WEB272 – SOMT Refolding

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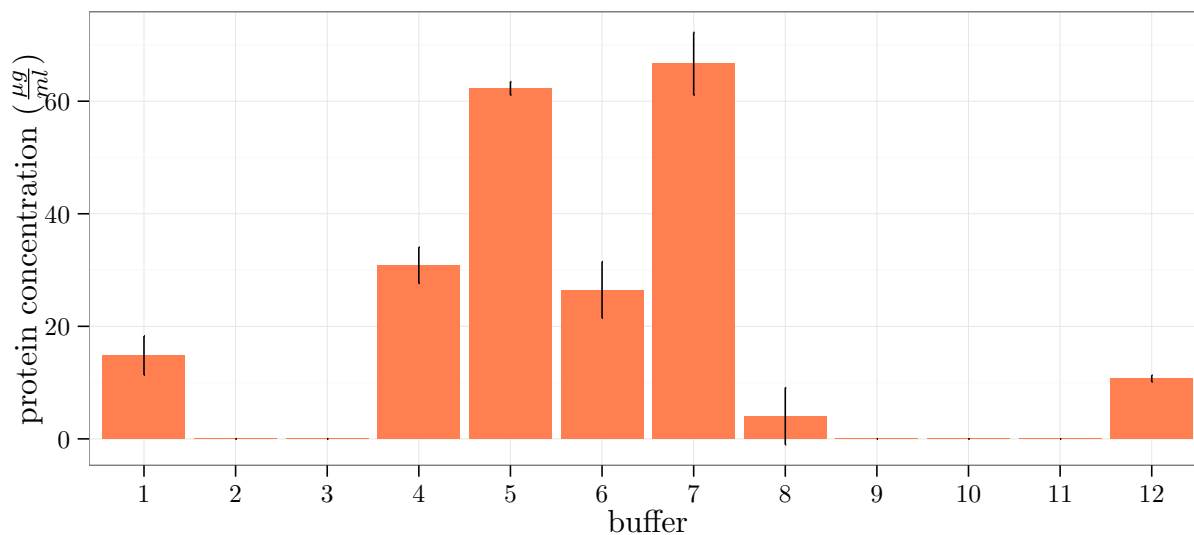
07/23/2015

Contents

After rebuffering protein concentrations were measured by Bradford:

1 Protein concetration

1.1 Regression tree
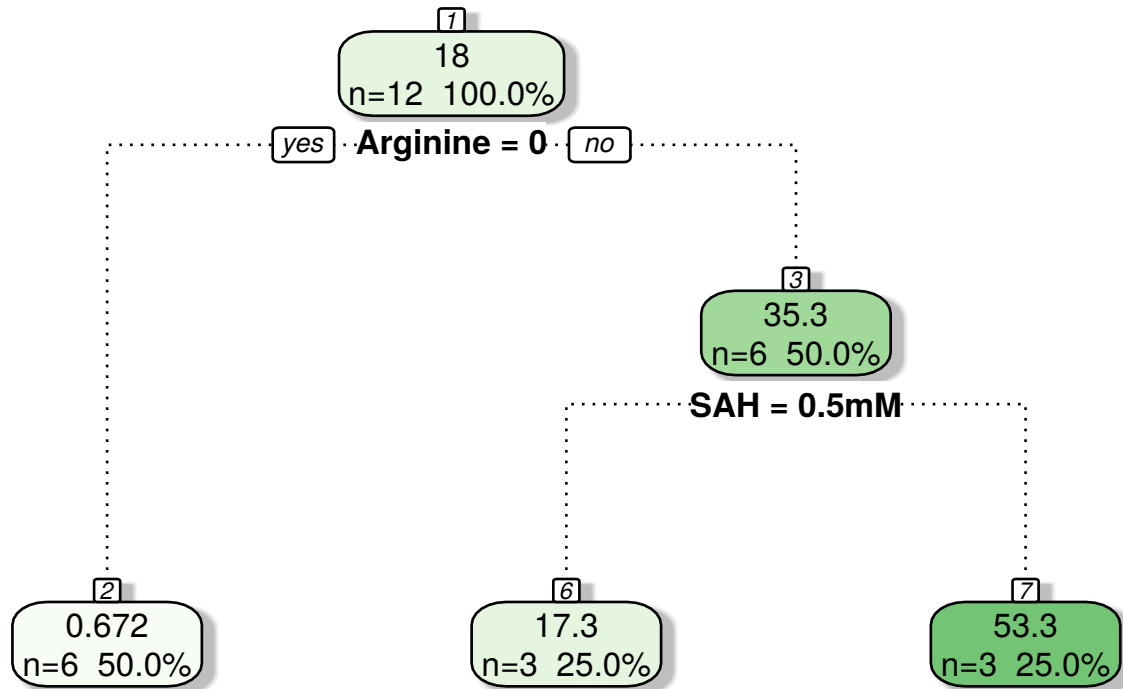
Next we build a regression tree. To see, which factors have the most influence on the protein concentration.

```
somttree2 <- rpart(BFmean ~ .,
                   data=df[,c(1:11,21)],
                   control = c(minsplit = 3,
```

```
                      minbucket = 2,
                      complexity = 0.001))
fancyRpartPlot(somttree2, digits=3)
```

```
                              ┌─┐
                              │1│
                              18
                          n=12  100.0%

              ┌─────┐                    ┌──┐
              │ yes │ ·  Arginine = 0  · │no│
              └─────┘                    └──┘

                                              ┌─┐
                                              │3│
                                             35.3
                                          n=6  50.0%

                                    SAH = 0.5mM

      ┌─┐                    ┌─┐                      ┌─┐
      │2│                    │6│                      │7│
     0.672                  17.3                     53.3
   n=6  50.0%            n=3  25.0%               n=3  25.0%
```
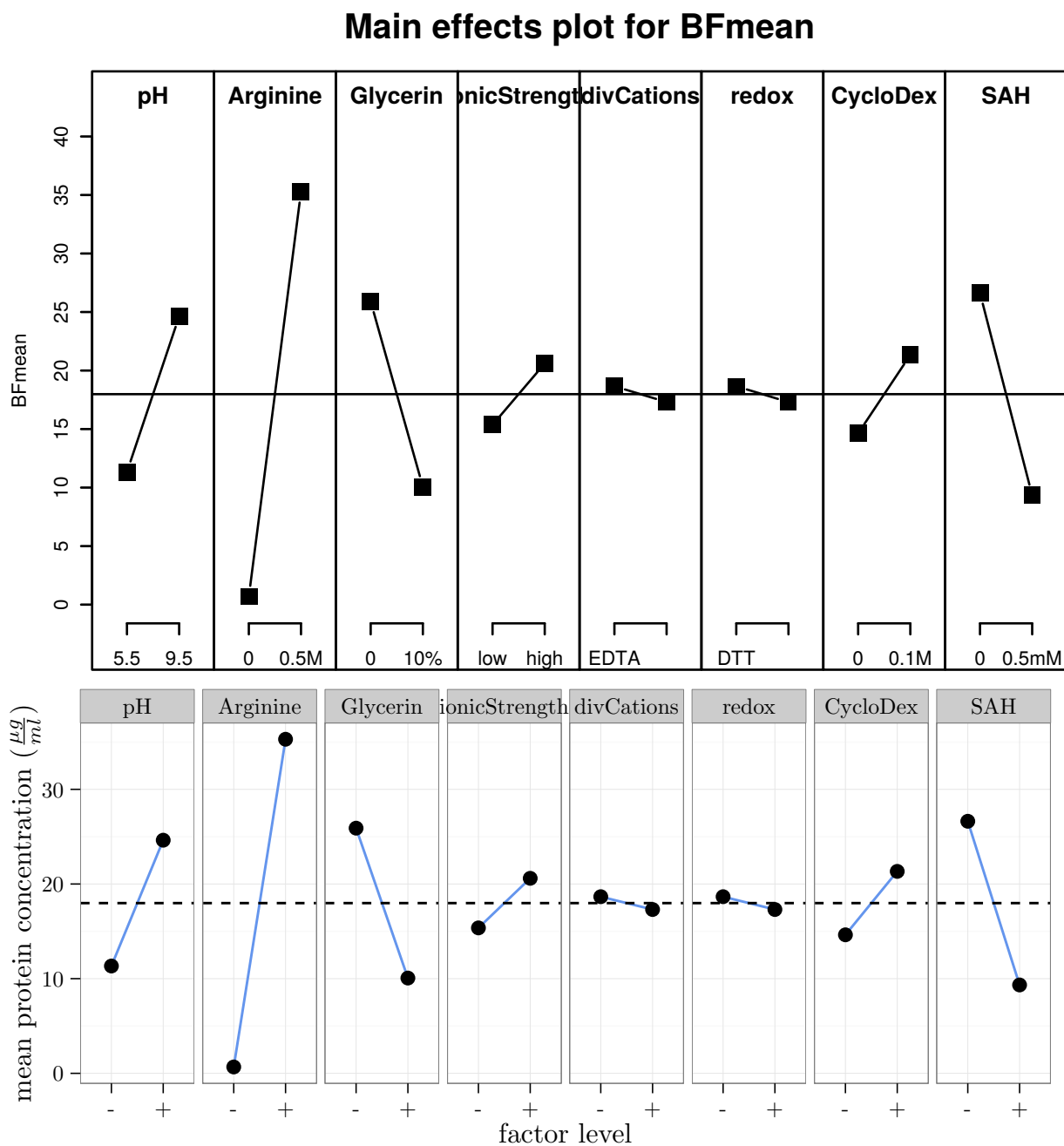
Rattle 2015-Jul-27 11:58:56 mori

Arginine seems to have the biggest impact on refolding efficiency (Arginine addition is better). Then comes SAH (no SAH is better).

1.2 Main effects plot

Main effects plot for BFmean
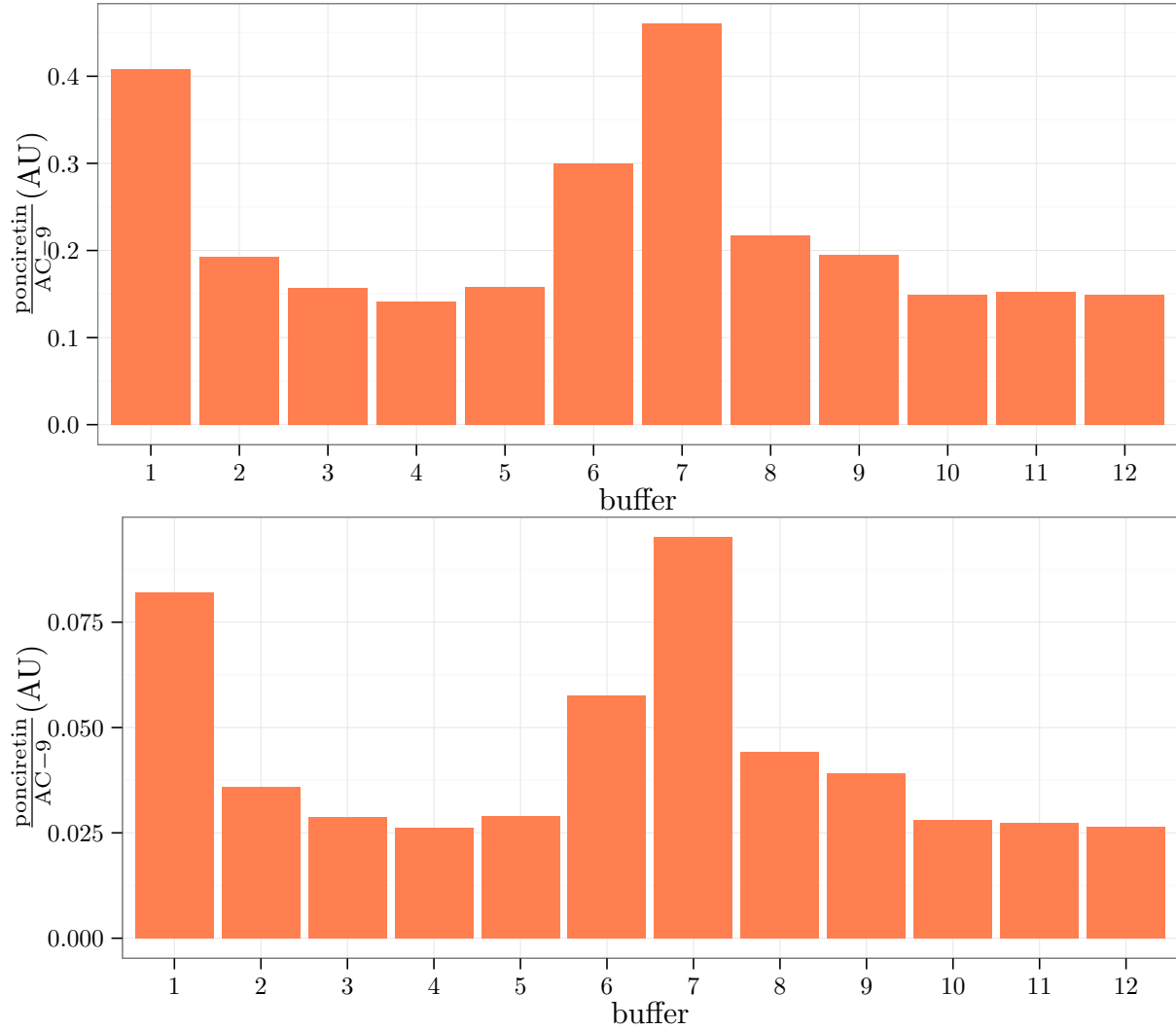
1.3 Statistical test

Test the statistical significance of main effects. Only Arginine is statistically significant to a p-value of 0.05. SAH to a p-value of 0.1.

% latex table generated in R 3.1.2 by xtable 1.7-4 package % Mon Jul 27 11:58:59 2015

```
## Error in eval(expr, envir, enclos): could not find function "LenthPlot"
```

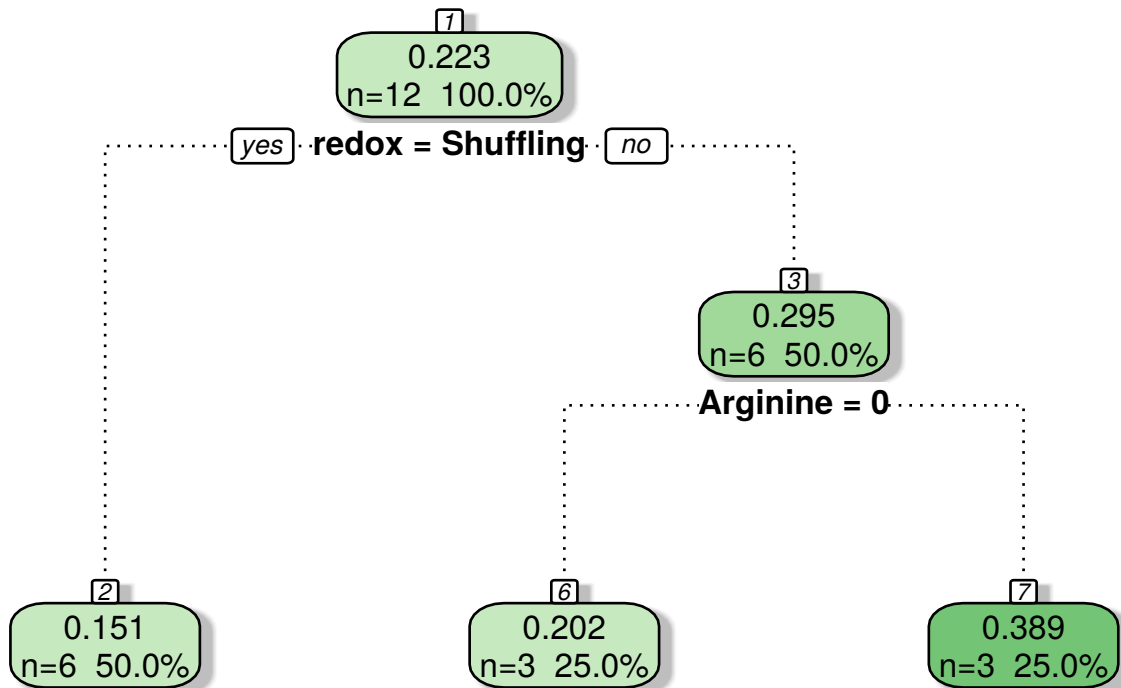|	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Arginine	1	3595.63	3595.63	24.56	0.0158
pH	1	529.87	529.87	3.62	0.1533
Glycerin	1	752.08	752.08	5.14	0.1083
ionicStrength	1	82.37	82.37	0.56	0.5077
divCations	1	5.49	5.49	0.04	0.8588
redox	1	5.52	5.52	0.04	0.8584
CycloDex	1	134.67	134.67	0.92	0.4083
SAH	1	896.83	896.83	6.13	0.0897
Residuals	3	439.26	146.42		

2 Protein volume activity

2.1 Regression tree

Next we build a regression tree. To see, which factors have the most influence the SOMT activity.

```
somttree2 <- rpart(P1_AC ~ .,
                data=df[,c(1:8,12)],
                control = c(minsplit = 3,
                            minbucket = 2,
                            complexity = 0.001))
fancyRpartPlot(somttree2, digits=3)
```
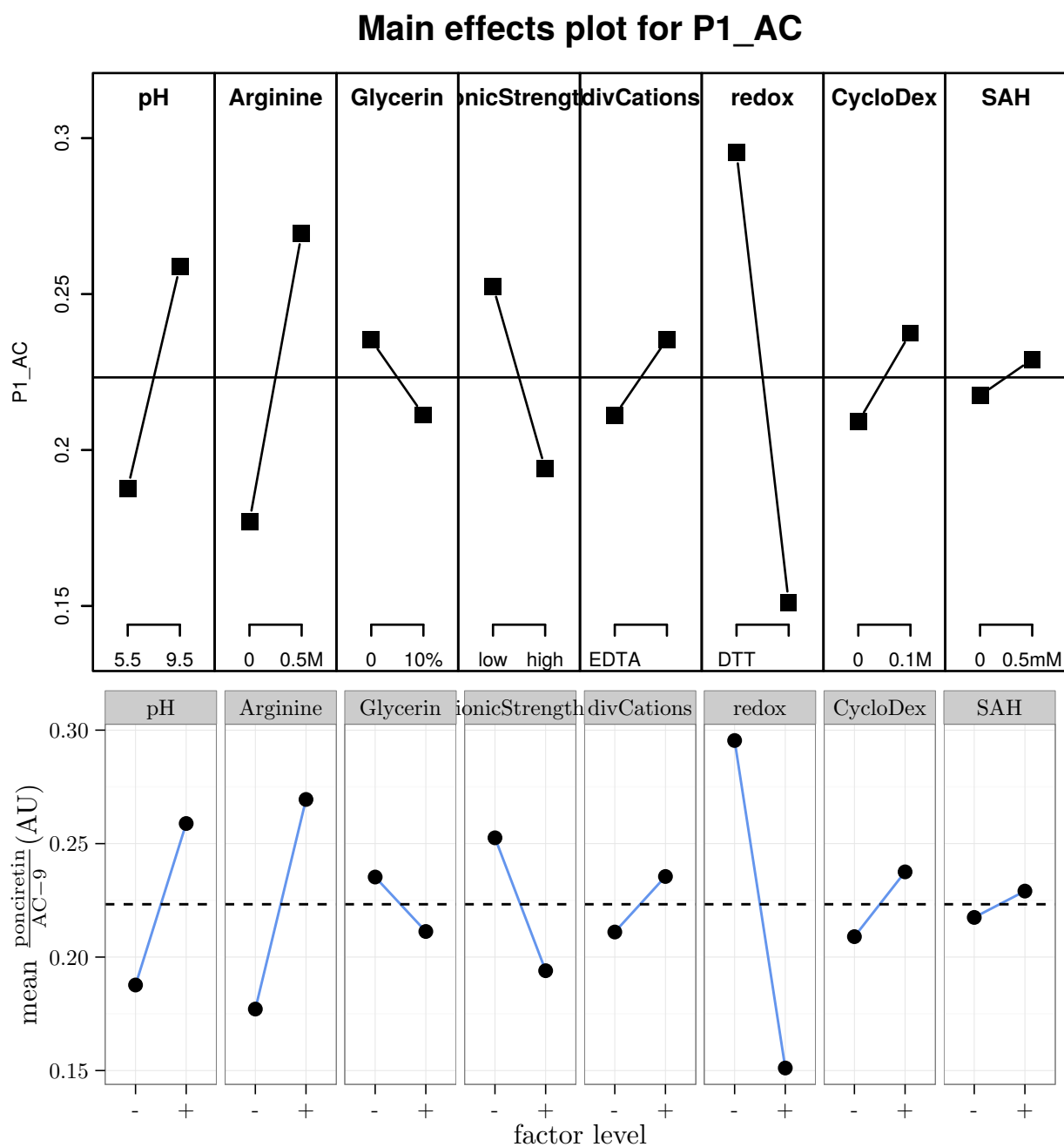
```
                            ┌1┐
                         0.223
                      n=12  100.0%

            yes ·········· redox = Shuffling ·· no ············

                                              ┌3┐
                                           0.295
                                        n=6  50.0%

                                  ········ Arginine = 0 ··········

    ┌2┐                    ┌6┐                        ┌7┐
 0.151                  0.202                      0.389
n=6  50.0%            n=3  25.0%                  n=3  25.0%
```

Rattle 2015-Jul-27 11:59:00 mori

The redox status seems to have the biggest impact on refolding efficiency measured by activity (reducing is better, DTT). Then comes arginine (arginine is better).

2.2   Main effects plot

Main effects plot for P1_AC

2.3   Statistical test

Test the statistical significance of main effects. Only Arginine is statistically significant to a p-value of 0.05. SAH to a p-value of 0.1.

% latex table generated in R 3.1.2 by xtable 1.7-4 package % Mon Jul 27 11:59:03 2015

```
## Error in eval(expr, envir, enclos): could not find function "LenthPlot"
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
pH	1	0.02	0.02	4.83	0.1153
Arginine	1	0.03	0.03	8.14	0.0649
Glycerin	1	0.00	0.00	0.55	0.5122
ionicStrength	1	0.01	0.01	3.27	0.1682
divCations	1	0.00	0.00	0.57	0.5047
redox	1	0.06	0.06	19.88	0.0210
CycloDex	1	0.00	0.00	0.78	0.4428
SAH	1	0.00	0.00	0.13	0.7439
Residuals	3	0.01	0.00		