Rich Gruss
In-Class 8-3

```
setwd('/Users/rgruss/git/CMDA/in_class/8')
load("fdata.RData")
attach(final)
model <- lm(ssc ~ som1 + som2 + som3 + som4 + som5 + som6 +
          som7 + som8 + som9 +som10 + som11 + som12 +som13 + som14 +
          age)


Residuals:
   Min     1Q  Median     3Q    Max
-4.0846 -0.9373 -0.2395  0.8615  5.1013

Coefficients:
          Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.930604   0.501616   1.855 0.064525 .
som1         0.204283   0.062278   3.280 0.001157 **
som2         0.326182   0.064194   5.081 6.53e-07 ***
som3         0.243625   0.033742   7.220 4.11e-12 ***
som4         0.153274   0.046042   3.329 0.000978 ***
som5         0.166983   0.071151   2.347 0.019566 *
som6         0.074954   0.083424   0.898 0.369641
som7         0.100937   0.081050   1.245 0.213947
som8        -0.009423   0.176722  -0.053 0.957510
som9         0.123674   0.089830   1.377 0.169593
som10        0.250056   0.073577   3.399 0.000767 ***
som11        0.179763   0.087164   2.062 0.040015 *
som12        0.204114   0.059449   3.433 0.000678 ***
som13        0.403307   0.046264   8.717  < 2e-16 ***
som14        0.197416   0.054433   3.627 0.000336 ***
age         -0.010667   0.016660  -0.640 0.522476
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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.533 on 307 degrees of freedom
Multiple R-squared:  0.7923,            Adjusted R-squared:  0.7822
F-statistic: 78.08 on 15 and 307 DF,  p-value: < 2.2e-16
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Interpretation: R-squared of .7 indicates that 70% of the variance is explained in a linear model that includes all 14 somatic markers along with age. The most important explanatory variables for the ssc scores are som13, som3, and som2, each of which is positively related to ssc score.