

Effect of digestion on composition and more

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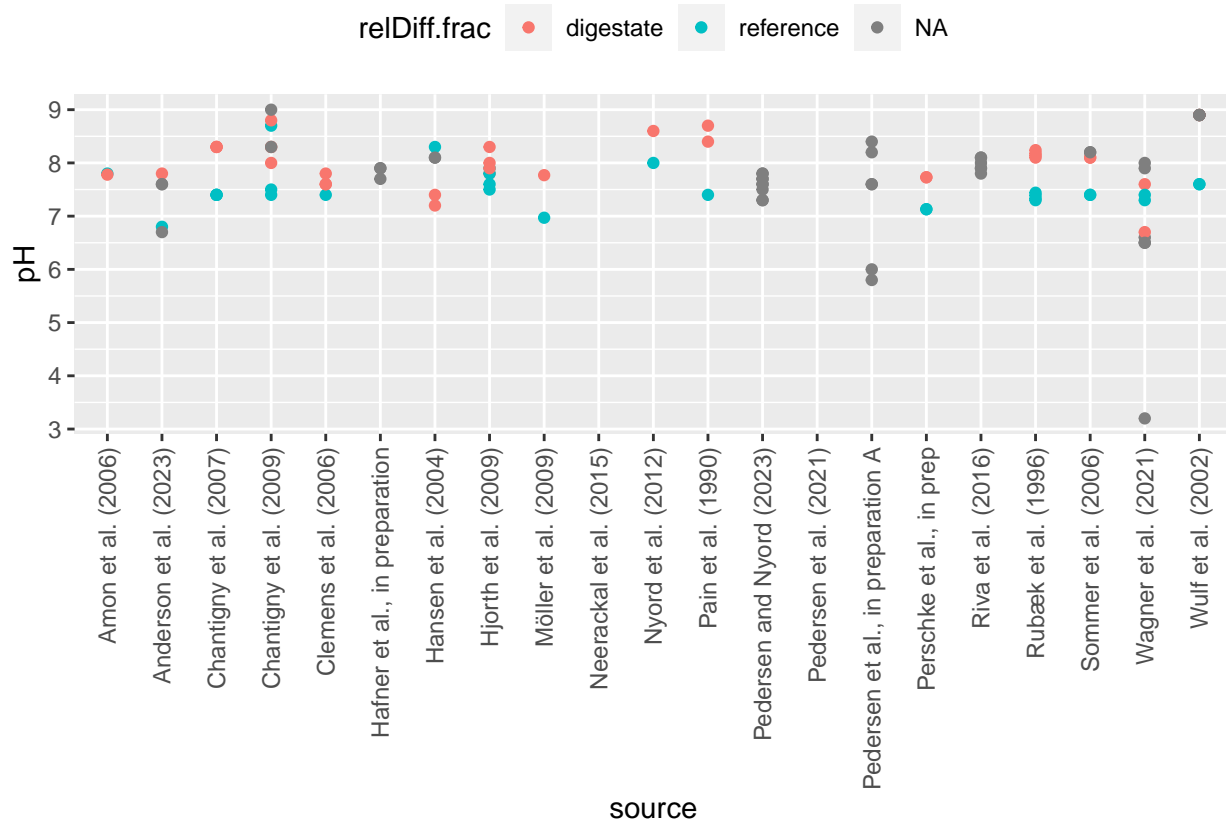
Vars

```
dw$d pH <- dw$pH.dig - dw$pH.ref
```

Plots

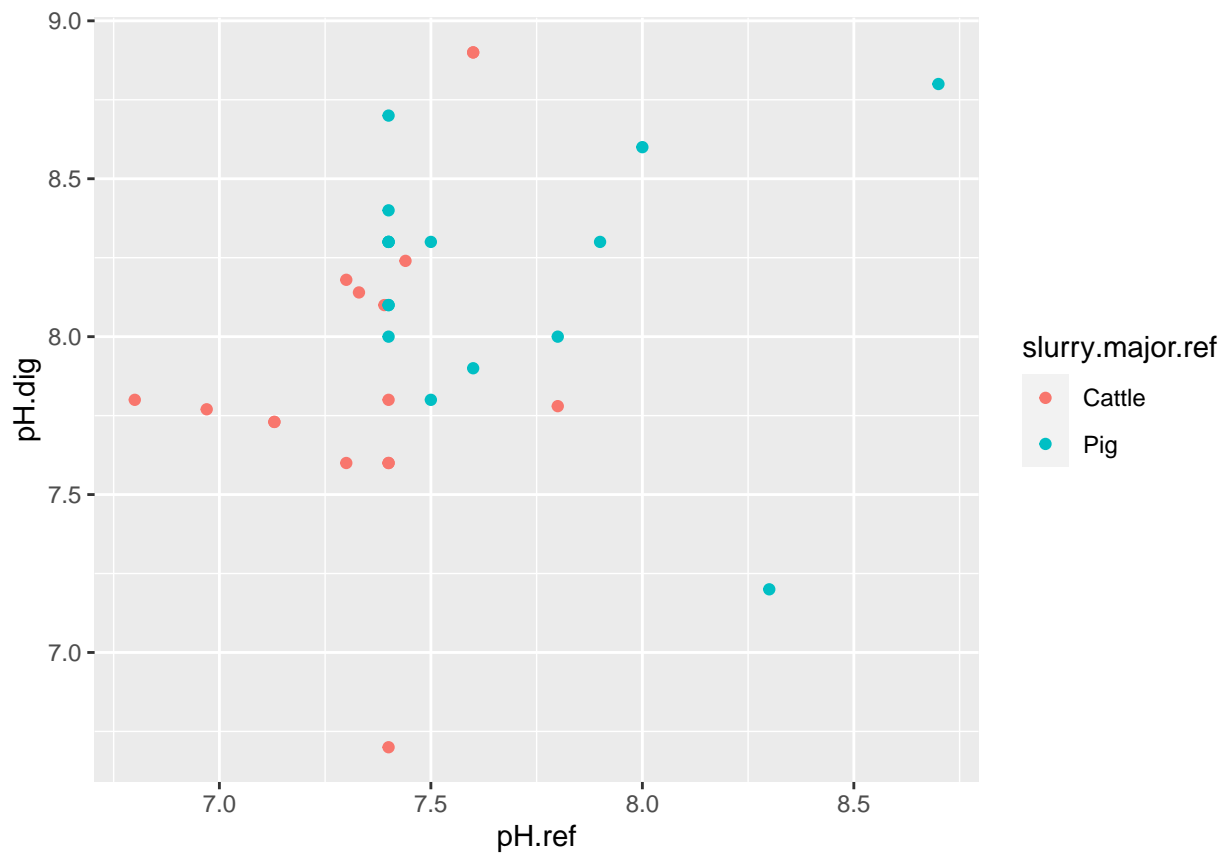
```
ggplot(dat, aes(source, pH, colour = relDiff.frac)) +  
  geom_point() +  
  theme(legend.position = 'top', axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1))
```

Warning: Removed 14 rows containing missing values (`geom_point()`).



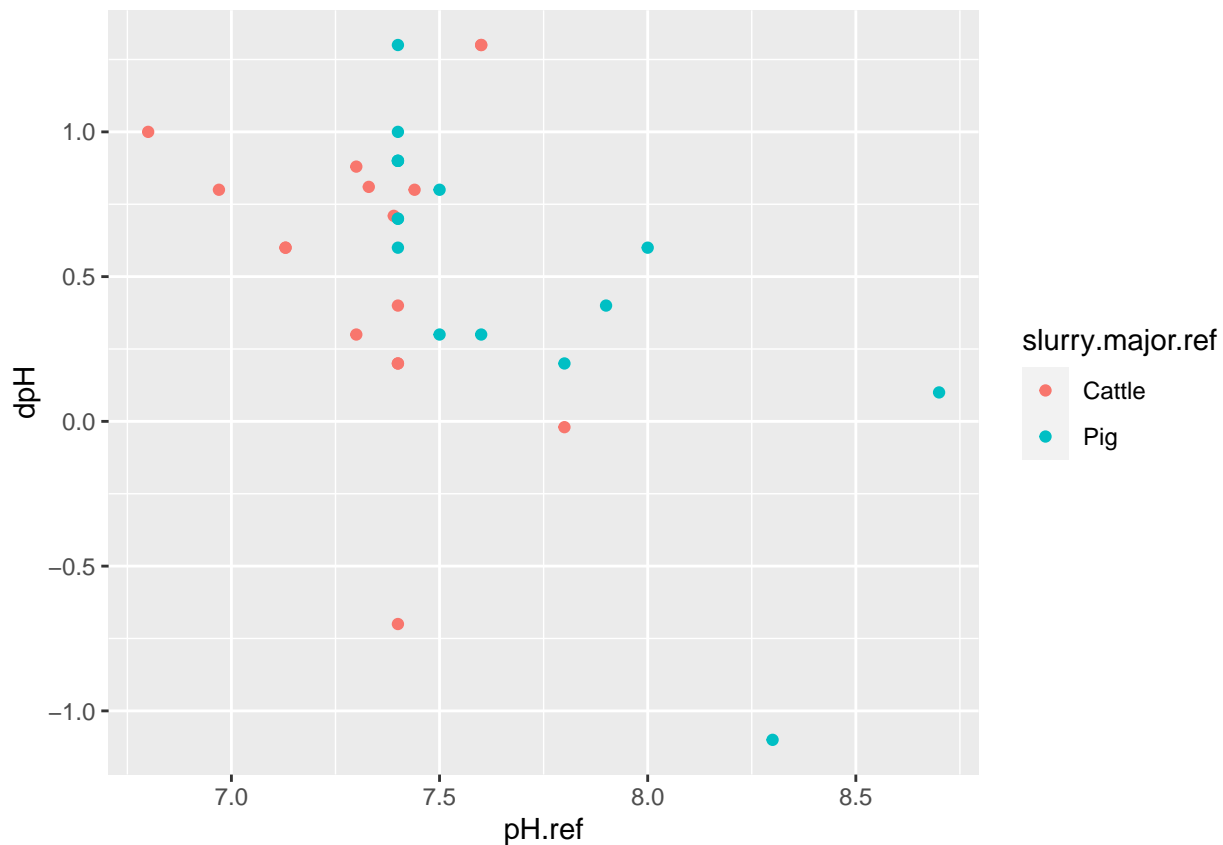
```
ggplot(dw, aes(pH.ref, pH.dig, colour = slurry.major.ref)) +  
  geom_point()
```

```
## Warning: Removed 8 rows containing missing values (`geom_point()`).
```



```
ggplot(dw, aes(pH.ref, dpH, colour = slurry.major.ref)) +  
  geom_point()
```

```
## Warning: Removed 8 rows containing missing values (`geom_point()`).
```



Stats

```
m1 <- lm(pH.dig ~ pH.ref + slurry.major.ref, data = dw)
summary(m1)
```

```
##
## Call:
## lm(formula = pH.dig ~ pH.ref + slurry.major.ref, data = dw)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.22242 -0.21802 -0.02809  0.23653  0.94021
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      6.5397     1.9091   3.425  0.00185 **
## pH.ref           0.1868     0.2597   0.719  0.47766
## slurry.major.refPig 0.2235     0.1834   1.218  0.23291
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4627 on 29 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.1081, Adjusted R-squared:  0.04655
## F-statistic: 1.757 on 2 and 29 DF,  p-value: 0.1905
```

```
m2 <- lm(pH.dig ~ pH.ref, data = dw)
summary(m2)
```

```
##
## Call:
## lm(formula = pH.dig ~ pH.ref, data = dw)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.32032 -0.20600  0.07968  0.27968  0.81368
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.5785     1.7525   3.183  0.00338 **
## pH.ref         0.3300     0.2335   1.413  0.16792
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4664 on 30 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.06241,    Adjusted R-squared:  0.03115
## F-statistic: 1.997 on 1 and 30 DF,  p-value: 0.1679
```

Try robust regression.

```
m3 <- MASS::rlm(pH.dig ~ pH.ref + slurry.major.ref, data = dw)
summary(m3)
```

```
##
## Call: rlm(formula = pH.dig ~ pH.ref + slurry.major.ref, data = dw)
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.21967 -0.25805 -0.01689  0.23664  0.92424
##
## Coefficients:
##              Value Std. Error t value
## (Intercept)    5.8444  1.4629   3.9951
## pH.ref          0.2804  0.1990   1.4091
## slurry.major.ref 0.2448  0.1405   1.7419
##
## Residual standard error: 0.3646 on 29 degrees of freedom
## (8 observations deleted due to missingness)
```

```
m4 <- MASS::rlm(pH.dig ~ pH.ref, data = dw)
summary(m4)
```

```
##
## Call: rlm(formula = pH.dig ~ pH.ref, data = dw)
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.33376 -0.22712  0.05298  0.23206  0.77509
##
## Coefficients:
##              Value Std. Error t value
## (Intercept)  4.6610  1.3478   3.4583
## pH.ref       0.4558  0.1796   2.5380
```

```
##
## Residual standard error: 0.34 on 30 degrees of freedom
## (8 observations deleted due to missingness)
```

Digestate pH does seem correlated with raw pH but only with robust regression. Issue seems to be a decrease in change in pH at higher raw pH.

```
t.test(dw$d pH)
```

```
##
## One Sample t-test
##
## data: dw$d pH
## t = 6.0685, df = 31, p-value = 1.01e-06
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.3688892 0.7423608
## sample estimates:
## mean of x
## 0.555625
```

Clearly pH does increase, according to a one-sample t-test. Compare among animal types.

```
m5 <- lm(d pH ~ slurry.major.ref, data = dw)
summary(m5)
```

```
##
## Call:
## lm(formula = d pH ~ slurry.major.ref, data = dw)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.63750 -0.24656  0.09937  0.32031  0.76250
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.57375    0.13154   4.362  0.00014 ***
## slurry.major.refPig -0.03625    0.18603  -0.195  0.84681
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5262 on 30 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.001264, Adjusted R-squared: -0.03203
## F-statistic: 0.03797 on 1 and 30 DF, p-value: 0.8468
```

But look at change in pH:

```
m6 <- lm(d pH ~ pH.ref + slurry.major.ref, data = dw)
summary(m6)
```

```
##
## Call:
## lm(formula = d pH ~ pH.ref + slurry.major.ref, data = dw)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.22242 -0.21802 -0.02809  0.23653  0.94021
```

```
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      6.5397      1.9091   3.425  0.00185 **
## pH.ref           -0.8132      0.2597  -3.131  0.00396 **
## slurry.major.refPig  0.2235      0.1834   1.218  0.23291
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4627 on 29 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.2535, Adjusted R-squared:  0.2021
## F-statistic: 4.925 on 2 and 29 DF,  p-value: 0.01441
```

```
m7 <- lm(dpH ~ pH.ref, data = dw)
summary(m7)
```

```
##
## Call:
## lm(formula = dpH ~ pH.ref, data = dw)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.32032 -0.20600  0.07968  0.27968  0.81368
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.5785      1.7525   3.183  0.00338 **
## pH.ref         -0.6700      0.2335  -2.869  0.00747 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4664 on 30 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.2153, Adjusted R-squared:  0.1892
## F-statistic: 8.233 on 1 and 30 DF,  p-value: 0.007466
```

```
m8 <- MASS::rlm(dpH ~ pH.ref + slurry.major.ref, data = dw)
summary(m8)
```

```
##
## Call: rlm(formula = dpH ~ pH.ref + slurry.major.ref, data = dw)
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.21967 -0.25805 -0.01689  0.23664  0.92424
##
## Coefficients:
##              Value Std. Error t value
## (Intercept)    5.8444   1.4629   3.9951
## pH.ref        -0.7196   0.1990  -3.6155
## slurry.major.refPig  0.2448   0.1405   1.7419
##
## Residual standard error: 0.3646 on 29 degrees of freedom
## (8 observations deleted due to missingness)
```

```
m9 <- MASS::rlm(dPH ~ pH.ref, data = dw)
summary(m9)
```

```
##
## Call: rlm(formula = dPH ~ pH.ref, data = dw)
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.33376 -0.22712  0.05298  0.23206  0.77509
##
## Coefficients:
##              Value Std. Error t value
## (Intercept)  4.6610   1.3478    3.4583
## pH.ref      -0.5442   0.1796   -3.0304
##
## Residual standard error: 0.34 on 30 degrees of freedom
## (8 observations deleted due to missingness)
```

Interestingly, the change in pH is negatively correlated with initial pH.

Change DM change.

```
dw$dDM <- dw$DM.dig - dw$DM.ref
t.test(dw$dDM)
```

```
##
## One Sample t-test
##
## data: dw$dDM
## t = -6.4365, df = 37, p-value = 1.614e-07
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -2.778377 -1.447939
## sample estimates:
## mean of x
## -2.113158
```

And DM clearly decreases.