

Stats 1: Effect of digestion on composition and more

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Vars

Difference in pH due to digestion.

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

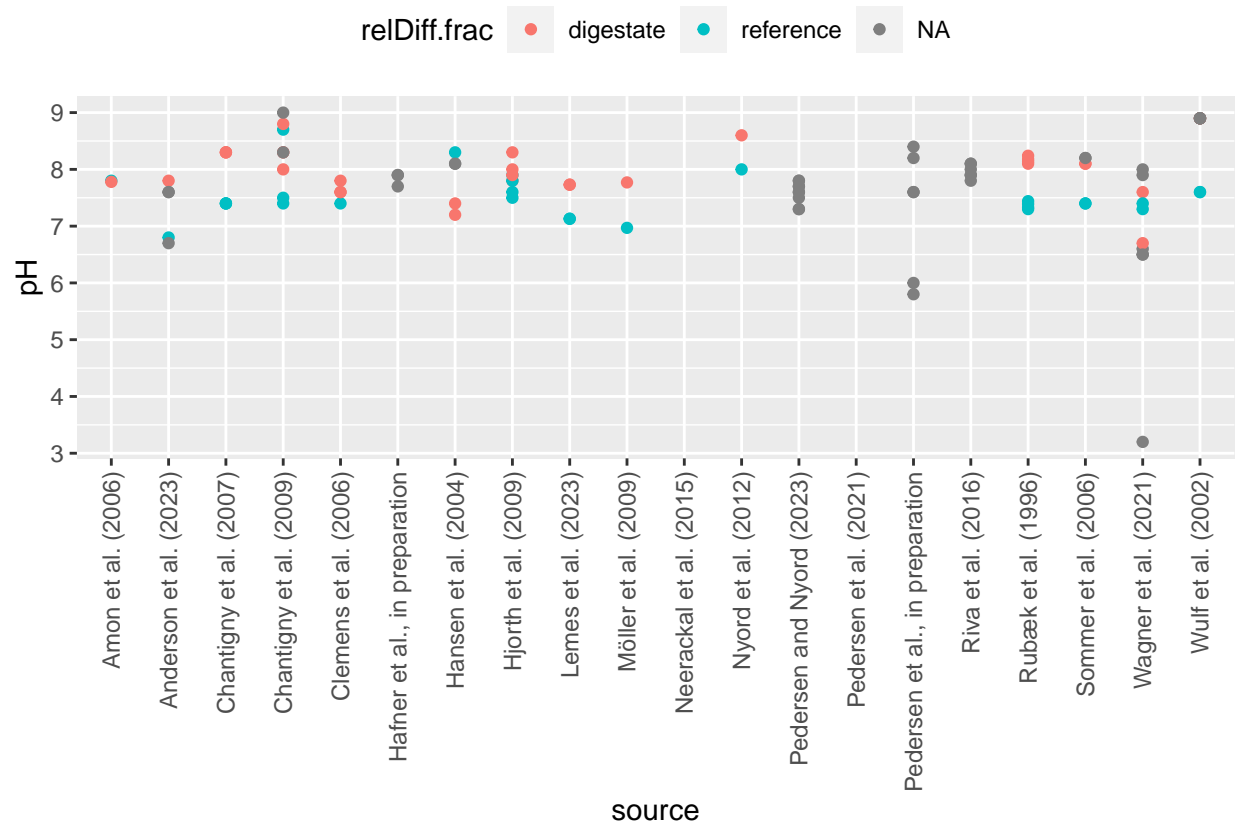
```
table(dw$source)
```

```
##  
##      Amon et al. (2006) Anderson et al. (2023) Chantigny et al. (2007) Chantigny et al. (2009) Cl  
##              1              1              3              3  
##      Hansen et al. (2004)   Hjorth et al. (2009)   Lemes et al. (2023)   Möller et al. (2009) Neer  
##              2              4              2              2  
##      Nyord et al. (2012)   Pedersen et al. (2021)   Rubæk et al. (1996)   Sommer et al. (2006)   W  
##              1              2              4              2  
##      Wulf et al. (2002)  
##              2
```

Plots

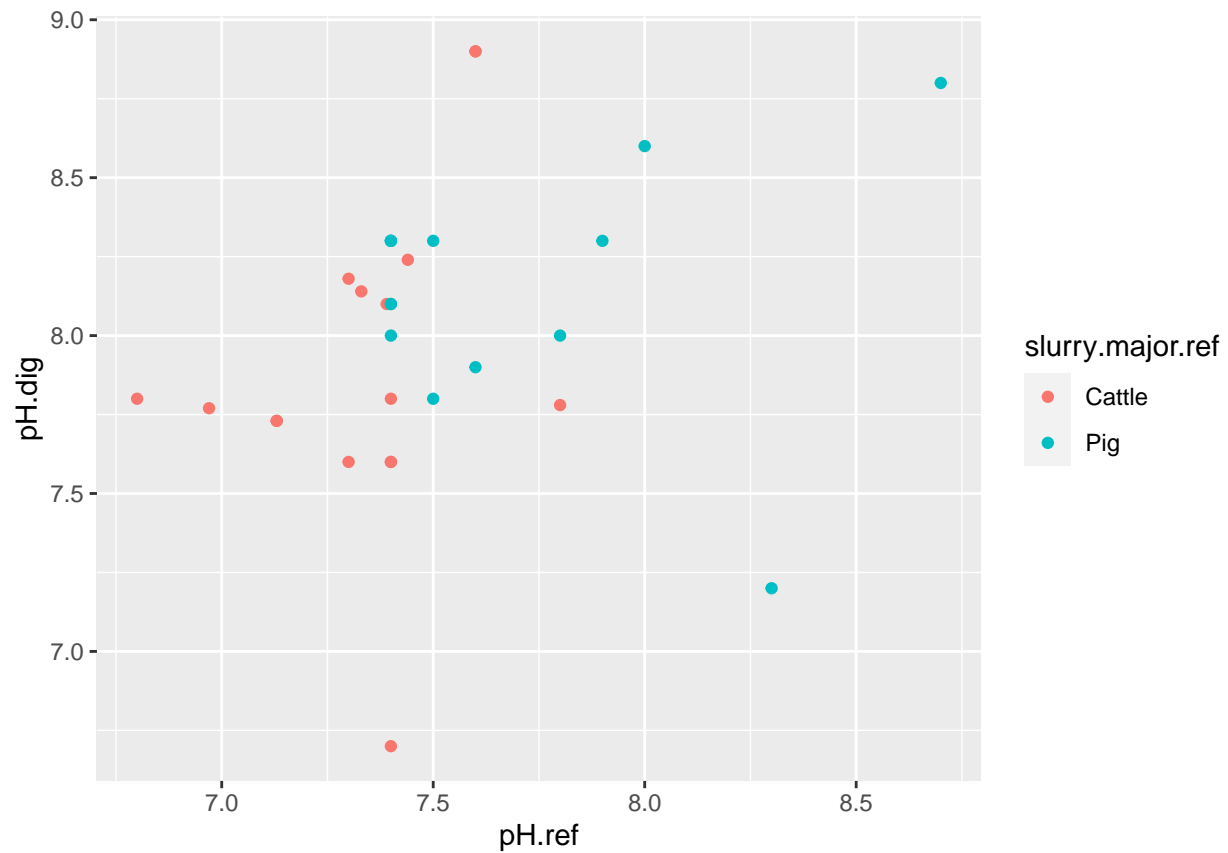
```
ggplot(dat, aes(source, pH, colour = relDiff.frac)) +  
  geom_point() +  
  theme(legend.position = 'top', axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1))
```

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



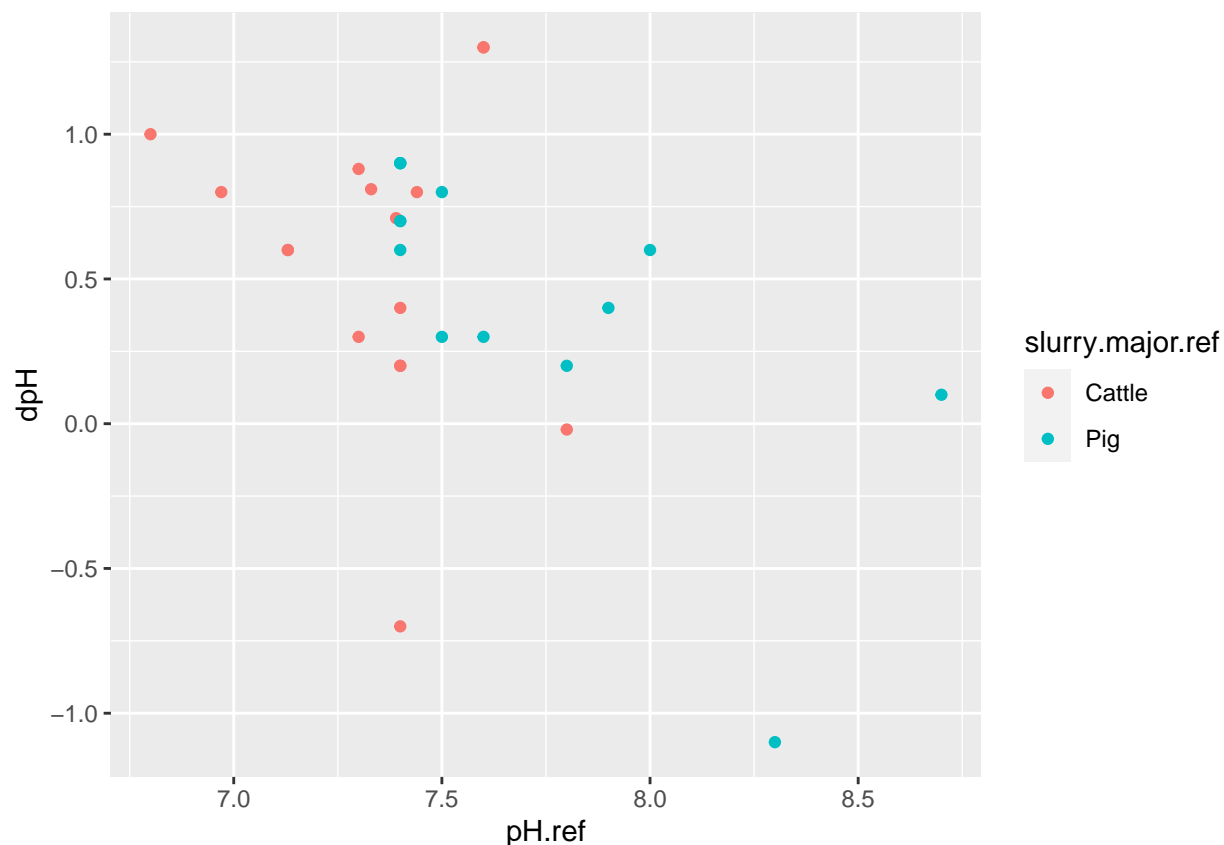
```
ggplot(dw, aes(pH.ref, pH.dig, colour = slurry.major.ref)) +
  geom_point()
```

```
## 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
## -1.22736 -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
```

```
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.

```
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)
```

```
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. So post digestion pH seems to be the same regardless of raw pH. Seems plausible. Say low raw pH is caused by a lot of VFAs, which then have no effect on digestate pH.

Simpler question: how does digestion change pH and DM?

```
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. Mixed-effects model more appropriate.

```
m5pH <- lmer(dpH ~ (1|source), data = dw)
summary(m5pH)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: dpH ~ (1 | source)
## Data: dw
##
## REML criterion at convergence: 32.6
##
## Scaled residuals:
##      Min      1Q   Median      3Q      Max
## -2.40843 -0.24053  0.08254  0.28675  1.94922
##
## Random effects:
## Groups Name Variance Std.Dev.
## source (Intercept) 0.30699 0.5541
## Residual 0.05266 0.2295
## Number of obs: 30, groups: source, 14
##
## Fixed effects:
```

```
##           Estimate Std. Error t value
## (Intercept)  0.4670    0.1554   3.005
```

```
confint(m5pH)
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %    97.5 %
## .sig01      0.3426621 0.8435668
## .sigma      0.1673777 0.3470989
## (Intercept) 0.1502382 0.7812450
```

Compare among animal types.

```
m6pH <- lmer(dpH ~ slurry.major.ref + (1|source), data = dw)
summary(m6pH)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: dpH ~ slurry.major.ref + (1 | source)
##      Data: dw
##
## REML criterion at convergence: 32.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4381 -0.2670  0.1201  0.2397  1.9352
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  source   (Intercept)  0.32301   0.5683
##  Residual                    0.05229   0.2287
## Number of obs: 30, groups:  source, 14
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      0.5678    0.2108   2.693
## slurry.major.refPig -0.2347    0.3211  -0.731
##
## Correlation of Fixed Effects:
##              (Intr)
## slrry.mjr.P -0.657
```

Not clearly smaller for pig.

But we don't care about standard deviation estimates, so simpler to explain mean by study.

```
dws <- aggregate2(dw, c('dpH', 'dDM'), by = 'source', FUN = list(mean = mean, n = function(x) sum(!is.na(x))))
```

```
t.test(dws$dpH.mean)
```

```
##
## One Sample t-test
##
## data: dws$d pH.mean
## t = 4.558, df = 11, p-value = 0.0008194
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.2907323 0.8337121
## sample estimates:
## mean of x
## 0.5622222
```

And repeat for DM:

```
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
```

Clearly DM does increase, according to a one-sample t-test. Mixed-effects model more appropriate.

```
m5DM <- lmer(dDM ~ (1|source), data = dw)
summary(m5DM)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: dDM ~ (1 | source)
## Data: dw
##
## REML criterion at convergence: 130.5
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -3.9984 -0.0775 -0.0079 0.1895 1.5780
##
## Random effects:
## Groups Name Variance Std.Dev.
## source (Intercept) 2.7817 1.6679
## Residual 0.9728 0.9863
## Number of obs: 36, groups: source, 16
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) -2.1976 0.4555 -4.824
```



```
confint(m5DM)
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %    97.5 %
## .sig01      1.0683971  2.496403
## .sigma      0.7464718  1.379687
## (Intercept) -3.1143616 -1.277186
```

Compare among animal types.

```
m6DM <- lmer(dDM ~ slurry.major.ref + (1|source), data = dw)
summary(m6DM)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: dDM ~ slurry.major.ref + (1 | source)
## Data: dw
##
## REML criterion at convergence: 125.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0063 -0.1773  0.0730  0.1991  1.6032
##
## Random effects:
## Groups Name Variance Std.Dev.
## source (Intercept) 2.3977  1.5485
## Residual 0.9613  0.9805
## Number of obs: 36, groups: source, 16
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    -2.7972     0.5416  -5.164
## slurry.major.refPig  1.5894     0.8828   1.800
##
## Correlation of Fixed Effects:
##              (Intr)
## slrry.mjr.P -0.614
```

Some evidence change is smaller for pigs.

We don't care about standard deviation estimates, so simpler to explain mean by study.

```
t.test(dws$dDM.mean)
```

```
##
## One Sample t-test
##
## data: dws$dDM.mean
## t = -5.4297, df = 13, p-value = 0.0001152
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
```

```
## -3.400268 -1.464613
## sample estimates:
## mean of x
## -2.43244
```