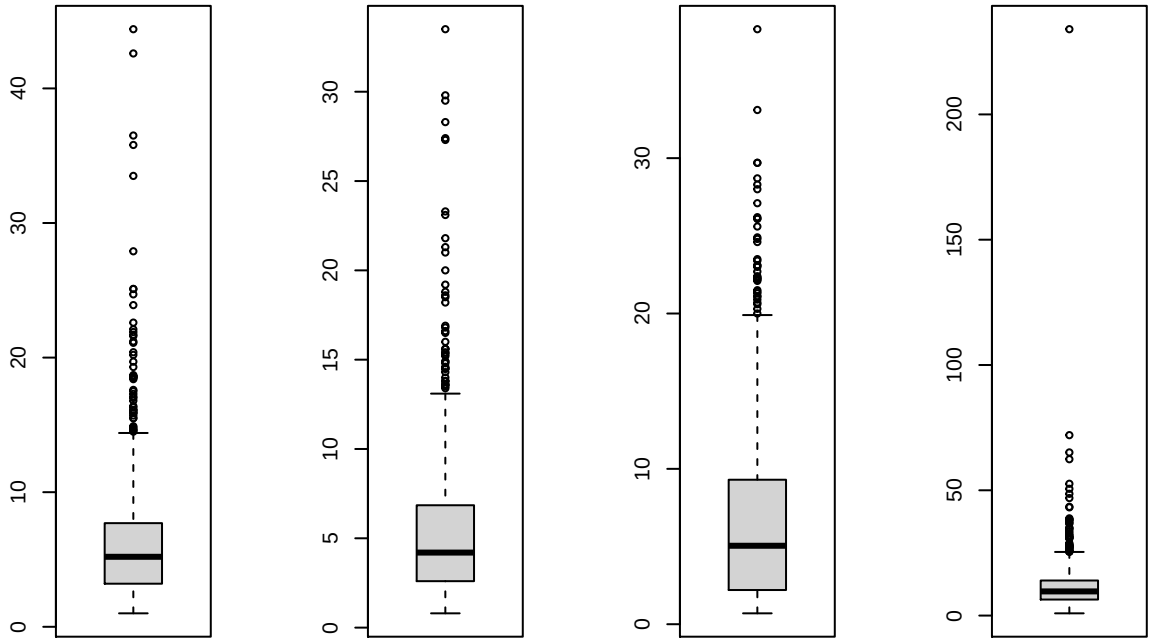
```
##      length          POP_PCB1         POP_PCB2         POP_PCB3
##  Min.   :0.5266   Min.   :  2000   Min.   :  2000   Min.   :  2000
##  1st Qu.:0.8754   1st Qu.:  9975   1st Qu.:  4800   1st Qu.:  3700
##  Median :1.0286   Median : 27600   Median : 11500   Median :  6200
##  Mean   :1.0543   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
```

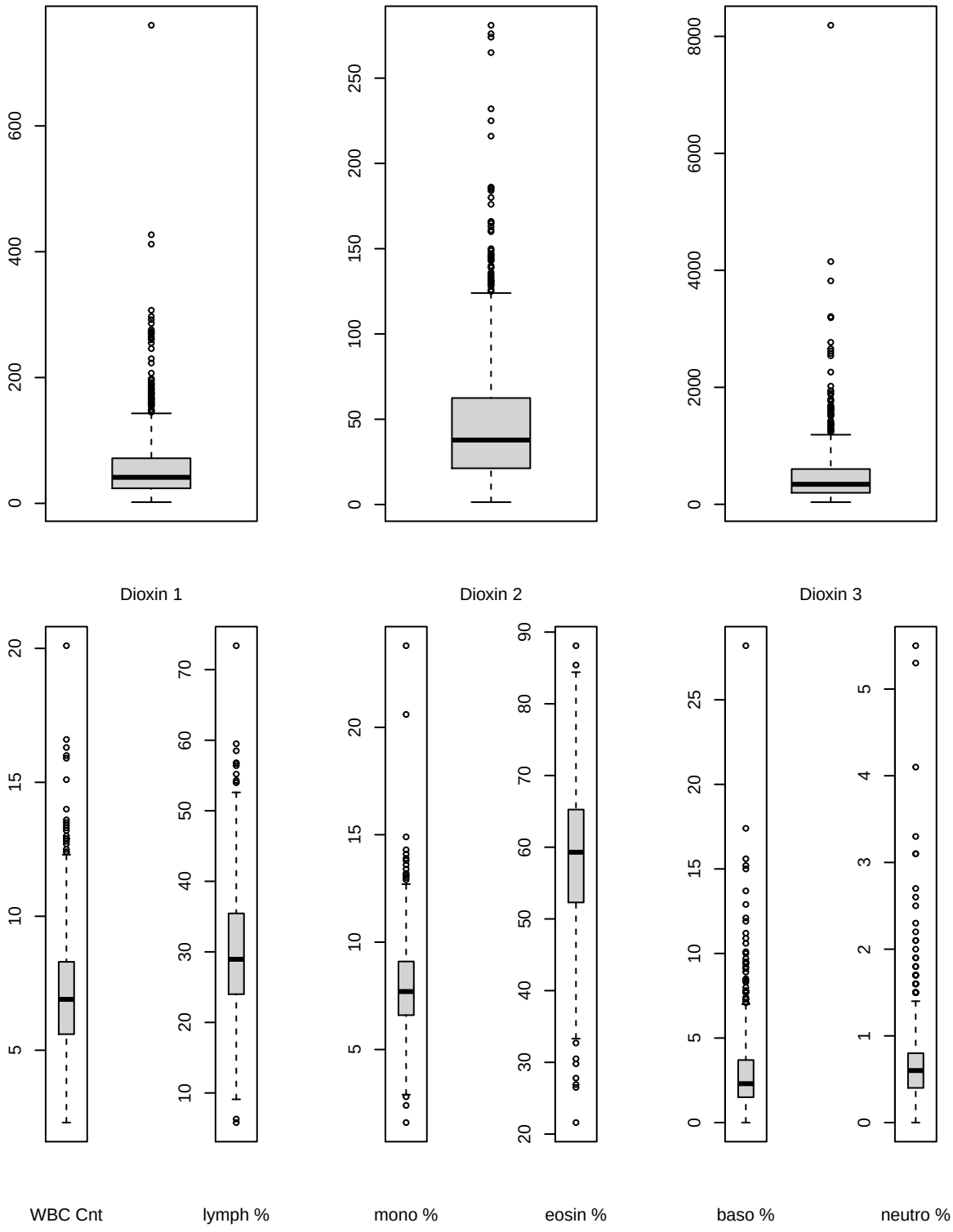
```
##  Mean   :0.6669   Mean   :28.09   4:167   White  :448
##  3rd Qu.:0.8000   3rd Qu.:31.17
##  Max.   :5.5000   Max.   :62.99
##      ageyrs         yrssmoke          smokenow     ln_lbxcot
##  Min.   :20.00   Min.   : 0.0   Non-Smoker:664   Min.   :-4.5099
##  1st Qu.:34.00   1st Qu.: 0.0   Smoker    :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
```

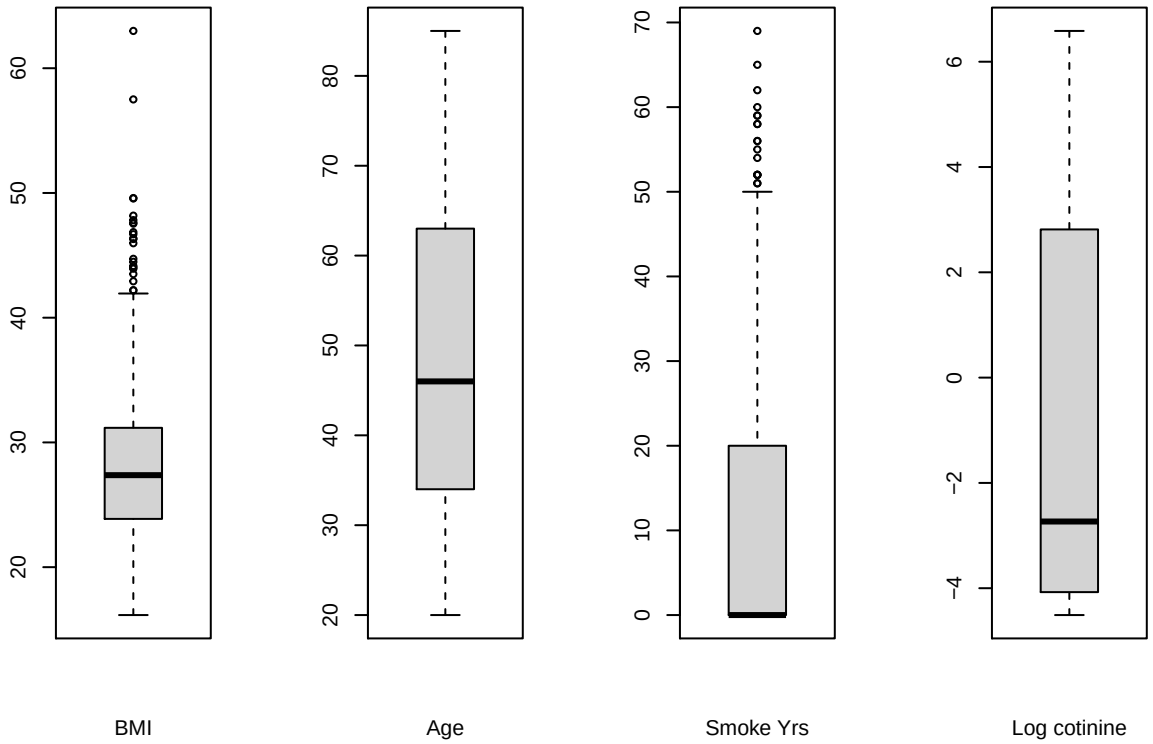
7.2 Boxplots




0
20000
40000
60000
80000
120000
PCB 7
0
50000
100000
150000
PCB 8
0
20000
40000
60000
80000
120000
PCB 9
0
50
100
150
PCB 10
0
200
400
600
800
PCB 11


0
10
20
30
40
Furan 1
0
5
10
15
20
25
30
Furan 2
0
10
20
30
Furan 3
0
50
100
150
200
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
```

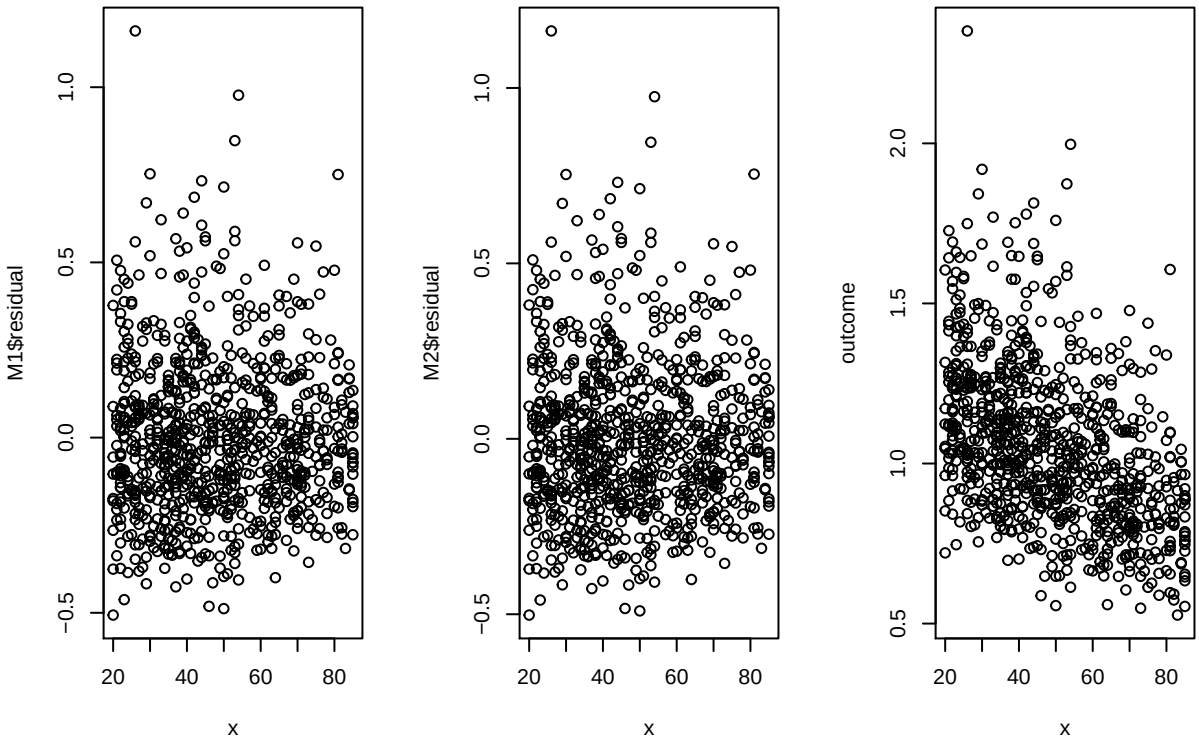
```r
max_WBC_idx = c()
for (c in 20:25) {
  max_WBC_idx[c-19] = which.max(pollutant_mat[, c])
}
max_WBC_idx
```

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

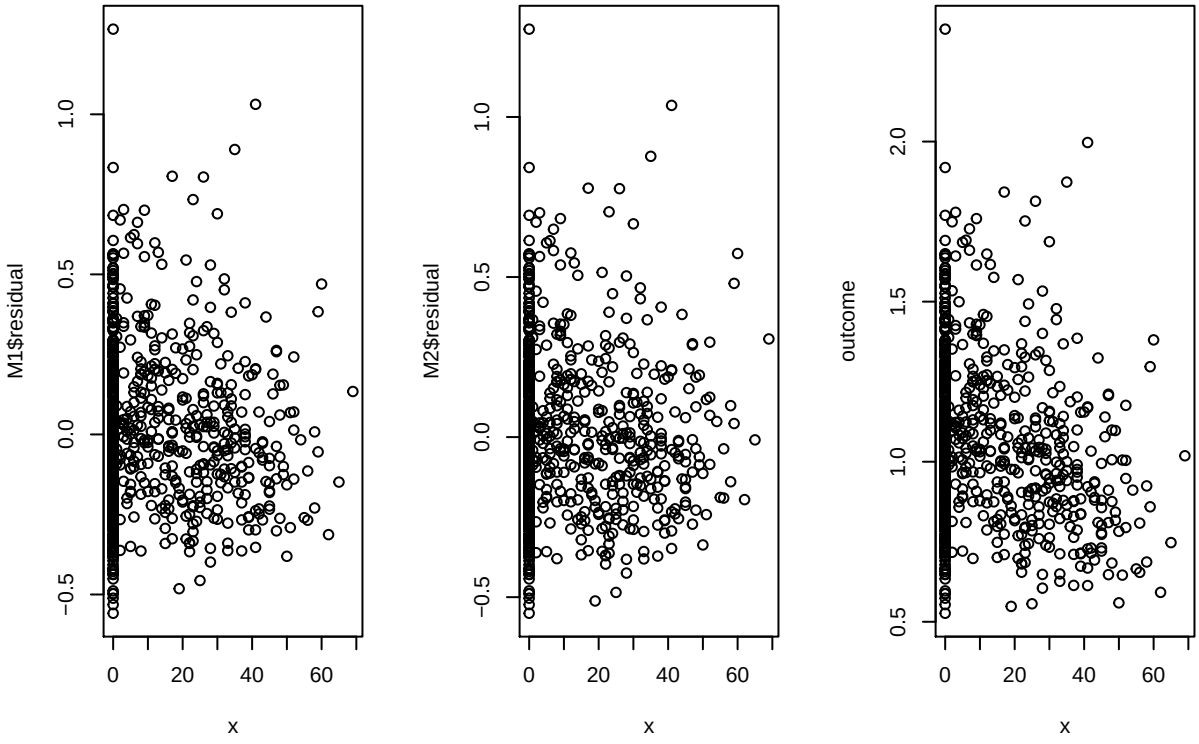
7.4 AvPlots

```r
# 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)
}
```

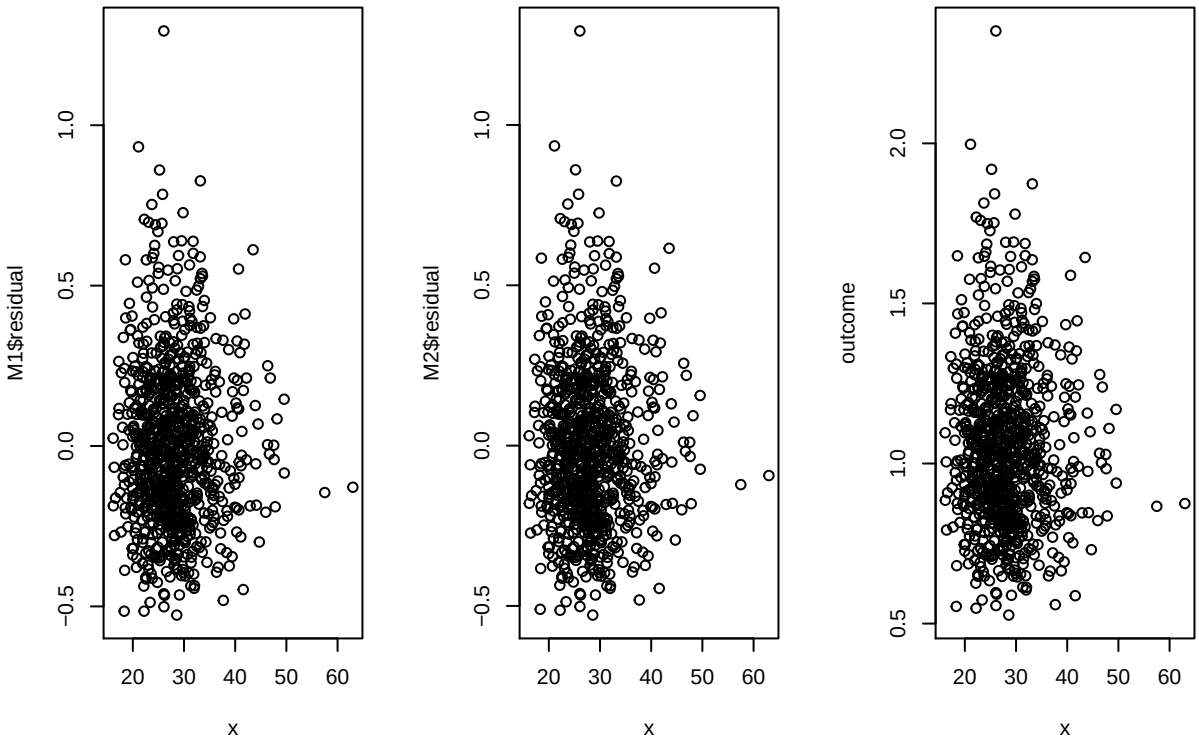
```
## [1] "residual for M1:  0.224172364185412"
## [1] "residual for M2:  0.22429269961392"
```



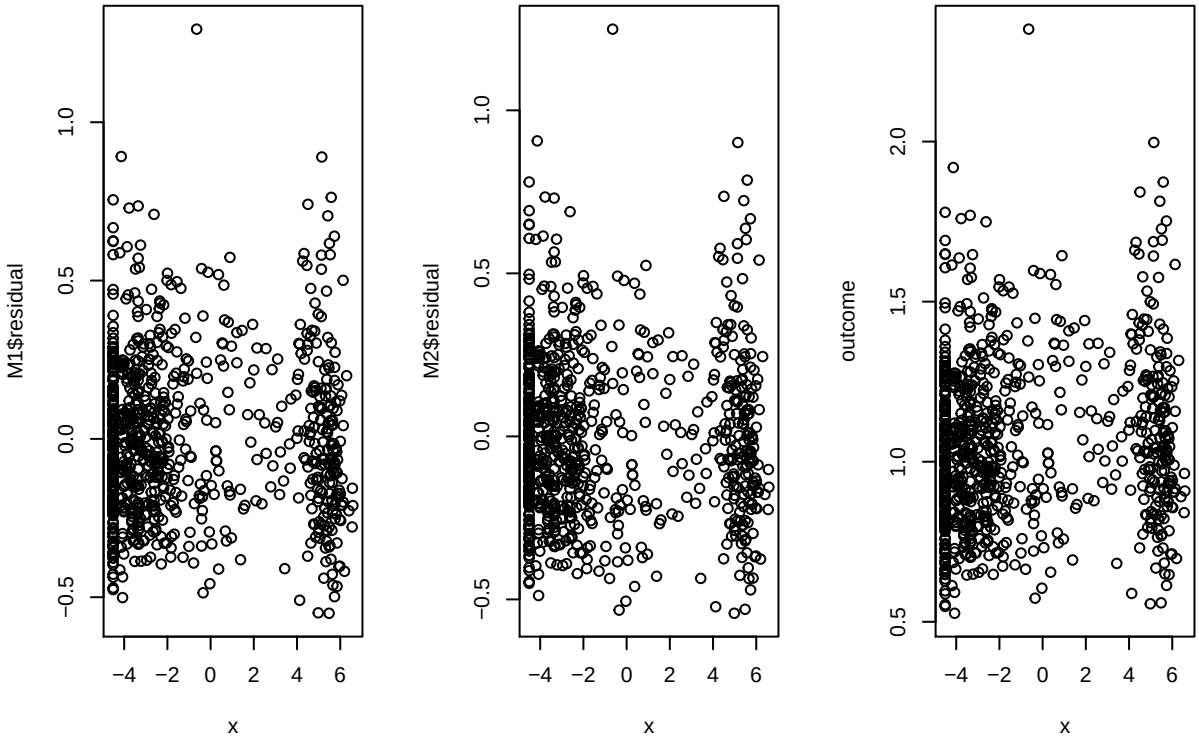

```
## [1] "residual for M1:  0.246320733146214"
## [1] "residual for M2:  0.245622720856213"
```



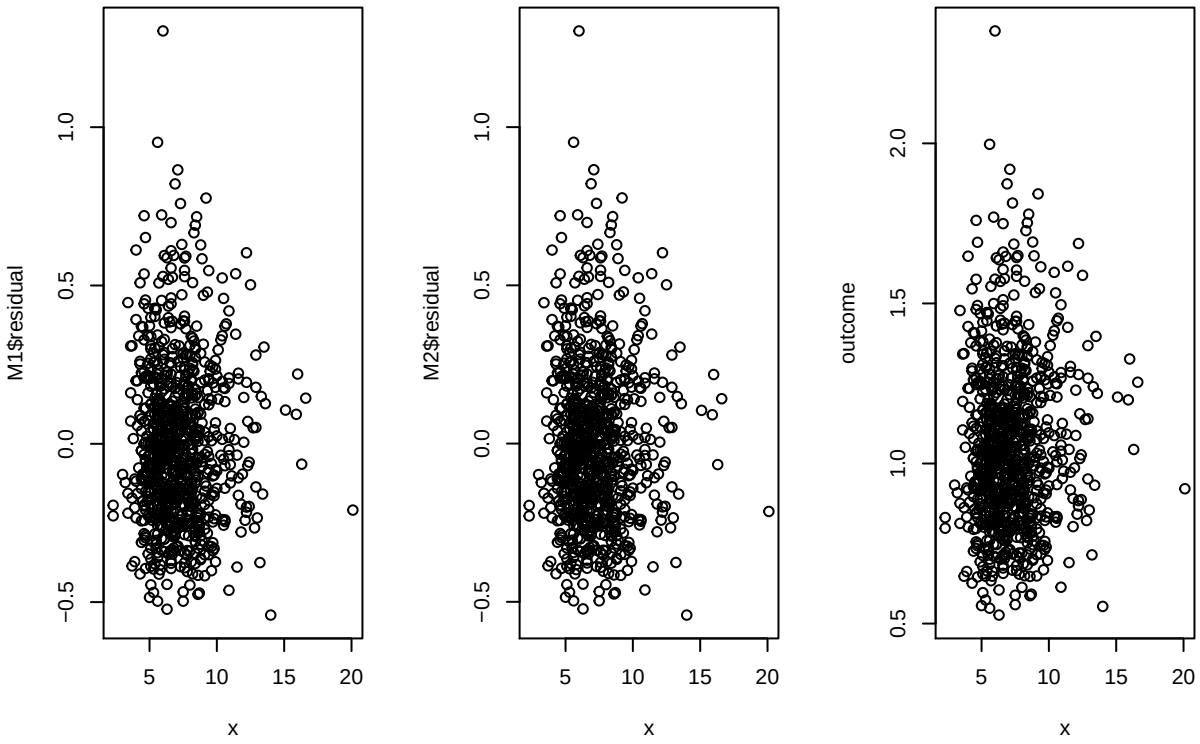

```
## [1] "residual for M1:  0.250228706427173"
## [1] "residual for M2:  0.25036248052387"
```



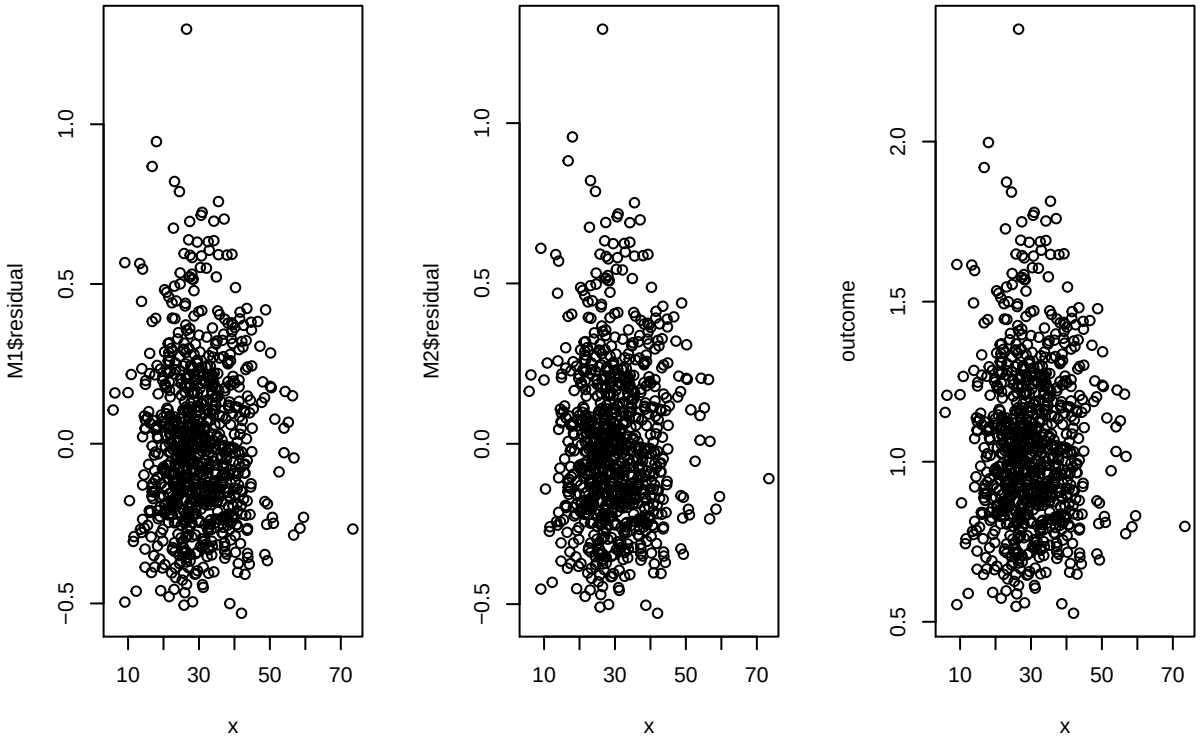

```
## [1] "residual for M1:  0.248212063673837"
## [1] "residual for M2:  0.24710732733351"
```



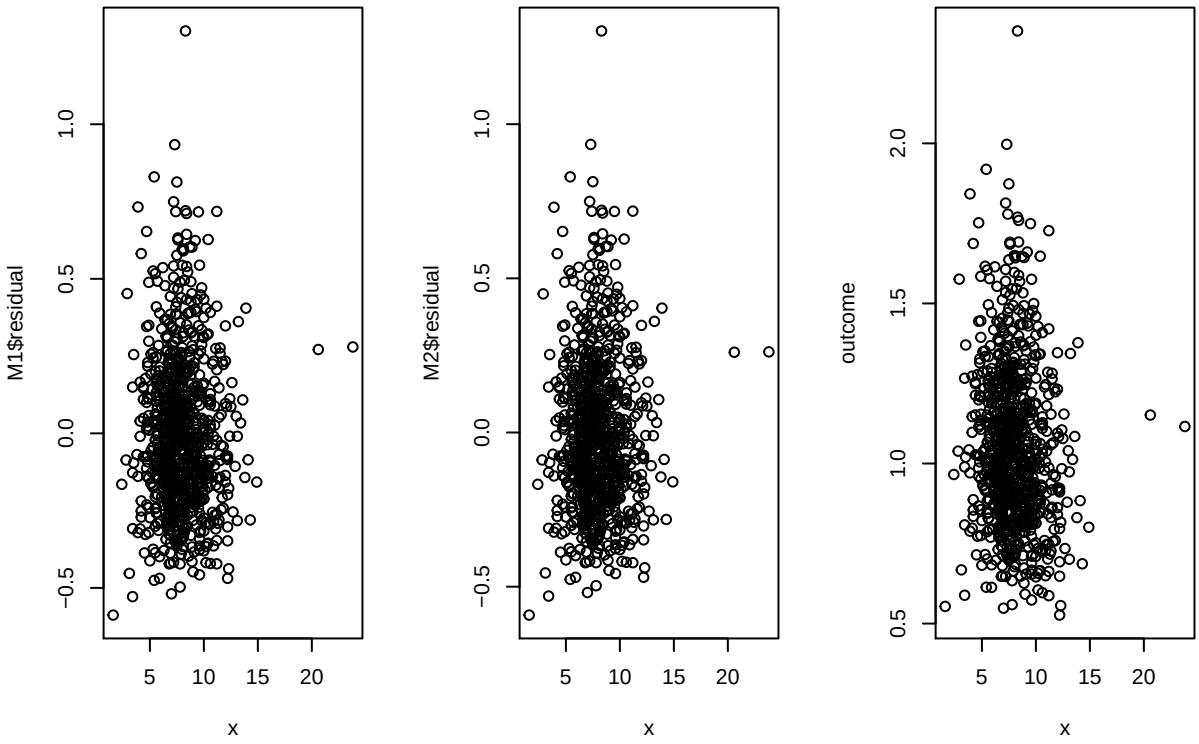

```
## [1] "residual for M1:  0.250065445847753"
## [1] "residual for M2:  0.250210403543218"
```



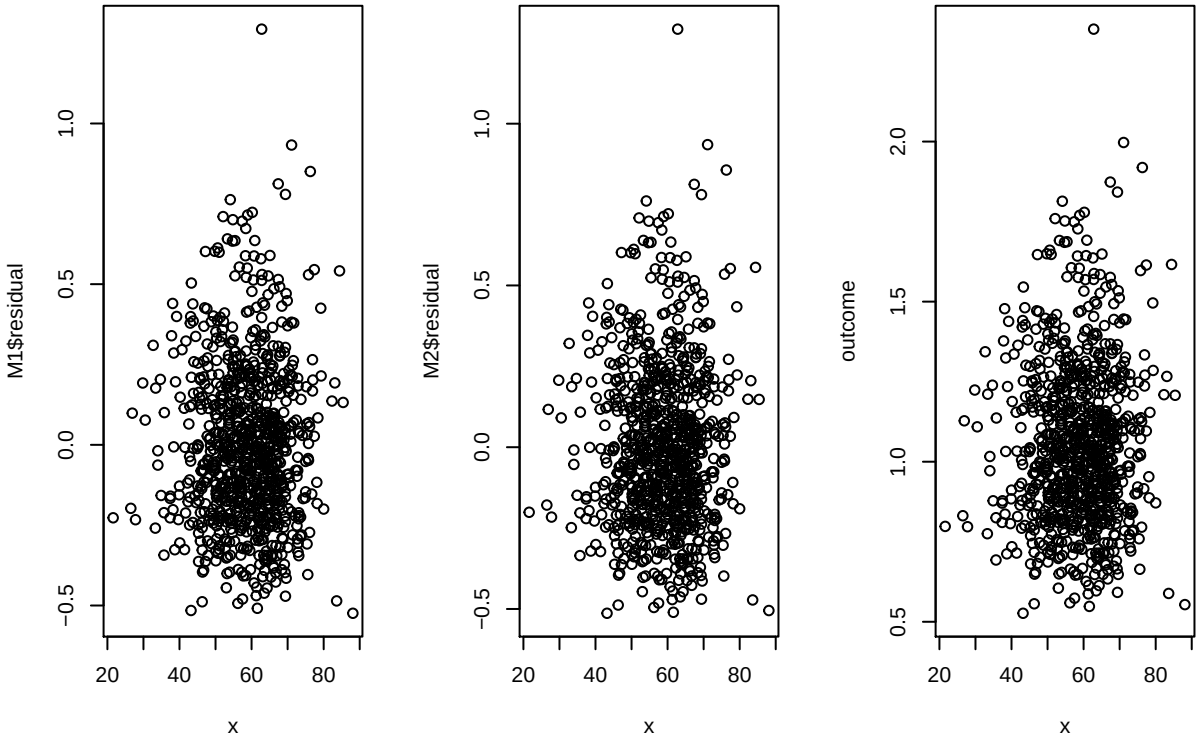

```
## [1] "residual for M1:  0.250373616826691"
## [1] "residual for M2:  0.250255208638358"
```



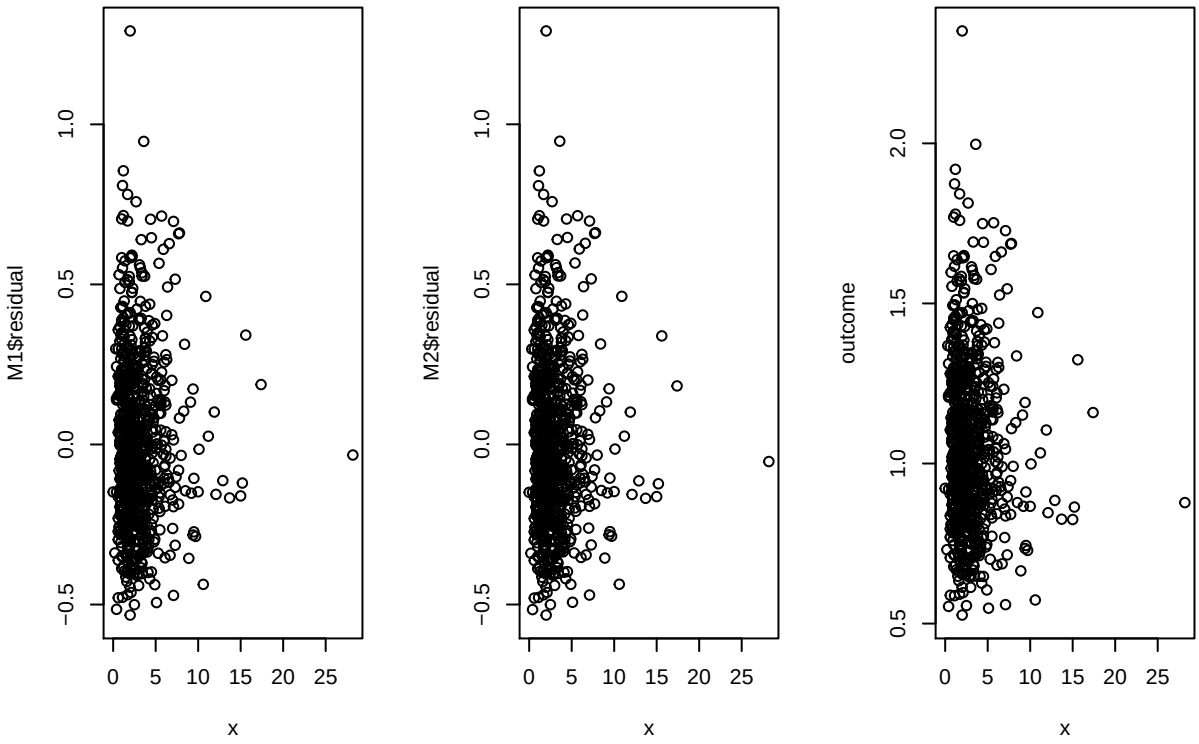

```
## [1] "residual for M1:  0.248704466454944"
## [1] "residual for M2:  0.248847192837983"
```



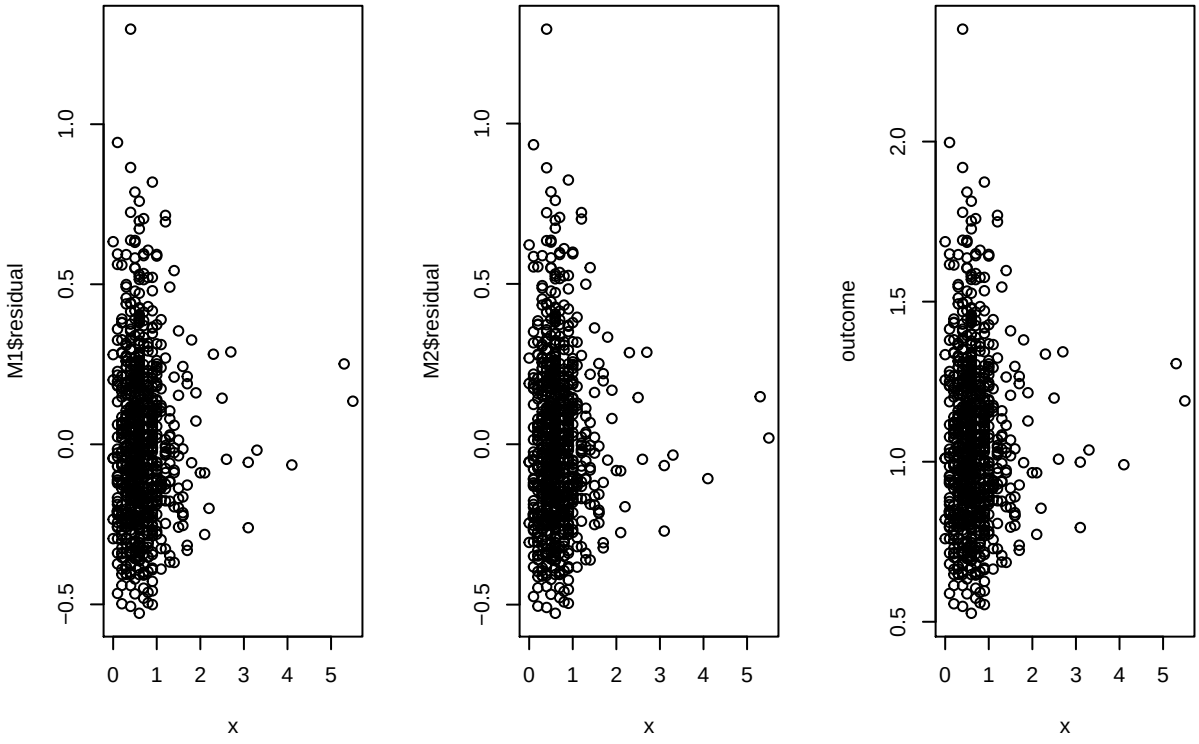

```
## [1] "residual for M1:  0.25026710930793"
## [1] "residual for M2:  0.250393729526099"
```



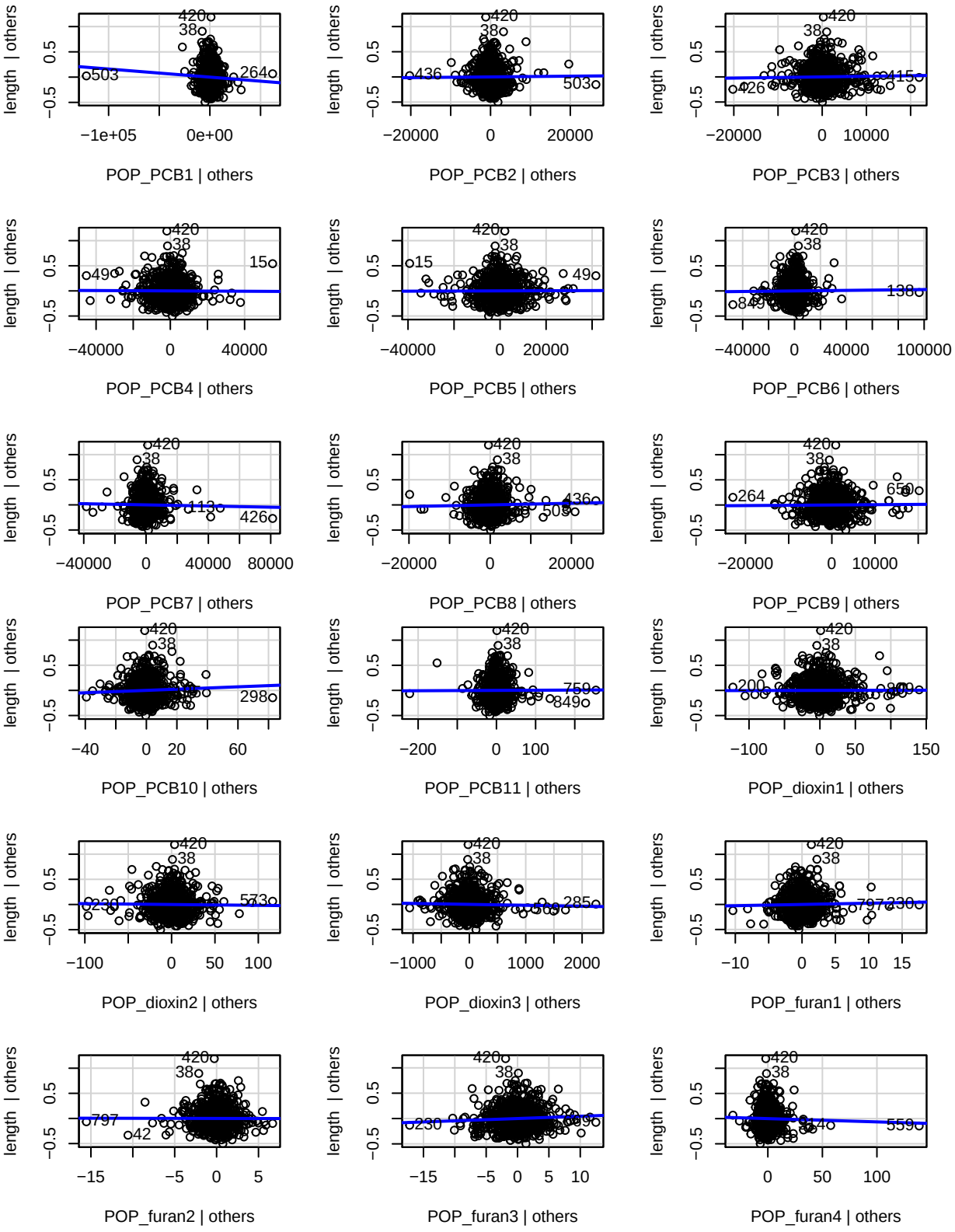

```
## [1] "residual for M1:  0.250043388210667"
## [1] "residual for M2:  0.25018695270193"
```

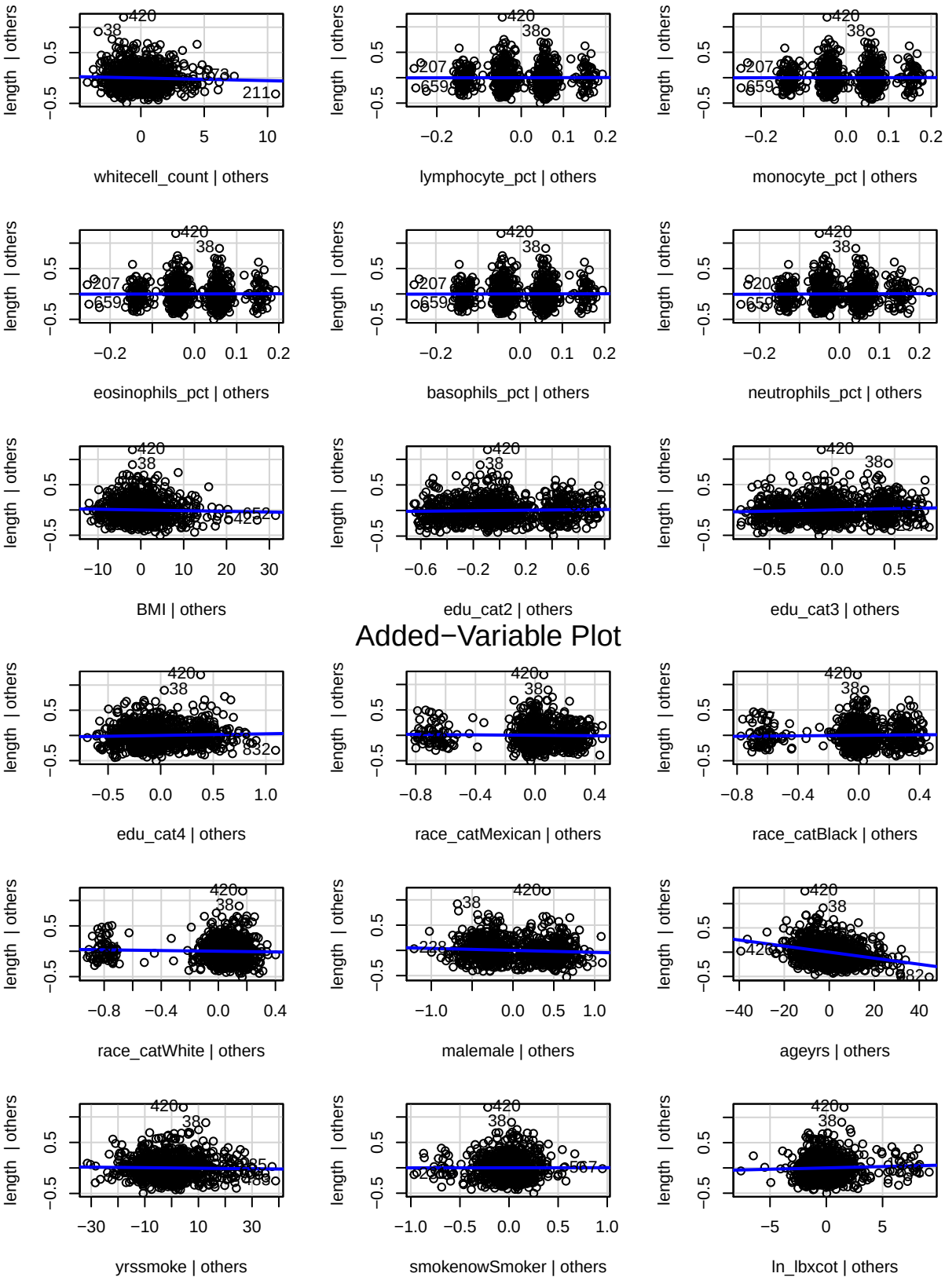



```
## [1] "residual for M1:  0.250382476371691"
## [1] "residual for M2:  0.25042580861039"
```



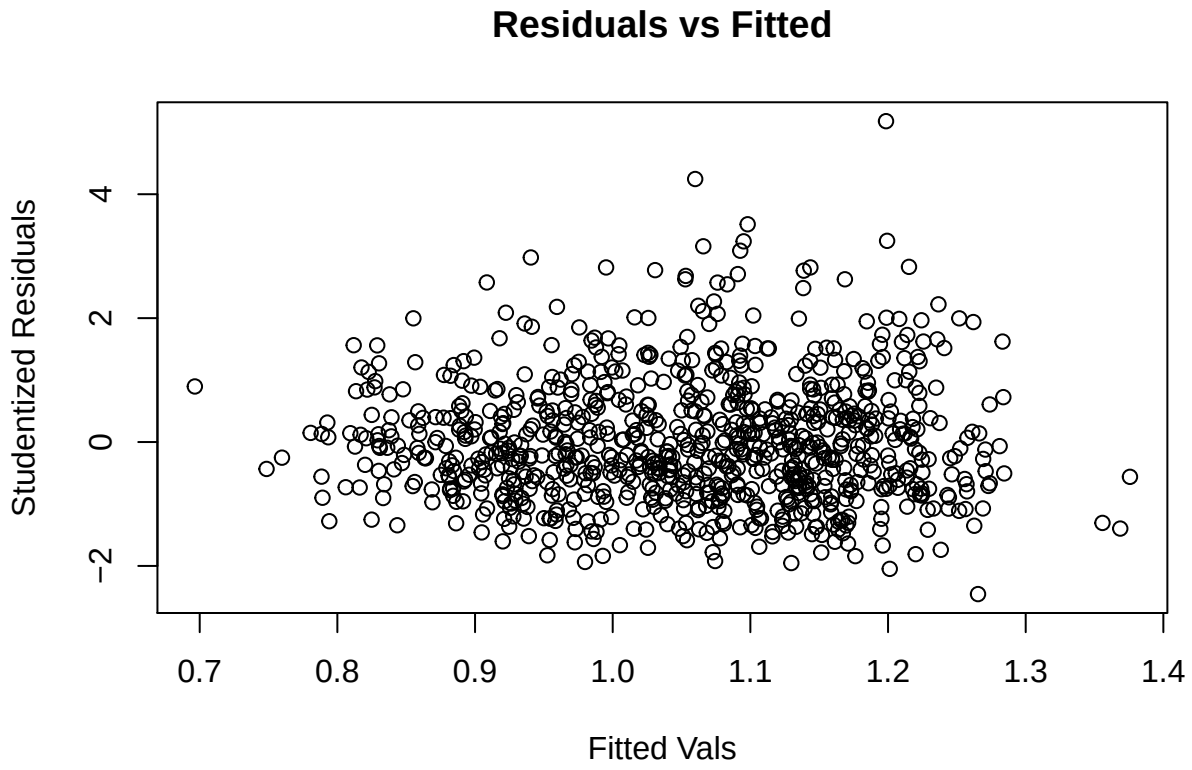

```
# testing non-linearity in MLR
library(car)
M <- lm (length ~ ., data=pollutants)
avPlots(M, main="Added-Variable Plot")
```


length | others
POP_PCB1 | others
POP_PCB2 | others
POP_PCB3 | others
POP_PCB4 | others
POP_PCB5 | others
POP_PCB6 | others
POP_PCB7 | others
POP_PCB8 | others
POP_PCB9 | others
POP_PCB10 | others
POP_PCB11 | others
POP_dioxin1 | others
POP_dioxin2 | others
POP_dioxin3 | others
POP_furan1 | others
POP_furan2 | others
POP_furan3 | others
POP_furan4 | others


length | others
whitecell_count | others
lymphocyte_pct | others
monocyte_pct | others
eosinophils_pct | others
basophils_pct | others
neutrophils_pct | others
BMI | others
edu_cat2 | others
edu_cat3 | others
Added−Variable Plot
edu_cat4 | others
race_catMexican | others
race_catBlack | others
race_catWhite | others
malemale | others
ageyrs | others
yrssmoke | others
smokenowSmoker | others
ln_lbxcot | others

7.5 Residuals vs Fitted plot

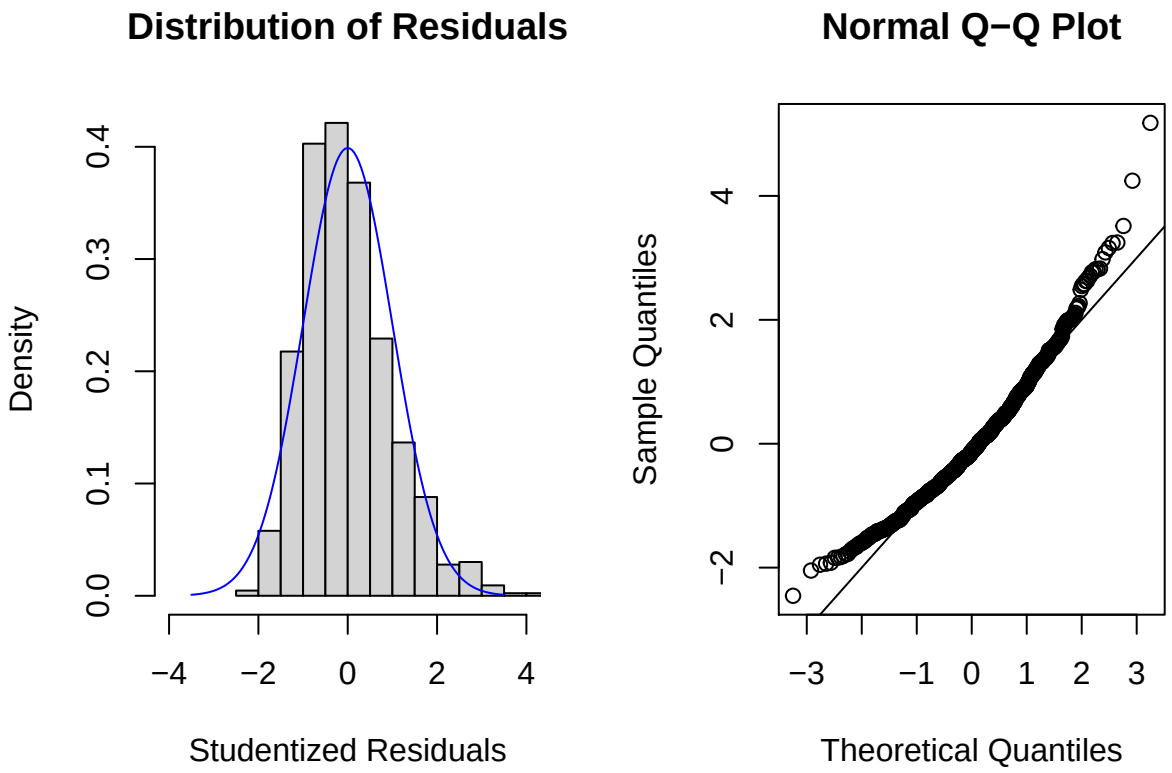
```
# Heteroskedasticity
## fit model
Mh <- lm(length ~ . - smokenow - race_cat
         - edu_cat - male , data = pollutants)
## residuals
res1 <- resid(Mh) # raw residuals
stud1 <- res1/(sigma(Mh)*sqrt(1-hatvalues(Mh))) # studentized residuals

## 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
```

```r
## qqplot of studentized residuals
qqnorm(stud1)
abline(0,1)
```



7.7 Model Summaries

7.7.1 Models Selected with Interactions

```r
summary(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)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.51670 -0.15495 -0.02971  0.12636  1.18096
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       1.305e+00  7.309e-02  17.856  < 2e-16 ***
## POP_PCB1         -7.505e-07  4.398e-07  -1.707  0.08839 .
## POP_PCB10         1.527e-03  9.448e-04   1.616  0.10655
## POP_furan3        3.658e-03  2.489e-03   1.470  0.14218
## whitecell_count -6.718e-03  4.665e-03  -1.440  0.15036
## eosinophils_pct   2.110e-03  1.043e-03   2.023  0.04350 *
## race_catMexican -1.834e-02  3.728e-02  -0.492  0.62286
```

```
## race_catBlack    5.185e-02  3.932e-02   1.319  0.18768
## race_catWhite   -1.286e-02  3.455e-02  -0.372  0.70976
## malemale        -5.164e-02  1.862e-02  -2.773  0.00572 **
## ageyrs          -6.727e-03  7.057e-04  -9.533  < 2e-16 ***
## ln_lbxcot        5.046e-03  2.503e-03   2.016  0.04425 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2226 on 638 degrees of freedom
## Multiple R-squared:  0.242,  Adjusted R-squared:  0.2289
## F-statistic: 18.52 on 11 and 638 DF,  p-value: < 2.2e-16
```

```
summary(MBIC_Interaction)
```

```
##
## Call:
## lm(formula = length ~ POP_PCB10 + male + ageyrs, data = train_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4908 -0.1554 -0.0272  0.1233  1.1811
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.3992875  0.0267275  52.354  < 2e-16 ***
## POP_PCB10    0.0017883  0.0006106   2.929  0.00352 **
## malemale    -0.0531973  0.0180434  -2.948  0.00331 **
## ageyrs      -0.0074571  0.0006478 -11.511  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2241 on 646 degrees of freedom
## Multiple R-squared:  0.222,  Adjusted R-squared:  0.2184
## F-statistic: 61.43 on 3 and 646 DF,  p-value: < 2.2e-16
```

7.7.2 Models after VIF Selection

```
summary(MAIC_reduced)
```

```
##
## Call:
## lm(formula = length ~ POP_dioxin3 + POP_furan3 + lymphocyte_pct +
##     race_cat + male + ageyrs + ln_lbxcot, data = train_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5093 -0.1532 -0.0305  0.1259  1.1978
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.436e+00  4.989e-02  28.773  < 2e-16 ***
## POP_dioxin3     -3.528e-05  2.355e-05  -1.499  0.13449
## POP_furan3       5.877e-03  2.021e-03   2.908  0.00376 **
## lymphocyte_pct  -1.801e-03  1.048e-03  -1.719  0.08615 .
```

```
## race_catMexican -1.633e-02  3.702e-02  -0.441  0.65919
## race_catBlack    5.850e-02  3.898e-02   1.501  0.13394
## race_catWhite   -1.014e-02  3.452e-02  -0.294  0.76906
## malemale        -5.309e-02  1.839e-02  -2.888  0.00401 **
## ageyrs          -6.600e-03  6.136e-04 -10.756  < 2e-16 ***
## ln_lbxcot        3.965e-03  2.419e-03   1.639  0.10171
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2228 on 640 degrees of freedom
## Multiple R-squared:  0.2381, Adjusted R-squared:  0.2274
## F-statistic: 22.23 on 9 and 640 DF,  p-value: < 2.2e-16
```

```
summary(MBIC_reduced)
```

```
##
## Call:
## lm(formula = length ~ POP_furan3 + ageyrs, data = train_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.52317 -0.16379 -0.02778  0.12409  1.15701
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.373603   0.025461  53.950   <2e-16 ***
## POP_furan3   0.005311   0.001881   2.823   0.0049 **
## ageyrs      -0.007226   0.000586 -12.331   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2251 on 647 degrees of freedom
## Multiple R-squared:  0.2136, Adjusted R-squared:  0.2111
## F-statistic: 87.84 on 2 and 647 DF,  p-value: < 2.2e-16
```

7.8 Results Model Coefficients

```
coef(cv_ridge_model1)
```

```
## 5 x 1 sparse Matrix of class "dgCMatrix"
##                          1
## (Intercept)  1.2330687211
## (Intercept)  .
## POP_PCB10   -0.0005356453
## malemale    -0.0271484294
## ageyrs      -0.0031085154
```

```
coef(cv_ridge_model3)
```

```
## 6 x 1 sparse Matrix of class "dgCMatrix"
##                          1
## (Intercept)  1.2464105180
## (Intercept)  .
## POP_furan3  -0.0006084626
```

```
## ageyrs      -0.0034406391
## ln_lbxcot    0.0037687481
## malemale    -0.0330128160
```

```
coef(cvfit_lasso_oh)
```

```
## 36 x 1 sparse Matrix of class "dgCMatrix"
##                                1
## (Intercept)          1.204264303
## POP_PCB3             .
## POP_PCB6             .
## POP_PCB7             .
## POP_PCB8             .
## POP_PCB9             .
## POP_PCB10            .
## POP_PCB11            .
## POP_dioxin1          .
## POP_dioxin2          .
## POP_dioxin3          .
## POP_furan1           .
## POP_furan2           .
## POP_furan3           .
## POP_furan4           .
## whitecell_count      .
## lymphocyte_pct       .
## monocyte_pct         .
## basophils_pct        .
## neutrophils_pct      .
## BMI                  .
## edu_cat_1            .
## edu_cat_2            .
## edu_cat_3            .
## edu_cat_4            .
## race_cat_Other       .
## race_cat_Mexican     .
## race_cat_Black       .
## race_cat_White       .
## male_female          .
## male_male            .
## ageyrs              -0.003017825
## yrssmoke             .
## smokenow_Non-Smoker  .
## smokenow_Smoker      .
## ln_lbxcot            .
```