Methods II: Homework 1

Tim Vigers

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```
# Load libraries
library(car)
```

```
## Loading required package: carData
```

```
library(nortest)
library(MASS)
# Read in data
hyponat <- read.table("/Users/timvigers/Documents/School/UC Denver/Biostatistics/Biostatistical Methods
```

1. Consider transforming covariates and the outcome.

a. Is categorization necessary for BMI?

The quadratic BMI term is significant, and the VIF values for the polynomials are large. This just shows that there is indeed a quadratic relationship and that the polynomial terms are collinear (as we were told in the question). When this is the case, it's correct to make the variable categorical as long as doing so makes scientific sense. In the case of BMI, it does make sense to split people into categorical groups like underweight, normal, and overweight. This removes the collinearity concern, and the model is still easily interpretable.

b. Should the number of previous marathons run be dichotomized?

The number of previous marathons is very skewed, which violates the assumption of normality. So, dichotomizing this variable at the median is a good idea.

c. Is there a quadratic relationship between weight change and sodium levels?

There does appear to be a quadratic relationship between weight change and sodium levels ($p = 0.00483$). However, the VIF isn't too high, so I don't think it's necessary to make it a categorical variable.

d. Should fluid frequency be treated as a continuous variable or 2 indicator variables?

The levels of fluidfr3 are 1 = every one mile, 2 = every two miles, and 3 = every third mile or more. I don't see how this could be treated as a continuous variable, so I think it's best to keep it as a categorical variable (indicator functions). You could maybe use total water intake as a continuous variable if that information was available, but this data can't be treated as continuous.

e. The authors only used weight change and excluded the self-reported variables from the multivariable analysis. Is this an issue?

I think this approach sort of makes sense. Weight difference is probably the best measure of fluid loss/intake (assuming they're consuming a negligible amount of solid food), and the other three variables are reporting similar information. When this is the case, dropping the self-reported variables makes sense as they're most likely the least accurate.

My main concern would be if one of those variables is really reporting different information, and by excluding them you're losing valuable data. Also, I worry a little bit about dropping 3 out of 4 variables, so it might be good to investigate the collinearity further and only drop 2.

f. Only running time was used in the multivariable model and not training pace since it is self-reported. Is this an issue?

I'm more comfortable with this than the previous question, since you're only looking at two variables, and they pretty clearly tell you the same information. If you ran the whole marathon quickly, it seems safe to assume that your training pace was also fast. And since it's self reported (and possibly hard to measure accurately yourself), you have to worry about inaccuracy or people intentionally overestimating how quickly they run.

g. Should the outcome sodium levels be log transformed?

Log transforming the outcome clearly doesn't change much (the log transformed outcome is still not normally distributed, and the histograms look very similar). So, I would keep the outcome as it is, especially since it's generally best to avoid transforming the outcome if possible.

2. Run the single variable analyses.

a. Which variables are associated with sodium levels at the 0.05 level of significance?

Based on the above output, the variables significantly associated with sodium are: female, lwobup01, fluidfr3, wtdiff (quadratic relationship), runtime, trainpse. So sex, whether you use anti-inflammatory medications, fluid intake frequency, weight change during the marathon, how quickly you run the marathon, and your training pace are all associated with sodium levels.

b. How do these univariate analyses compare to the original paper where sodium levels were dichotomous?

The paper concluded that "considerable weight gain while running, a long racing time, and bodymass index extremes were associated with hyponatremia, whereas female sex, composition of fluids ingested, and use of nonsteroidal anti-inflammatory drugs were not." So our analyses agree that weight change and running time are associated with sodium. However, we did not find that BMI was associated (when treated as a continuous or a categorical variable), and did find that sex and use of NSAIDs were.

3. Multivariable analyses with stepwise regression based on AIC

a. What predictors are included in the final model?

Using both forward and backward stepwise regression based in AIC, change in weight and anti-inflammatory usage are both associated with sodium level, and so is BMI category.

b.

There are a couple of problems with this method. First, it's possible that some variables are significant in a multiple regression model, but are not significant when tested on their own. Second, it doesn't take polynomial associations (e.g. BMI) or collinearity into account. Lastly, this way of approaching things doesn't really think about the scientific question. All of the variables in this data set make sense to test, but many data sets include lots of variables that don't make sense with the question at hand, so just using this approach without thinking can end up including nonsensical variables in the model.

4. Partial F test with all covariates with a p-value less than 0.1

a. What predictors are included in the final model?

The only variable included after partial F tests is weight difference.

b. What are the results of the F test?

The reduced model is not significantly different from the full model.

5. Why do you think that there are more significant covariates in the final model for a binary outcome than there are for a continuous outcome?

By turning the outcome into a categorical variable, you're throwing out a lot of information, and this inceases the risk of a false positive. You lose a lot of statistical power by dichotomizing a variable, which makes some intuitive sense if you think about it as a reduction in sample size.

Code

```
# Problem 1a
polymod <- lm(sodium ~ bmi + I(bmi^2),data = hyponat)
summary(polymod)
```

```
##
## Call:
## lm(formula = sodium ~ bmi + I(bmi^2), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.4019  -2.8199   0.1535   3.0960  15.2932
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 85.94424   13.62912   6.306 8.24e-10 ***
## bmi          4.56748    1.14186   4.000 7.66e-05 ***
## I(bmi^2)    -0.09440    0.02371  -3.981 8.26e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.78 on 367 degrees of freedom
## Multiple R-squared:  0.04179,    Adjusted R-squared:  0.03657
## F-statistic: 8.003 on 2 and 367 DF,  p-value: 0.0003964
```

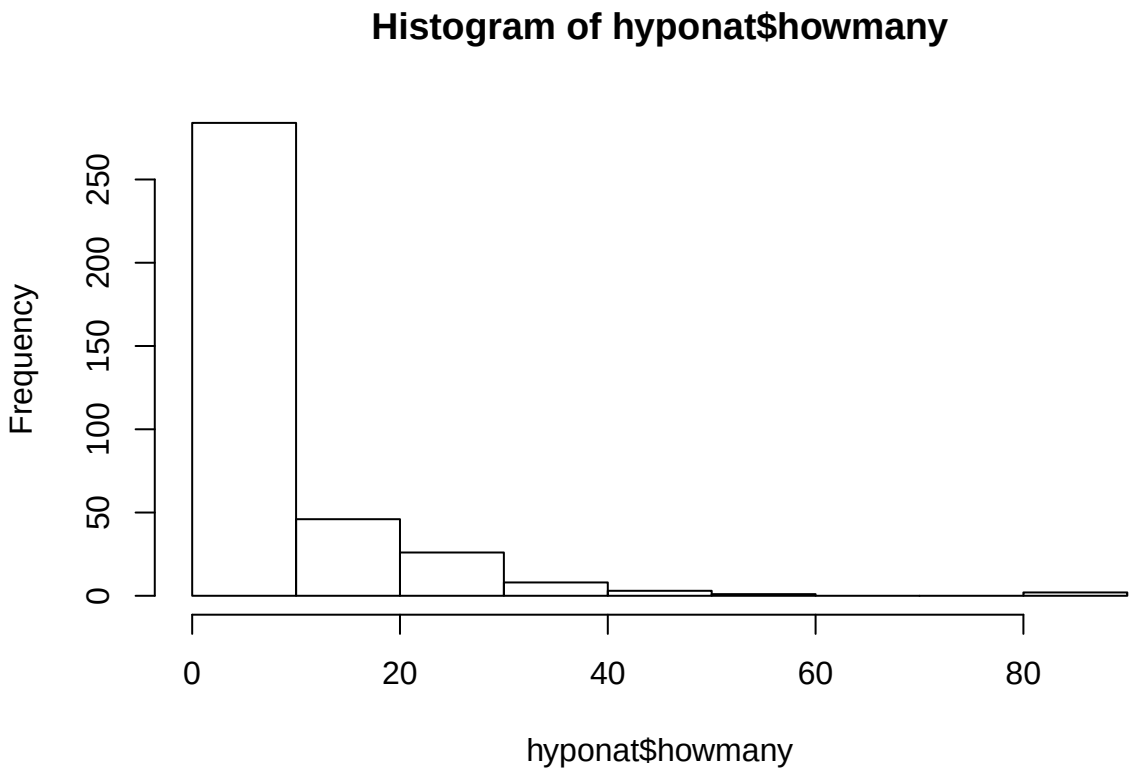
```
vif(polymod)
```

```
##      bmi I(bmi^2)
## 155.9472 155.9472
```

```
hyponat$bmiC <- cut(hyponat$bmi,c(0,20,25,Inf))
category <- lm(sodium ~ bmiC, data = hyponat)
summary(category)
```

```
##
## Call:
## lm(formula = sodium ~ bmiC, data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.8314  -2.8314   0.1686   3.1686  15.1686
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  138.2973     0.7921 174.604  < 2e-16 ***
## bmiC(20,25]    2.5341     0.8476   2.990  0.00298 **
## bmiC(25,Inf]   1.5617     0.9617   1.624  0.10528
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.818 on 367 degrees of freedom
## Multiple R-squared:  0.02669,    Adjusted R-squared:  0.02139
## F-statistic: 5.032 on 2 and 367 DF,  p-value: 0.006984
```

```r
# Problem 1b
hist(hyponat$howmany)
```




```r
# Problem 1c
fit <- lm(sodium ~ poly(wtdiff,2), data = hyponat)
summary(fit)
```

```
##
## Call:
## lm(formula = sodium ~ poly(wtdiff, 2), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -24.0835  -2.4685   0.3256   2.6527  14.2696
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       140.373      0.224 626.688  < 2e-16 ***
## poly(wtdiff, 2)1  -42.313      4.309  -9.821  < 2e-16 ***
## poly(wtdiff, 2)2  -12.216      4.309  -2.835  0.00483 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.309 on 367 degrees of freedom
## Multiple R-squared:  0.2216, Adjusted R-squared:  0.2174
## F-statistic: 52.24 on 2 and 367 DF,  p-value: < 2.2e-16
```

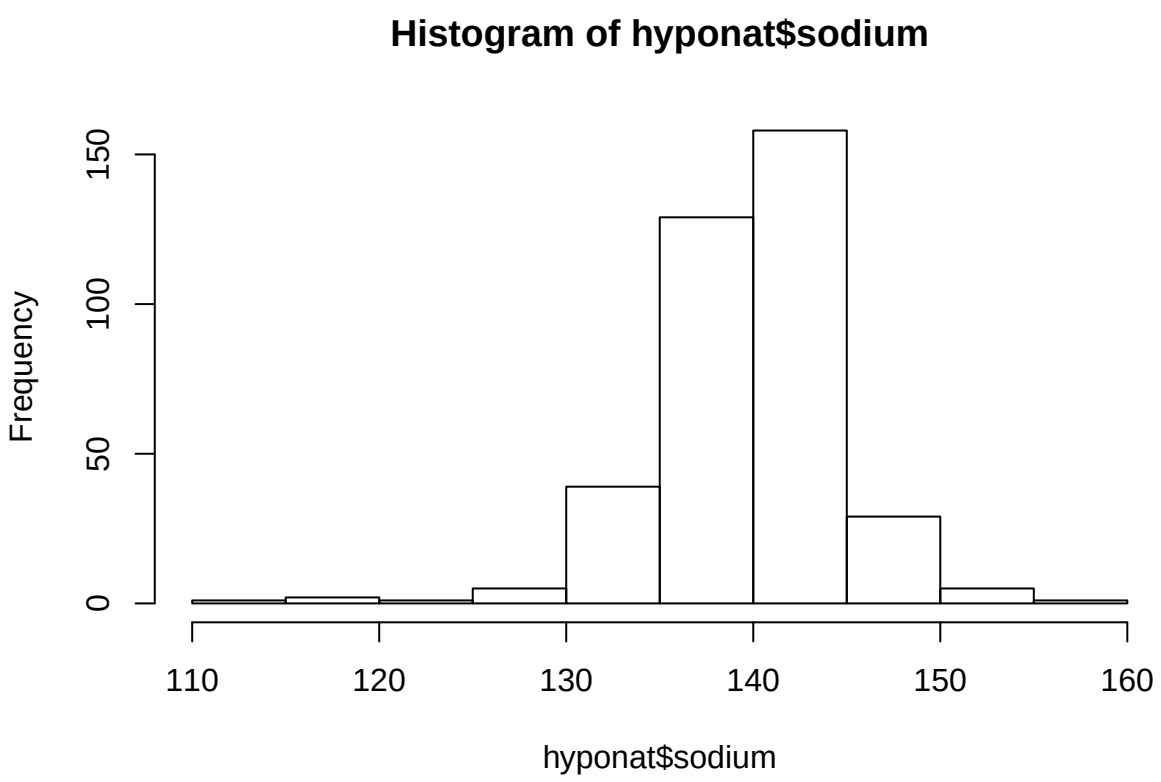
```r
weightmod <- lm(sodium ~ wtdiff + I(wtdiff^2),data = hyponat)
vif(weightmod)
```

```
##      wtdiff I(wtdiff^2)
##    1.255001    1.255001
```

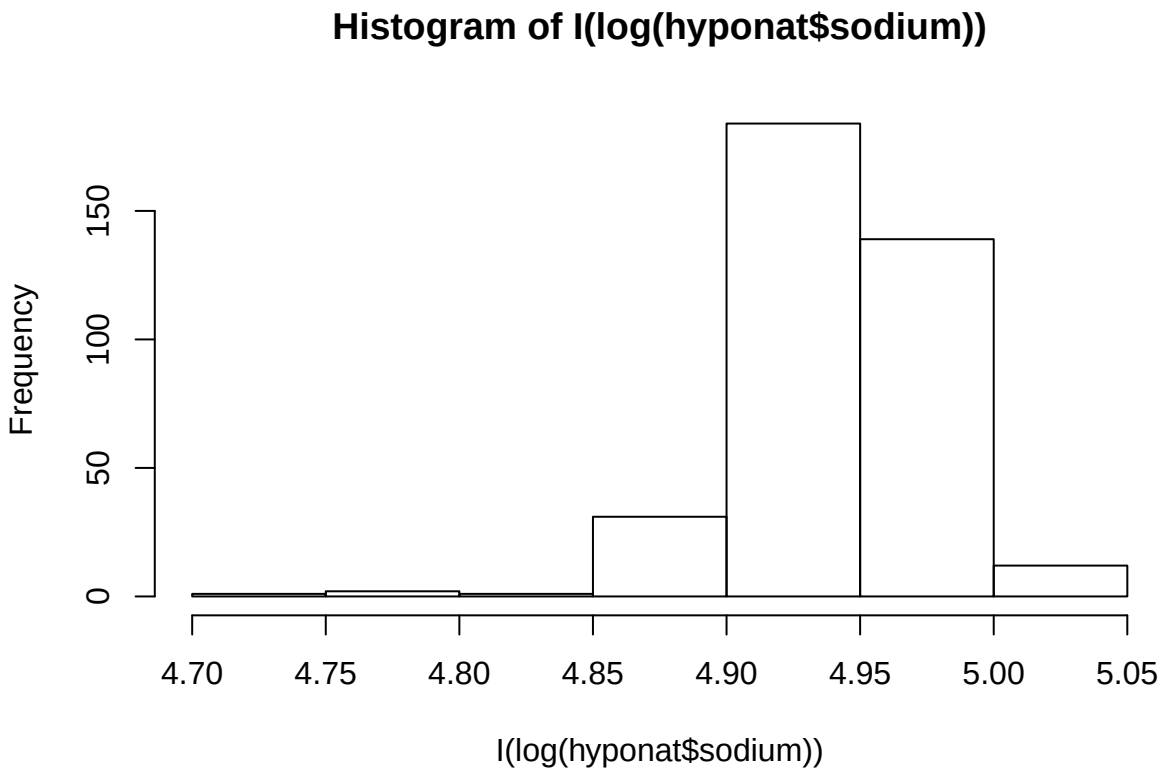
```r
# Problem 1d
hyponat$fluidfr3 <- as.factor(hyponat$fluidfr3)
catmod <- lm(sodium ~ fluidfr3, data = hyponat)
summary(catmod)
```

```
##
## Call:
## lm(formula = sodium ~ fluidfr3, data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.7480  -2.7368   0.2632   3.2520  15.2632
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 139.7368     0.3316 421.356  < 2e-16 ***
## fluidfr32     1.0112     0.5394   1.875 0.061645 .
## fluidfr33     3.1455     0.8866   3.548 0.000439 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.794 on 367 degrees of freedom
## Multiple R-squared:  0.03617,    Adjusted R-squared:  0.03091
## F-statistic: 6.885 on 2 and 367 DF,  p-value: 0.00116
```

```r
# Problem 1g - log transform sodium levels
hist(hyponat$sodium)
```



```r
hist(I(log(hyponat$sodium)))
```




```r
lillie.test(hyponat$sodium)
```

```
##
##  Lilliefors (Kolmogorov-Smirnov) normality test
##
## data:  hyponat$sodium
## D = 0.10252, p-value = 5.076e-10
```

```r
lillie.test(I(log(hyponat$sodium)))
```

```
##
##  Lilliefors (Kolmogorov-Smirnov) normality test
##
## data:  I(log(hyponat$sodium))
## D = 0.11078, p-value = 8.407e-12
```

```r
# Probem 2 - univariate analysis
vars <- colnames(hyponat)[-c(which(colnames(hyponat)=="sodium"))]
univar <- lapply(vars, function(x){
  summary(lm(as.formula(paste0("sodium ~ ",x)), data = hyponat))
})
univar
```

```
## [[1]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -25.1339  -2.1339  -0.0206   2.9794  14.9794
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 141.0206     0.3075 458.603  < 2e-16 ***
## female       -1.8867     0.5249  -3.595 0.000369 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.793 on 368 degrees of freedom
## Multiple R-squared:  0.03392,    Adjusted R-squared:  0.0313
## F-statistic: 12.92 on 1 and 368 DF,  p-value: 0.000369
##
##
## [[2]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.5557  -2.4258   0.4443   3.3860  15.5432
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 140.58045    0.31964 439.812   <2e-16 ***
## howmany      -0.02474    0.02327  -1.063    0.288
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.869 on 368 degrees of freedom
## Multiple R-squared:  0.003062,   Adjusted R-squared:  0.000353
## F-statistic:  1.13 on 1 and 368 DF,  p-value: 0.2884
##
##
## [[3]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.2152  -2.3795   0.4178   3.1970  15.6206
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 139.64576    1.07859 129.471   <2e-16 ***
## age           0.01898    0.02736   0.694    0.488
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.874 on 368 degrees of freedom
## Multiple R-squared:  0.001306,   Adjusted R-squared:  -0.001408
```

```
## F-statistic: 0.4811 on 1 and 368 DF,  p-value: 0.4883
##
##
## [[4]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -25.7711  -2.0888   0.2289   2.9112  16.2289
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 141.0888     0.3717 379.563  < 2e-16 ***
## lwobup01     -1.3176     0.5043  -2.613  0.00935 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.832 on 368 degrees of freedom
## Multiple R-squared:  0.01821,    Adjusted R-squared:  0.01554
## F-statistic: 6.826 on 1 and 368 DF,  p-value: 0.009353
##
##
## [[5]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.2390  -2.2390   0.2551   3.1316  15.2551
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 140.7449     0.4921 285.997   <2e-16 ***
## wateld01     -0.5059     0.5740  -0.881    0.379
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.872 on 368 degrees of freedom
## Multiple R-squared:  0.002107,   Adjusted R-squared:  -0.0006048
## F-statistic: 0.777 on 1 and 368 DF,  p-value: 0.3786
##
##
## [[6]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.4699  -2.4699   0.5301   3.4571  16.2381
##
```

```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 140.4699     0.2602 539.873   <2e-16 ***
## urinat3p     -1.7080     1.0922  -1.564    0.119
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.861 on 368 degrees of freedom
## Multiple R-squared:  0.006602,   Adjusted R-squared:  0.003903
## F-statistic: 2.446 on 1 and 368 DF,  p-value: 0.1187
##
##
## [[7]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.7480  -2.7368   0.2632   3.2520  15.2632
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 139.7368     0.3316 421.356  < 2e-16 ***
## fluidfr32     1.0112     0.5394   1.875 0.061645 .
## fluidfr33     3.1455     0.8866   3.548 0.000439 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.794 on 367 degrees of freedom
## Multiple R-squared:  0.03617,    Adjusted R-squared:  0.03091
## F-statistic: 6.885 on 2 and 367 DF,  p-value: 0.00116
##
##
## [[8]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -24.1017  -2.5612   0.3042   2.5762  14.5866
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 139.4968     0.2434 573.117   <2e-16 ***
## wtdiff       -1.4092     0.1449  -9.728   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.35 on 368 degrees of freedom
## Multiple R-squared:  0.2046, Adjusted R-squared:  0.2024
## F-statistic: 94.64 on 1 and 368 DF,  p-value: < 2.2e-16
##
```

```
##
## [[9]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.7264  -2.5159   0.1344   2.7186  16.6333
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 144.802143   1.420510 101.937  < 2e-16 ***
## runtime      -0.019501   0.006157  -3.168  0.00167 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.812 on 368 degrees of freedom
## Multiple R-squared:  0.02654,    Adjusted R-squared:  0.0239
## F-statistic: 10.03 on 1 and 368 DF,  p-value: 0.001666
##
##
## [[10]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.4851  -2.4851   0.1256   2.8313  16.0718
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 146.712879   1.968890  74.516  < 2e-16 ***
## trainpse     -0.012975   0.003997  -3.246  0.00128 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.809 on 368 degrees of freedom
## Multiple R-squared:  0.02784,    Adjusted R-squared:  0.0252
## F-statistic: 10.54 on 1 and 368 DF,  p-value: 0.001276
##
##
## [[11]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -26.310  -2.382   0.535   3.271  15.668
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept) 139.54400    2.16471  64.463   <2e-16 ***
## bmi           0.03596    0.09326   0.386      0.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.876 on 368 degrees of freedom
## Multiple R-squared:  0.0004039,  Adjusted R-squared:  -0.002312
## F-statistic: 0.1487 on 1 and 368 DF,  p-value: 0.7
##
##
## [[12]]
##
## Call:
## lm(formula = as.formula(paste0("sodium ~ ", x)), data = hyponat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.8314  -2.8314   0.1686   3.1686  15.1686
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  138.2973     0.7921 174.604  < 2e-16 ***
## bmiC(20,25]    2.5341     0.8476   2.990  0.00298 **
## bmiC(25,Inf]   1.5617     0.9617   1.624  0.10528
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.818 on 367 degrees of freedom
## Multiple R-squared:  0.02669,    Adjusted R-squared:  0.02139
## F-statistic: 5.032 on 2 and 367 DF,  p-value: 0.006984
```

```
# Problem 3 - stepwise AIC
sigvars <- c("female","lwobup01","fluidfr3","wtdiff","runtime","trainpse","bmiC")
sigvars <- paste(sigvars,collapse = " + ")
formula <- as.formula(paste0("sodium ~ ",sigvars))
stepwise <- stepAIC(lm(formula, data = hyponat),direction = "both",trace = 0)
stepwise
```

```
##
## Call:
## lm(formula = sodium ~ lwobup01 + wtdiff + bmiC, data = hyponat)
##
## Coefficients:
##  (Intercept)      lwobup01        wtdiff   bmiC(20,25]  bmiC(25,Inf]
##     138.7320       -0.7481       -1.3379        1.4928        0.8858
```

```
# Problem 4 - partial F test
sigvars
```

```
## [1] "female + lwobup01 + fluidfr3 + wtdiff + runtime + trainpse + bmiC"
```

```
full <- lm(sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) + runtime + trainpse + bmiC,data
# Remove bmiC
mod1 <- lm(sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) + runtime + trainpse,data = hyp
anova(full,mod1)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) +
##     runtime + trainpse + bmiC
## Model 2: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) +
##     runtime + trainpse
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    359 6552.9
## 2    361 6627.4 -2   -74.563 2.0425 0.1312
```

```
# Remove trainpse
mod2 <- lm(sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) + runtime,data = hyponat)
anova(mod1,mod2)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) +
##     runtime + trainpse
## Model 2: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) +
##     runtime
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    361 6627.4
## 2    362 6633.4 -1   -5.9738 0.3254 0.5687
```

```
# Remove runtime
mod3 <- lm(sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2),data = hyponat)
anova(mod2,mod3)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) +
##     runtime
## Model 2: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2)
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    362 6633.4
## 2    363 6651.0 -1   -17.639 0.9626 0.3272
```

```
# Remove weight difference
mod4 <- lm(sodium ~ female + lwobup01 + fluidfr3,data = hyponat)
anova(mod3,mod4)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2)
## Model 2: sodium ~ female + lwobup01 + fluidfr3
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1    363 6651.0
## 2    365 8109.4 -2   -1458.4 39.798 2.358e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Put weight difference back in
mod5 <- lm(sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2),data = hyponat)
anova(mod4,mod5)
```

```
## Analysis of Variance Table
##
```

```
## Model 1: sodium ~ female + lwobup01 + fluidfr3
## Model 2: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2)
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1    365 8109.4
## 2    363 6651.0  2    1458.4 39.798 2.358e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Remove fluid frequency
mod6 <- lm(sodium ~ female + lwobup01 + wtdiff + I(wtdiff^2),data = hyponat)
anova(mod5,mod6)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2)
## Model 2: sodium ~ female + lwobup01 + wtdiff + I(wtdiff^2)
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    363 6651.0
## 2    365 6703.3 -2   -52.284 1.4268 0.2414
```

```
# Remove NSAIDs
mod7 <- lm(sodium ~ female + wtdiff + I(wtdiff^2),data = hyponat)
anova(mod6,mod7)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ female + lwobup01 + wtdiff + I(wtdiff^2)
## Model 2: sodium ~ female + wtdiff + I(wtdiff^2)
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1    365 6703.3
## 2    366 6769.1 -1    -65.81 3.5834 0.05915 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Remove female
mod8 <- lm(sodium ~ wtdiff + I(wtdiff^2),data = hyponat)
anova(mod7,mod8)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ female + wtdiff + I(wtdiff^2)
## Model 2: sodium ~ wtdiff + I(wtdiff^2)
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    366 6769.1
## 2    367 6812.9 -1   -43.757 2.3659 0.1249
```

```
anova(mod8,full)
```

```
## Analysis of Variance Table
##
## Model 1: sodium ~ wtdiff + I(wtdiff^2)
## Model 2: sodium ~ female + lwobup01 + fluidfr3 + wtdiff + I(wtdiff^2) +
##     runtime + trainpse + bmiC
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1    367 6812.9
## 2    359 6552.9  8    260.03 1.7807 0.07954 .
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```