

Effect of digestion on composition and more

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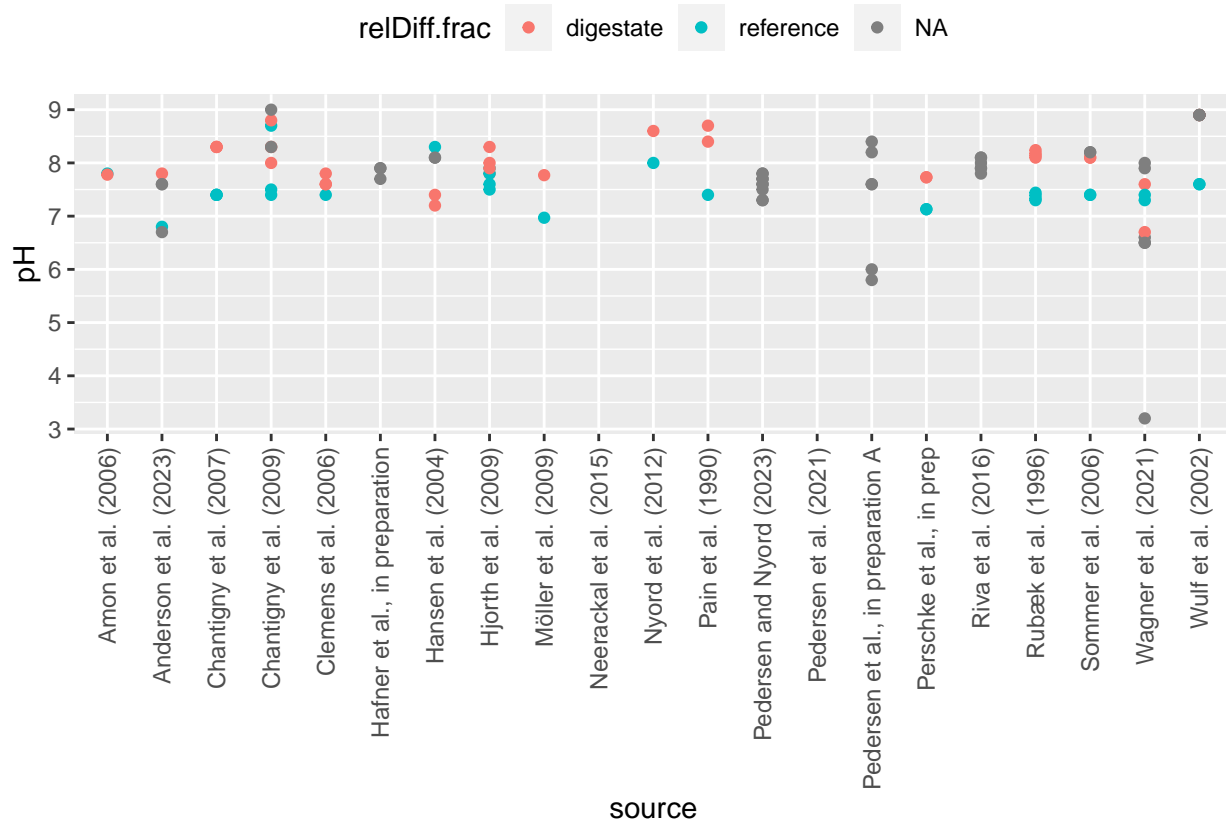
Vars

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

Plots

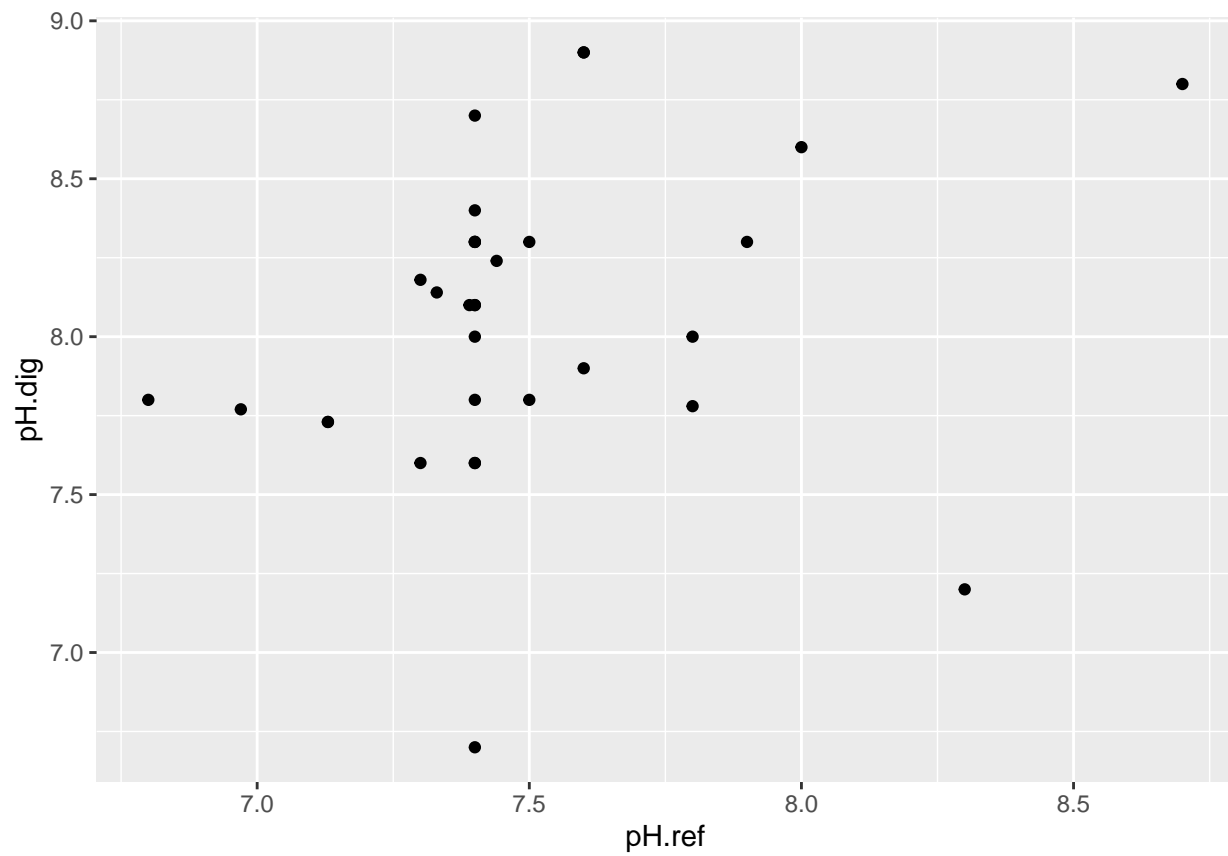
```
ggplot(dat, aes(source, pH, colour = relDiff.frac)) +  
  geom_point() +  
  theme(legend.position = 'top', axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1))
```

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



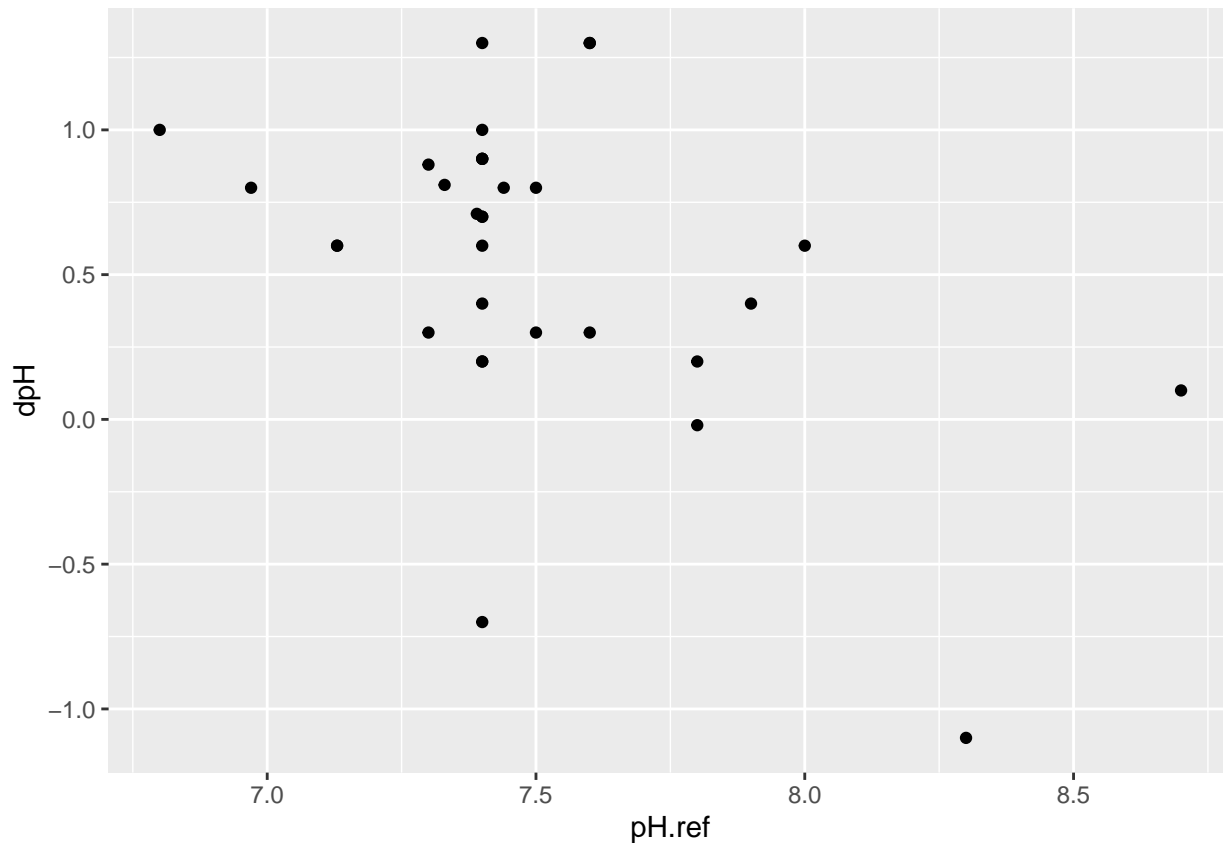
```
ggplot(dw, aes(pH.ref, pH.dig)) +  
  geom_point()
```

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



```
ggplot(dw, aes(pH.ref, dpH)) +  
  geom_point()
```

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



Stats

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

```
##
## 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.

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

```
##
## 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 decrease in change in pH at higher raw pH.

```
t.test(dw$dpH)
```

```
##
## One Sample t-test
##
## data: dw$dpH
## 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.

But look at change in pH:

```
m3 <- lm(dpH ~ pH.ref, data = dw)
summary(m3)
```

```
##
## 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
```

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

```
##
## 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.