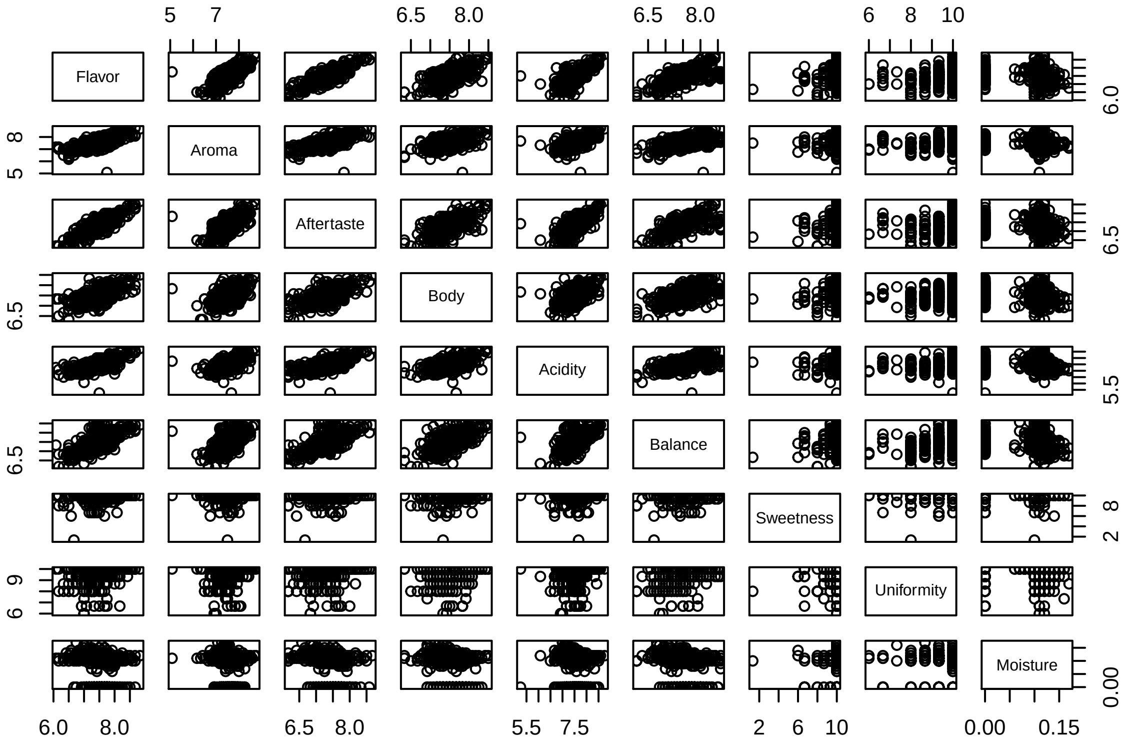
```r
## Coffee example  (Coffee Quality Institute, 2018) continued
coffee <- read.csv("coffee_arabica.csv")

# cor(coffee) # doesn't work as there's a categorical variable
cor(coffee[,-1]) # e.g., remove first column
```

```
##                  Aroma     Flavor Aftertaste        Body     Acidity    Balance
## Aroma       1.00000000  0.7339782  0.6892744  0.56699932  0.60115765  0.6156508
## Flavor      0.73397820  1.0000000  0.8582783  0.67694834  0.73845546  0.7324530
## Aftertaste  0.68927440  0.8582783  1.0000000  0.67407704  0.69408861  0.7657979
## Body        0.56699932  0.6769483  0.6740770  1.00000000  0.60795391  0.6924568
## Acidity     0.60115765  0.7384555  0.6940886  0.60795391  1.00000000  0.6417994
## Balance     0.61565084  0.7324530  0.7657979  0.69245676  0.64179938  1.0000000
## Sweetness   0.06955938  0.1345364  0.1185760  0.03977892  0.06906093  0.1016718
## Uniformity  0.14785498  0.2132347  0.2143116  0.07195778  0.14876428  0.2180726
## Moisture   -0.11567549 -0.1327342 -0.1745366 -0.21009097 -0.10391684 -0.2161964
##             Sweetness Uniformity    Moisture
## Aroma      0.06955938 0.14785498 -0.11567549
## Flavor     0.13453644 0.21323472 -0.13273418
## Aftertaste 0.11857600 0.21431157 -0.17453658
## Body       0.03977892 0.07195778 -0.21009097
## Acidity    0.06906093 0.14876428 -0.10391684
## Balance    0.10167183 0.21807265 -0.21619640
## Sweetness  1.00000000 0.34756414  0.08049300
## Uniformity 0.34756414 1.00000000  0.02105693
## Moisture   0.08049300 0.02105693  1.00000000
```

```r
# pairs without response: pairs(coffee[,-1])
# pairs with response, this is what we want
pairs(~ Flavor + Aroma + Aftertaste + Body +
        Acidity + Balance + Sweetness + Uniformity + Moisture, data=coffee)
```



```r
# Code our own indicators, so that we can more easily interpret VIFs
# 1 = wet, 0 otherwise
coffee$wet <- ifelse(coffee$Processing.Method == 'Washed / Wet', 1, 0)
# 1 = semi/dry, 0 otherwise
coffee$semi <- ifelse(coffee$Processing.Method == 'Semi-washed / Semi-pulped',
                      1, 0)
```

Model:

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3} + \beta_4 x_{i4} + \beta_5 x_{i5} + \beta_6 x_{i6} + \beta_7 x_{i7} + \beta_8 x_{i8} + \beta_9 x_{i9} + \beta_{10} x_{i(10)} + \varepsilon_i$$

where

- $y =$ flavour
- $x_1 = 1$ if wet, 0 otherwise
- $x_2 = 1$ if semi, 0 otherwise
- $x_3 =$ Aroma
- $x_4 =$ Aftertaste
- $x_5 =$ Body
- $x_6 =$ Acidity
- $x_7 =$ Balance
- $x_8 =$ Sweetness
- $x_9 =$ Uniformity

- $x_{10} =$ Moisture

```r
# Full MLR with our own coded indicators
mfull <- lm(Flavor~ wet + semi + Aroma + Aftertaste +
      Body + Acidity + Balance + Sweetness + Uniformity + Moisture, dat=coffee)
summary(mfull)
```

```
##
## Call:
## lm(formula = Flavor ~ wet + semi + Aroma + Aftertaste + Body +
##     Acidity + Balance + Sweetness + Uniformity + Moisture, data = coffee)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.68587 -0.08465  0.00079  0.08910  0.63633
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.728757   0.168516  -4.325 1.67e-05 ***
## wet         -0.033061   0.011024  -2.999  0.00277 **
## semi        -0.001396   0.022021  -0.063  0.94947
## Aroma        0.220302   0.020447  10.774  < 2e-16 ***
## Aftertaste   0.468759   0.023912  19.603  < 2e-16 ***
## Body         0.096140   0.024334   3.951 8.28e-05 ***
## Acidity      0.216751   0.021194  10.227  < 2e-16 ***
## Balance      0.046806   0.022558   2.075  0.03823 *
## Sweetness    0.025507   0.010150   2.513  0.01211 *
## Uniformity   0.016297   0.009803   1.663  0.09669 .
## Moisture     0.169012   0.102480   1.649  0.09938 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.148 on 1108 degrees of freedom
## Multiple R-squared:  0.8091, Adjusted R-squared:  0.8073
## F-statistic: 469.5 on 10 and 1108 DF,  p-value: < 2.2e-16
```

```r
# Full MLR alternative, using factor command
mfull_alternative <- lm(Flavor~ factor(Processing.Method) + Aroma + Aftertaste +
      Body + Acidity + Balance + Sweetness + Uniformity + Moisture, dat=coffee)
```

Suppose we want to check the VIF for $j = 1$; that is, x_1. Now, we fit:

$$x_{i1} = \alpha_0 + \alpha_2 x_{i2} + \alpha_3 x_{i3} + \alpha_4 x_{i4} + \alpha_5 x_{i5} + \alpha_6 x_{i6} + \alpha_7 x_{i7} + \alpha_8 x_{i8} + \alpha_9 x_{i9} + \alpha_{10} x_{i(10)} + \varepsilon_i$$

```r
wet_reg <- lm(wet ~ semi + Aroma + Aftertaste + Body + Acidity + Balance +
                Sweetness + Uniformity + Moisture,dat=coffee)
summary(wet_reg)
```

```
##
## Call:
## lm(formula = wet ~ semi + Aroma + Aftertaste + Body + Acidity +
##     Balance + Sweetness + Uniformity + Moisture, data = coffee)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.0015 -0.0283  0.1770  0.2522  0.7704
```

```
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.81748    0.45838   1.783 0.074794 .
## semi        -0.75675    0.05551 -13.632  < 2e-16 ***
## Aroma        0.09690    0.05562   1.742 0.081774 .
## Aftertaste  -0.13169    0.06502  -2.026 0.043054 *
## Body        -0.21885    0.06596  -3.318 0.000936 ***
## Acidity      0.18696    0.05746   3.254 0.001173 **
## Balance     -0.10804    0.06136  -1.761 0.078563 .
## Sweetness    0.08373    0.02753   3.041 0.002413 **
## Uniformity   0.03547    0.02668   1.329 0.184053
## Moisture     0.59486    0.27858   2.135 0.032956 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4031 on 1109 degrees of freedom
## Multiple R-squared:  0.1911, Adjusted R-squared:  0.1845
## F-statistic: 29.11 on 9 and 1109 DF,  p-value: < 2.2e-16
```

```r
r2_wet <- summary(wet_reg)$r.squared
r2_wet
```

```
## [1] 0.191077
```

R_j: In our case, $R_1 = 0.191077$.

```r
VIF_wet <- 1 / (1 - r2_wet)
VIF_wet
```

```
## [1] 1.236212
```

VIF_j: $\text{VIF}_1 = 1.236212$. Interpretation: in a regression with all the variables compared to a regression with just this one, the estimated variance has increased by a factor of 1.24, which is not a very large inflation. The variable wet is not very linearly correlated or dependent on the other predictors that we have in the model.

```r
Aroma_reg <- lm(Aroma ~ wet + semi + Aftertaste +
      Body + Acidity + Balance + Sweetness + Uniformity + Moisture, dat=coffee)
r2_Aroma <- summary(Aroma_reg)$r.squared
r2_Aroma
```

```
## [1] 0.5204716
```

```r
VIF_Aroma <- 1 / (1 - r2_Aroma)
VIF_Aroma
```

```
## [1] 2.085382
```

$R_3 = 0.5204716$, $\text{VIF}_3 = 2.085382$.

```r
Aftertaste_reg <- lm(Aftertaste ~ wet + semi + Aroma +
       Body + Acidity + Balance + Sweetness + Uniformity + Moisture, dat=coffee)
r2_Aftertaste <- summary(Aftertaste_reg)$r.squared
r2_Aftertaste
```

```
## [1] 0.7101012
```

```r
VIF_Aftertaste <- 1 / (1 - r2_Aftertaste)
VIF_Aftertaste
```

```
## [1] 3.449479
```

```
library(car)
```

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

```
vif(mfull) # VIF function in the "car" library
```

```
##        wet        semi       Aroma Aftertaste        Body    Acidity    Balance
##   1.236212    1.178004   2.085382   3.449479    2.317728   2.232210   3.002813
##  Sweetness Uniformity   Moisture
##   1.159602    1.209901   1.086101
```

No serious signs of inflation, all VIFs are less than 10.

```
## Python in FL everglades example (2017)
## Sex, length, total mass, fat mass, and specimen condition data for
## 248 Burmese pythons (Python bivittatus) collected in the Florida Everglades

python <- read.csv("FLpython.csv")
head(python)
```

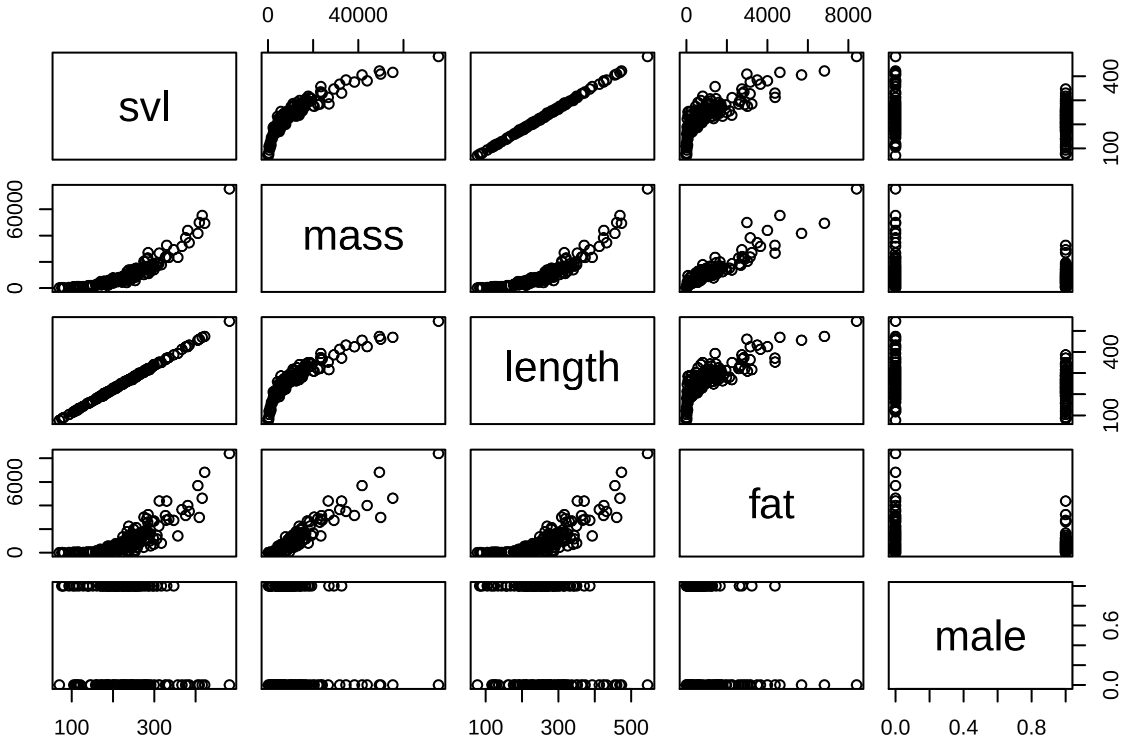
```
##   sex  svl mass length    fat
## 1   F 70.0  186   77.5  6.000
## 2   M 76.0  310   83.8 11.000
## 3   M 77.0  260   86.1  6.000
## 4   M 78.0  262   87.1  8.000
## 5   M 81.0  306   91.1  4.000
## 6   M 93.5  605  104.6 18.959
```

```
python$male <- ifelse(python$sex == 'M', 1, 0) # 1 = M, 0 =F

cor(python[,-1])
```

```
##               svl       mass     length        fat       male
## svl     1.0000000  0.8843022  0.9994935  0.8098652 -0.1602418
## mass    0.8843022  1.0000000  0.8858256  0.9419114 -0.2190993
## length  0.9994935  0.8858256  1.0000000  0.8114658 -0.1593512
## fat     0.8098652  0.9419114  0.8114658  1.0000000 -0.2933111
## male   -0.1602418 -0.2190993 -0.1593512 -0.2933111  1.0000000
```

```
pairs(python[,-1])
```



```r
mpf <- lm(fat ~ male + svl + mass + length, data = python)
summary(mpf)
```

```
##
## Call:
## lm(formula = fat ~ male + svl + mass + length, data = python)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2445.77  -137.41    -5.29   110.00  1527.27
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.021e+02  1.331e+02   1.518    0.130
## male        -1.971e+02  4.732e+01  -4.165 4.32e-05 ***
## svl         -3.370e+00  1.125e+01  -0.300    0.765
## mass         1.178e-01  5.302e-03  22.210  < 2e-16 ***
## length       1.594e+00  1.010e+01   0.158    0.875
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 360.9 on 243 degrees of freedom
## Multiple R-squared:  0.897,  Adjusted R-squared:  0.8953
## F-statistic:   529 on 4 and 243 DF,  p-value: < 2.2e-16
```

```r
vif(mpf)
```

```
##        male          svl         mass       length 
##    1.058699  994.546545    4.813078 1007.484200
```

```r
mpf_l <- lm(length ~ male + svl + mass, data=python)
1/(1-summary(mpf_l)$r.squared)
```

```
## [1] 1007.484
```

Misleading conclusion: svl and length are both irrelevant (this is not the case). Also, the standard errors are very large.

```r
# remove "length" based on VIF
mpf2 <- lm(fat ~ male + mass + svl, data = python)
summary(mpf2)
```

```
## 
## Call:
## lm(formula = fat ~ male + mass + svl, data = python)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -2444.44  -137.38    -6.66   109.22  1530.81 
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  204.09840  132.30121   1.543   0.1242    
## male        -196.71705   47.16396  -4.171 4.22e-05 ***
## mass           0.11788    0.00524  22.495  < 2e-16 ***
## svl           -1.59841    0.76433  -2.091   0.0375 *  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 360.2 on 244 degrees of freedom
## Multiple R-squared:  0.897,  Adjusted R-squared:  0.8957 
## F-statistic: 708.2 on 3 and 244 DF,  p-value: < 2.2e-16
```

```r
vif(mpf2)
```

```
##     male     mass      svl 
## 1.056139 4.720065 4.611903
```

Svl now has a significant *t*-statistic.