

# Induced vs Constitutive Project: Univariate repeated analysis of biochemical assays

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*October 27, 2017*

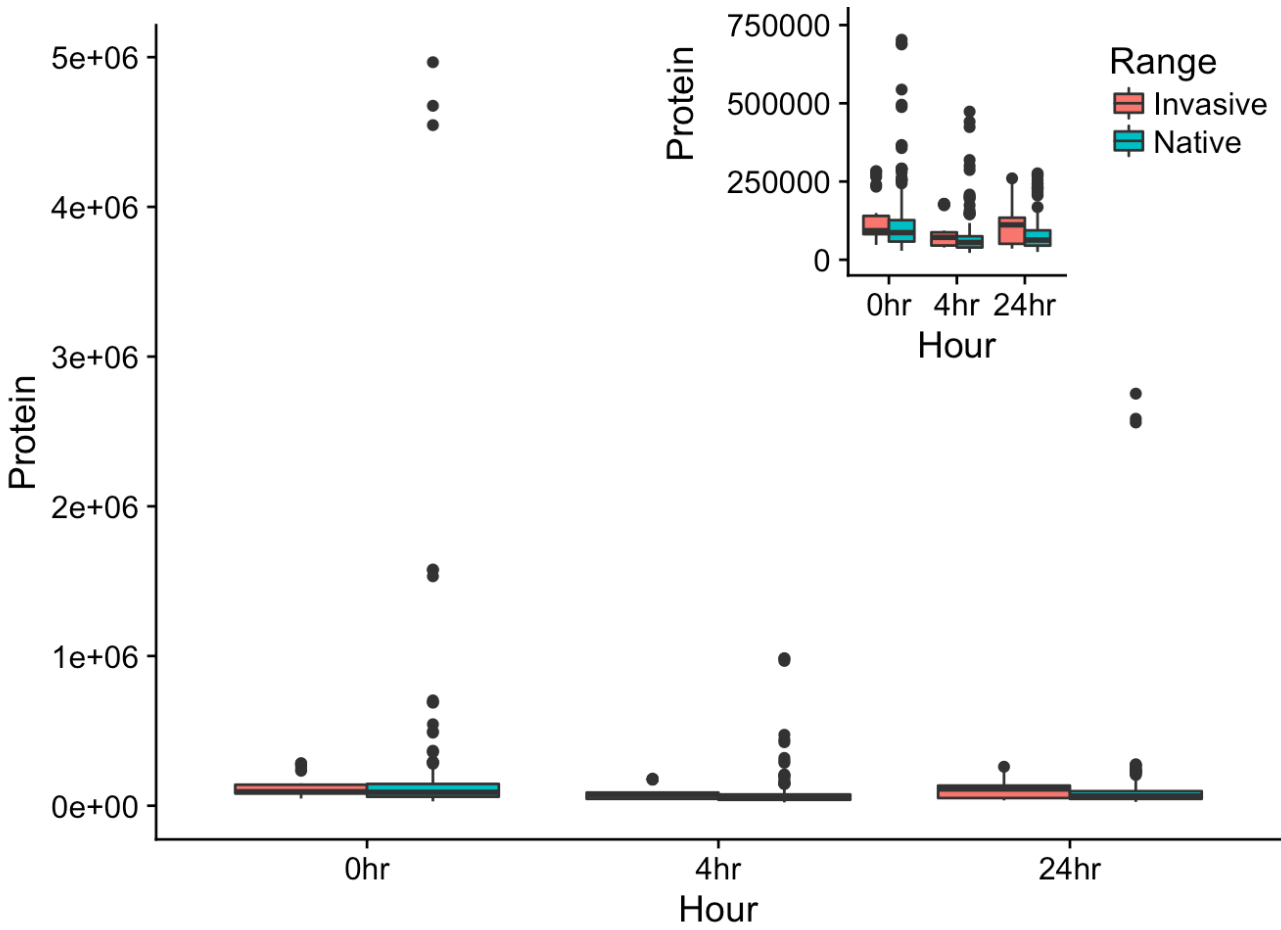
## Results of the univariate analyses for each biochemical assay

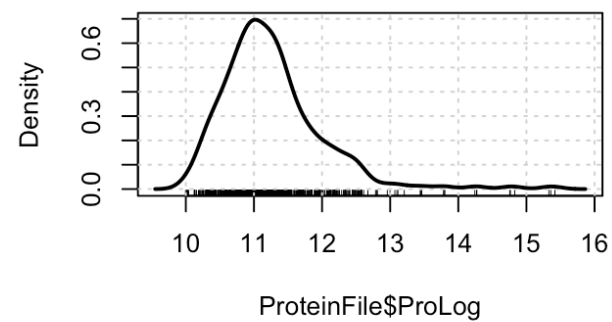
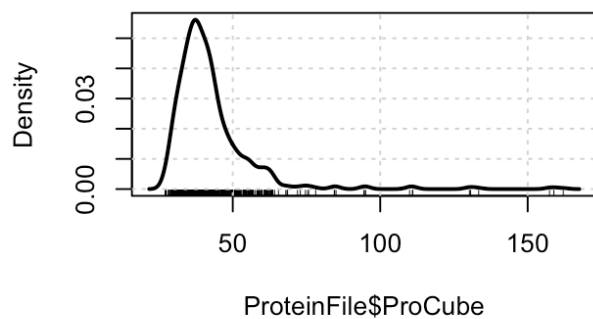
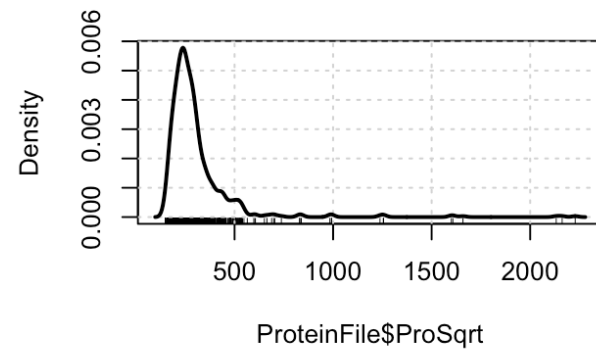
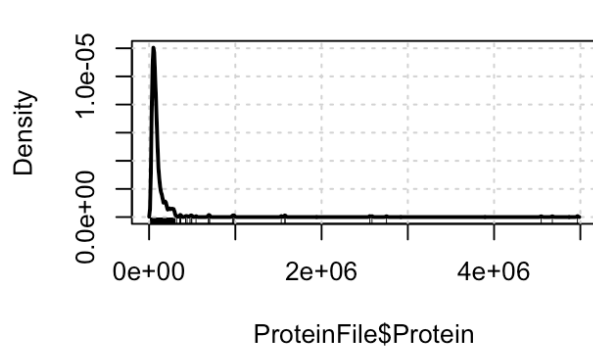
Prior to running the multivariate analysis, I looked at each assay separately as a repeated measures test.

```
library(ggplot2)
library(data.table)
library(scales)
library(plyr)
library(dplyr)
library(reshape2)
library(lme4)
library(effects)
library(multcomp)
library(lmerTest)
library(piecewiseSEM)
library(car)
library(gridExtra)
library(cowplot)
library(Rmisc)
```

## Protein Quantification Analysis

Boxplots to examine for homogeneity of variances and density plots for normal distributions

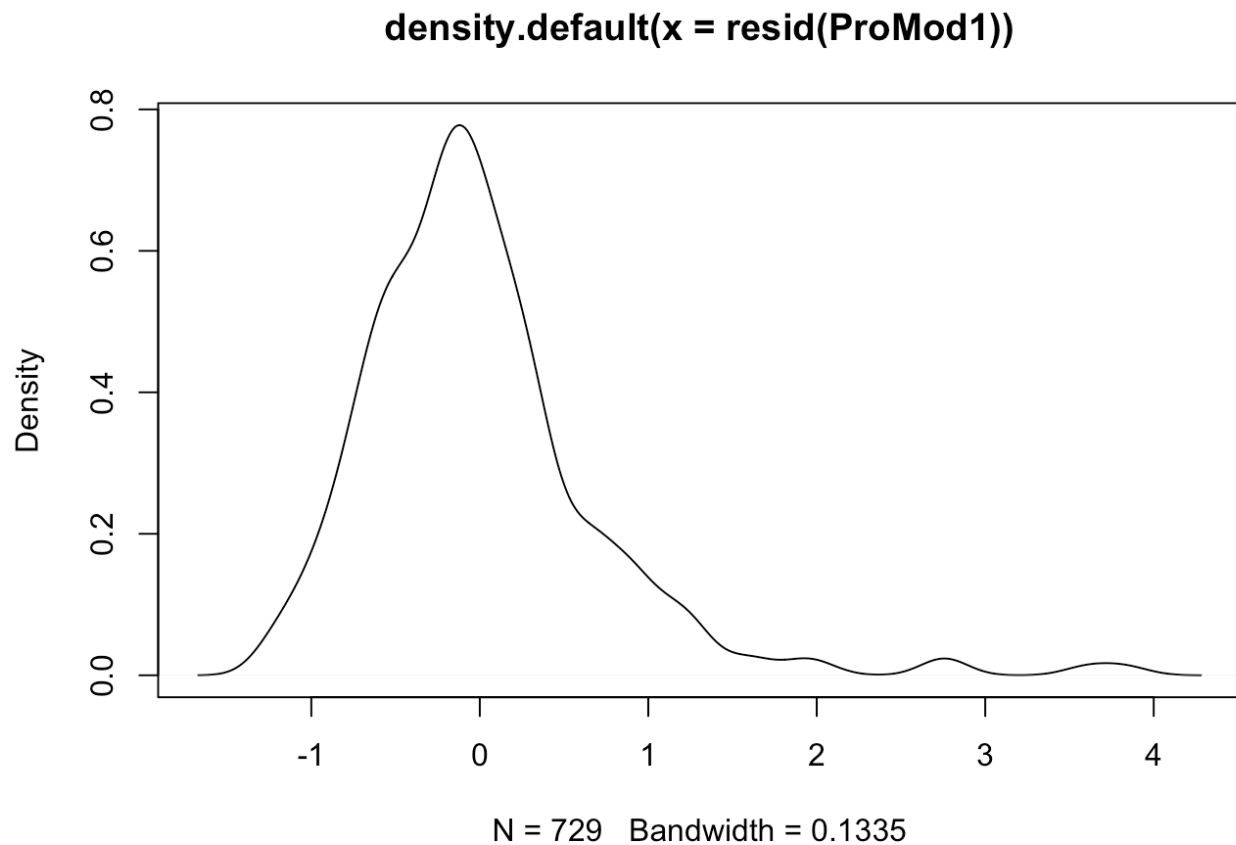




Results of the univariate repeated measures

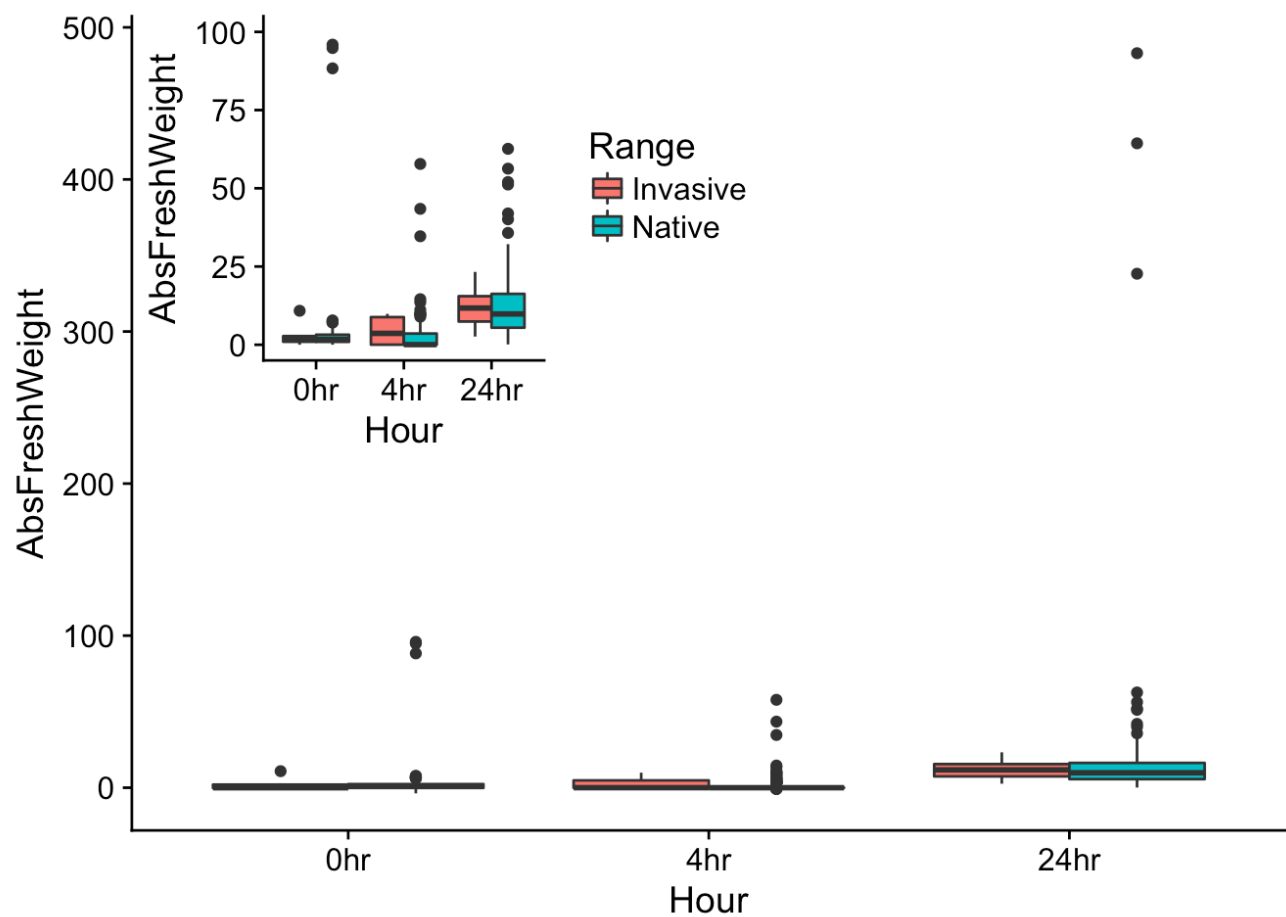
```
ProMod1 <- lm(cbind(ProteinHr0, ProteinHr4, ProteinHr24) ~ Range, data = ProteinW  
ide)
```

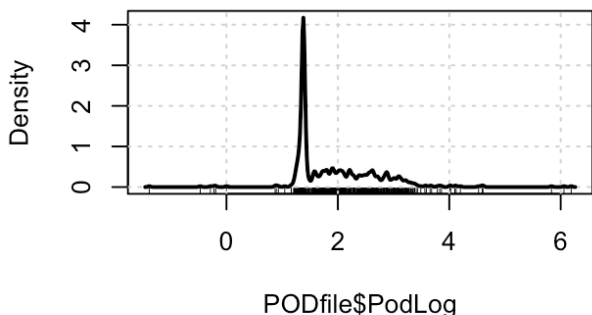
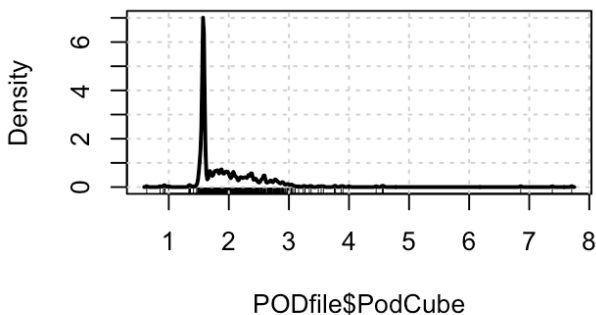
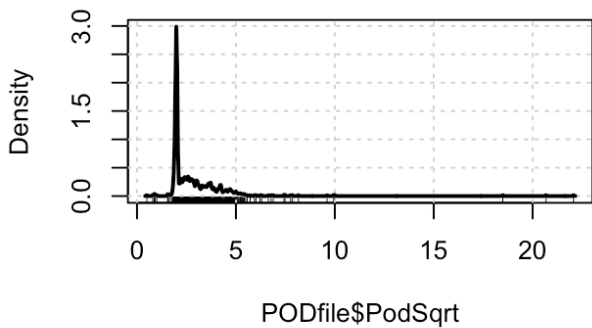
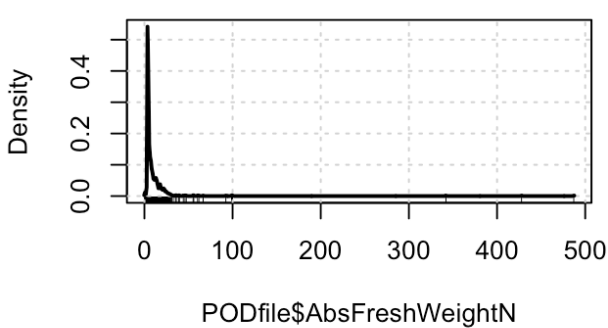
Residuals:



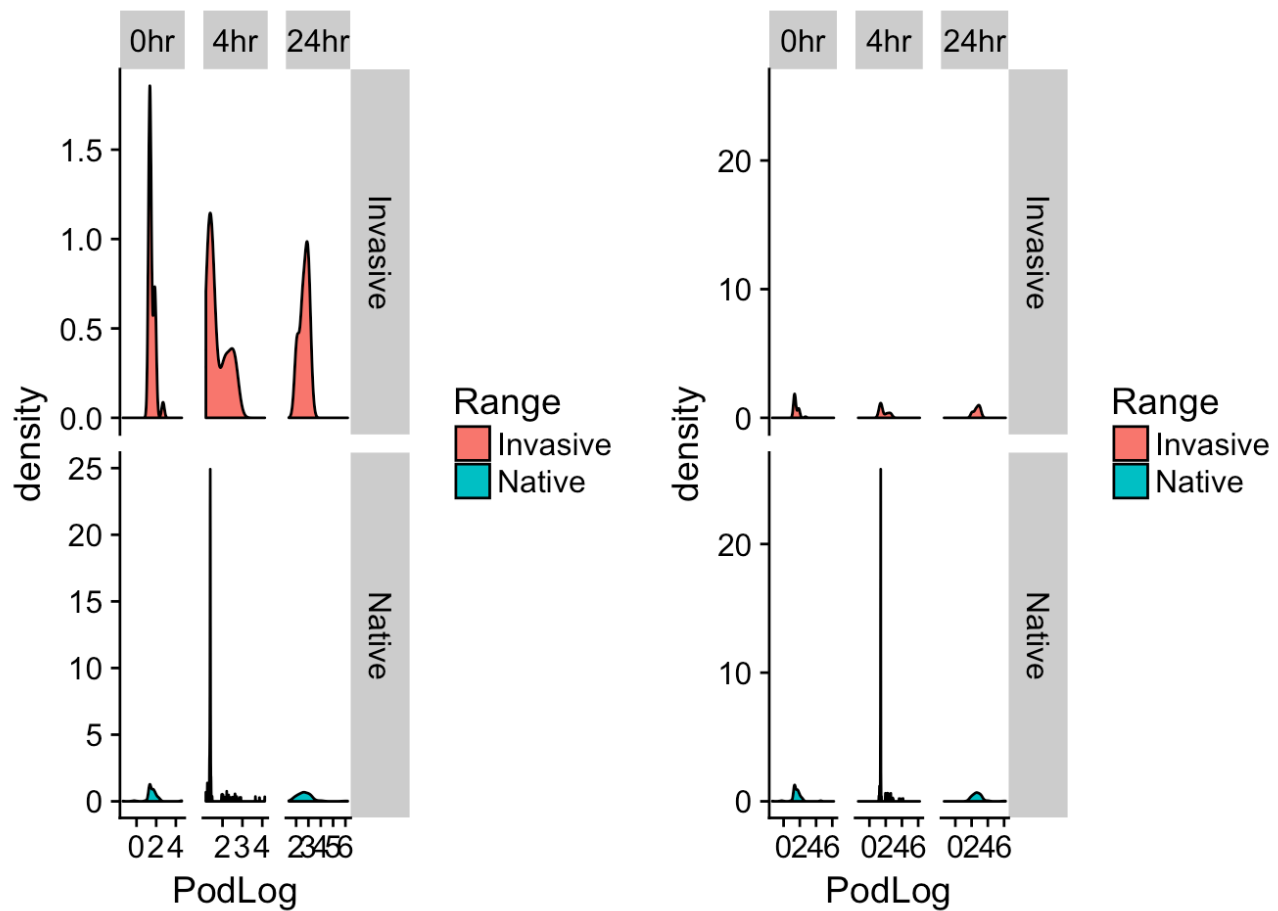
```
##
## Type II Repeated Measures MANOVA Tests: Pillai test statistic
##
##      Df test stat approx F num Df den Df    Pr(>F)
## (Intercept)    1  0.99824   136641      1   241 < 2.2e-16 ***
## Range          1  0.01886      5      1   241  0.03235 *
## blockD         1  0.24001     38      2   240 4.979e-15 ***
## Range:blockD   1  0.00388      0      2   240  0.62683
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Peroxidase Activity Assay





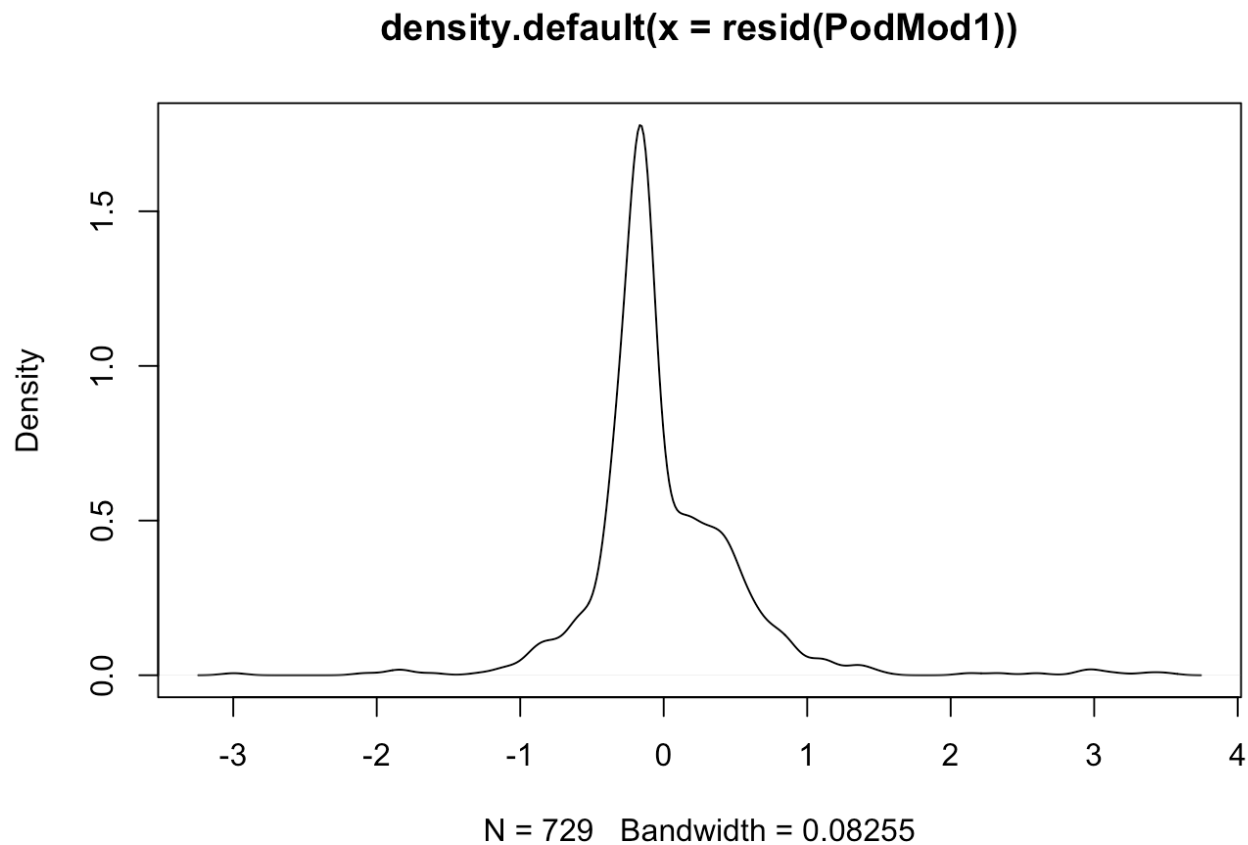
These looked a little odd so I broke them down by range. Graph on the right is at same scale, left is to give better view of distribution



Results of the univariate repeated measures

```
PodMod1 <- lm(cbind(PODHr0, PODHr4, PODHr24) ~ Range, data = PODWide)
```

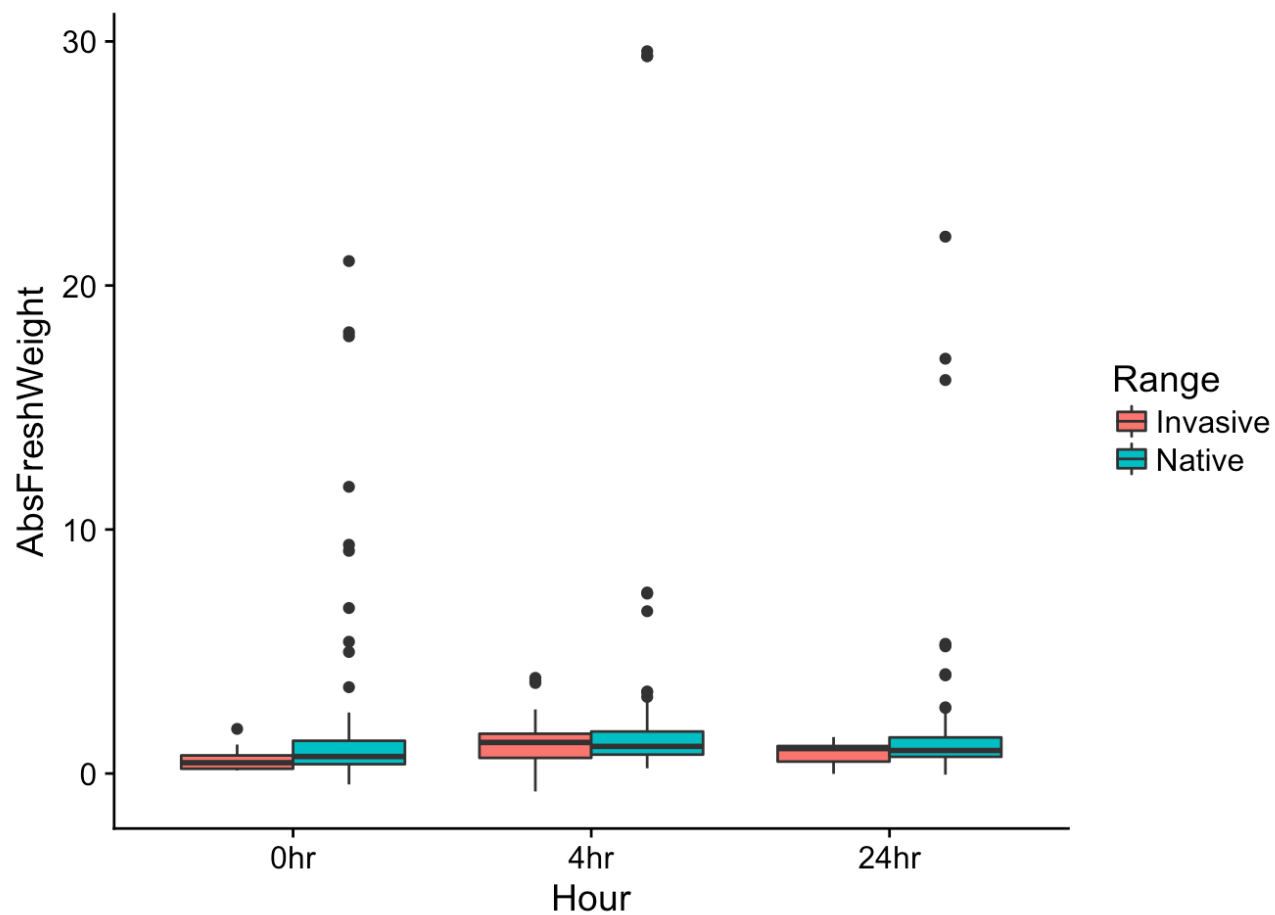
Residuals:

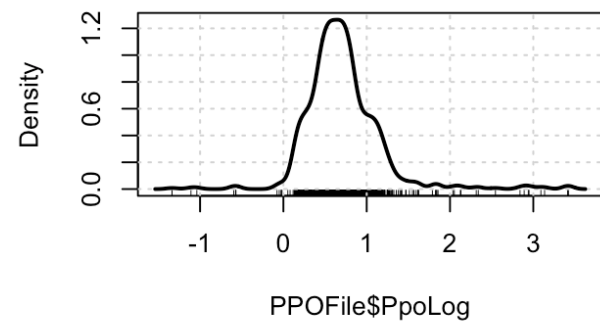
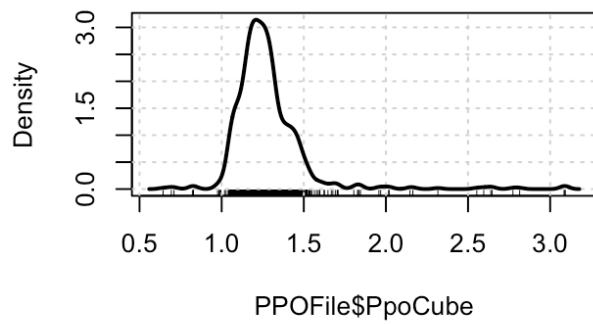
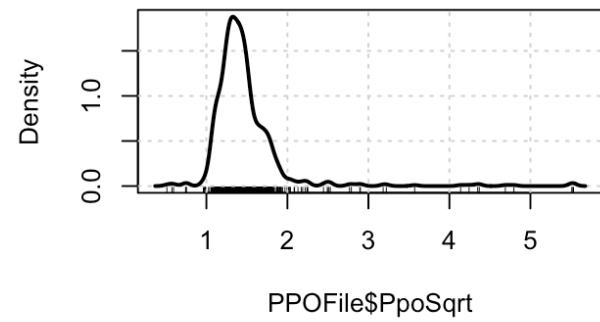
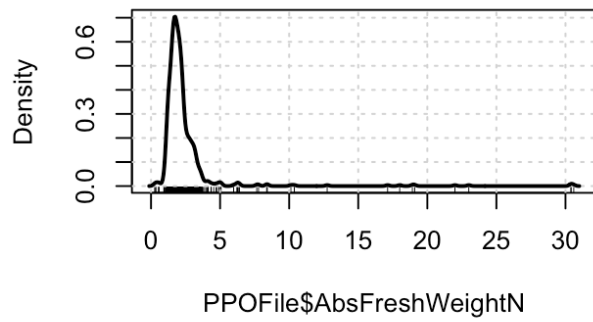


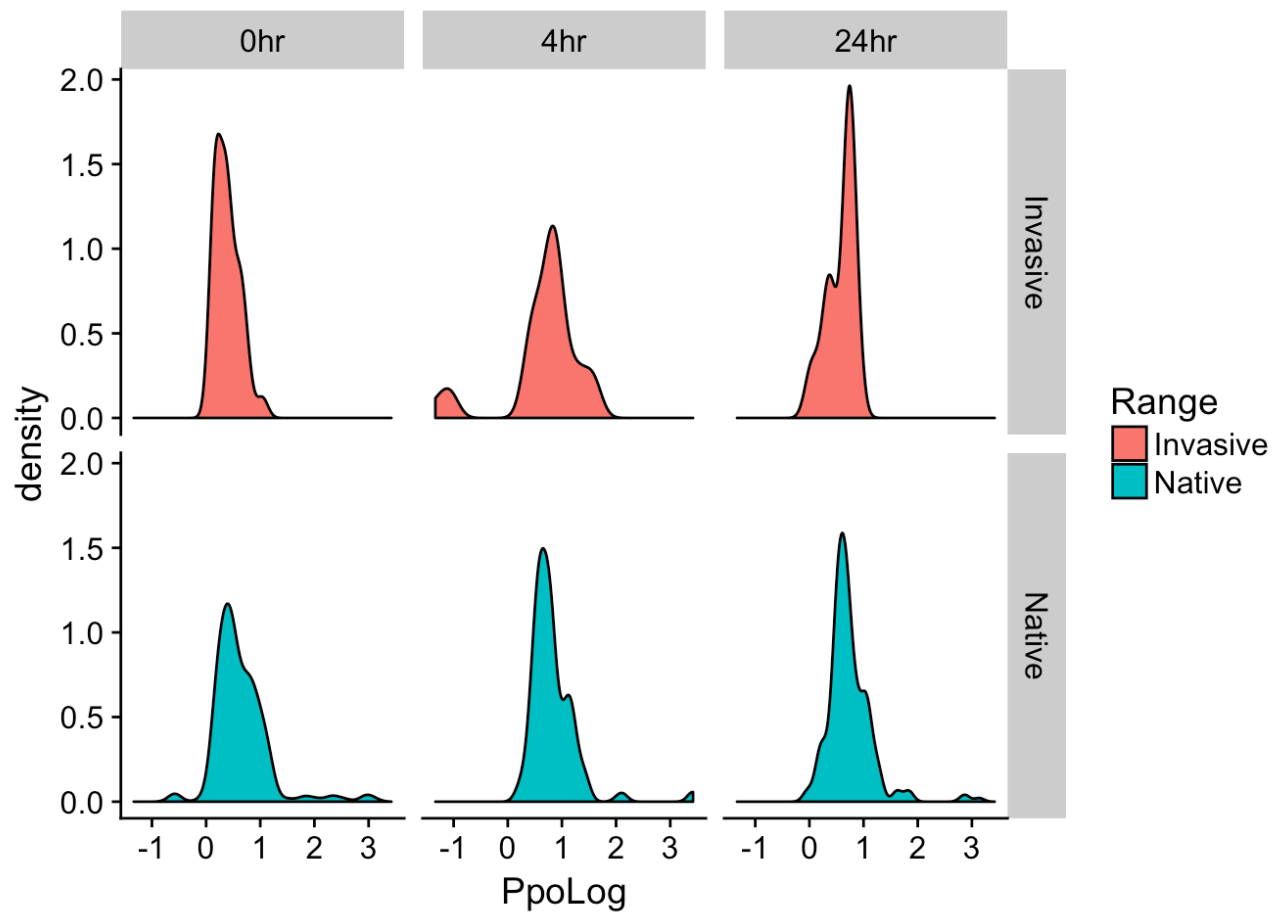
```
##
## Type II Repeated Measures MANOVA Tests: Pillai test statistic
##
##      Df test stat approx F num Df den Df  Pr(>F)
## (Intercept)    1   0.96493   6630.6     1   241 < 2e-16 ***
## Range          1   0.00101     0.2     1   241 0.62198
## blockD         1   0.80547   496.9     2   240 < 2e-16 ***
## Range:blockD   1   0.03572     4.4     2   240 0.01271 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Polyphenol Oxidase Activity





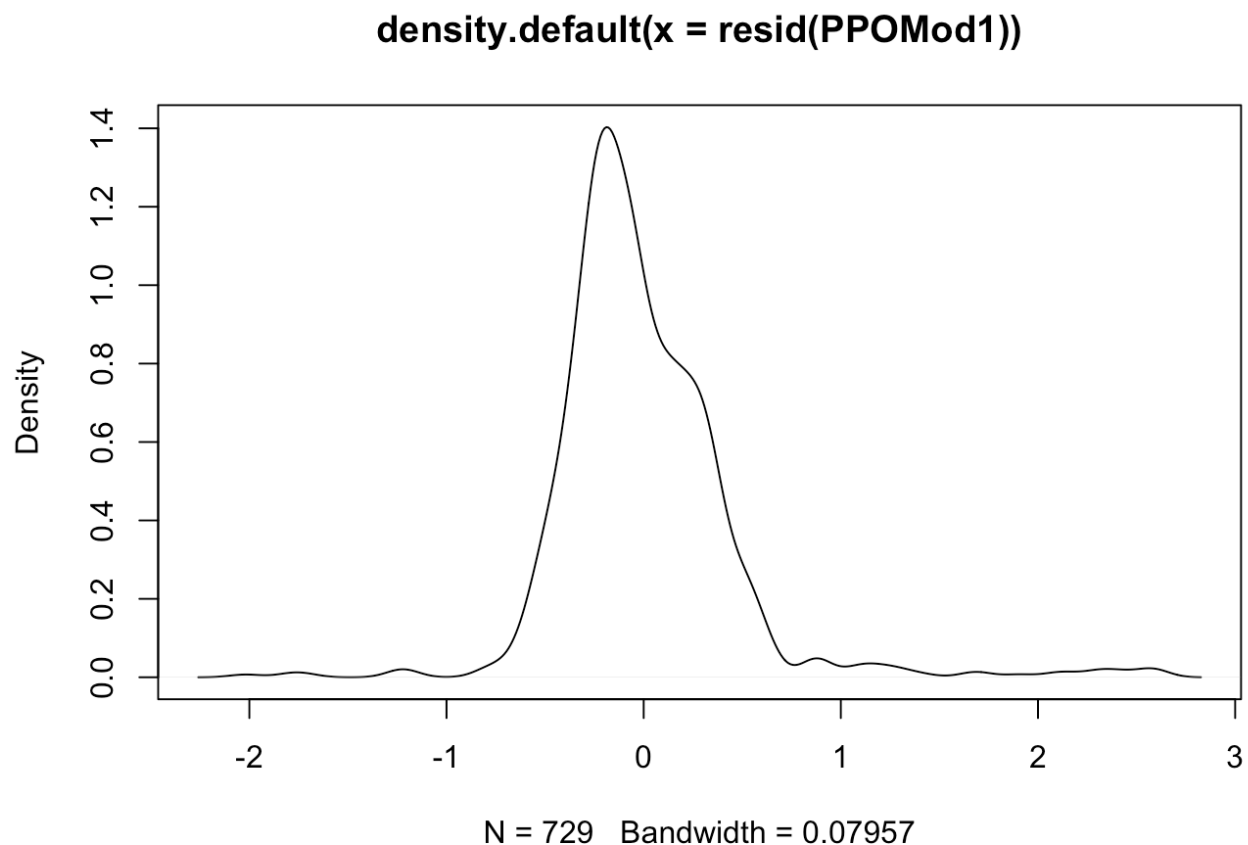




Results of the univariate repeated measures

```
PPOMod1 <- lm(cbind(PPOHr0, PPOHr4, PPOHr24) ~ Range, data = PPOWide)
```

Residuals:



```
##
## Type II Repeated Measures MANOVA Tests: Pillai test statistic
##
```

	Df	test stat	approx F	num Df	den Df	Pr(>F)
## (Intercept)	1	0.88625	1877.64	1	241	< 2.2e-16 ***
## Range	1	0.06083	15.61	1	241	0.0001023 ***
## blockD	1	0.07883	10.27	2	240	5.256e-05 ***
## Range:blockD	1	0.00298	0.36	2	240	0.6992842

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