Effect of digestion on composition and more

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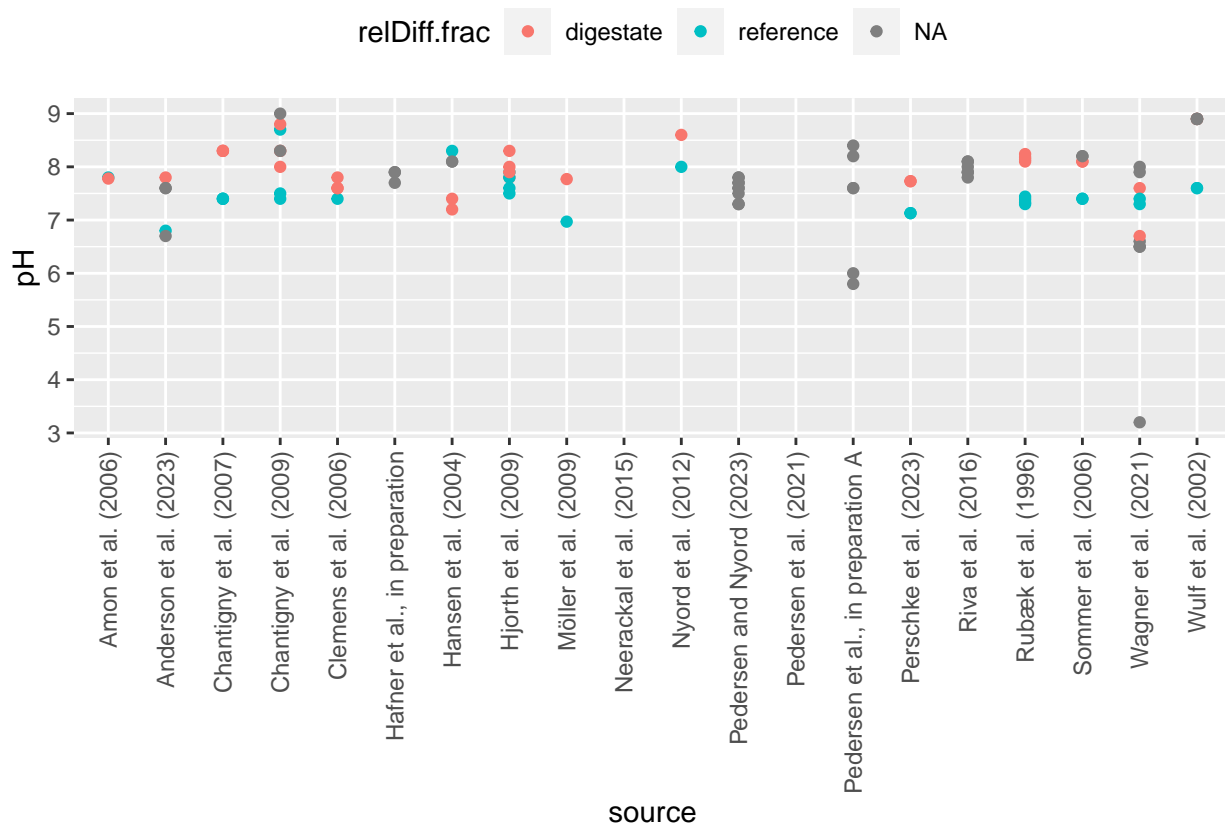
Vars

```
dw$dpH <- dw$pH.dig - dw$pH.ref
```
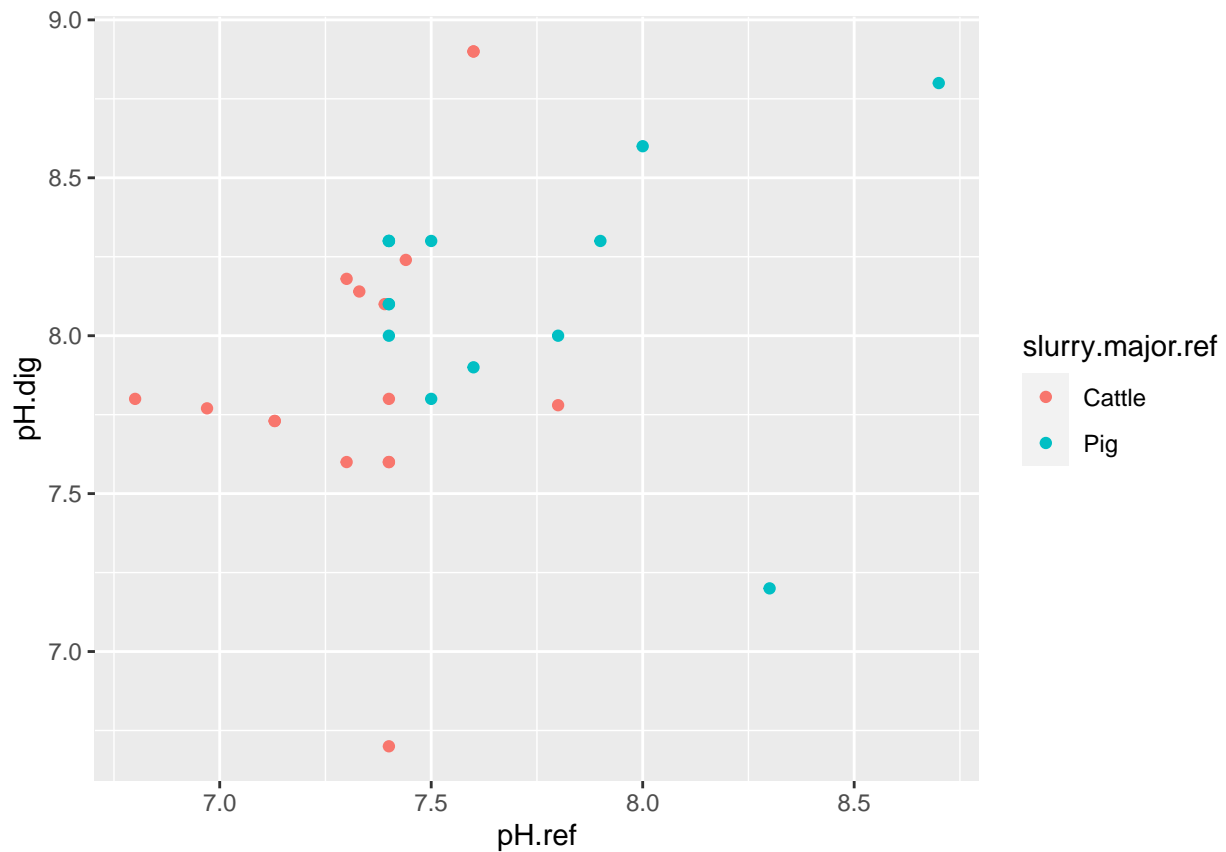
Plots

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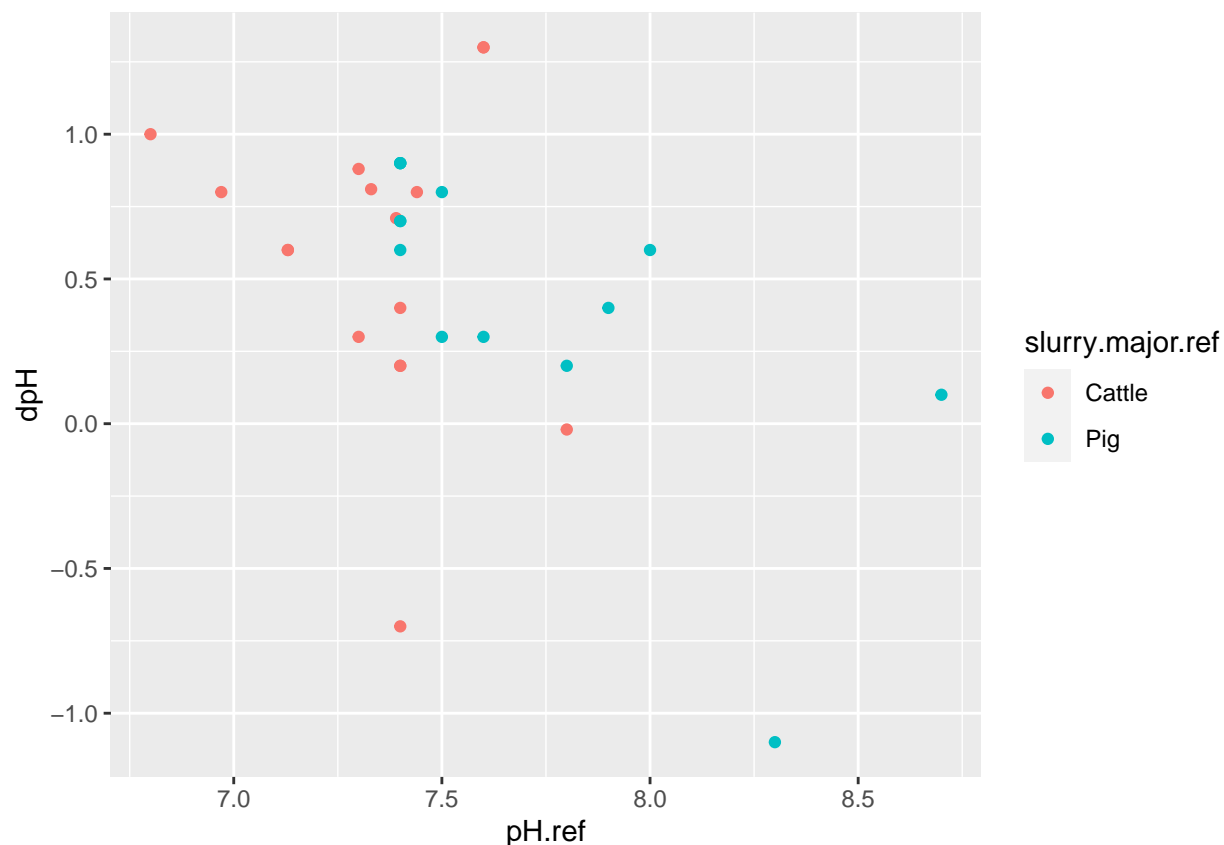
```
ggplot(dw, aes(pH.ref, pH.dig, colour = slurry.major.ref)) +
  geom_point()
```

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).

dpH

pH.ref

slurry.major.ref
- Cattle
- Pig

Stats

```r
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
## -1.22736 -0.20649  0.03326  0.23480  0.91961
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)           5.9652     1.9543   3.052  0.00505 **
## pH.ref                0.2652     0.2659   0.997  0.32753
## slurry.major.refPig   0.1378     0.1939   0.711  0.48317
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4623 on 27 degrees of freedom
##   (8 observations deleted due to missingness)
## Multiple R-squared:  0.09634,    Adjusted R-squared:  0.0294
## F-statistic: 1.439 on 2 and 27 DF,  p-value: 0.2547
```

```r
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
## -1.28218 -0.17555  0.07506  0.27243  0.84633
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.3369     1.7277   3.089   0.0045 **
## pH.ref        0.3575     0.2300   1.554   0.1314
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4582 on 28 degrees of freedom
##   (8 observations deleted due to missingness)
## Multiple R-squared:  0.07942,    Adjusted R-squared:  0.04654
## F-statistic: 2.416 on 1 and 28 DF,  p-value: 0.1314
```

Try robust regression.

```r
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
## -1.226190 -0.255524  0.008057  0.208057  0.902945
##
## Coefficients:
##                   Value  Std. Error t value
## (Intercept)       5.3042 1.3889     3.8189
## pH.ref            0.3543 0.1890     1.8750
## slurry.major.refPig 0.1658 0.1378   1.2030
##
## Residual standard error: 0.3501 on 27 degrees of freedom
##   (8 observations deleted due to missingness)
```

```r
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
## -1.30077 -0.19951  0.07298  0.22510  0.80426
##
## Coefficients:
##             Value  Std. Error t value
## (Intercept) 4.4867 1.2497     3.5902
## pH.ref      0.4749 0.1664     2.8544
```

```
##
## Residual standard error: 0.3313 on 28 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$dpH)
```

```
##
##  One Sample t-test
##
## data:  dw$dpH
## t = 5.5511, df = 29, p-value = 5.492e-06
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.3258861 0.7061139
## sample estimates:
## mean of x
##     0.516
```

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

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

```
##
## Call:
## lm(formula = dpH ~ slurry.major.ref, data = dw)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.5500 -0.2309  0.1431  0.2922  0.7262
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.5738     0.1285   4.463  0.00012 ***
## slurry.major.refPig -0.1237     0.1882  -0.658  0.51614
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5142 on 28 degrees of freedom
##   (8 observations deleted due to missingness)
## Multiple R-squared:  0.01521,    Adjusted R-squared:  -0.01996
## F-statistic: 0.4325 on 1 and 28 DF,  p-value: 0.5161
```

But look at change in pH:

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

```
##
## Call:
## lm(formula = dpH ~ pH.ref + slurry.major.ref, data = dw)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.22736 -0.20649  0.03326  0.23480  0.91961
```

```
## 
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          5.9652     1.9543   3.052  0.00505 **
## pH.ref              -0.7348     0.2659  -2.764  0.01017 *
## slurry.major.refPig  0.1378     0.1939   0.711  0.48317
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.4623 on 27 degrees of freedom
##   (8 observations deleted due to missingness)
## Multiple R-squared:  0.2324, Adjusted R-squared:  0.1755
## F-statistic: 4.086 on 2 and 27 DF,  p-value: 0.02816
m7 <- lm(dpH ~ pH.ref, data = dw)
summary(m7)
```

```
## 
## Call:
## lm(formula = dpH ~ pH.ref, data = dw)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.28218 -0.17555  0.07506  0.27243  0.84633
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.3369     1.7277   3.089   0.0045 **
## pH.ref       -0.6425     0.2300  -2.794   0.0093 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.4582 on 28 degrees of freedom
##   (8 observations deleted due to missingness)
## Multiple R-squared:  0.218,  Adjusted R-squared:   0.19
## F-statistic: 7.805 on 1 and 28 DF,  p-value: 0.009295
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
## -1.226190 -0.255524  0.008057  0.208057  0.902945
## 
## Coefficients:
##                     Value   Std. Error t value
## (Intercept)          5.3042  1.3889      3.8189
## pH.ref              -0.6457  0.1890     -3.4167
## slurry.major.refPig  0.1658  0.1378      1.2030
## 
## Residual standard error: 0.3501 on 27 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
## -1.30077 -0.19951  0.07298  0.22510  0.80426
##
## Coefficients:
##             Value   Std. Error t value
## (Intercept)  4.4867  1.2497     3.5902
## pH.ref      -0.5251  0.1664    -3.1565
##
## Residual standard error: 0.3313 on 28 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 = -6.6101, df = 35, p-value = 1.224e-07
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -2.909077 -1.542034
## sample estimates:
## mean of x
## -2.225556
```

And DM clearly decreases.