Statistical Analyses for Van Meter et al 2016

Contents

intro

Statistical analysis and results presentation and discussion for total concentrations of parent active ingredients (atrazine, imidacloprid, fipronil, triadimenon, pendimethalin).

```
## [1] "R version 3.0.2 (2013-09-25)"
```

```
##
## Attaching package: 'dplyr'
##
## The following object is masked from 'package:MASS':
##
##     select
##
## The following objects are masked from 'package:stats':
##
##     filter, lag
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

data prep

```
##  [1] "Day"         "Row"         "Column"      "Pesticide"   "SoilType"
##  [6] "BodyBurden"  "Soil"        "Weight"      "Total"       "Formulation"
## [11] "Parent"
```

```
## [1] "integer"

##   [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
##  [36] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
##  [71] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
## [106] 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
## [141] 3 3 3 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
## [176] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
## [211] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
## [246] 3 3 3 3 3 3 3 0 0 0 0 1 1 1 1 1 1 1 1
## Levels: 0 1 2 3

## [1] "integer"

##   [1] 1 1 3 5 6 7 1 2 2 4 5 7 1 1 2 5 6 6 1 2 4 5 5 7 1 1 3 5 6 7 1 2 2 4 5
##  [36] 7 1 1 2 5 6 6 1 2 4 5 5 7 1 1 3 5 6 7 1 2 2 4 5 7 1 1 2 5 6 6 1 2 4 5
##  [71] 5 7 1 1 3 5 6 7 1 2 2 4 5 7 1 1 2 5 6 6 1 2 4 5 5 7 1 2 5 6 6 7 2 2 4
## [106] 4 6 7 1 1 4 7 7 7 2 3 5 6 6 7 1 1 4 7 7 7 2 3 5 6 6 7 1 1 4 7 7 7 2 3
## [141] 5 6 6 7 1 1 2 4 5 7 2 2 2 5 6 7 1 3 4 4 6 6 1 3 5 6 6 7 1 1 2 4 5 7 2
## [176] 2 2 5 6 7 1 3 4 4 6 6 1 3 5 6 6 7 1 1 2 4 5 7 2 2 2 5 6 7 1 3 4 4 6 6
## [211] 1 3 5 6 6 7 1 1 2 4 5 7 2 2 2 5 6 7 1 3 4 4 6 6 1 3 5 6 6 7 2 3 3 4 5
## [246] 7 1 3 3 5 5 5 1 1 4 7 7 7 2 3 5 6 6 7
## Levels: 1 2 3 4 5 6 7

## [1] "factor"

## [1] "factor"

## [1] "factor"

## [1] "numeric"

## [1] "numeric"

## [1] "numeric"

## [1] "integer"

##   [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0
##  [36] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##  [71] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1
## [106] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [141] 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0
## [176] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [211] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1
## [246] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## Levels: 0 1

## [1] "integer"
```

```
##   [1] 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0
##  [36] 0 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1
##  [71] 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0
## [106] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [141] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0
## [176] 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1
## [211] 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0
## [246] 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1
## Levels: 0 1
```

```
## [1] "integer"
```

```
##   [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0
##  [36] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##  [71] 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [106] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0
## [141] 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0
## [176] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [211] 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [246] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## Levels: 0 1
```

koc data

```
##  [1] ATZTOT   ATZDEA   STAUGDEA ATZDIA   STAUGDIA ATZ      Imid
##  [8] FipTOT   Fip      FipS     TNDTOT   TDLA     STRIKEA  TDLB
## [15] STRIKEB  TDN      Pendi
## 17 Levels: ATZ ATZDEA ATZDIA ATZTOT Fip FipS FipTOT Imid ... TNDTOT
```

```
## [1] PLE OLS
## Levels: OLS PLE
```

summary stats for exposure data

Summary statistics for data set.

```
str(frog.soil)
```

```
## 'data.frame':    264 obs. of  16 variables:
##  $ Pesticide             : Factor w/ 17 levels "ATZ","ATZDEA",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ SoilType              : Factor w/ 2 levels "OLS","PLE": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Day                   : Factor w/ 4 levels "0","1","2","3": 3 3 3 3 3 3 3 3 3 3 ...
##  $ Row                   : Factor w/ 7 levels "1","2","3","4",..: 2 4 5 7 1 2 4 5 5 7 ...
##  $ Column                : Factor w/ 10 levels "","A","B","C",..: 10 3 9 6 6 8 10 2 8 5 ...
##  $ BodyBurden            : num  0.728 0.27 0.237 1.9 0.566 ...
##  $ Soil                  : num  16.6 12.3 21.6 29.2 14.2 ...
##  $ Weight                : num  11.1 12 17.4 11.8 11.1 ...
##  $ Total                 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Formulation           : Factor w/ 2 levels "0","1": 1 1 1 1 2 2 2 2 2 2 ...
```

```
##  $ Parent                : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ bowlbcf               : num  0.044 0.022 0.011 0.065 0.0398 ...
##  $ surface_area_total    : num  4.57 4.76 5.91 4.71 4.55 ...
##  $ surface_area_footprint: num  3.3 3.5 4.82 3.46 3.28 ...
##  $ expKoc                : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ litKoc                : num  NA NA NA NA NA NA NA NA NA NA ...
```

```
head(frog.soil)
```

```
##   Pesticide SoilType Day Row Column BodyBurden     Soil  Weight Total
## 1       ATZ      OLS   2   2      I  0.7282998 16.55151 11.1447     0
## 2       ATZ      OLS   2   4      B  0.2703513 12.28110 11.9615     0
## 3       ATZ      OLS   2   5      H  0.2365494 21.60190 17.3882     0
## 4       ATZ      OLS   2   7      E  1.8995641 29.24066 11.7687     0
## 5       ATZ      OLS   2   1      E  0.5662302 14.23919 11.0822     0
## 6       ATZ      OLS   2   2      G  1.9850391 19.48325 10.0690     0
##   Formulation Parent    bowlbcf surface_area_total surface_area_footprint
## 1           0      1 0.04400201           4.567885               3.299112
## 2           0      1 0.02201361           4.758833               3.503537
## 3           0      1 0.01095040           5.909763               4.815101
## 4           0      1 0.06496310           4.714269               3.455478
## 5           1      1 0.03976562           4.553036               3.283379
## 6           1      1 0.10188442           4.307167               3.026407
##   expKoc litKoc
## 1     NA     NA
## 2     NA     NA
## 3     NA     NA
## 4     NA     NA
## 5     NA     NA
## 6     NA     NA
```

```
#View(frog.soil.total.ai)
#using dplyr
frog.soil.group <- group_by(frog.soil, Pesticide, SoilType, Formulation, Parent)
str(frog.soil.group)
```

```
## Classes 'grouped_df', 'tbl_df', 'tbl' and 'data.frame':  264 obs. of  16 variables:
##  $ Pesticide             : Factor w/ 17 levels "ATZ","ATZDEA",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ SoilType              : Factor w/ 2 levels "OLS","PLE": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Day                   : Factor w/ 4 levels "0","1","2","3": 3 3 3 3 3 3 3 3 3 3 ...
##  $ Row                   : Factor w/ 7 levels "1","2","3","4",..: 2 4 5 7 1 2 4 5 5 7 ...
##  $ Column                : Factor w/ 10 levels "","A","B","C",..: 10 3 9 6 6 8 10 2 8 5 ...
##  $ BodyBurden            : num  0.728 0.27 0.237 1.9 0.566 ...
##  $ Soil                  : num  16.6 12.3 21.6 29.2 14.2 ...
##  $ Weight                : num  11.1 12 17.4 11.8 11.1 ...
##  $ Total                 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Formulation           : Factor w/ 2 levels "0","1": 1 1 1 1 2 2 2 2 2 2 ...
##  $ Parent                : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ bowlbcf               : num  0.044 0.022 0.011 0.065 0.0398 ...
##  $ surface_area_total    : num  4.57 4.76 5.91 4.71 4.55 ...
##  $ surface_area_footprint: num  3.3 3.5 4.82 3.46 3.28 ...
##  $ expKoc                : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ litKoc                : num  NA NA NA NA NA NA NA NA NA NA ...
```

```
##  - attr(*, "vars")=List of 4
##   ..$ : symbol Pesticide
##   ..$ : symbol SoilType
##   ..$ : symbol Formulation
##   ..$ : symbol Parent
##  - attr(*, "drop")= logi TRUE
##  - attr(*, "indices")=List of 44
##   ..$ : int  0 1 2 3 10 11
##   ..$ : int  4 5 6 7 8 9
##   ..$ : int  18 19 20 21 22 23
##   ..$ : int  12 13 14 15 16 17
##   ..$ : int  24 25 26 27 28 29
##   ..$ : int  30 31 32 33 34 35
##   ..$ : int  36 37 38 39 40 41
##   ..$ : int  42 43 44 45 46 47
##   ..$ : int  48 49 56 57 58 59
##   ..$ : int  50 51 52 53 54 55
##   ..$ : int  60 61 62 63 64 65
##   ..$ : int  66 67 68 69 70 71
##   ..$ : int  72 73 74 75 76 77
##   ..$ : int  78 79 80 81 82 83
##   ..$ : int  84 85 86 87 88 89
##   ..$ : int  90 91 92 93 94 95
##   ..$ : int  96 97 98 99 100 101
##   ..$ : int  102 103 104 105 106 107
##   ..$ : int  108 109 110 111 112 113
##   ..$ : int  114 115 116 117 118 119
##   ..$ : int  120 121 122 123 124 125
##   ..$ : int  126 127 128 129 130 131
##   ..$ : int  132 133 134 135 136 137
##   ..$ : int  138 139 140 141 142 143
##   ..$ : int  144 145 146 147 148 149
##   ..$ : int  150 151 152 153 154 155
##   ..$ : int  156 157 158 159 160 161
##   ..$ : int  162 163 164 165 166 167
##   ..$ : int  168 169 170 171 172 173
##   ..$ : int  174 175 176 177 178 179
##   ..$ : int  180 181 182 183 184 185
##   ..$ : int  186 187 188 189 190 191
##   ..$ : int  192 193 194 195 196 197
##   ..$ : int  198 199 200 201 202 203
##   ..$ : int  204 205 206 207 208 209
##   ..$ : int  210 211 212 213 214 215
##   ..$ : int  216 217 218 219 220 221
##   ..$ : int  222 223 224 225 226 227
##   ..$ : int  228 229 230 231 232 233
##   ..$ : int  234 235 236 237 238 239
##   ..$ : int  246 247 248 249 250 251
##   ..$ : int  240 241 242 243 244 245
##   ..$ : int  252 255 256 257 258 259
##   ..$ : int  253 254 260 261 262 263
##  - attr(*, "group_sizes")= int  6 6 6 6 6 6 6 6 6 6 ...
##  - attr(*, "biggest_group_size")= int 6
##  - attr(*, "labels")='data.frame':   44 obs. of  4 variables:
```

```
##   ..$ Pesticide  : Factor w/ 17 levels "ATZ","ATZDEA",..: 1 1 1 1 2 2 3 3 4 4 ...
##   ..$ SoilType   : Factor w/ 2 levels "OLS","PLE": 1 1 2 2 1 2 1 2 1 1 ...
##   ..$ Formulation: Factor w/ 2 levels "0","1": 1 2 1 2 1 1 1 1 1 2 ...
##   ..$ Parent     : Factor w/ 2 levels "0","1": 2 2 2 2 1 1 1 1 2 2 ...
##   ..- attr(*, "vars")=List of 4
##   .. ..$ : symbol Pesticide
##   .. ..$ : symbol SoilType
##   .. ..$ : symbol Formulation
##   .. ..$ : symbol Parent
```

```
frog.soil.group
```

```
## Source: local data frame [264 x 16]
## Groups: Pesticide, SoilType, Formulation, Parent
##
##    Pesticide SoilType Day Row Column BodyBurden      Soil  Weight Total
## 1        ATZ      OLS   2   2      I  0.7282998 16.551513 11.1447     0
## 2        ATZ      OLS   2   4      B  0.2703513 12.281098 11.9615     0
## 3        ATZ      OLS   2   5      H  0.2365494 21.601898 17.3882     0
## 4        ATZ      OLS   2   7      E  1.8995641 29.240663 11.7687     0
## 5        ATZ      OLS   2   1      E  0.5662302 14.239191 11.0822     0
## 6        ATZ      OLS   2   2      G  1.9850391 19.483245 10.0690     0
## 7        ATZ      OLS   2   4      I  0.2670444 18.094682 11.0174     0
## 8        ATZ      OLS   2   5      A  0.2356130 18.492963 12.3638     0
## 9        ATZ      OLS   2   5      G  0.3124082  7.940987 10.1878     0
## 10       ATZ      OLS   2   7      D  0.2438387 16.933410 11.5272     0
## ..       ...      ... ... ...    ...        ...       ...     ...   ...
## Variables not shown: Formulation (fctr), Parent (fctr), bowlbcf (dbl),
##   surface_area_total (dbl), surface_area_footprint (dbl), expKoc (dbl),
##   litKoc (dbl)
```

```
frog.soil.means <- summarise(frog.soil.group,
            count = n(),
            FrogMean = mean(BodyBurden),
            FrogSD = sd(BodyBurden),
            SoilMean = mean(Soil),
            SoilSD = sd(Soil)
  )
frog.soil.means
```

```
## Source: local data frame [44 x 9]
## Groups: Pesticide, SoilType, Formulation
##
##    Pesticide SoilType Formulation Parent count   FrogMean      FrogSD
## 1        ATZ      OLS           0      1     6 0.81375385 0.654947835
## 2        ATZ      OLS           1      1     6 0.60169561 0.688861900
## 3        ATZ      PLE           0      1     6 0.43815022 0.230781640
## 4        ATZ      PLE           1      1     6 0.52394830 0.336497915
## 5     ATZDEA      OLS           0      0     6 0.56841980 0.853934956
## 6     ATZDEA      PLE           0      0     6 0.11582458 0.098357479
## 7     ATZDIA      OLS           0      0     6 0.56823951 0.846310211
## 8     ATZDIA      PLE           0      0     6 0.07990814 0.074451822
## 9     ATZTOT      OLS           0      1     6 1.95041316 2.301128614
```

```
## 10    ATZTOT      OLS           1      1     6 0.82672856 0.663118510
## 11    ATZTOT      PLE           0      1     6 0.63388293 0.354753198
## 12    ATZTOT      PLE           1      1     6 0.69718557 0.337418123
## 13       Fip      OLS           0      1     6 0.09692212 0.050364156
## 14       Fip      PLE           0      1     6 0.05474889 0.033710850
## 15      FipS      OLS           0      0     6 0.06154416 0.031688542
## 16      FipS      PLE           0      0     6 0.03365841 0.025023420
## 17    FipTOT      OLS           0      1     6 0.15846628 0.078824431
## 18    FipTOT      PLE           0      1     6 0.08840730 0.055028527
## 19      Imid      OLS           0      1     6 0.03531090 0.021642805
## 20      Imid      PLE           0      1     6 0.04027054 0.025656606
## 21     Pendi      OLS           0      1     6 3.69828962 2.012556828
## 22     Pendi      OLS           1      1     6 1.73652917 1.007560748
## 23     Pendi      PLE           0      1     6 2.94789191 1.421463716
## 24     Pendi      PLE           1      1     6 3.03225651 1.606078090
## 25  STAUGDEA      OLS           1      0     6 0.09659701 0.065142138
## 26  STAUGDEA      PLE           1      0     6 0.09044778 0.036584069
## 27  STAUGDIA      OLS           1      0     6 0.12843594 0.118047484
## 28  STAUGDIA      PLE           1      0     6 0.08278948 0.026913238
## 29   STRIKEA      OLS           1      0     6 0.04013783 0.057736717
## 30   STRIKEA      PLE           1      0     6 0.01052381 0.021706468
## 31   STRIKEB      OLS           1      0     6 0.08923070 0.102226784
## 32   STRIKEB      PLE           1      0     6 0.03710196 0.041024425
## 33      TDLA      OLS           0      0     6 0.07845052 0.046822014
## 34      TDLA      PLE           0      0     6 0.02754424 0.041536786
## 35      TDLB      OLS           0      0     6 0.16031762 0.070661612
## 36      TDLB      PLE           0      0     6 0.08023899 0.054961891
## 37       TDN      OLS           0      1     6 0.08926025 0.042368742
## 38       TDN      OLS           1      1     6 0.05391972 0.007921897
## 39       TDN      PLE           0      1     6 0.07315779 0.031544457
## 40       TDN      PLE           1      1     6 0.05642193 0.024150822
## 41    TNDTOT      OLS           0      1     6 0.32802839 0.107117899
## 42    TNDTOT      OLS           1      1     6 0.18390695 0.153054256
## 43    TNDTOT      PLE           0      1     6 0.18201386 0.124224013
## 44    TNDTOT      PLE           1      1     6 0.11034839 0.063776177
## Variables not shown: SoilMean (dbl), SoilSD (dbl)
```

```
#View(frog.soil.means)

#Merge means and other statistics back into larger file.
frog.soil <- merge(frog.soil,frog.soil.means)

#treatment bcf
frog.soil$treatbcf <- frog.soil$BodyBurden/frog.soil$SoilMean
```

Setup of the main data set frog.soil:

```
dim(frog.soil)
```

```
## [1] 264  22
```

```r
str(frog.soil)
```

```
## 'data.frame':    264 obs. of  22 variables:
##  $ Pesticide             : Factor w/ 17 levels "ATZ","ATZDEA",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ SoilType              : Factor w/ 2 levels "OLS","PLE": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Formulation           : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 2 2 2 2 ...
##  $ Parent                : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ Day                   : Factor w/ 4 levels "0","1","2","3": 3 3 3 3 3 3 3 3 3 3 ...
##  $ Row                   : Factor w/ 7 levels "1","2","3","4",..: 2 4 5 7 1 2 1 2 5 7 ...
##  $ Column                : Factor w/ 10 levels "","A","B","C",..: 10 3 9 6 3 7 6 8 8 5 ...
##  $ BodyBurden            : num  0.728 0.27 0.237 1.9 0.472 ...
##  $ Soil                  : num  16.6 12.3 21.6 29.2 29.7 ...
##  $ Weight                : num  11.14 11.96 17.39 11.77 9.56 ...
##  $ Total                 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ bowlbcf               : num  0.044 0.022 0.011 0.065 0.0159 ...
##  $ surface_area_total    : num  4.57 4.76 5.91 4.71 4.18 ...
##  $ surface_area_footprint: num  3.3 3.5 4.82 3.46 2.9 ...
##  $ expKoc                : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ litKoc                : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ count                 : int  6 6 6 6 6 6 6 6 6 6 ...
##  $ FrogMean              : num  0.814 0.814 0.814 0.814 0.814 ...
##  $ FrogSD                : num  0.655 0.655 0.655 0.655 0.655 ...
##  $ SoilMean              : num  21.2 21.2 21.2 21.2 21.2 ...
##  $ SoilSD                : num  7.08 7.08 7.08 7.08 7.08 ...
##  $ treatbcf              : num  0.0344 0.0128 0.0112 0.0897 0.0223 ...
```

conditional data sets for subset analyses

Create additional subsets.

```r
## [1] 96 22
```

```r
##  [1] "Pesticide"              "SoilType"
##  [3] "Formulation"            "Parent"
##  [5] "Day"                    "Row"
##  [7] "Column"                 "BodyBurden"
##  [9] "Soil"                   "Weight"
## [11] "Total"                  "bowlbcf"
## [13] "surface_area_total"     "surface_area_footprint"
## [15] "expKoc"                 "litKoc"
## [17] "count"                  "FrogMean"
## [19] "FrogSD"                 "SoilMean"
## [21] "SoilSD"                 "treatbcf"
```

```r
## [1] 60 22
```

```r
##  [1] "Pesticide"              "SoilType"
##  [3] "Formulation"            "Parent"
##  [5] "Day"                    "Row"
##  [7] "Column"                 "BodyBurden"
```

```
##  [9] "Soil"                  "Weight"
## [11] "Total"                 "bowlbcf"
## [13] "surface_area_total"    "surface_area_footprint"
## [15] "expKoc"                "litKoc"
## [17] "count"                 "FrogMean"
## [19] "FrogSD"                "SoilMean"
## [21] "SoilSD"                "treatbcf"
```

```
## [1] 48 22
```

```
##  [1] "Pesticide"             "SoilType"
##  [3] "Formulation"           "Parent"
##  [5] "Day"                   "Row"
##  [7] "Column"                "BodyBurden"
##  [9] "Soil"                  "Weight"
## [11] "Total"                 "bowlbcf"
## [13] "surface_area_total"    "surface_area_footprint"
## [15] "expKoc"                "litKoc"
## [17] "count"                 "FrogMean"
## [19] "FrogSD"                "SoilMean"
## [21] "SoilSD"                "treatbcf"
```

statistical analyese (anova, etc.)

Analysis of total analyte concentrations data set.

```
##################
#analyses
##################
#randomized block design for bowlbcfs
bowlbcf.total.aov <- aov(bowlbcf ~ Pesticide + SoilType + Formulation +
                           surface_area_total + expKoc, data = frog.soil.total)
summary(bowlbcf.total.aov)
```

```
##                    Df Sum Sq Mean Sq F value   Pr(>F)
## Pesticide           4 0.8852 0.22130  16.231 5.76e-10 ***
## SoilType            1 0.0262 0.02617   1.919    0.169
## Formulation         1 0.0300 0.03000   2.200    0.142
## surface_area_total  1 0.0062 0.00615   0.451    0.504
## expKoc              1 0.0005 0.00051   0.038    0.847
## Residuals          87 1.1862 0.01363
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#randomized block design for bowlbcfs
treatbcf.total.aov <- aov(treatbcf ~ Pesticide + SoilType + Formulation +
                           surface_area_total + expKoc, data = frog.soil.total)
summary(treatbcf.total.aov)
```

```
##                    Df Sum Sq Mean Sq F value   Pr(>F)
## Pesticide           4 0.6790 0.16975  23.153 4.73e-13 ***
```

```
## SoilType            1 0.0131 0.01306   1.781    0.186
## Formulation         1 0.0145 0.01451   1.979    0.163
## surface_area_total  1 0.0146 0.01459   1.990    0.162
## expKoc              1 0.0077 0.00772   1.053    0.308
## Residuals          87 0.6379 0.00733
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A paired comparison design is implemented to examine the impacts of soil type and surface area. The paired comparison design is essentially a randomized block design where the blocking variable (pesticides) has size 2 and is therefore treated as a nuisance variable. This accounts for the large variation in treatment application rates across the different pesticides tested. The paired comparison design on the bowl bcf finds soil type significant, but not amphibian surface area.

We evaluate 3 different ways: with bowlbcfs, where each frog tissue concentration is divided by its soil concentration, mean bcf, where each frog tissue concentration is divided by the mean of the soil concentrations for that treatment, and by body.burden where soil concentration is used as an additional covariate.

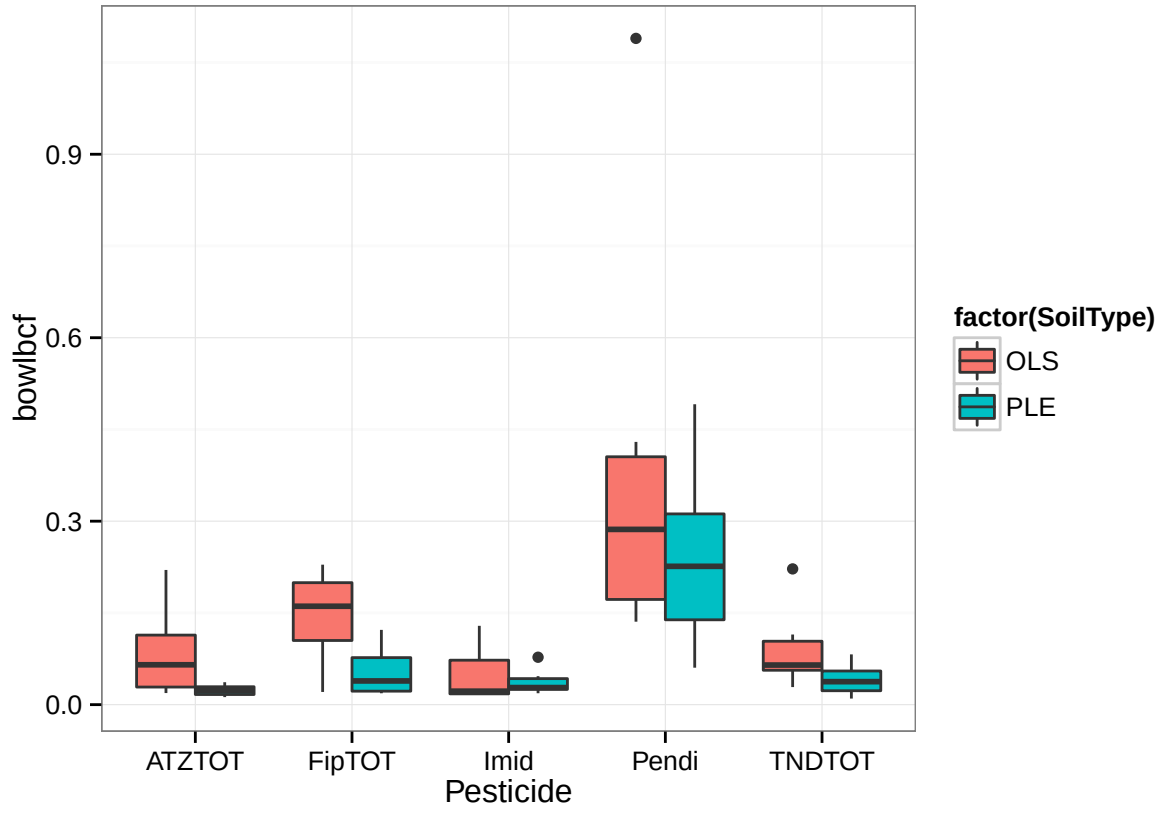
```
# is imidacloprid being factored in correctly for the aov
bowlbcf.total.ai.aov <- aov(bowlbcf ~ Pesticide + SoilType + surface_area_total + expKoc,
                            data = frog.soil.total.ai)
summary(bowlbcf.total.ai.aov)
```

```
##                    Df Sum Sq Mean Sq F value   Pr(>F)
## Pesticide           4 0.6372 0.15929   9.456 8.03e-06 ***
## SoilType            1 0.0821 0.08211   4.875   0.0317 *
## surface_area_total  1 0.0015 0.00154   0.091   0.7638
## expKoc              1 0.0304 0.03035   1.802   0.1853
## Residuals          52 0.8759 0.01684
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# more significant if imidacloprid is dropped (but not necessary)
bowlbcf.total.noimid.aov <- aov(bowlbcf ~ Pesticide + SoilType + surface_area_total,
                                data = frog.soil.total.noimid)
summary(bowlbcf.total.noimid.aov)
```

```
##                    Df Sum Sq Mean Sq F value   Pr(>F)
## Pesticide           3 0.5563 0.18543   8.857 0.000115 ***
## SoilType            1 0.0961 0.09613   4.592 0.037968 *
## surface_area_total  1 0.0001 0.00013   0.006 0.936840
## Residuals          42 0.8793 0.02094
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
qplot(Pesticide, bowlbcf, fill=factor(SoilType), data=frog.soil.total.ai, geom="boxplot", position="dod
```




```
#### the winner - aov and boxplot for Van Meter et al. ##############################
#bcfs found by dividing the frog of each experimental unit by the average concentration
#of the soil over the treatment
treatbcf.total.ai.aov <- aov(treatbcf ~ Pesticide + SoilType + expKoc,
                             data = frog.soil.total.ai)
summary(treatbcf.total.ai.aov)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## Pesticide    4 0.4257 0.10642  18.180 1.87e-09 ***
## SoilType     1 0.0644 0.06438  10.999  0.00165 **
## expKoc       1 0.0201 0.02012   3.438  0.06928 .
## Residuals   53 0.3102 0.00585
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
model.tables(treatbcf.total.ai.aov)
```

```
## Warning in replications(paste("~", xx), data = mf): non-factors ignored:
## expKoc
```

```
## Tables of effects
##
##  Pesticide
## Pesticide
```

```
##   ATZTOT   FipTOT     Imid    Pendi   TNDTOT
## -0.04343 -0.00611 -0.06732  0.16376 -0.04691
##
##  SoilType
## SoilType
##      OLS      PLE
##  0.03276 -0.03276
##
##  expKoc
## expKoc
##    1.733    2.303    2.556    2.634    2.864     3.01    3.025    3.645
##  0.03371  0.01133  0.01813 -0.01133  0.00399 -0.00823  0.00823 -0.01813
##    4.242    6.425
## -0.00399 -0.03371
```

```
#for reporting - http://www.bodowinter.com/tutorial/bw_anova_general.pdf
#soiltype
# p = 0.00165, F= 10.999, df1 = 1, df2 = 53

#tukey as anova post-hoc proxy
TukeyHSD(treatbcf.total.ai.aov)
```

```
## Warning in replications(paste("~", xx), data = mf): non-factors ignored:
## expKoc
```

```
## Warning in TukeyHSD.aov(treatbcf.total.ai.aov): 'which' specified some
## non-factors which will be dropped
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = treatbcf ~ Pesticide + SoilType + expKoc, data = frog.soil.total.ai)
##
## $Pesticide
##                        diff         lwr         upr     p adj
## FipTOT-ATZTOT  0.037321911 -0.05088198  0.12552581 0.7542455
## Imid-ATZTOT   -0.023891382 -0.11209528  0.06431251 0.9394943
## Pendi-ATZTOT   0.207189936  0.11898604  0.29539383 0.0000002
## TNDTOT-ATZTOT -0.003481293 -0.09168519  0.08472260 0.9999639
## Imid-FipTOT   -0.061213293 -0.14941719  0.02699060 0.2996226
## Pendi-FipTOT   0.169868025  0.08166413  0.25807192 0.0000135
## TNDTOT-FipTOT -0.040803204 -0.12900710  0.04740069 0.6884923
## Pendi-Imid     0.231081318  0.14287742  0.31928521 0.0000000
## TNDTOT-Imid    0.020410089 -0.06779381  0.10861398 0.9652483
## TNDTOT-Pendi  -0.210671229 -0.29887512 -0.12246733 0.0000001
##
## $SoilType
##                diff        lwr         upr     p adj
## PLE-OLS -0.06551572 -0.1051385 -0.02589299 0.0016508
```

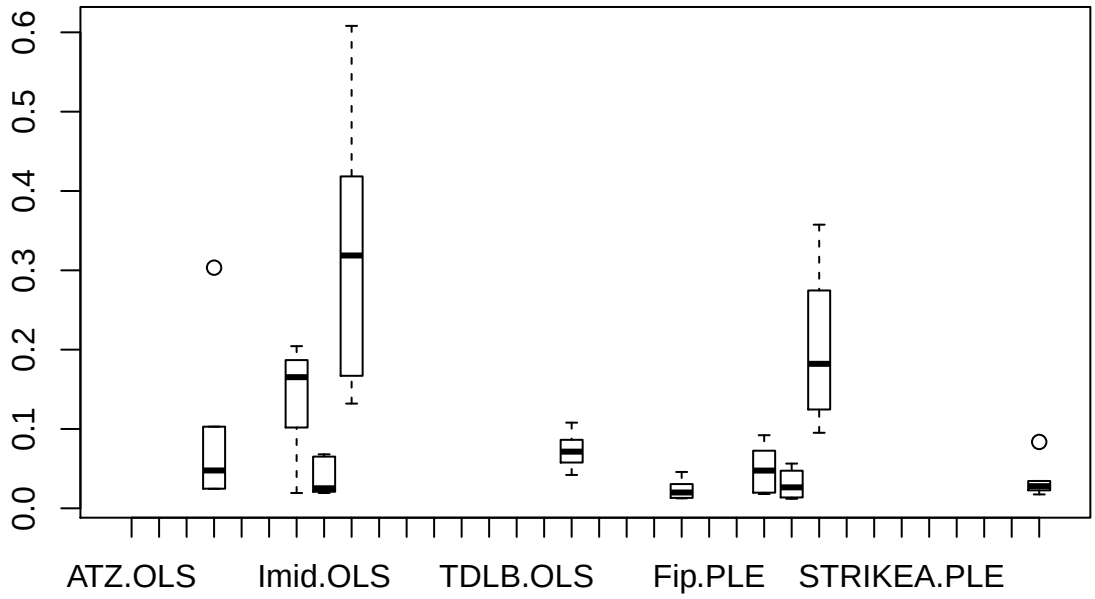
```
#figure 1 of Van Meter et al. manuscript
#pdf(paste(frogsoildir,"rvm2016_fig1.pdf", sep=""))
```

```
png(paste(frogsoildir,"rvm2016_fig1.png", sep=""))
  boxplot(treatbcf ~ Pesticide + SoilType, data =frog.soil.total.ai)
  pesticides <- c("Atrazine", "Fipronil", "Imidacloprid", "Pendimethalin", "Triadimenon")
  qplot(x=Pesticide, y=treatbcf, fill=factor(SoilType), xlab="", ylab="Bioconcentration Factor",
        data=frog.soil.total.ai, geom="boxplot", position="dodge") +
        theme_bw() +  scale_x_discrete(breaks=c("ATZTOT", "FipTOT", "Imid", "Pendi", "TNDTOT"), labels=
        guides(fill=guide_legend(title="Soil Type")) + theme(legend.position="top")
dev.off()
```

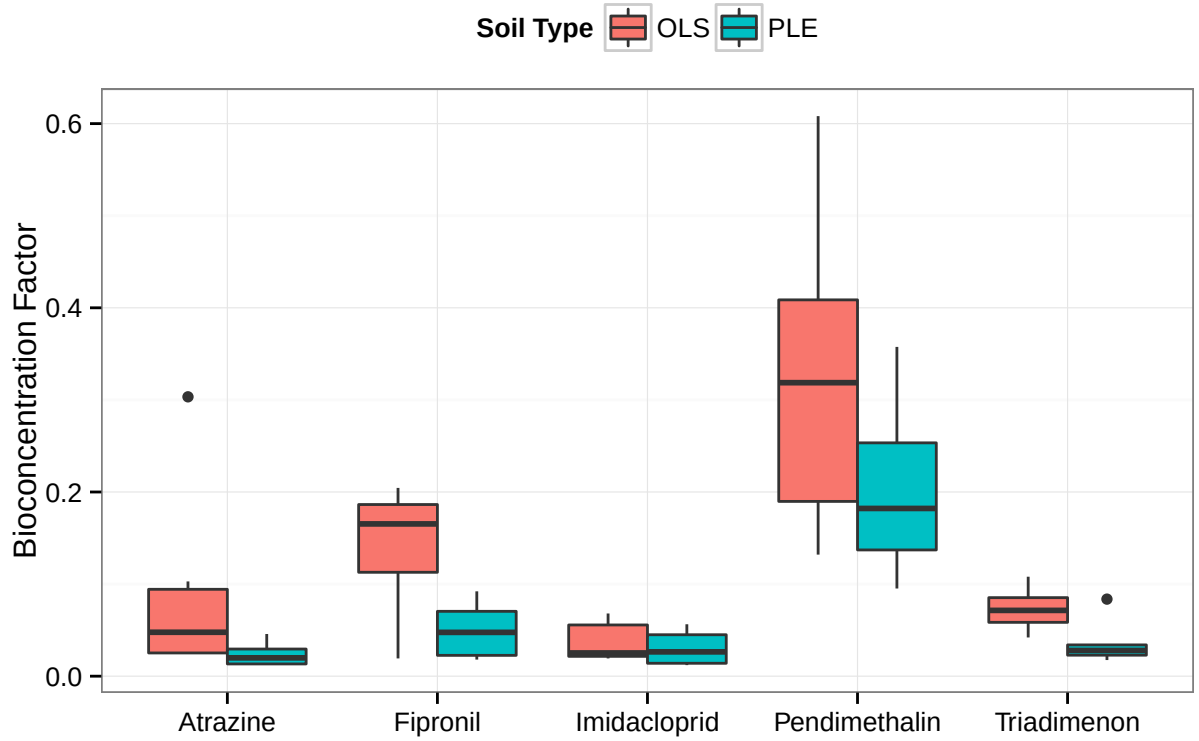
```
## pdf
##   2
```

```
####################################

  boxplot(treatbcf ~ Pesticide + SoilType, data =frog.soil.total.ai)
```




```
  pesticides <- c("Atrazine", "Fipronil", "Imidacloprid", "Pendimethalin", "Triadimenon")
  qplot(x=Pesticide, y=treatbcf, fill=factor(SoilType), xlab="", ylab="Bioconcentration Factor",
        data=frog.soil.total.ai, geom="boxplot", position="dodge") +
        theme_bw() +  scale_x_discrete(breaks=c("ATZTOT", "FipTOT", "Imid", "Pendi", "TNDTOT"), labels=
        guides(fill=guide_legend(title="Soil Type")) + theme(legend.position="top")
```



some additional stuff we did not use

```
#Bartlett test to test the null hypothesis of equal group variances
bartlett.test(treatbcf ~ Pesticide, data =frog.soil.total.ai)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  treatbcf by Pesticide
## Bartlett's K-squared = 44.5486, df = 4, p-value = 4.935e-09
```

```
#no sale! for pesticides
bartlett.test(treatbcf ~ SoilType, data = frog.soil.total.ai)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  treatbcf by SoilType
## Bartlett's K-squared = 7.5497, df = 1, p-value = 0.006002
```

```
#also rejected for soil type, but not grouped by pesticide
```

```r
#the oneway.test( ) applies a Welch correction for nonhomogeneity
oneway.test(treatbcf ~ Pesticide + SoilType, data =frog.soil.total.ai)
```

```
##
##  One-way analysis of means (not assuming equal variances)
##
## data:  treatbcf and Pesticide + SoilType
## F = 6.0442, num df = 9.000, denom df = 20.078, p-value = 0.0003999
```

```r
#nonparameteric kruskal test
kruskal.test(treatbcf ~ Pesticide, data =frog.soil.total.ai)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  treatbcf by Pesticide
## Kruskal-Wallis chi-squared = 27.9798, df = 4, p-value = 1.259e-05
```

```r
kruskal.test(treatbcf ~ SoilType, data =frog.soil.total.ai)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  treatbcf by SoilType
## Kruskal-Wallis chi-squared = 7.0035, df = 1, p-value = 0.008135
```

```r
treatbcf.total.noimid.aov <- aov(treatbcf ~ Pesticide + SoilType + surface_area_total,
                                 data = frog.soil.total.noimid)
summary(treatbcf.total.noimid.aov)
```

```
##                    Df Sum Sq Mean Sq F value   Pr(>F)
## Pesticide           3 0.3577 0.11924  16.072 4.18e-07 ***
## SoilType            1 0.0771 0.07711  10.394  0.00245 **
## surface_area_total  1 0.0014 0.00142   0.192  0.66354
## Residuals          42 0.3116 0.00742
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can also consider the pairwise t-test. For this we need the means of the pesticide treatements by soil for the test. Doesn't make any sense.