

Summary of solid manure data

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```
names(dat)
```

```
## [1] "source"          "abs.emis.info"    "incorp.info"
## [4] "timing.info"      "location"         "manure.source"
## [7] "man.type"        "manure.source.det" "meas.meth"
## [10] "meas.meth.det"   "meas.scale"       "duration"
## [13] "house.inf"       "stor.meth"        "stor.cov"
## [16] "stor.cov.type"   "stor.length"      "man.treat"
## [19] "DM"             "pH"               "TAN"
## [22] "totN"           "X23"              "app.meth"
## [25] "incorp"          "incorp.set"       "incorp.meth"
## [28] "incorp.depth"    "incorp.time"      "amount"
## [31] "season"         "temp.app"         "temp.avg"
## [34] "pres"           "soil.type"        "soil.clay"
## [37] "crop"           "soil.dens"        "soil.water"
## [40] "emis.perc.TAN"   "emis.perc.N"      "emis.source"
## [43] "emis.ID"        "notes"            "row.in.file"
## [46] "fTAN"           "manure.source.nm" "incorp.depth.nm"
## [49] "meas.meth.nm"    "season.nm"        "source.key"
```

Counts

First plot counts:

```
kable(table(dat$meas.meth, exclude = NULL))
```

Var1	Freq
dynamic chamber	141
micromet	53
NA	1

```
kable(table(dat$manure.source, exclude = NULL))
```

Var1	Freq
cattle	47
pig	66
poultry	81
NA	1

```
kable(table(dat[, c('man.type', 'manure.source')], exclude = NULL))
```

	cattle	pig	poultry	NA
broiler litter	0	0	5	0
deep litter	12	2	0	0
farmyard manure	26	58	0	0
fiber	3	4	0	0
fresh solid manure	1	0	0	0
litter	0	0	43	0
manure	0	0	1	0
solid	2	2	4	0
NA	3	0	28	1

```
kable(table(dat[, c('meas.meth', 'manure.source')], exclude = NULL))
```

	cattle	pig	poultry	NA
dynamic chamber	30	62	49	0
micromet	17	4	32	0
NA	0	0	0	1

Then studies:

```
dat.study <- dat[!duplicated(dat[, c('source', 'meas.meth', 'manure.source'))], ]
kable(table(dat.study$meas.meth, exclude = NULL))
```

Var1	Freq
dynamic chamber	18
micromet	15
NA	1

```
kable(table(dat.study$manure.source, exclude = NULL))
```

Var1	Freq
cattle	12
pig	9
poultry	12
NA	1

```
kable(table(dat.study[, c('man.type', 'manure.source')], exclude = NULL))
```

	cattle	pig	poultry	NA
broiler litter	0	0	1	0
deep litter	3	1	0	0
farmyard manure	4	5	0	0
fiber	2	2	0	0
litter	0	0	6	0

	cattle	pig	poultry	NA
solid	2	1	1	0
NA	1	0	4	1

```
kable(table(dat.study[, c('meas.meth', 'manure.source')], exclude = NULL))
```

	cattle	pig	poultry	NA
dynamic chamber	5	7	6	0
micromet	7	2	6	0
NA	0	0	0	1

Easier combined?

```
kable(
  aggregate2(as.data.frame(dat), 'source',
    by = c('meas.meth', 'manure.source'),
    FUN = list(n.plots = length, n.studies = function(x) length(unique(x))))
)
```

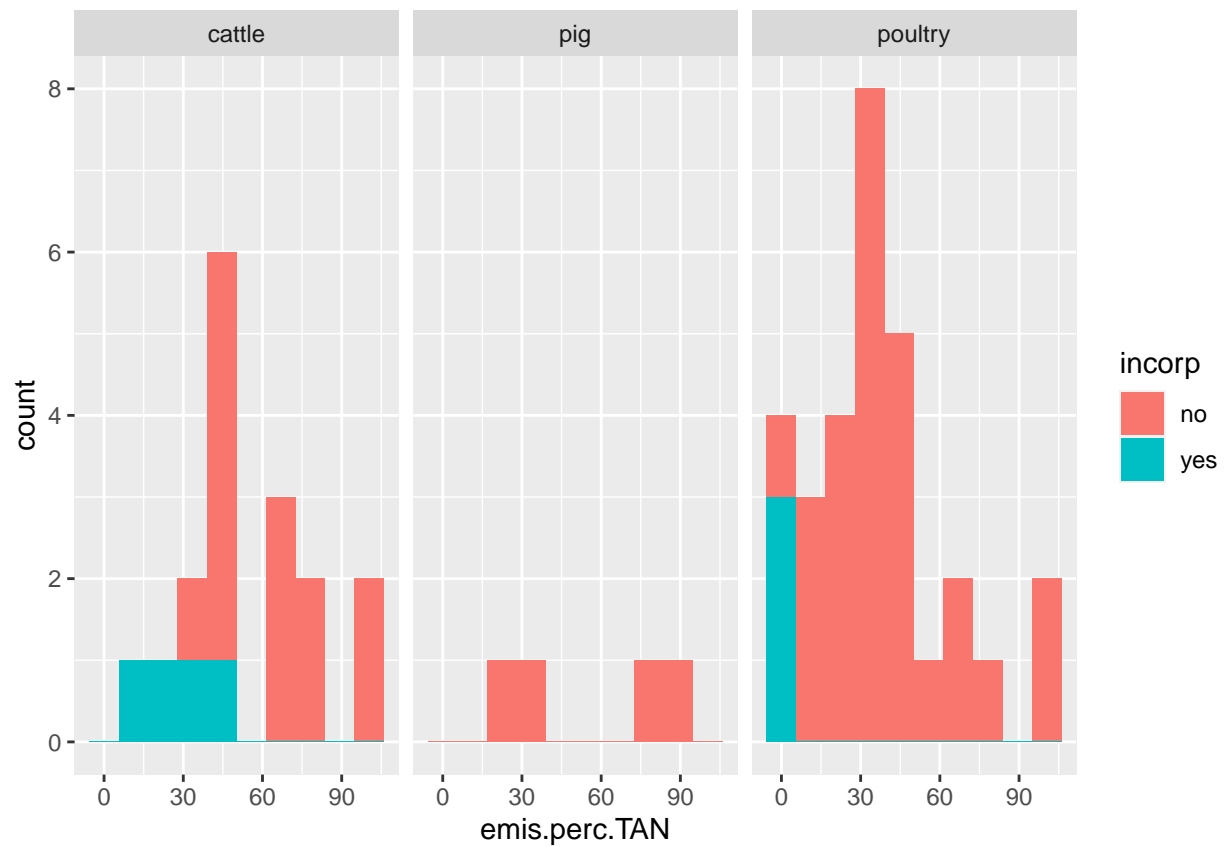
meas.meth	manure.source	source.n.plots	source.n.studies
dynamic chamber	cattle	30	5
micromet	cattle	17	7
dynamic chamber	pig	62	7
micromet	pig	4	2
dynamic chamber	poultry	49	6
micromet	poultry	32	6

Emission factors and other variables for micromet observations only

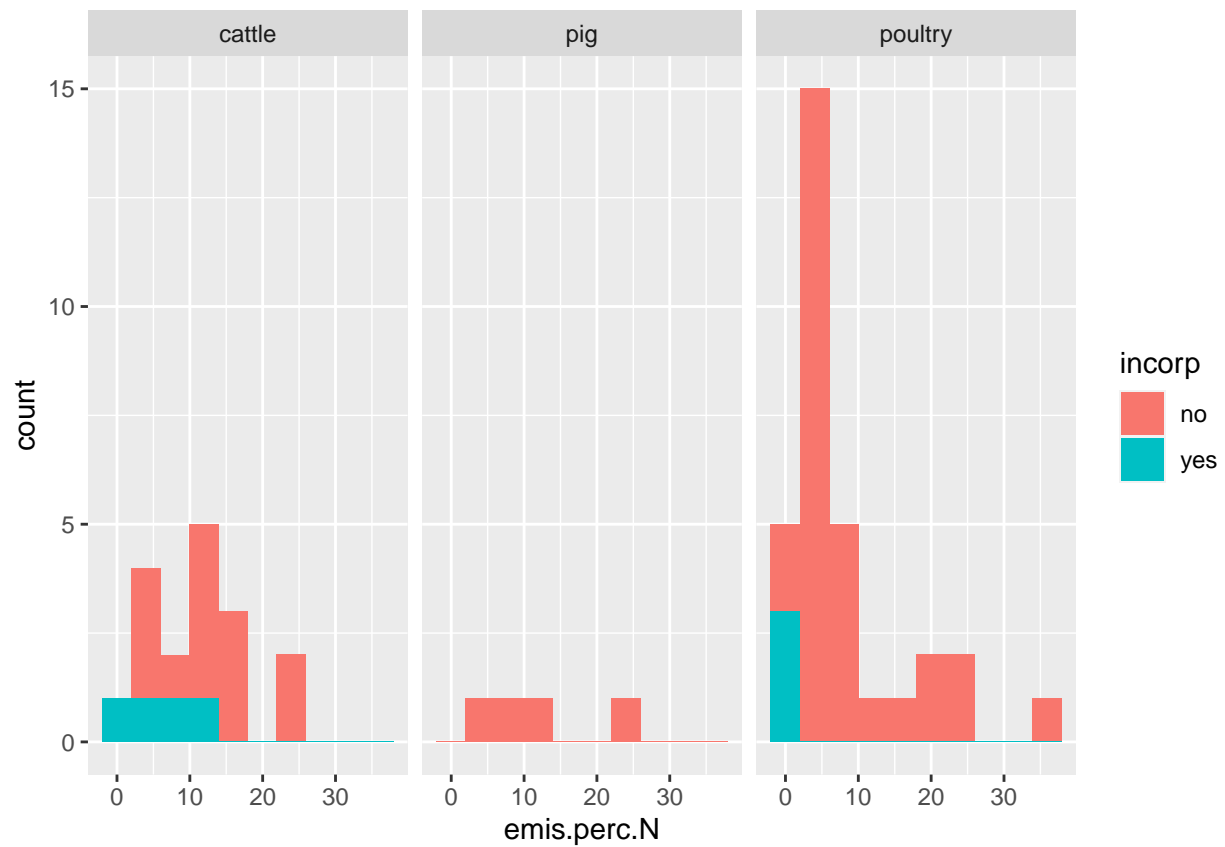
```
datmm <- subset(dat, meas.meth == 'micromet')
```

```
ggplot(datmm, aes(emis.perc.TAN, fill = incorp)) +
  geom_histogram(bins = 10) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 2 rows containing non-finite values (`stat_bin()`).
```

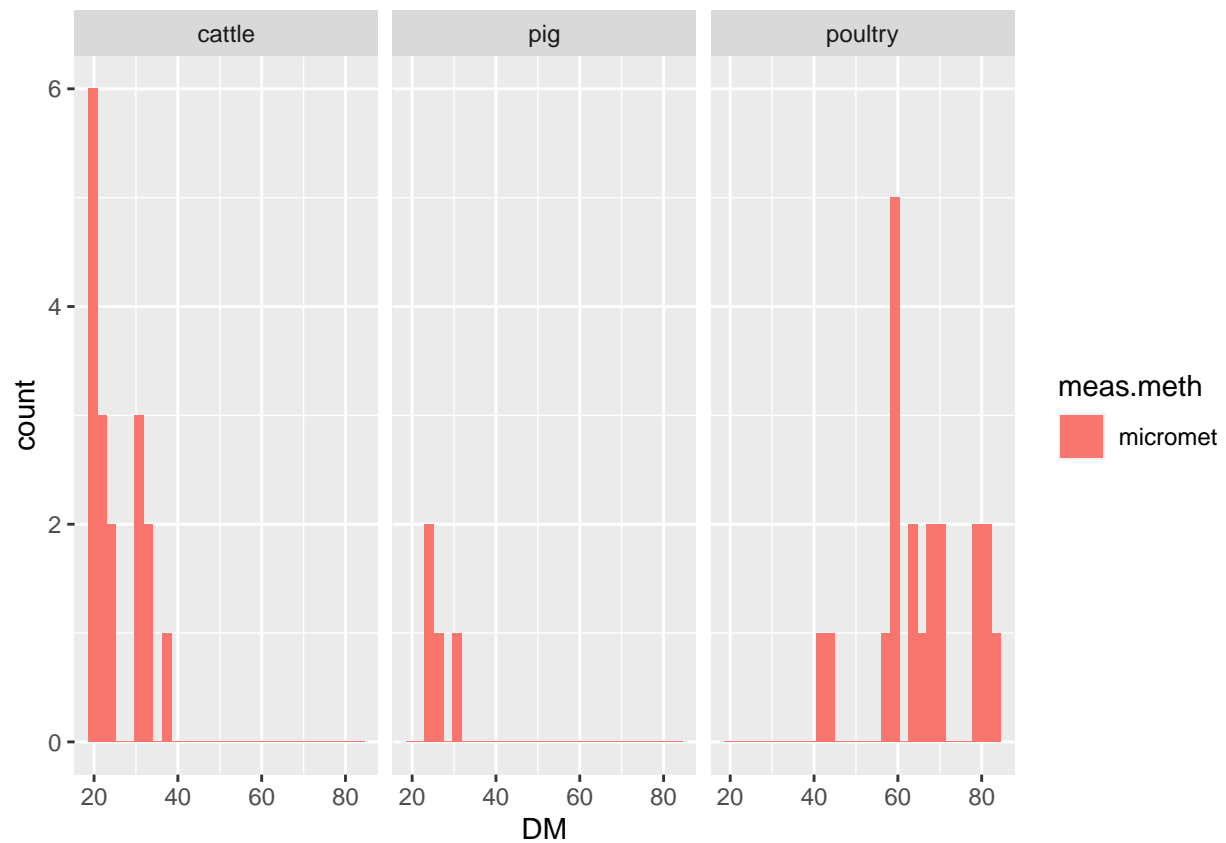


```
ggplot(datmm, aes(emis.perc.N, fill = incorp)) +
  geom_histogram(bins = 10) +
  facet_wrap(~ manure.source, scales = 'fixed')
```



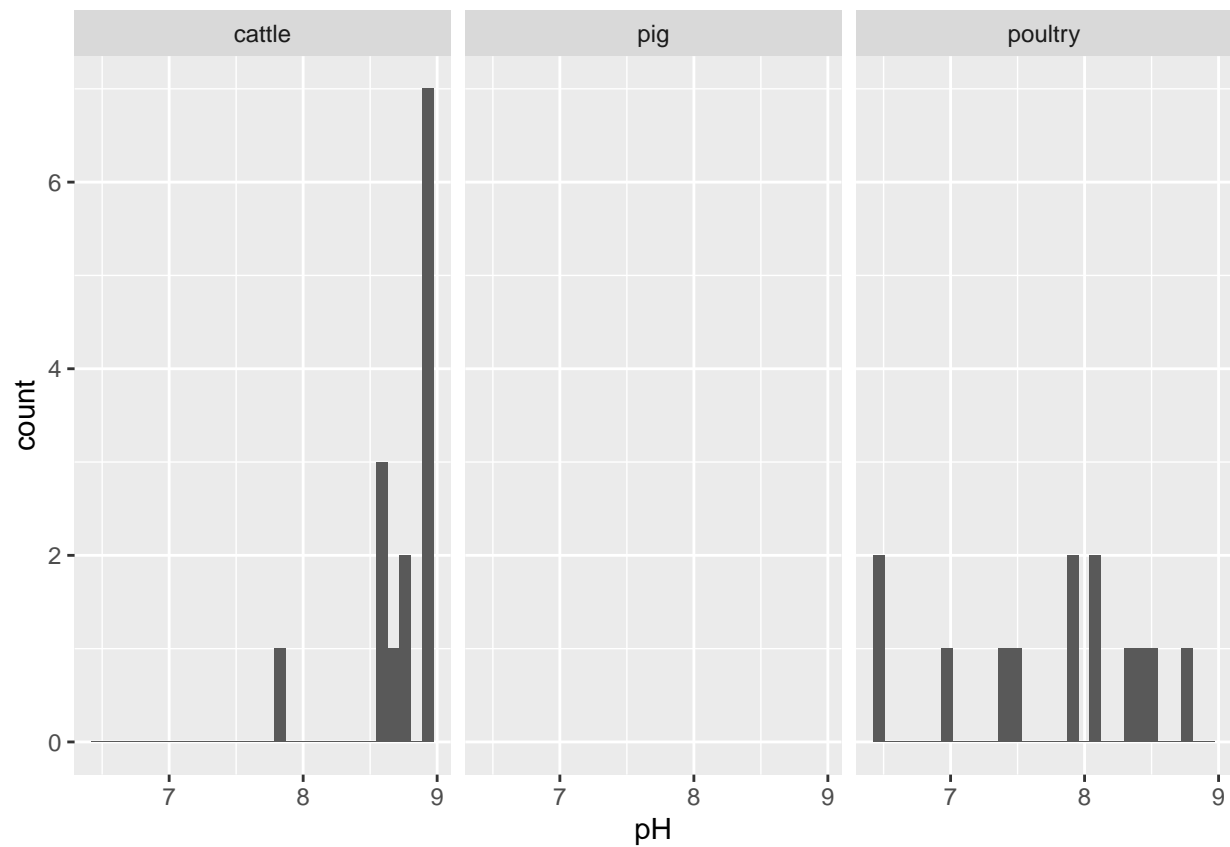
```
ggplot(datmm, aes(DM, fill = meas.meth)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

Warning: Removed 12 rows containing non-finite values (`stat_bin()`).



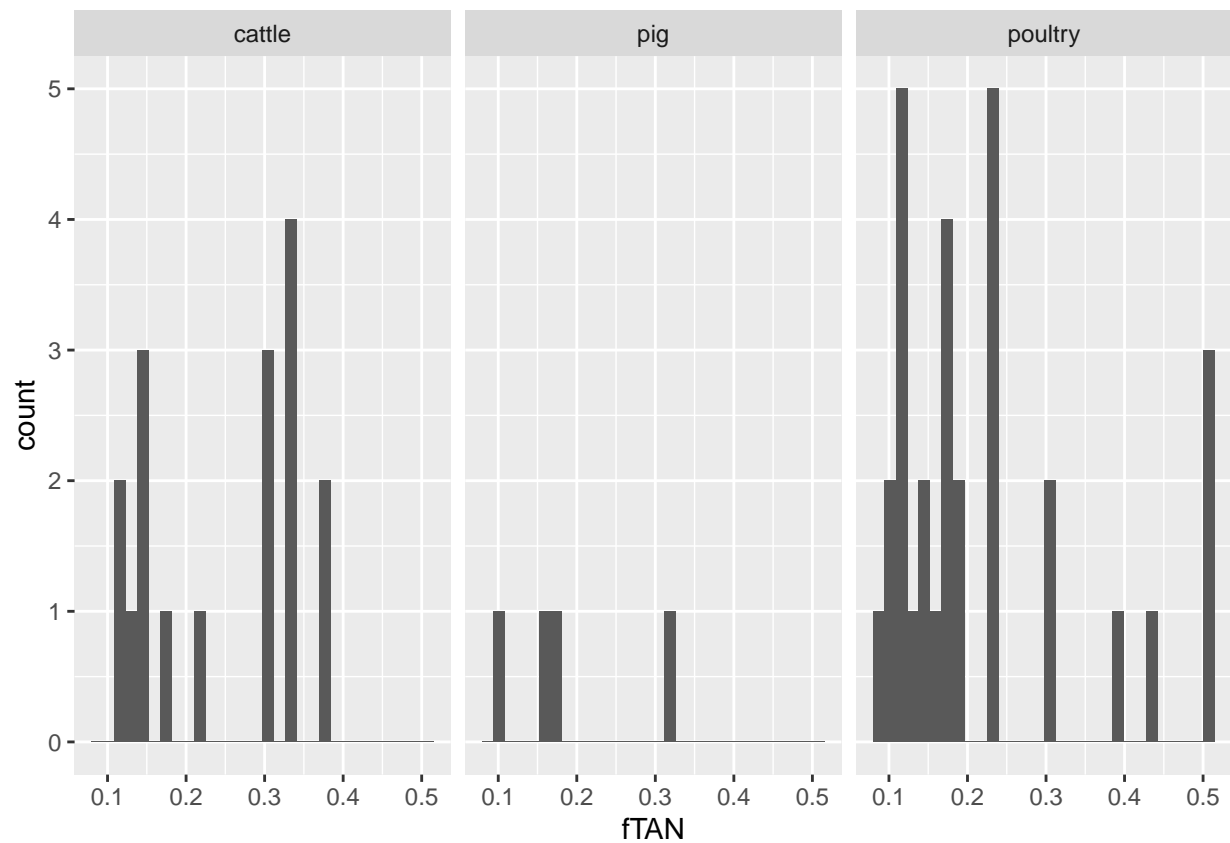
```
ggplot(datmm, aes(pH)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

Warning: Removed 26 rows containing non-finite values (`stat_bin()`).



```
ggplot(datmm, aes(fTAN)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

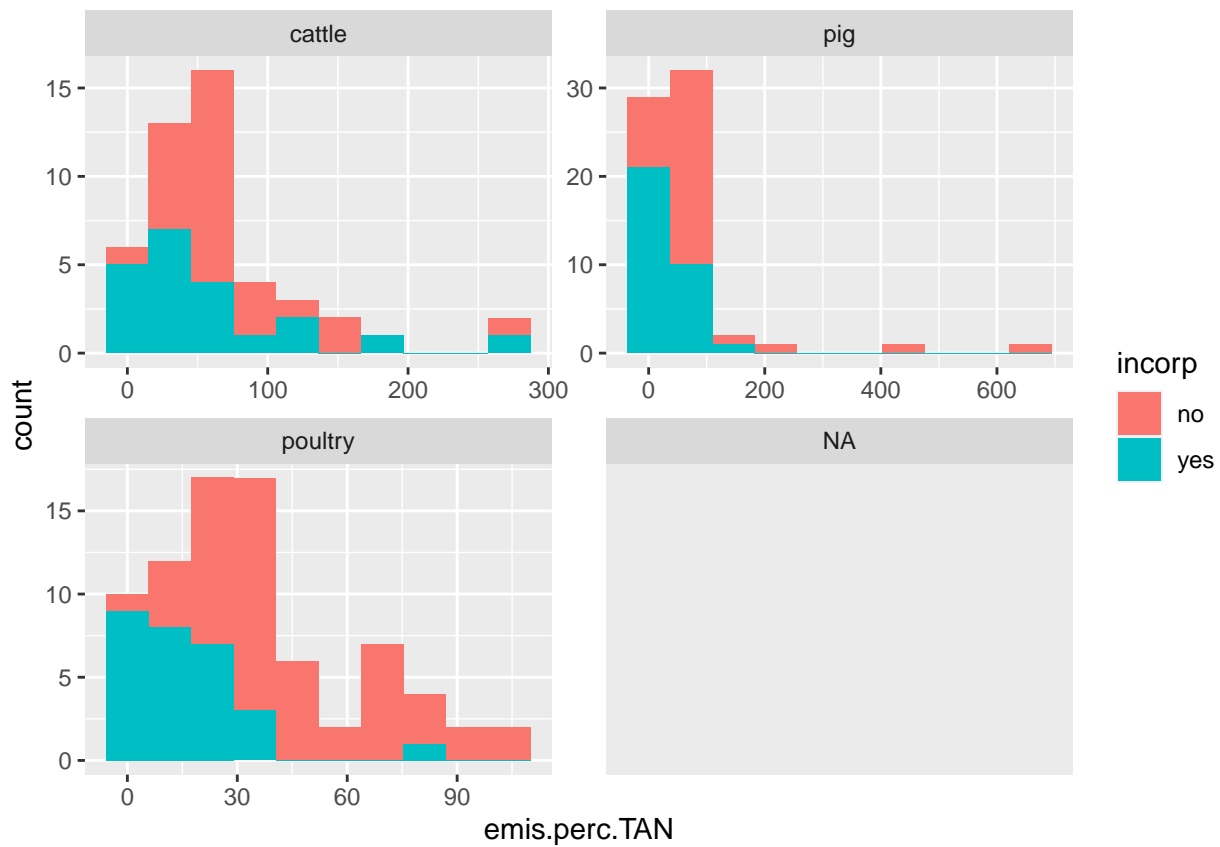
Warning: Removed 2 rows containing non-finite values (`stat_bin()`).



Emission factors and other variables for all observations

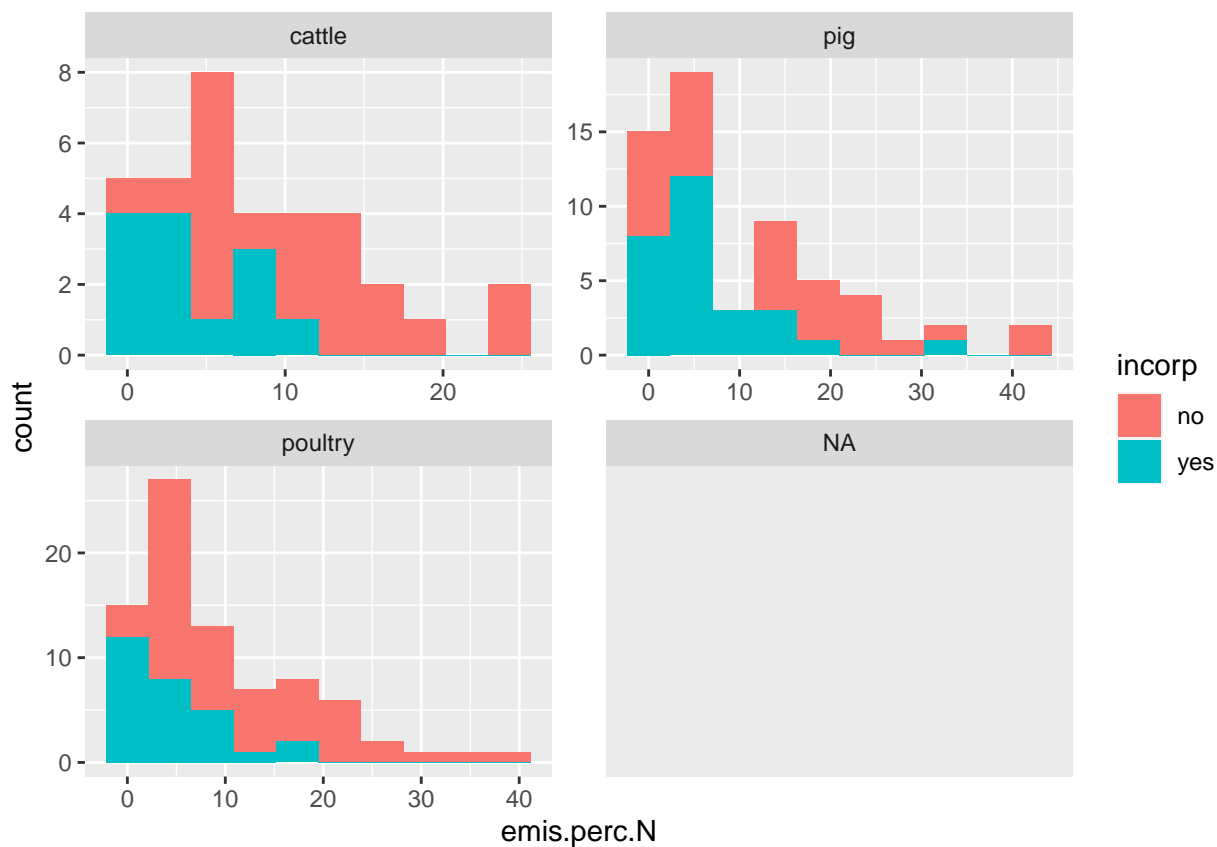
```
ggplot(dat, aes(emis.perc.TAN, fill = incorp)) +  
  geom_histogram(bins = 10) +  
  facet_wrap(~ manure.source, scales = 'free')
```

```
## Warning: Removed 3 rows containing non-finite values (`stat_bin()`).
```

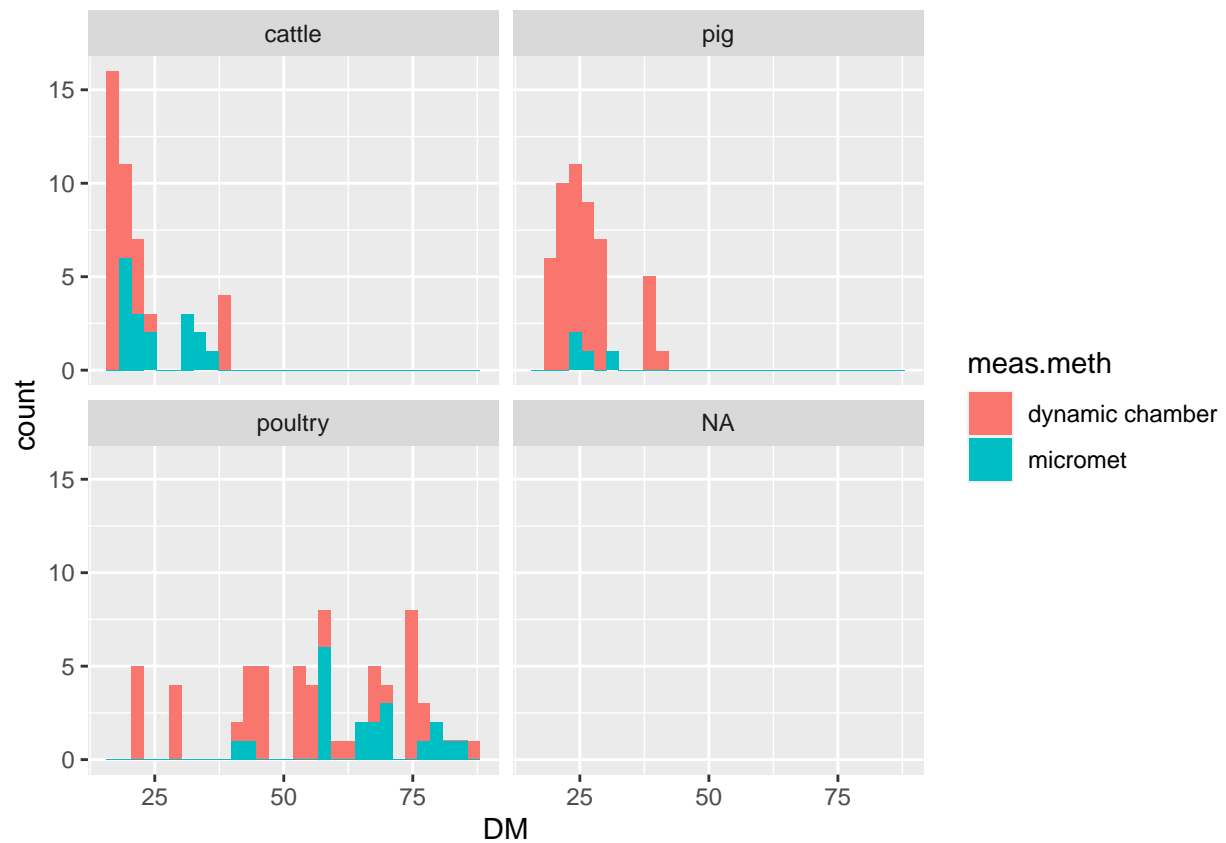
```
ggplot(dat, aes(emis.perc.N, fill = incorp)) +
  geom_histogram(bins = 10) +
  facet_wrap(~ manure.source, scales = 'free')
```

```
## Warning: Removed 19 rows containing non-finite values (`stat_bin()`).
```



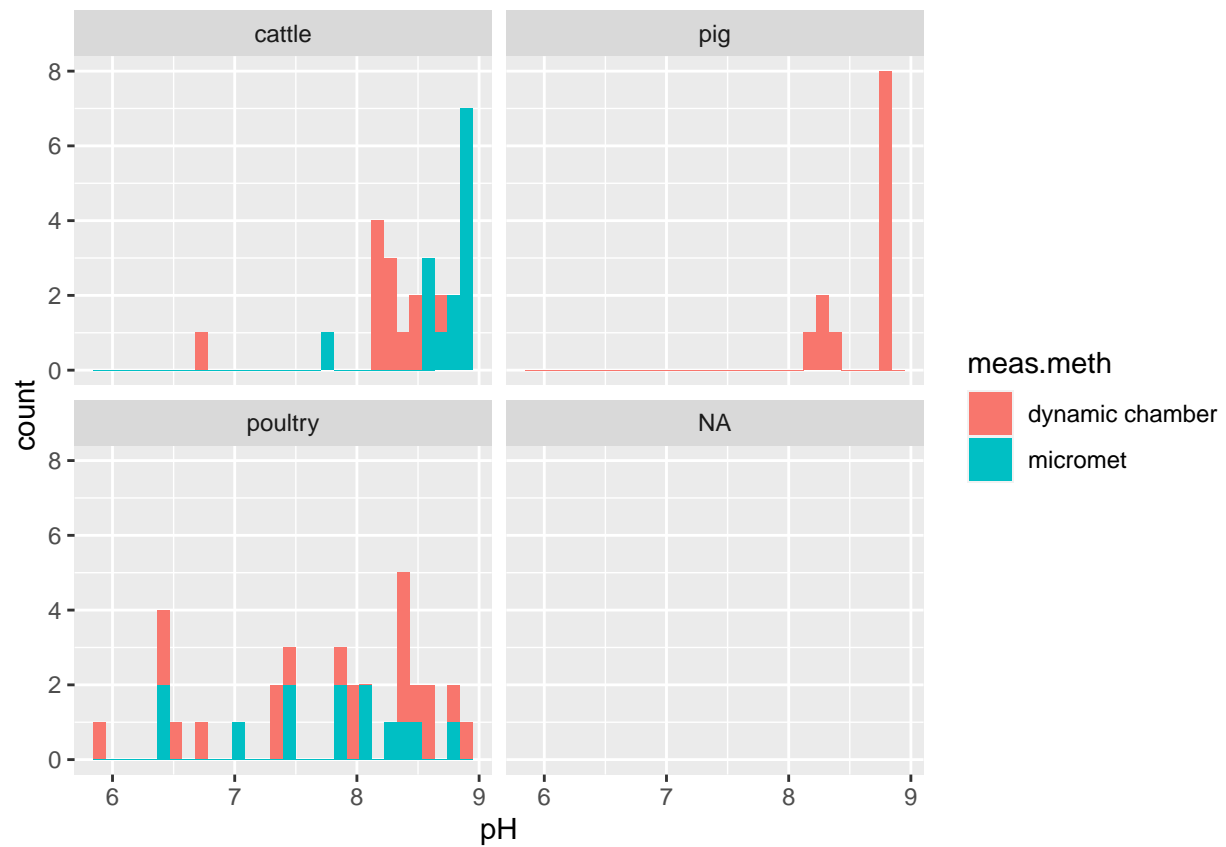
```
ggplot(dat, aes(DM, fill = meas.meth)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 31 rows containing non-finite values (`stat_bin()`).
```



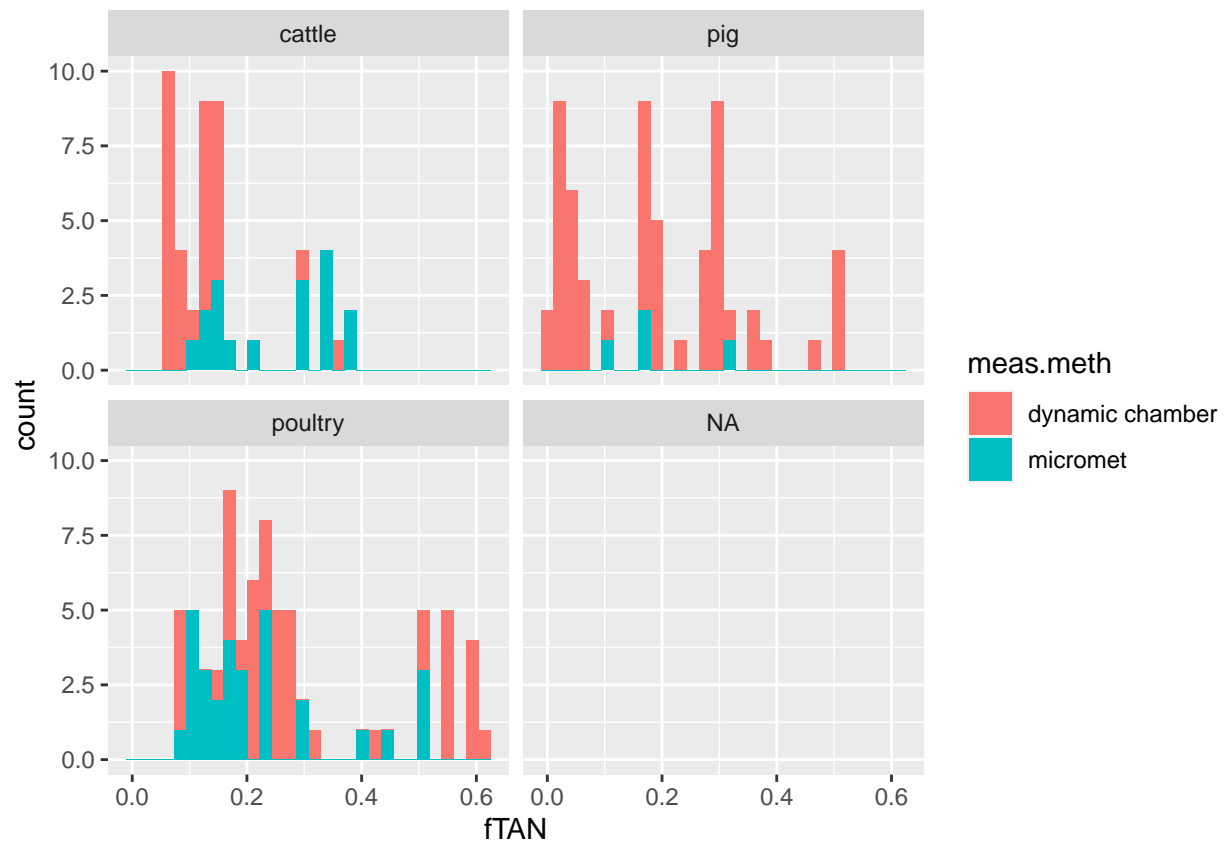
```
ggplot(dat, aes(pH, fill = meas.meth)) +  
  geom_histogram(bins = 30) +  
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 124 rows containing non-finite values (`stat_bin()`).
```



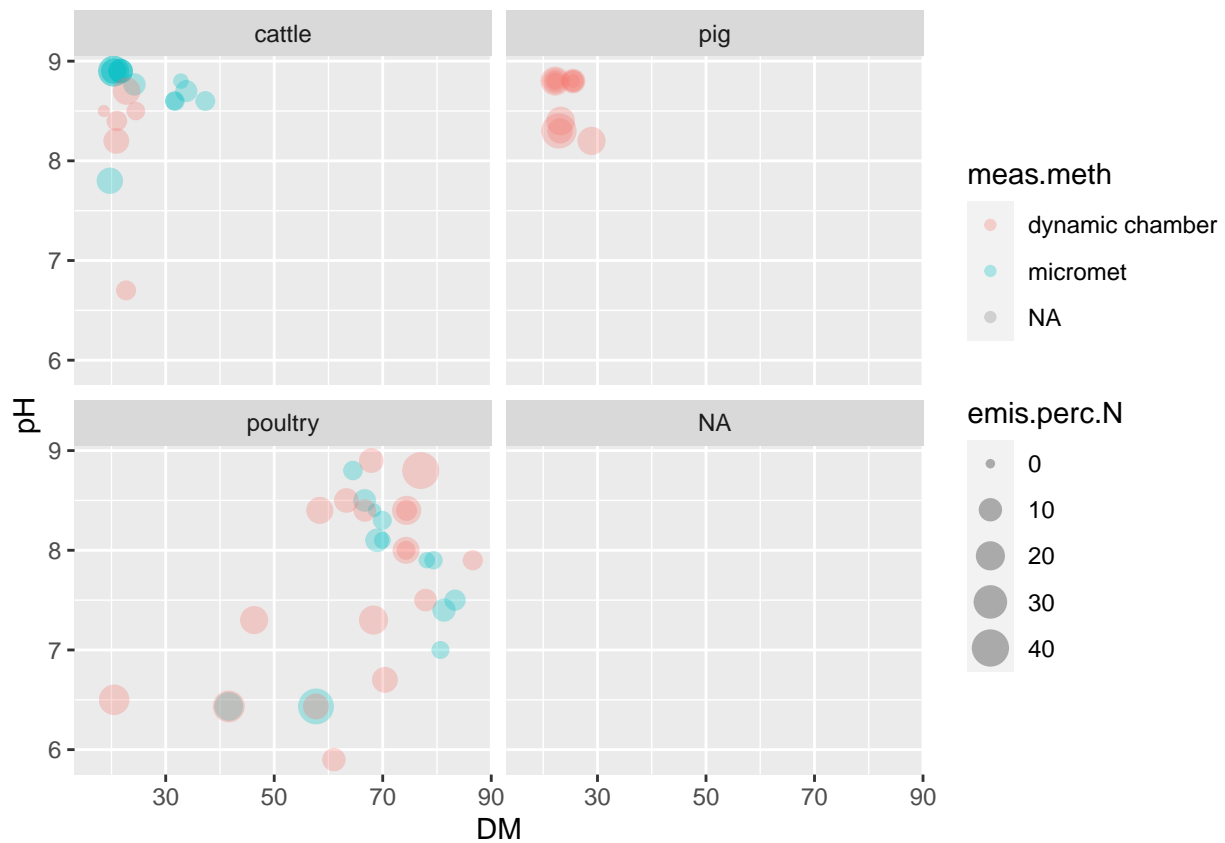
```
ggplot(dat, aes(fTAN, fill = meas.meth)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

Warning: Removed 14 rows containing non-finite values (`stat_bin()`).



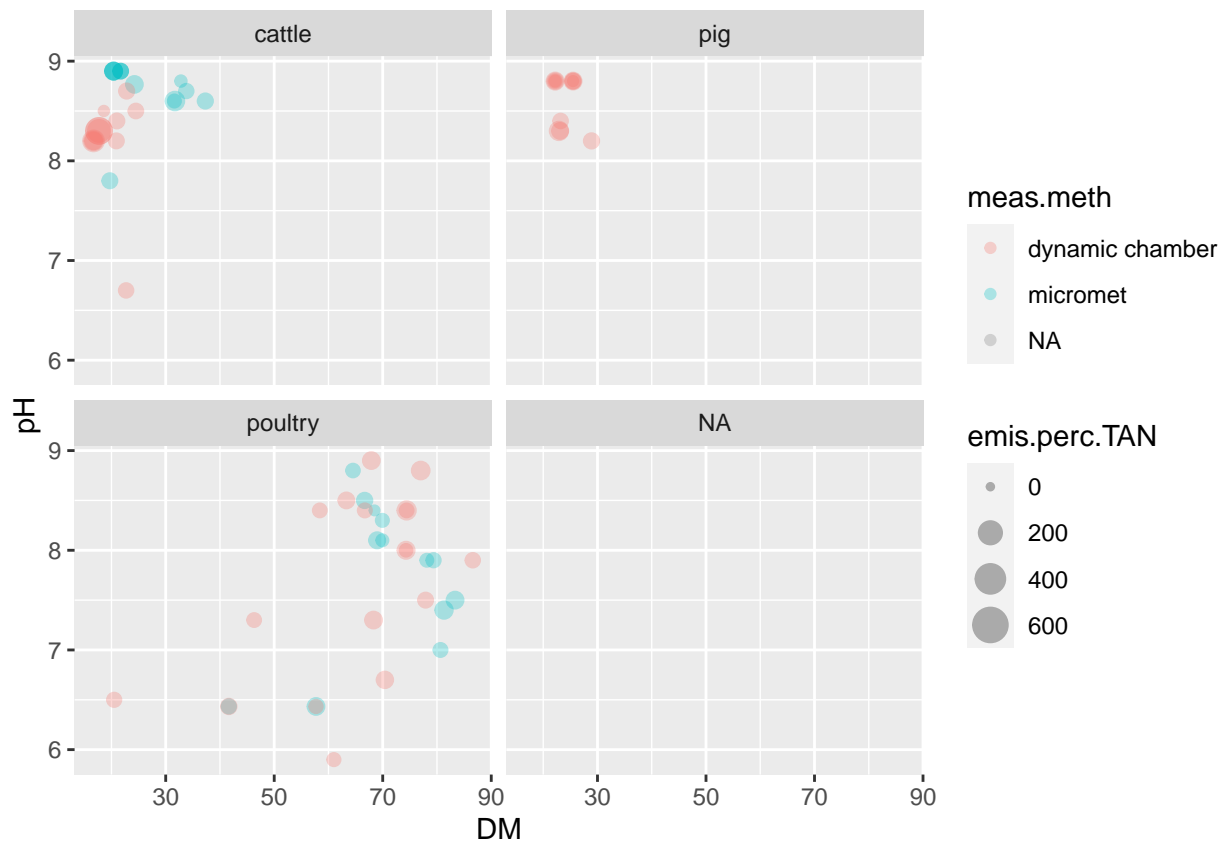
```
ggplot(dat, aes(DM, pH, size = emis.perc.N, colour = meas.meth)) +
  geom_point(alpha = 0.3) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 132 rows containing missing values (`geom_point()`).
```



```
ggplot(dat, aes(DM, pH, size = emis.perc.TAN, colour = meas.meth)) +
  geom_point(alpha = 0.3) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 126 rows containing missing values (`geom_point()`).
```

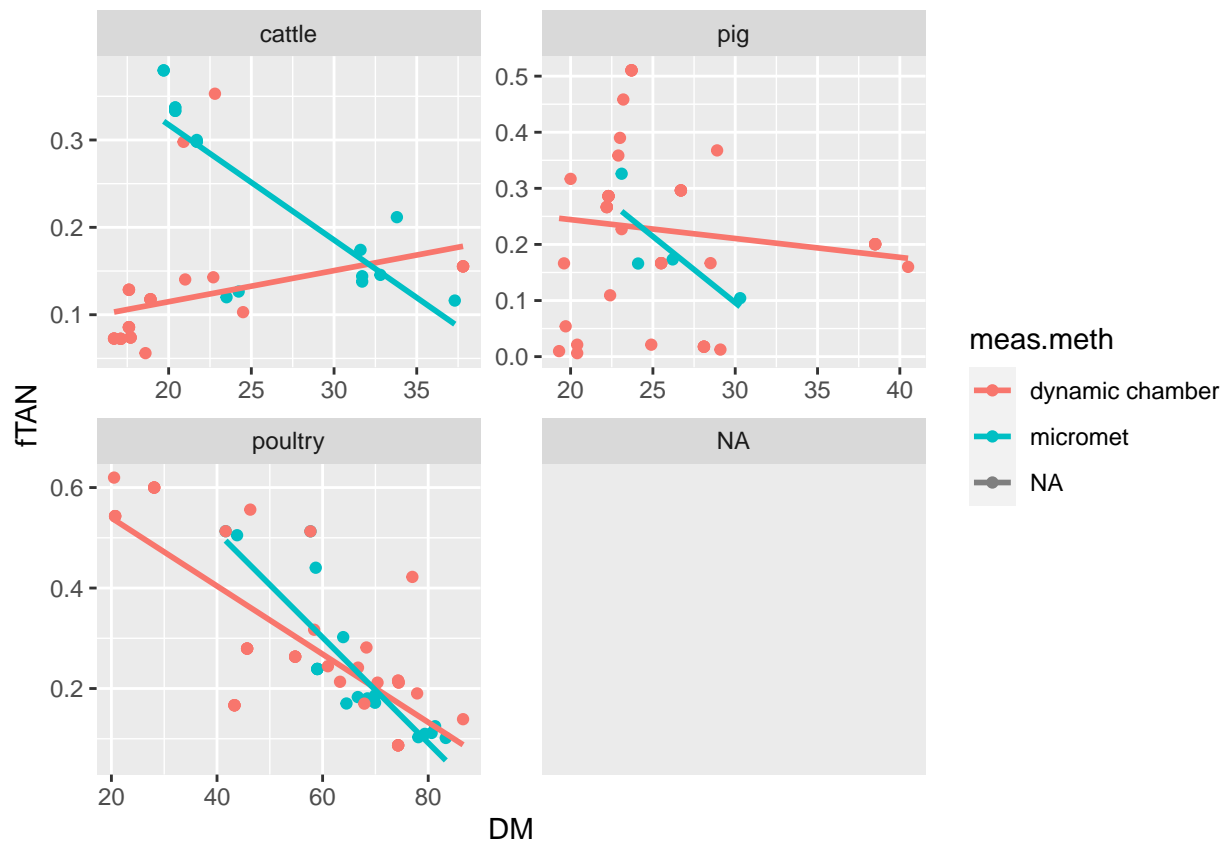


```
ggplot(dat, aes(DM, fTAN, colour = meas.meth)) +
  geom_point() +
  geom_smooth(method = lm, se = FALSE) +
  facet_wrap(~ manure.source, scales = 'free')
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

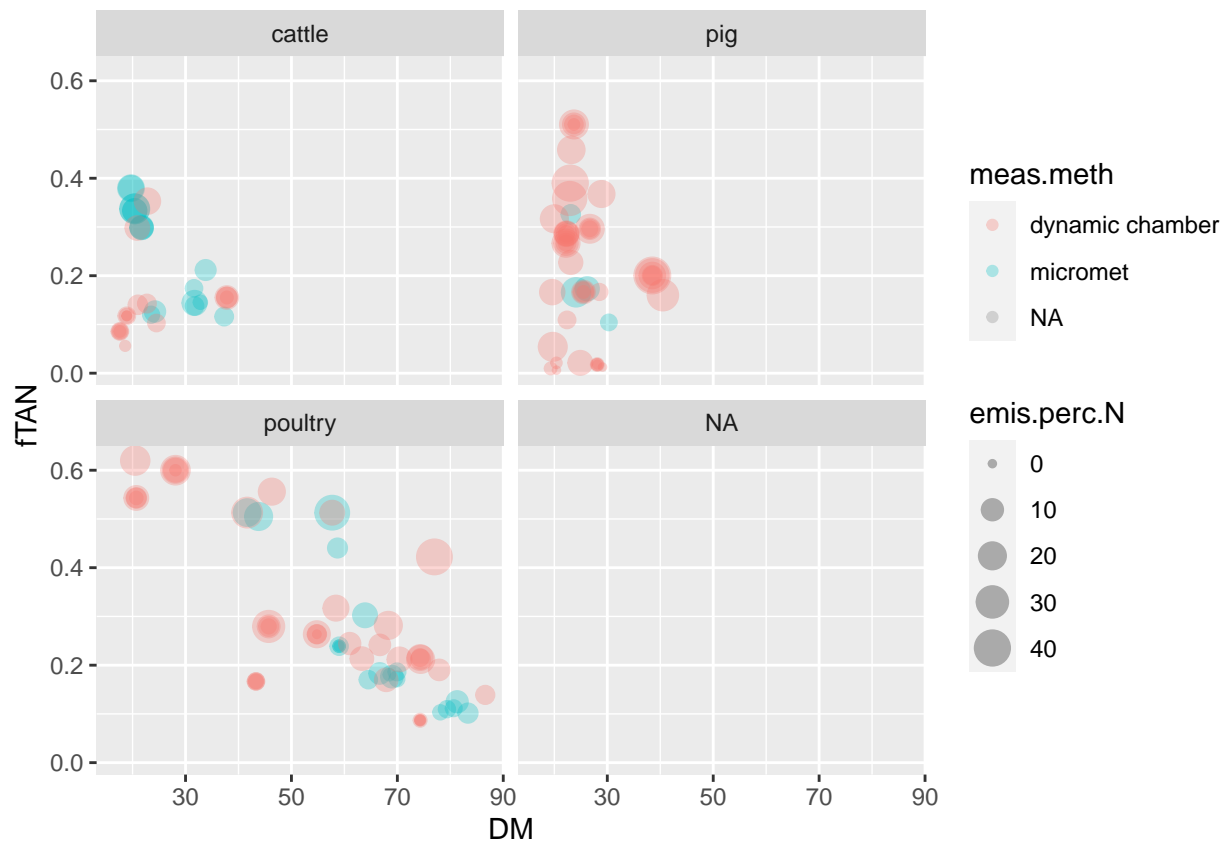
```
## Warning: Removed 36 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 36 rows containing missing values (`geom_point()`).
```



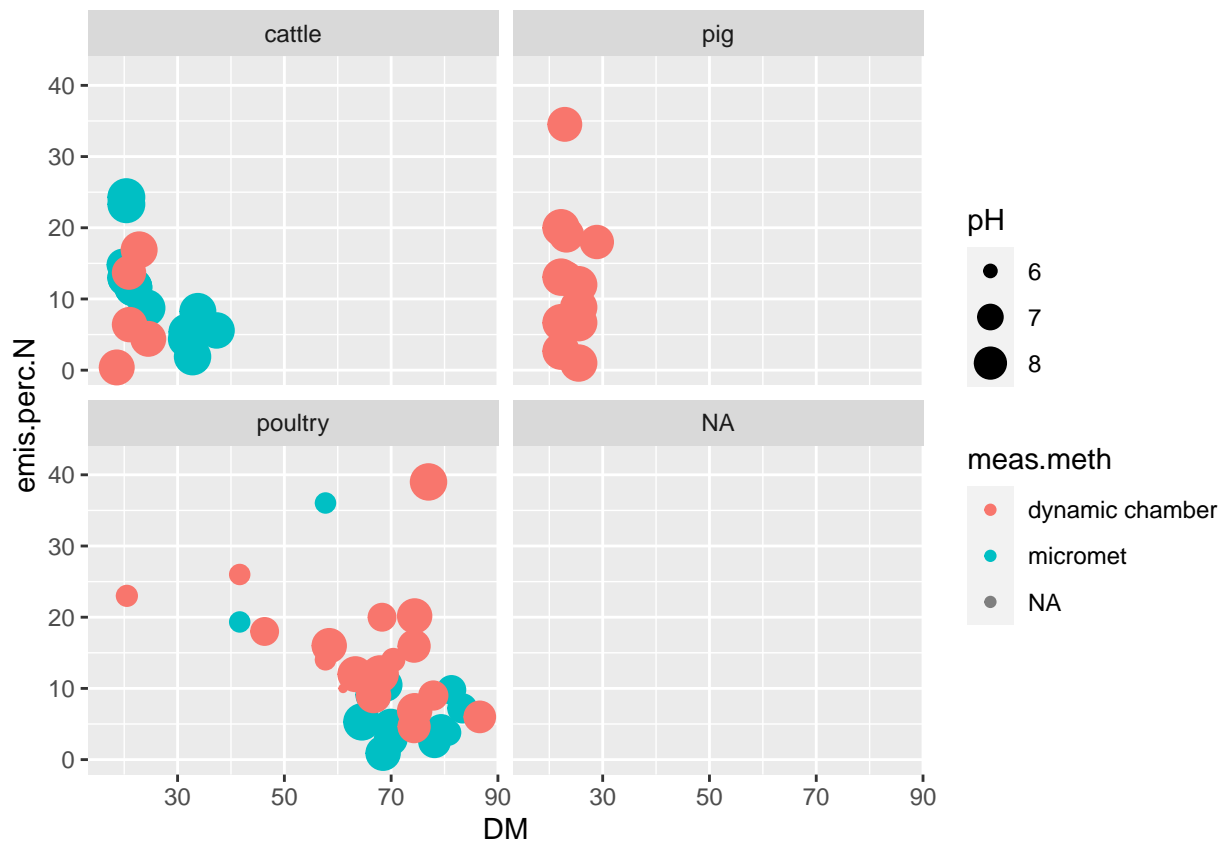
```
ggplot(dat, aes(DM, fTAN, size = emis.perc.N, colour = meas.meth)) +
  geom_point(alpha = 0.3) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 48 rows containing missing values (`geom_point()`).
```

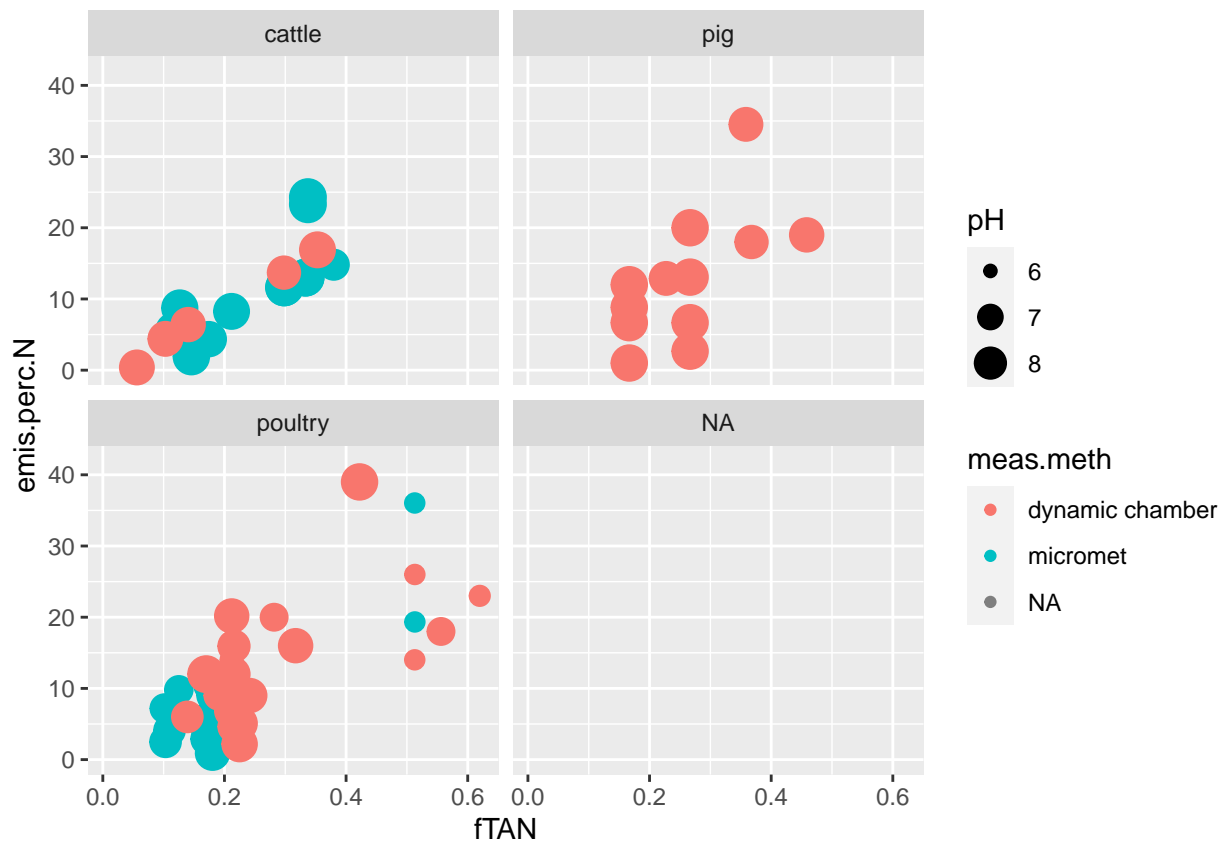
```
ggplot(dat, aes(DM, emis.perc.N, size = pH, colour = meas.meth)) +
  geom_point() +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 132 rows containing missing values (`geom_point()`).
```



```
ggplot(dat, aes(fTAN, emis.perc.N, size = pH, colour = meas.meth)) +
  geom_point() +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## Warning: Removed 130 rows containing missing values (`geom_point()`).
```



Variable summary

```
dfsumm(as.data.frame(dat))
```

```
##
## 195 rows and 51 columns
## 195 unique rows
##
## Class          source abs.emis.info incorp.info timing.info
## Minimum        Balsari et al. (2008a)      0      0      0
## Maximum        Williams et al. (2003)      1      1      1
## Mean            <NA>      0.242      0.598      0.582
## Unique (excl. NA) 25      2      2      2
## Missing values    1      1      1      1
## Sorted           FALSE      FALSE      FALSE      FALSE
##
## Class          location manure.source man.type
## Minimum        Canada, British Columbia cattle broiler litter
## Maximum        UK      poultry      solid
## Mean            <NA>      <NA>      <NA>
## Unique (excl. NA) 11      3      8
## Missing values    1      1      32
## Sorted           FALSE      FALSE      FALSE
##
## manure.source.det meas.meth meas.meth.det meas.scale
```

```

## Class                character      character      character  character
## Minimum              beef dynamic chamber      IHF field plot
## Maximum              turkey      micromet      wind tunnel laboratory
## Mean                 <NA>          <NA>          <NA>          <NA>
## Unique (excl. NA)    5              2              4              2
## Missing values       126            1              37             1
## Sorted               FALSE          FALSE          FALSE          FALSE
##
##
## duration house.inf      stor.meth stor.cov
## Class                character character      character character
## Minimum              120  outdoor 1 L container, 5C, laboratory      no
## Maximum              96  outdoor      stockpile      yes
## Mean                 <NA>  <NA>          <NA>          <NA>
## Unique (excl. NA)    19      1              8              2
## Missing values       33      193            129            161
## Sorted               FALSE      TRUE          FALSE          FALSE
##
##
## stor.cov.type      stor.length man.treat      DM      pH
## Class                character      character character numeric numeric
## Minimum              plastic sheeting      0  wetted      16.7      5.9
## Maximum              plastic sheeting several months      wetted      86.6      8.9
## Mean                 <NA>          <NA>          <NA>      37.7      8.17
## Unique (excl. NA)    1              7              1      80      22
## Missing values       182            145            193      31      124
## Sorted               TRUE          FALSE      TRUE  FALSE  FALSE
##
##
## TAN      totN      X23  app.meth      incorp incorp.set
## Class      numeric numeric numeric character character      numeric
## Minimum    0.0389      2.1      2.6 broadcast      no      1
## Maximum    18.9      59.3      9.4 broadcast      yes      12
## Mean       3.15      14.2      4.68      <NA>      <NA>      4.29
## Unique (excl. NA)  96      103      13      1      2      12
## Missing values    14      12      180      23      1      80
## Sorted          FALSE  FALSE  FALSE      TRUE  FALSE  FALSE
##
##
##
## incorp.meth incorp.depth
## Class                character      character
## Minimum              disc      deep
## Maximum              vaste-tandcultivator (fixed tine cultivator)      shallow
## Mean                 <NA>          <NA>
## Unique (excl. NA)    13              3
## Missing values       114            87
## Sorted               FALSE          FALSE
##
##
## incorp.time amount      season temp.app temp.avg      pres
## Class                character numeric character numeric numeric numeric
## Minimum              2.5      autumn      10      2.4      4
## Maximum              6      70.6      winter      31      27.8      119
## Mean                 <NA>      21.8      <NA>      22.7      14.1      41
## Unique (excl. NA)    8      89      5      8      28      17
## Missing values       109      6      0      179      117      176
## Sorted               FALSE  FALSE  FALSE  FALSE  FALSE  FALSE
##
##
## soil.type soil.clay      crop soil.dens soil.water

```

```

## Class          character  numeric character  numeric  numeric
## Minimum        caly soil    1.94    grass    0.75    0.09
## Maximum        silt loam    64      stubble   4.5     0.28
## Mean           <NA>        22.3    <NA>     1.85    0.166
## Unique (excl. NA) 8         9       3        3       13
## Missing values   83        120     117     186     175
## Sorted          FALSE     FALSE    FALSE    FALSE    FALSE
##
##
## emis.perc.TAN emis.perc.N emis.source
## Class          numeric    numeric  character
## Minimum        0         0      Figure 14
## Maximum        658       42      Table 7
## Mean           52.8      9.35     <NA>
## Unique (excl. NA) 173     151     19
## Missing values   3       19       1
## Sorted          FALSE     FALSE    FALSE
##
##
## emis.ID
## Class          character
## Minimum        Aerobic, 24 h/Pig FYM, 1999, Uncompacted 24
## Maximum        Winter 2001, PP
## Mean           <NA>
## Unique (excl. NA) 135
## Missing values   54
## Sorted          FALSE
##
##
## Class
## Minimum
## Maximum        Same data as in Sommer and Hansen (2022). Hansen and Birkmose writes that the soil
## Mean
## Unique (excl. NA)
## Missing values
## Sorted
##
## row.in.file    fTAN manure.source.nm incorp.depth.nm
## Class          numeric numeric    character    character
## Minimum        4 0.00621    Cattle      Deep
## Maximum        198 0.62     Poultry     Shallow
## Mean           101 0.219    <NA>        <NA>
## Unique (excl. NA) 195 104    3           3
## Missing values   0 14      1           87
## Sorted          FALSE  FALSE    FALSE       FALSE
##
##
## meas.meth.nm season.nm source.key
## Class          character  factor    factor
## Minimum        Dynamic chamber Spring     1
## Maximum        Micrometeorological Unknown    25
## Mean           <NA>      Autumn     16
## Unique (excl. NA) 2       5         25
## Missing values   1       0         1
## Sorted          FALSE    FALSE    FALSE
##

```