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))))
)
```

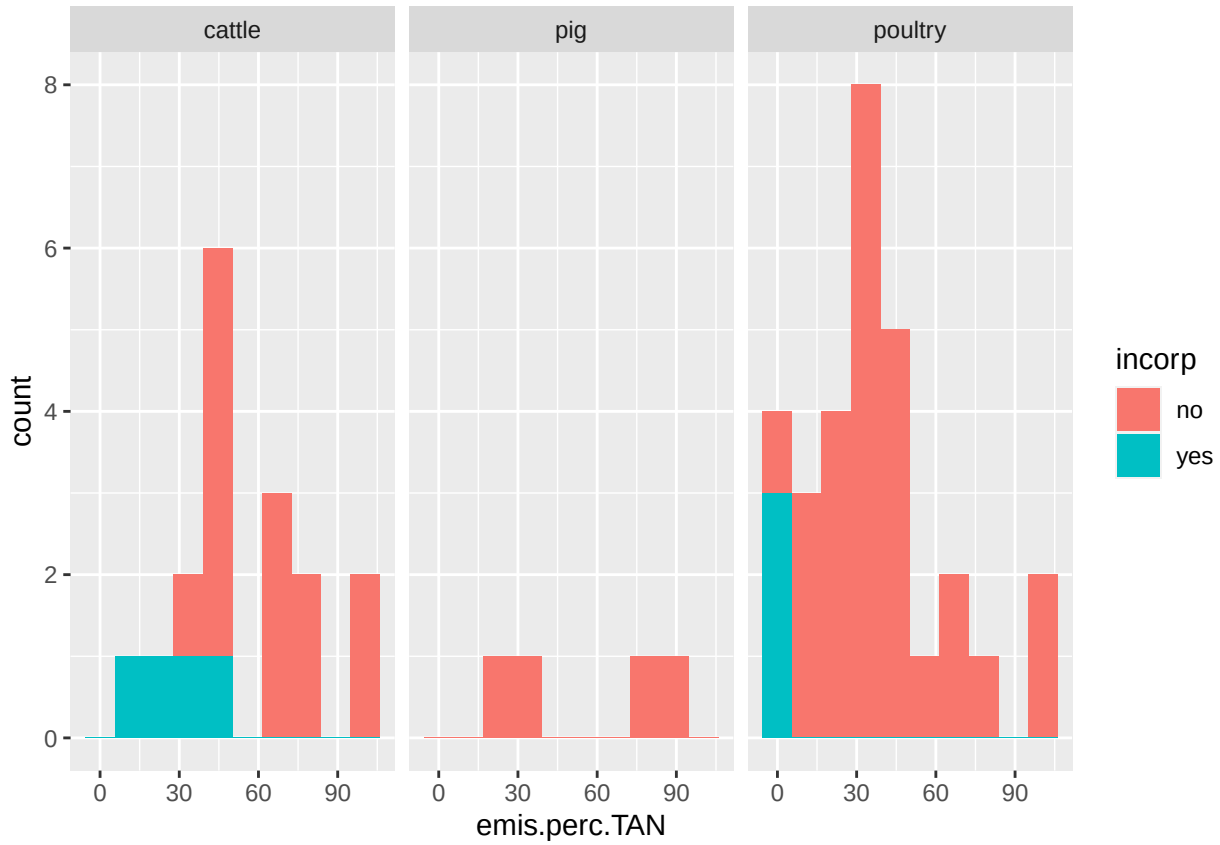
meas.meth	manure.source	source.n.plots	source.n.studies
dynamic chamber	cattle	30	5
micromet	cattle	17	7
dynamic chamber	pig	62	7
micromet	pig	4	2
dynamic chamber	poultry	49	6
micromet	poultry	32	6

Emission factors and other variables for micromet observations only

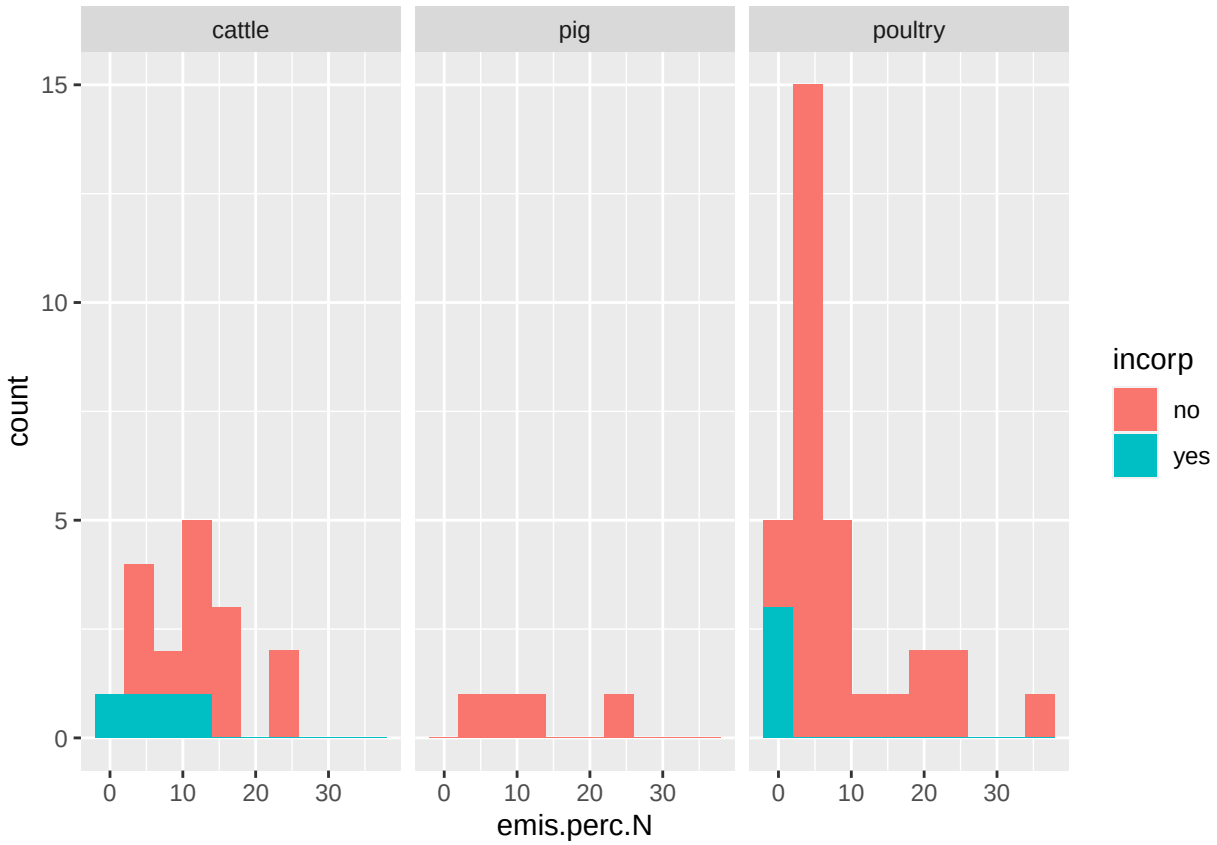
```
datmm <- subset(dat, meas.meth == 'micromet')
```

```
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()`).
```

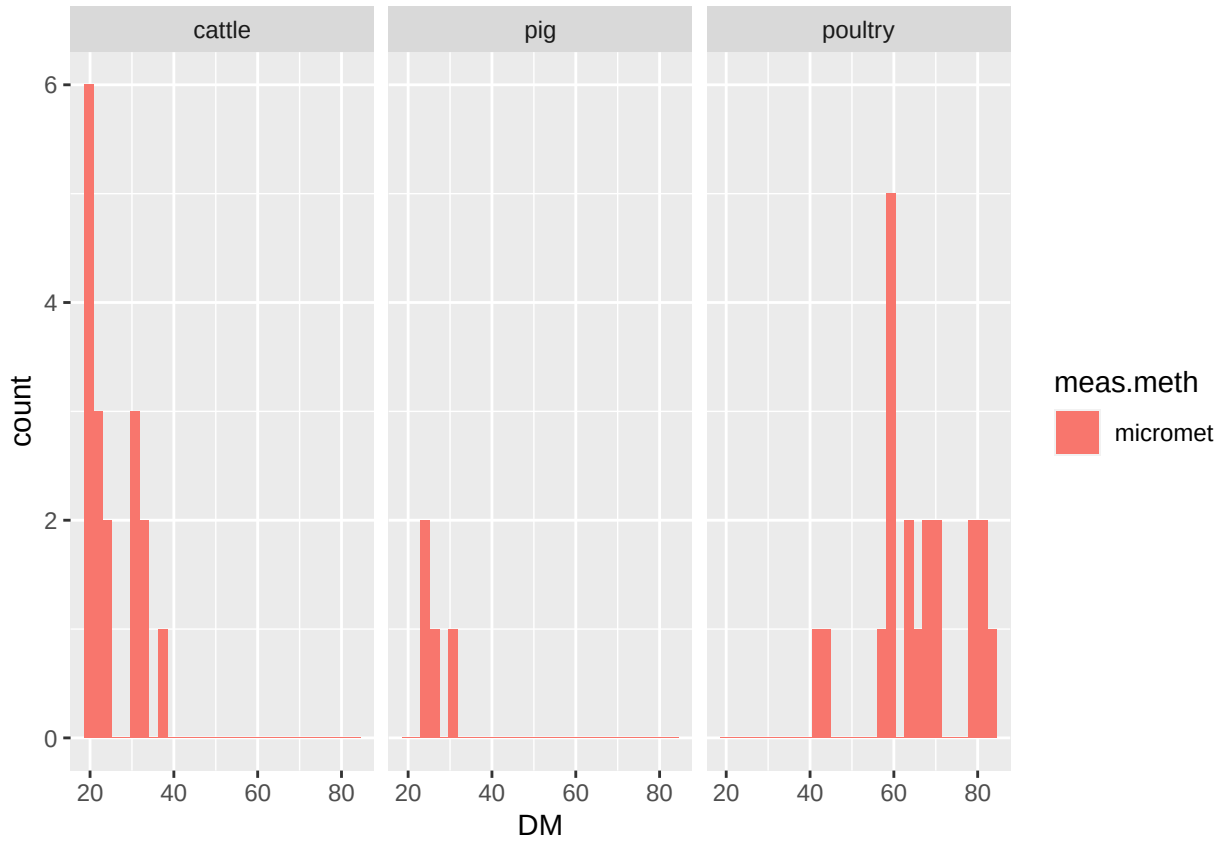



```
ggplot(datmm, aes(emis.perc.N, fill = incorp)) +
  geom_histogram(bins = 10) +
  facet_wrap(~ manure.source, scales = 'fixed')
```



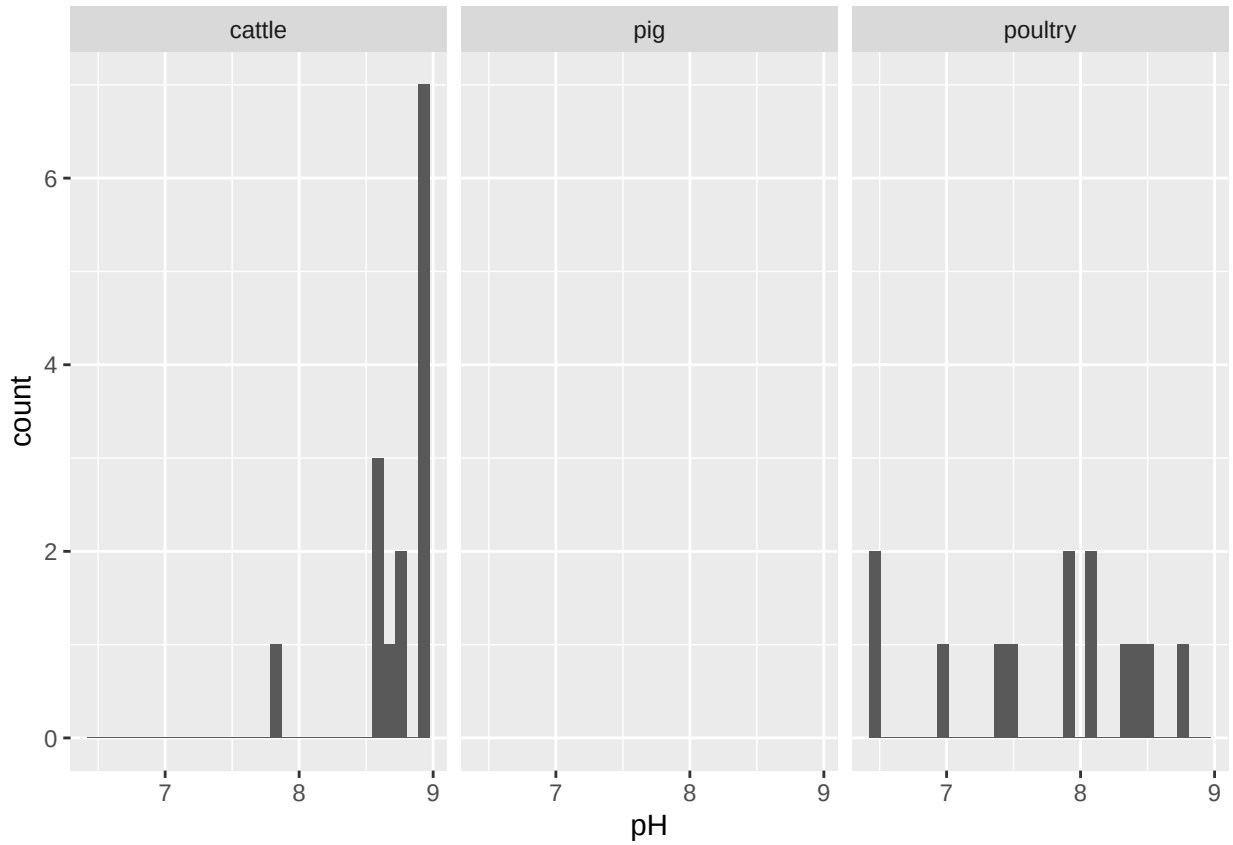

```
ggplot(datmm, aes(DM, fill = meas.meth)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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



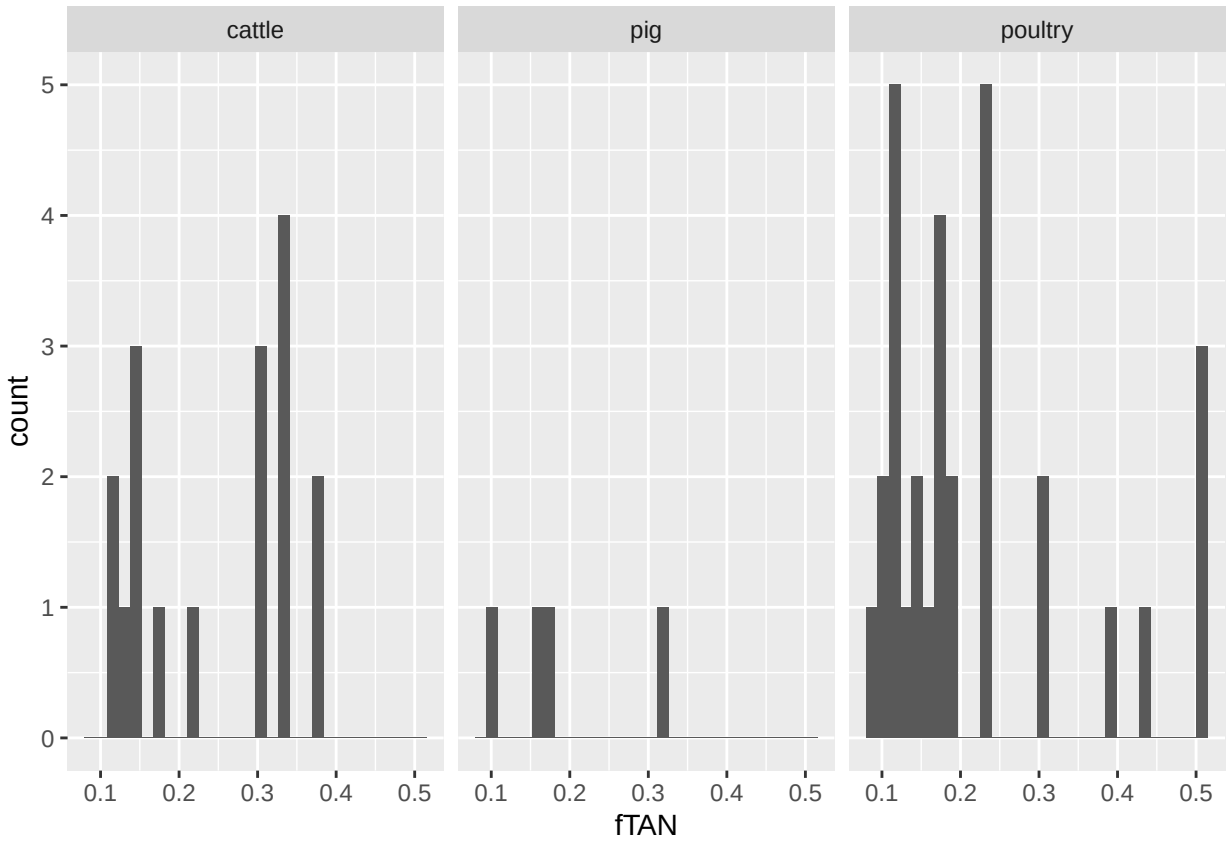

```
ggplot(datmm, aes(pH)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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




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

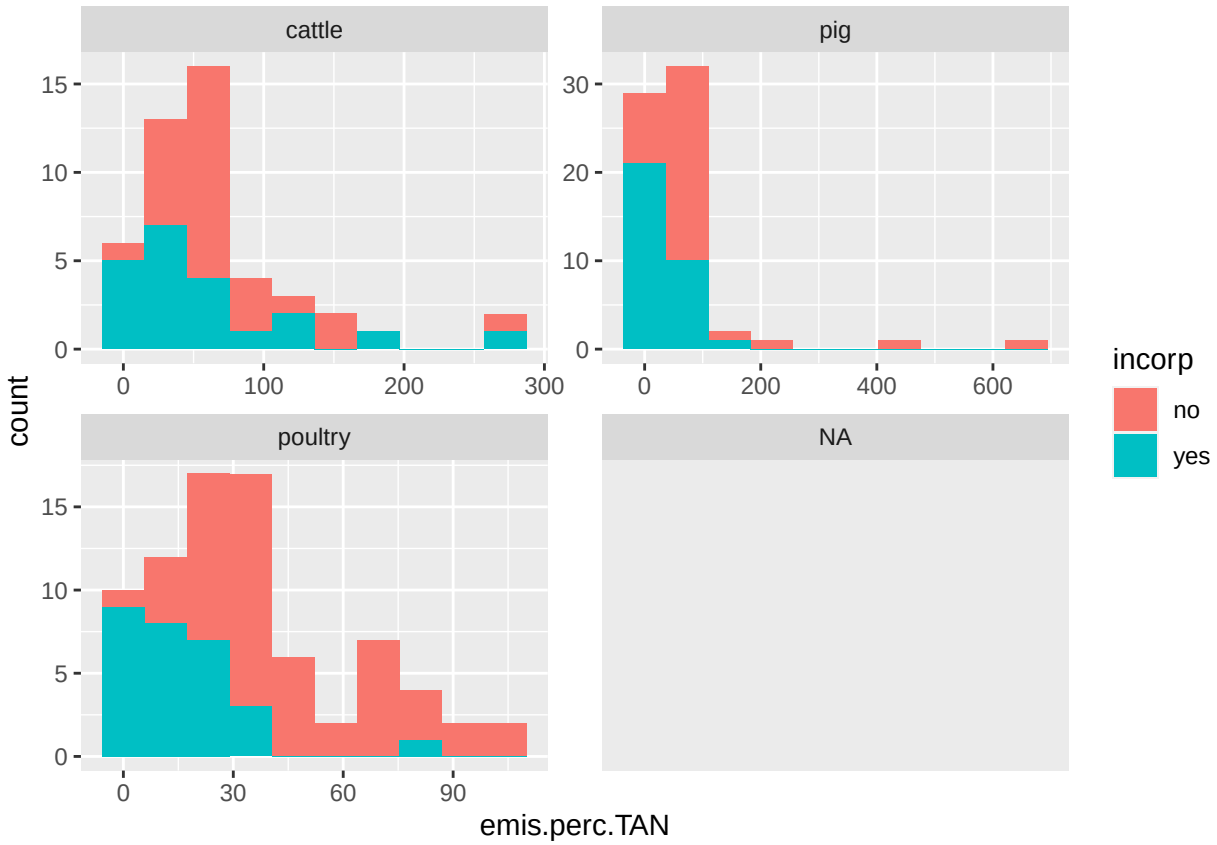
```
## Warning: Removed 2 rows containing non-finite values (`stat_bin()`).
```



Emission factors and other variables for all observations

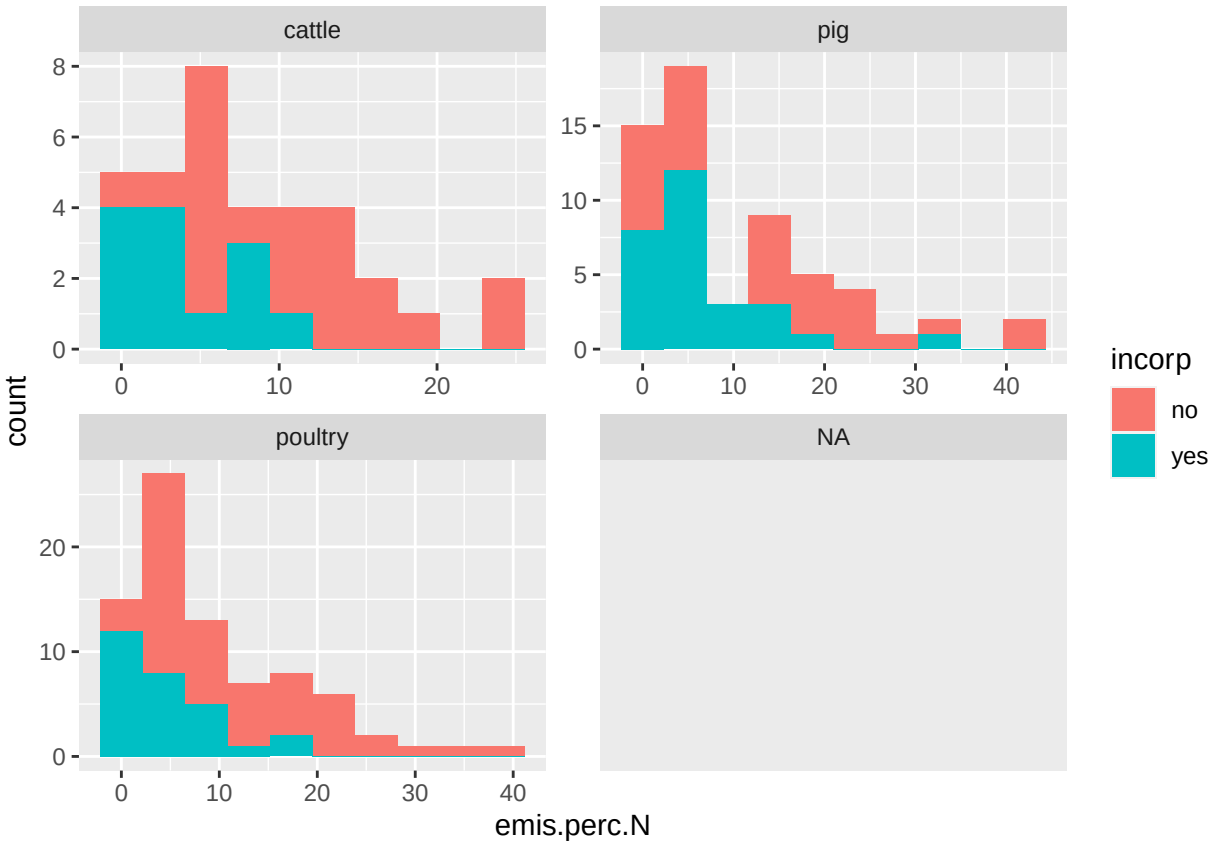
```
ggplot(dat, aes(emis.perc.TAN, fill = incorp)) +
  geom_histogram(bins = 10) +
  facet_wrap(~ manure.source, scales = 'free')
```

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



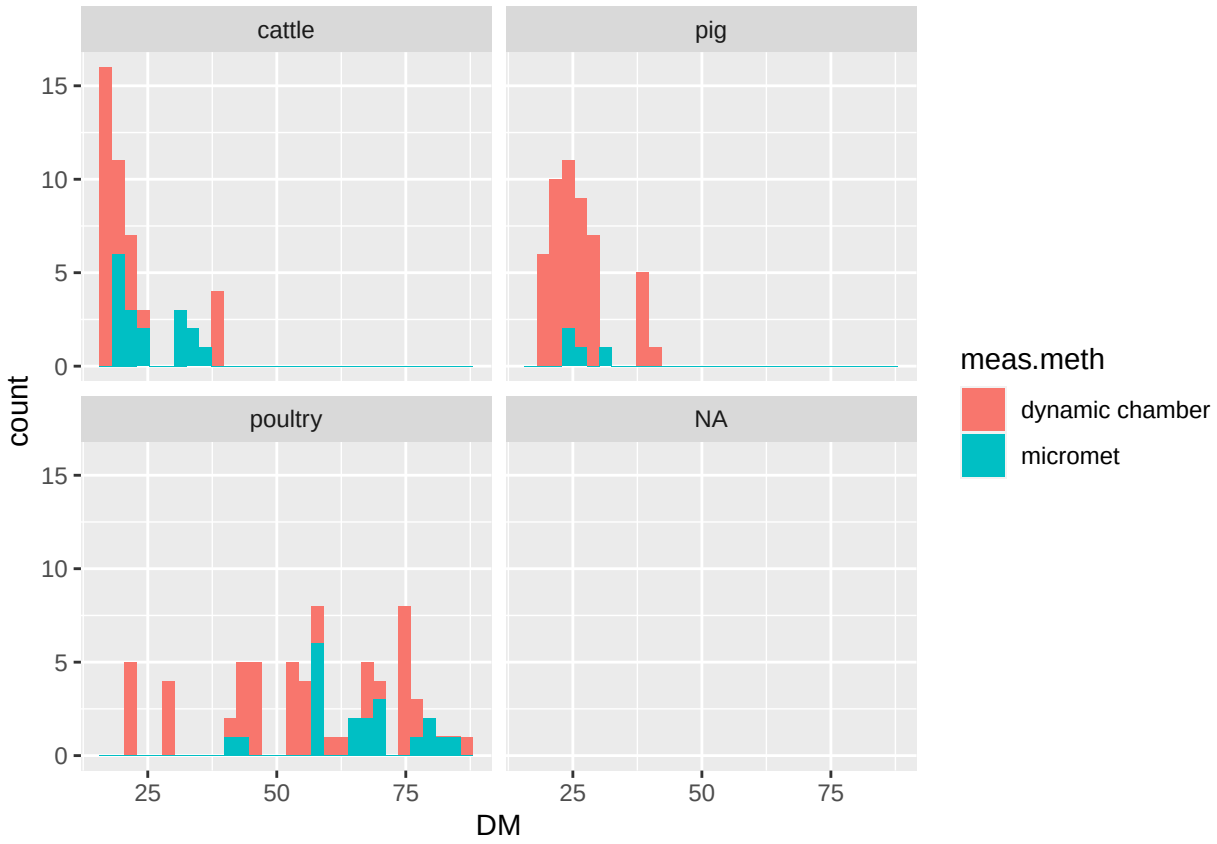

```
ggplot(dat, aes(emis.perc.N, fill = incorp)) +
  geom_histogram(bins = 10) +
  facet_wrap(~ manure.source, scales = 'free')
```

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



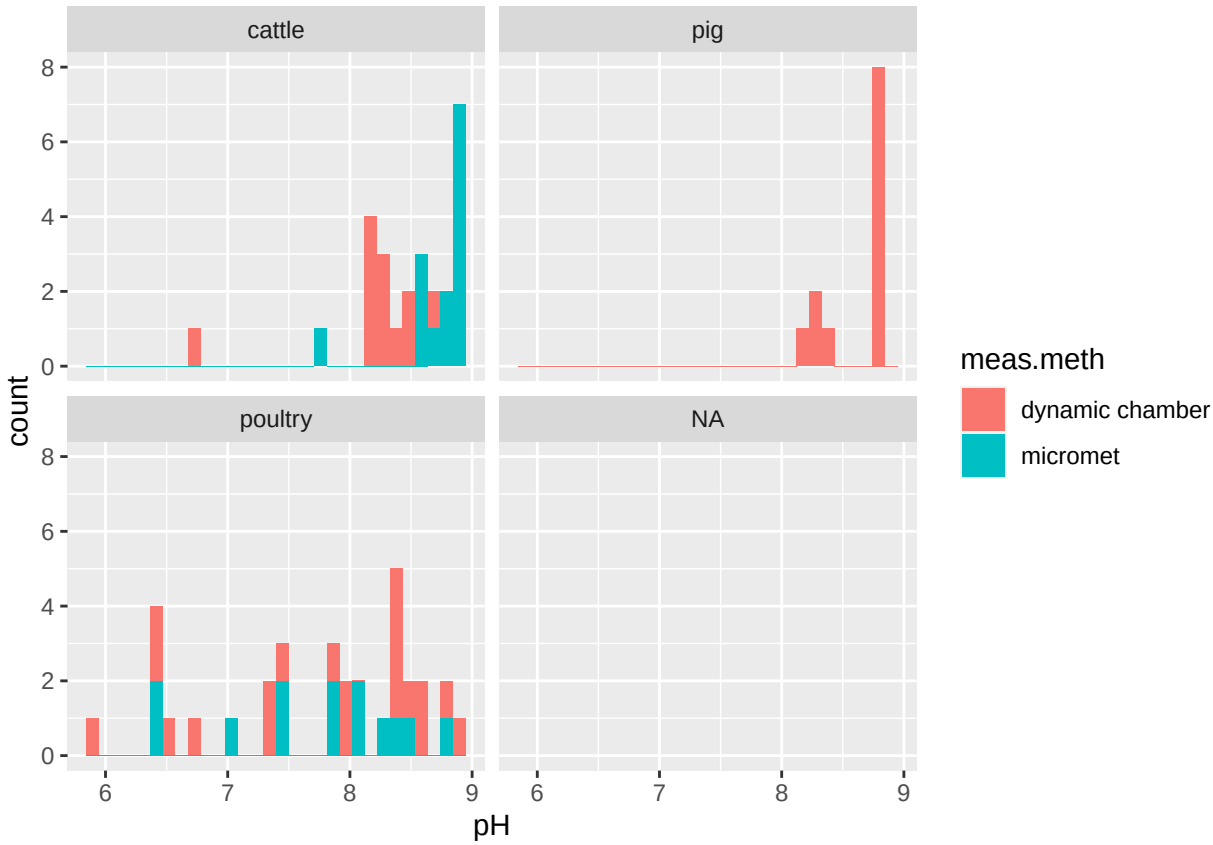

```
ggplot(dat, aes(DM, fill = meas.meth)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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



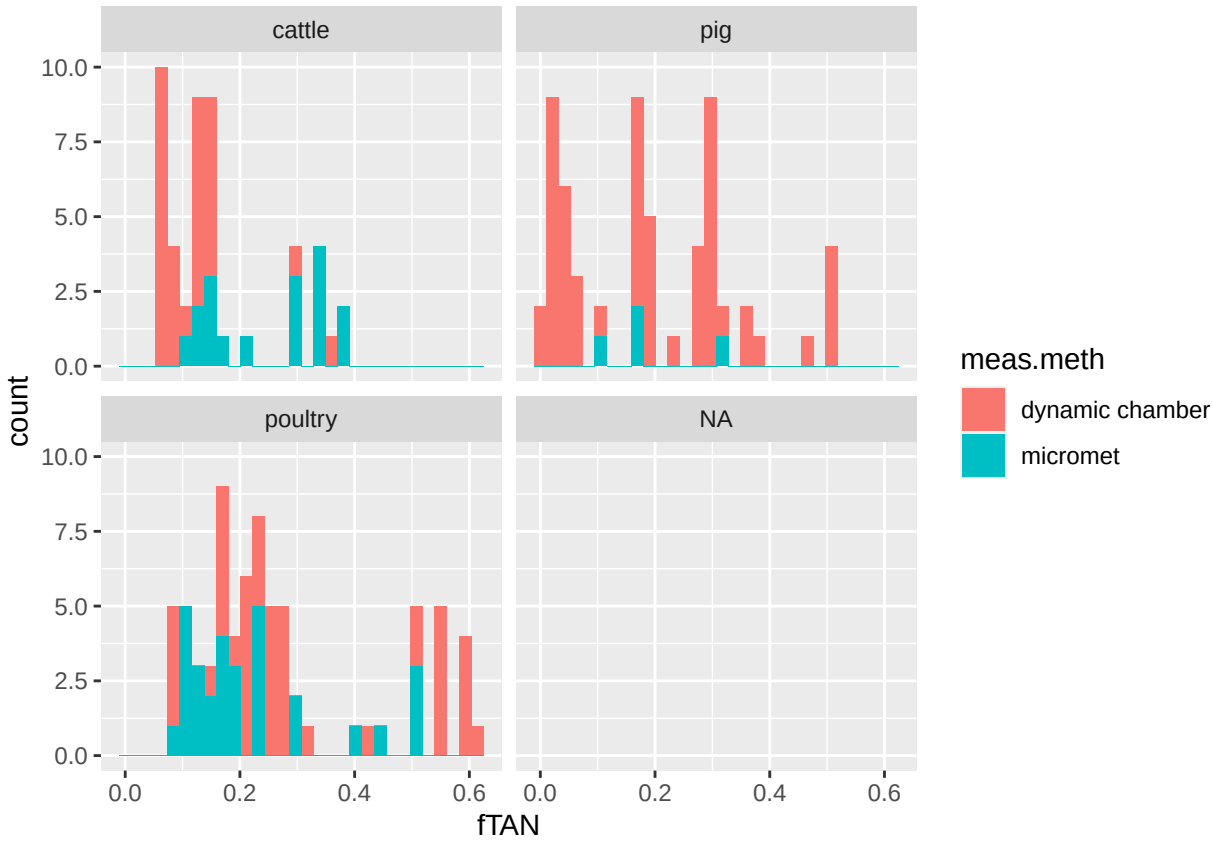

```
ggplot(dat, aes(pH, fill = meas.meth)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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



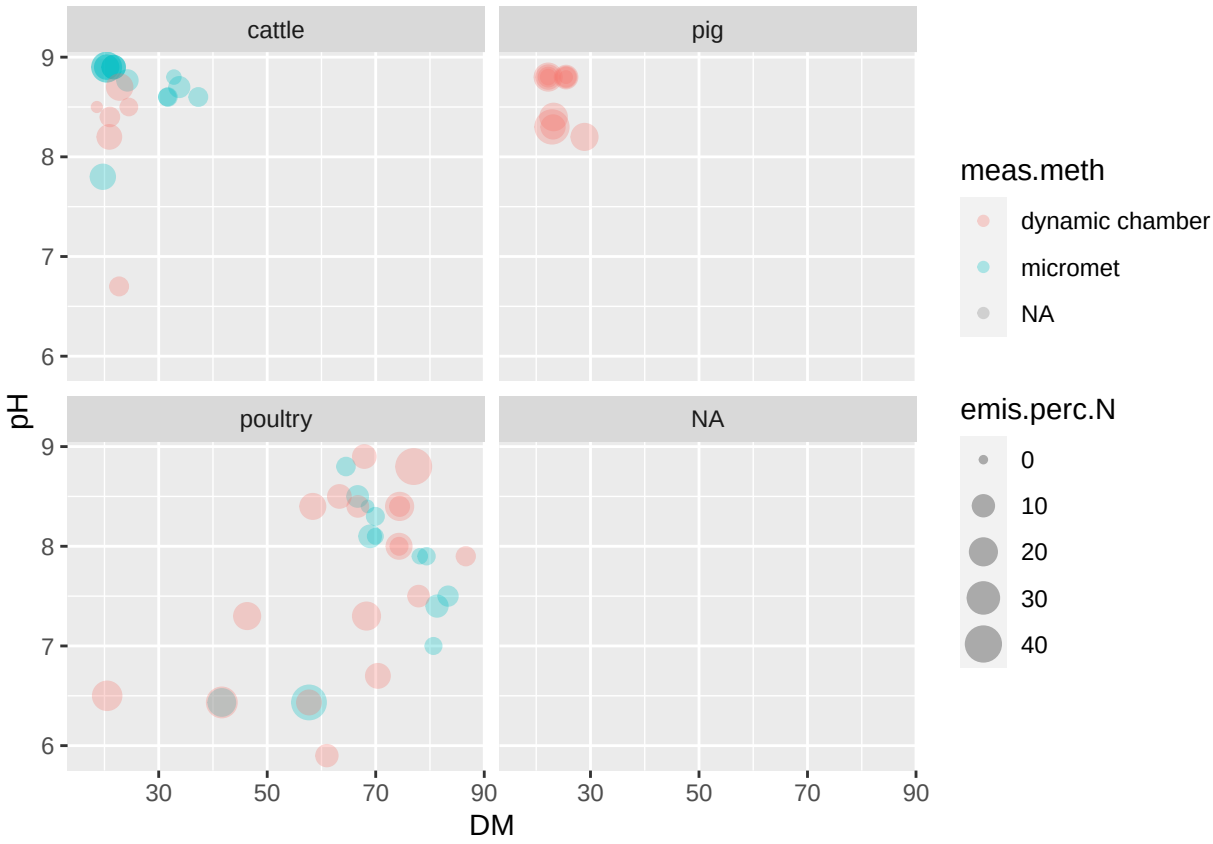

```
ggplot(dat, aes(fTAN, fill = meas.meth)) +
  geom_histogram(bins = 30) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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



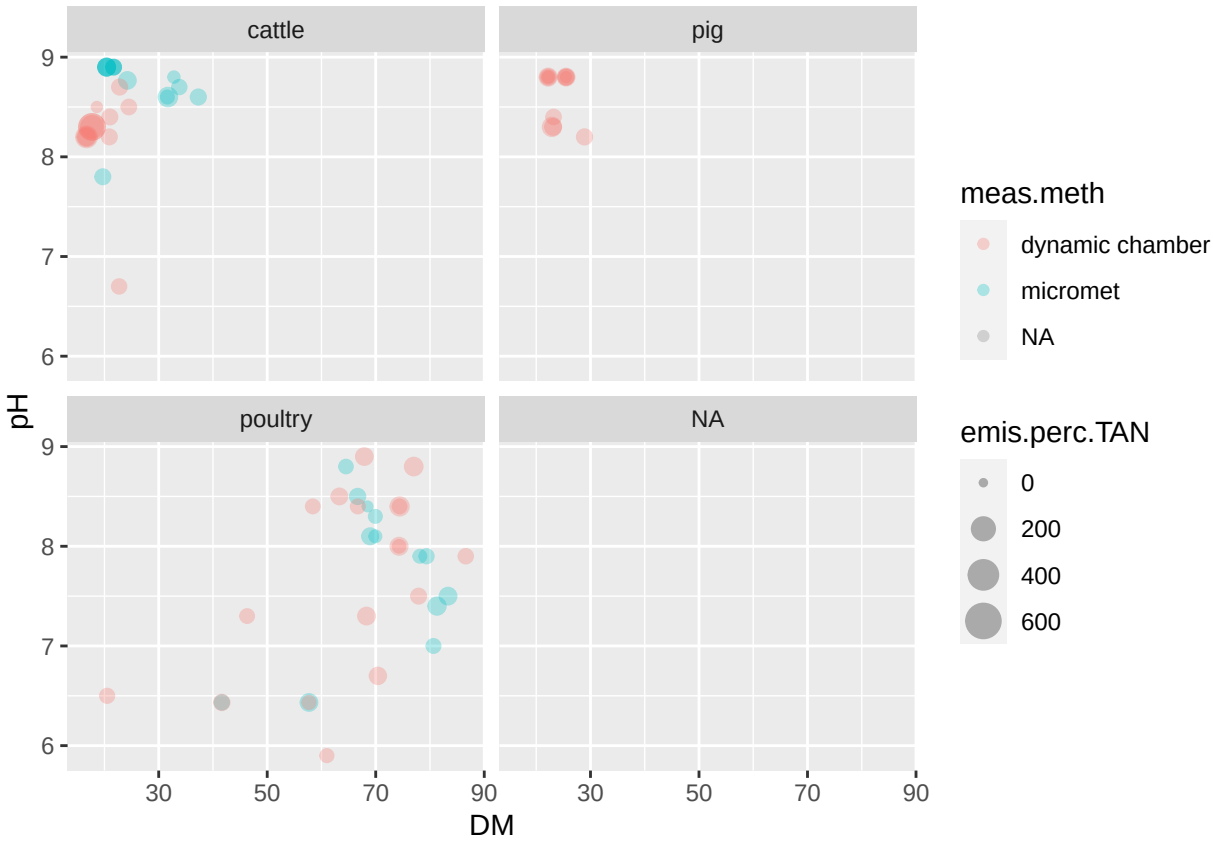

```
ggplot(dat, aes(DM, pH, size = emis.perc.N, colour = meas.meth)) +
  geom_point(alpha = 0.3) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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



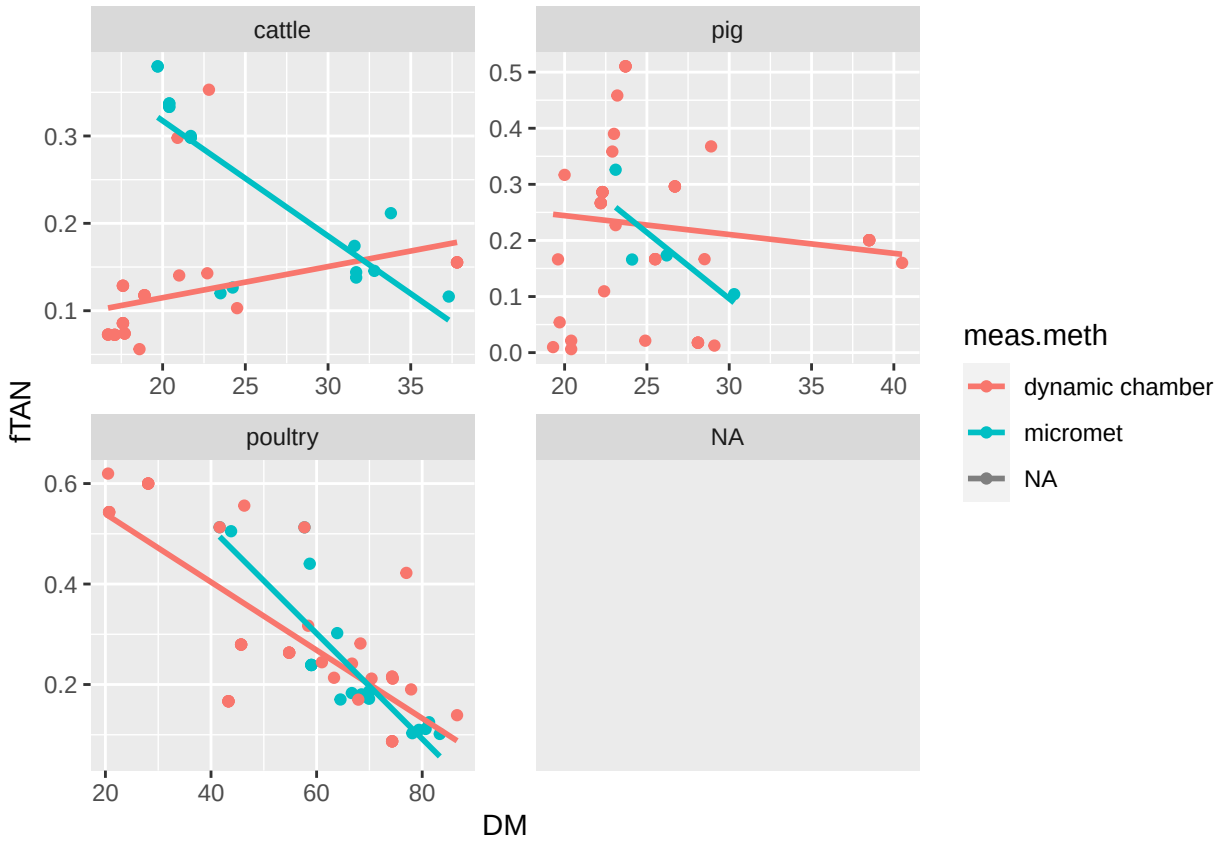

```
ggplot(dat, aes(DM, pH, size = emis.perc.TAN, colour = meas.meth)) +
  geom_point(alpha = 0.3) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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



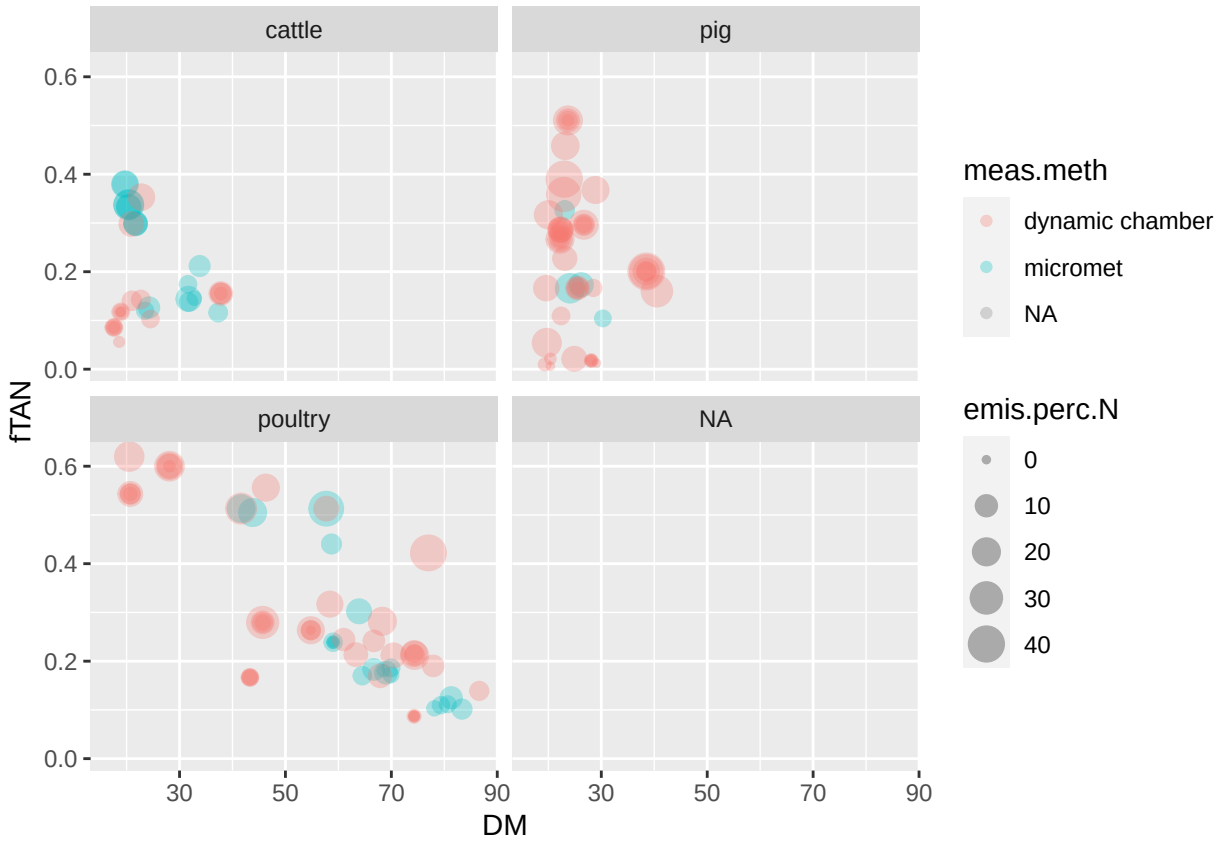

```
ggplot(dat, aes(DM, fTAN, colour = meas.meth)) +
  geom_point() +
  geom_smooth(method = lm, se = FALSE) +
  facet_wrap(~ manure.source, scales = 'free')
```

```
## `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()`).
```



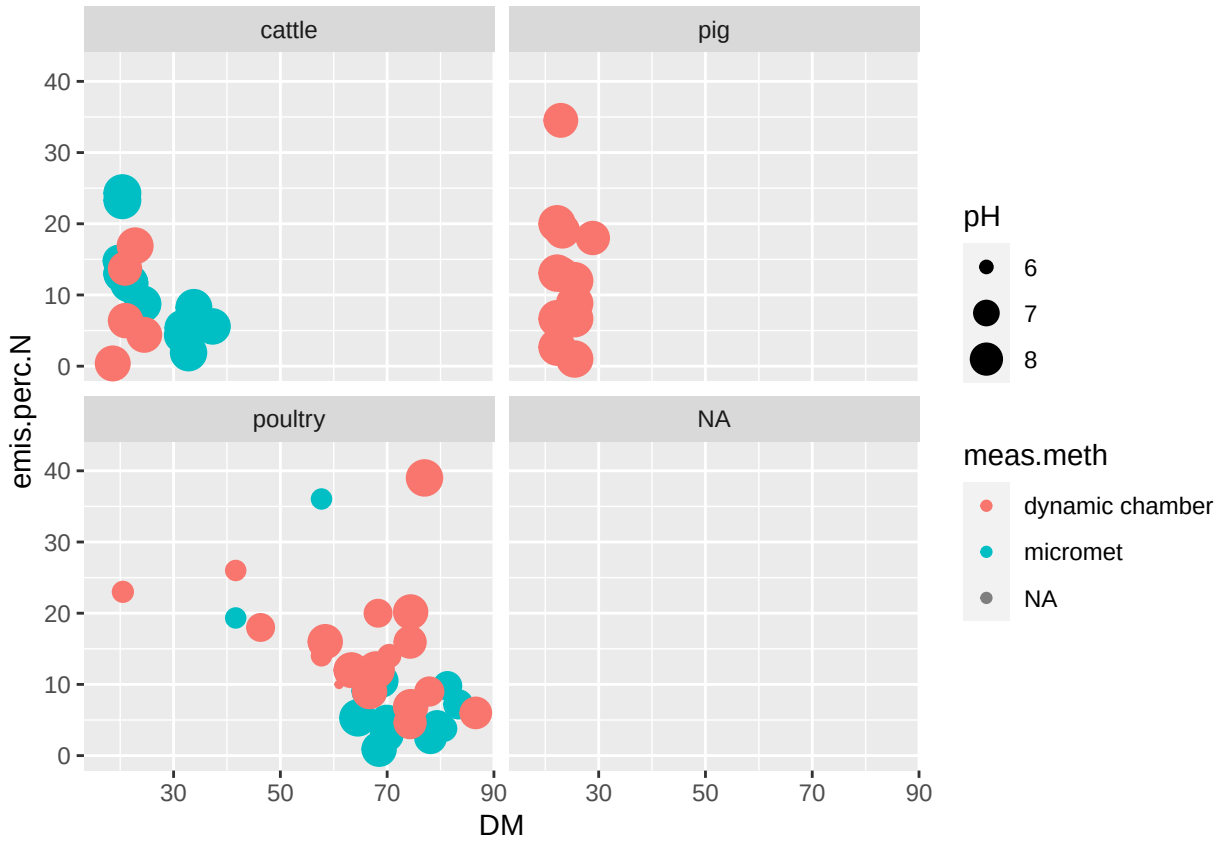

```
ggplot(dat, aes(DM, fTAN, size = emis.perc.N, colour = meas.meth)) +
  geom_point(alpha = 0.3) +
  facet_wrap(~ manure.source, scales = 'fixed')
```

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



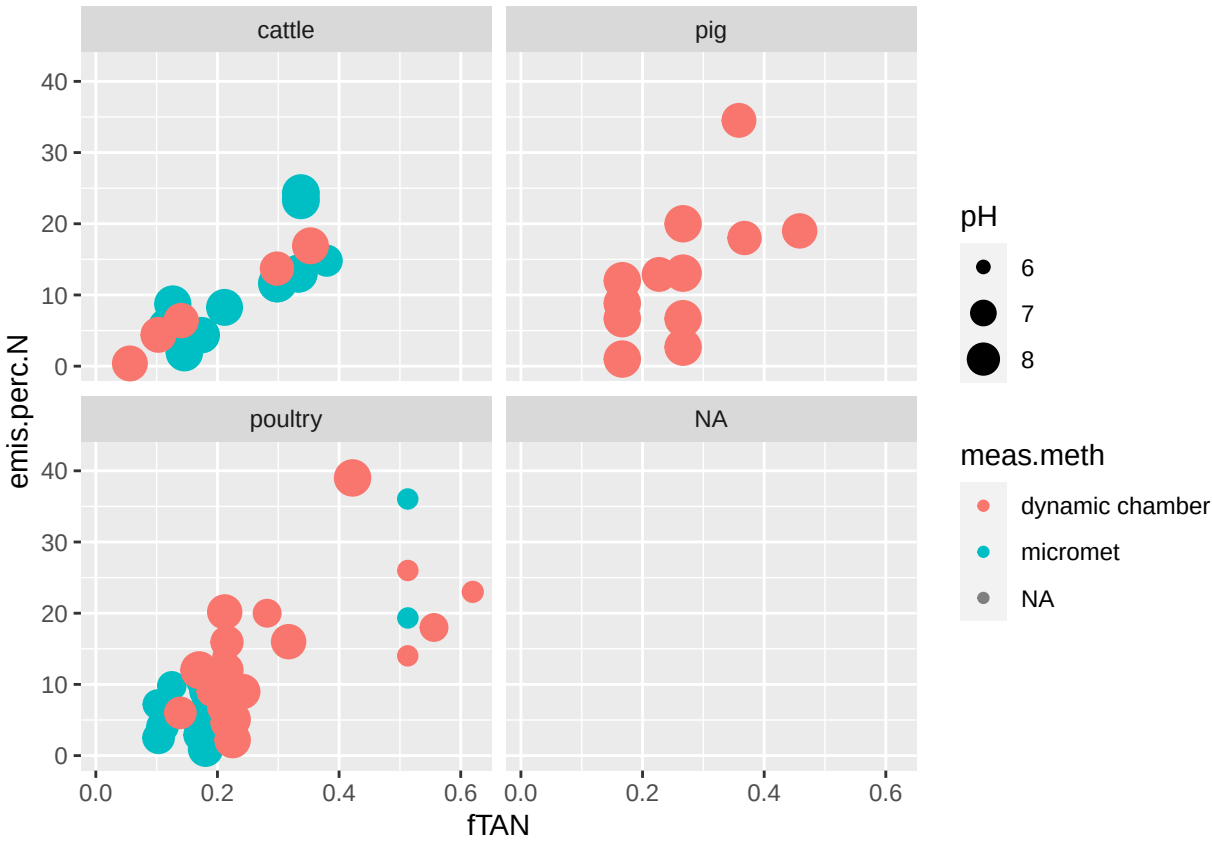

```
ggplot(dat, aes(DM, emis.perc.N, size = pH, colour = meas.meth)) +
  geom_point() +
  facet_wrap(~ manure.source, scales = 'fixed')
```

```
## 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
##                                    source abs.emis.info incorp.info
## Class                           character       numeric     numeric
## Minimum            Balsari et al. (2008a)             0           0
## Maximum            Williams et al. (2003)             1           1
## Mean                                 <NA>         0.242       0.598
## Unique (excld. NA)                     25             2           2
## Missing values                          1             1           1
## Sorted                              FALSE         FALSE       FALSE
##
##                     timing.info                 location manure.source
## Class                   numeric                character     character
## Minimum                       0 Canada, British Colombia        cattle
## Maximum                       1                       UK       poultry
## Mean                      0.469                     <NA>          <NA>
## Unique (excld. NA)            2                       11             3
## Missing values                1                        1             1
## Sorted                    FALSE                    FALSE         FALSE
##
##                         man.type manure.source.det       meas.meth
```

```
## Class                  character         character       character
## Minimum            broiler litter              beef dynamic chamber
## Maximum                   solid            turkey        micromet
## Mean                      <NA>              <NA>            <NA>
## Unique (excld. NA)           8                 5               2
## Missing values              32               126               1
## Sorted                   FALSE             FALSE           FALSE
##
##                    meas.meth.det meas.scale  duration house.inf
## Class                  character  character character character
## Minimum                      IHF field plot       120   outdoor
## Maximum            wind tunnel laboratory        96   outdoor
## Mean                        <NA>       <NA>      <NA>      <NA>
## Unique (excld. NA)             4          2        19         1
## Missing values                37          1        33       193
## Sorted                     FALSE      FALSE     FALSE      TRUE
##
##                                      stor.meth  stor.cov    stor.cov.type
## Class                                character character        character
## Minimum            1 L container, 5C, laboratory        no plastic sheeting
## Maximum                                stockpile       yes plastic sheeting
## Mean                                       <NA>      <NA>              <NA>
## Unique (excld. NA)                            8         2                 1
## Missing values                              129       161               182
## Sorted                                    FALSE     FALSE              TRUE
##
##                       stor.length man.treat      DM      pH     TAN    totN
## Class                   character character numeric numeric numeric numeric
## Minimum                         0    wetted    16.7     5.9  0.0389     2.1
## Maximum            several months    wetted    86.6     8.9    18.9    59.3
## Mean                        <NA>      <NA>    37.7    8.17    3.15    14.2
## Unique (excld. NA)             7         1      80      22      96     103
## Missing values               145       193      31     124      14      12
## Sorted                     FALSE      TRUE   FALSE   FALSE   FALSE   FALSE
##
##                          X23  app.meth    incorp incorp.set
## Class                numeric character character    numeric
## Minimum                  2.6 broadcast        no          1
## Maximum                  9.4 broadcast       yes         12
## Mean                    4.68      <NA>      <NA>       4.29
## Unique (excld. NA)        13         1         2         12
## Missing values           180        23         1         80
## Sorted                 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 (excld. 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 (excld. 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 (excld. 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 (excld. 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 (excld. NA)                                     135
## Missing values                                          54
## Sorted                                               FALSE
##
##
## Class
## Minimum
## Maximum            Same data as in Sommer and Hansen (2022). Hansen and Birkmose writes that the soi
## Mean
## Unique (excld. 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 (excld. 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 (excld. NA)                  2         5         25
## Missing values                      1         0          1
## Sorted                          FALSE     FALSE      FALSE
##
```