USDA

United States Department of Agriculture

Expanding the Toolkit for Soil Scientists

The *Algorithms for Quantitative Pedology* {aqp} R package

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Big Data with Soil Survey, Capacity Building

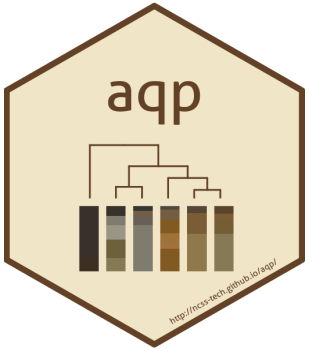
Natural Resources Conservation Service

nrcs.usda.gov/

The {aqp} R package

R is a freely available language and environment for statistical computing and graphics.

The {aqp} **R** package provides functions to support data-driven tasks such as visualization, aggregation, and classification of soil profiles. The code is open-source and under active development by members of the National Cooperative Soil Survey.



Project Homepage: http://ncss-tech.github.io/AQP/

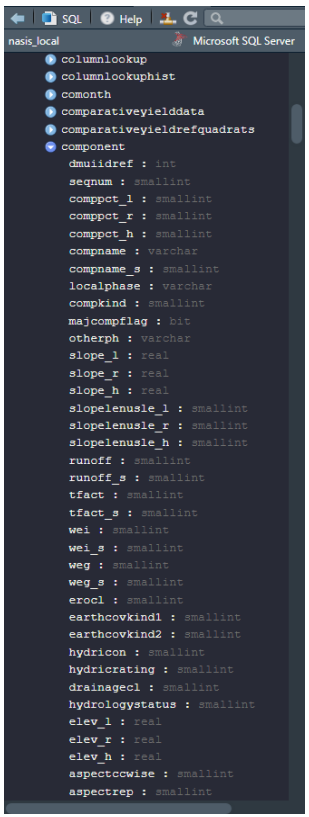
{aqp} on Comprehensive R Archive Network (CRAN; *stable*)

- http://cran.r-project.org/web/packages/aqp/

{aqp} on GitHub (*development*):

- http://github.com/ncss-tech/aqp/

Soil Data Inputs



You can load data from any source that **R** supports!

The {`soilDB`} package has several ways to get soil data!

- `fetchSDA`, `fetchSDA_spatial`, `SDA_query` & `SDA_spatialQuery` for SSURGO from Soil Data Access (SDA)
- `fetchKSSL` for querying a snapshot of the Kellogg Soil Survey Laboratory (KSSL) database
- `fetchOSD` for series type location profiles and narratives from Official Series Descriptions (OSDs)
- `fetchNASIS` for NASIS pedons / components from a local database

Natural Resources Conservation Service

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{aqp} SoilProfileCollection

```
library(aqp) # load aqp package

# load sample dataset CA serpentinite Soils
# (McGahan et al., 2009)
data(sp4, package = "aqp") # see ?sp4 for metadata
```

{aqp} SoilProfileCollection

```
library(aqp) # load aqp package

# load sample dataset CA serpentinite Soils
# (McGahan et al., 2009)
data(sp4, package = "aqp") # see ?sp4 for metadata
```

```
head(sp4, n = 8)
```

```
##       id name top bottom   K   Mg  Ca CEC_7 ex_Ca_to_Mg sand silt clay   CF
## 1 colusa    A   0      3 0.3 25.7 9.0  23.0         0.35   46   33   21 0.12
## 2 colusa  ABt   3      8 0.2 23.7 5.6  21.4         0.23   42   31   27 0.27
## 3 colusa  Bt1   8     30 0.1 23.2 1.9  23.7         0.08   40   28   32 0.27
## 4 colusa  Bt2  30     42 0.1 44.3 0.3  43.0         0.01   27   18   55 0.16
## 5  glenn    A   0      9 0.2 21.9 4.4  18.8         0.20   54   20   25 0.55
## 6  glenn   Bt   9     34 0.3 18.9 4.5  27.5         0.20   49   18   34 0.84
## 7  kings    A   0      4 0.2 12.1 1.4  23.7         0.58   43   55    3 0.50
## 8  kings  Bt1   4     13 0.6 12.1 7.0  18.0         0.51   36   49   15 0.75
```

Optional: use `data.table` or `tibble`!

```
sp4 ← data.table::as.data.table(sp4)
head(sp4)
```

```
##         id name top bottom   K   Mg  Ca CEC_7 sand silt clay   CF
## 1: colusa    A   0      3 0.3 25.7 9.0  23.0   46   33   21 0.12
## 2: colusa  ABt   3      8 0.2 23.7 5.6  21.4   42   31   27 0.27
## 3: colusa  Bt1   8     30 0.1 23.2 1.9  23.7   40   28   32 0.27
## 4: colusa  Bt2  30     42 0.1 44.3 0.3  43.0   27   18   55 0.16
## 5:  glenn    A   0      9 0.2 21.9 4.4  18.8   54   20   25 0.55
## 6:  glenn   Bt   9     34 0.3 18.9 4.5  27.5   49   18   34 0.84
```

Optional: use `data.table` or `tibble`!

```
sp4 ← data.table::as.data.table(sp4)
head(sp4)
```

```
##         id name top bottom   K   Mg  Ca CEC_7 sand silt clay   CF
## 1: colusa    A   0      3 0.3 25.7 9.0  23.0   46   33   21 0.12
## 2: colusa  ABt   3      8 0.2 23.7 5.6  21.4   42   31   27 0.27
## 3: colusa  Bt1   8     30 0.1 23.2 1.9  23.7   40   28   32 0.27
## 4: colusa  Bt2  30     42 0.1 44.3 0.3  43.0   27   18   55 0.16
## 5:  glenn    A   0      9 0.2 21.9 4.4  18.8   54   20   25 0.55
## 6:  glenn   Bt   9     34 0.3 18.9 4.5  27.5   49   18   34 0.84
```

```
sp4 ← tibble::as_tibble(sp4)
head(sp4)
```

```
## # A tibble: 6 x 10
##   id     name    top bottom     K    Mg    Ca CEC_7  sand  silt
##   <chr>  <chr> <int>  <int> <dbl> <dbl> <dbl> <dbl> <int> <int>
## 1 colusa A         0      3   0.3  25.7   9    23       46    33
## 2 colusa ABt       3      8   0.2  23.7   5.6  21.4     42    31
## 3 colusa Bt1       8     30   0.1  23.2   1.9  23.7     40    28
## 4 colusa Bt2      30     42   0.1  44.3   0.3  43       27    18
## 5 glenn  A         0      9   0.2  21.9   4.4  18.8     54    20
## 6 glenn  Bt        9     34   0.3  18.9   4.5  27.5     49    18
```

{aqp} Methods (basics)

"Promote" *data.frame*-like horizon data to a *SoilProfileCollection* object.

```
class(sp4)
```

```
## [1] "tbl_df"     "tbl"        "data.frame"
```

{aqp} Methods (basics)

"Promote" *data.frame*-like horizon data to a *SoilProfileCollection* object.

```
class(sp4)
```

```
## [1] "tbl_df"     "tbl"        "data.frame"
```

```
depths(sp4) ← id ~ top + bottom # specify site ID, top and bottom depth
```

{aqp} Methods (basics)

"Promote" *data.frame*-like horizon data to a *SoilProfileCollection* object.

```
class(sp4)
```

```
## [1] "tbl_df"     "tbl"        "data.frame"
```

```
depths(sp4) ← id ~ top + bottom # specify site ID, top and bottom depth
```

```
class(sp4) # sp4 promoted from tbl_df → SoilProfileCollection
```

```
## [1] "SoilProfileCollection"
## attr(,"package")
## [1] "aqp"
```

{aqp} Methods (basics)

"Promote" *data.frame*-like horizon data to a *SoilProfileCollection* object.

```
class(sp4)
```

```
## [1] "tbl_df"     "tbl"        "data.frame"
```

```
depths(sp4) ← id ~ top + bottom # specify site ID, top and bottom depth
```

```
class(sp4) # sp4 promoted from tbl_df → SoilProfileCollection
```

```
## [1] "SoilProfileCollection"
## attr(,"package")
## [1] "aqp"
```

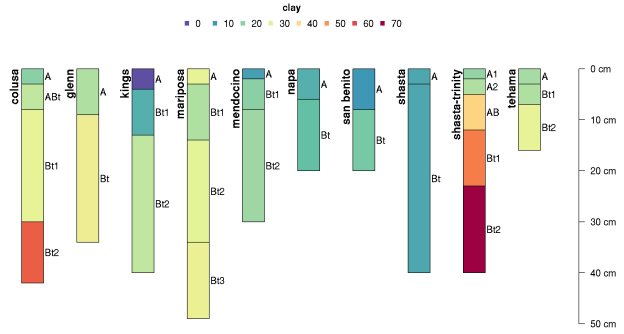
```
str(profile_id(sp4), vec.len = 3) # view first 3 profile IDs
```

```
##  chr [1:10] "colusa" "glenn" "kings" ...
```

{aqp} Methods (site data)

plot

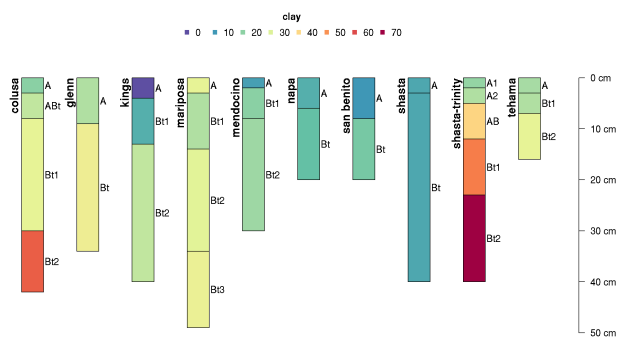
```
plot(sp4, # plot % clay content
     color = 'clay',
     id.style = 'side',
     cex.names = 1)
```



{aqp} Methods (site data)

plot

```
plot(sp4, # plot % clay content
     color = 'clay',
     id.style = 'side',
     cex.names = 1)
```



site

```
site(sp4) # "site" data
```

```
## # A tibble: 10 x 1
##    id
##    <chr>
##  1 colusa
##  2 glenn
##  3 kings
##  4 mariposa
##  5 mendocino
##  6 napa
##  7 san benito
##  8 shasta
##  9 shasta-trinity
## 10 tehama
```

{aqp} Methods (horizon data)

horizons

```
horizons(sp4) # "horizon" data
```

```
## # A tibble: 30 x 13
##    id       name    top bottom     K    Mg    Ca CEC_7  sand  silt  clay    CF h
##    <chr>    <chr> <int>  <int> <dbl> <dbl> <dbl> <dbl> <int> <int> <int> <dbl> <
##  1 colusa   A         0      3   0.3  25.7   9    23      46    33    21  0.12 1
##  2 colusa   ABt       3      8   0.2  23.7   5.6  21.4    42    31    27  0.27 2
##  3 colusa   Bt1       8     30   0.1  23.2   1.9  23.7    40    28    32  0.27 3
##  4 colusa   Bt2      30     42   0.1  44.3   0.3  43      27    18    55  0.16 4
##  5 glenn    A         0      9   0.2  21.9   4.4  18.8    54    20    25  0.55 5
##  6 glenn    Bt        9     34   0.3  18.9   4.5  27.5    49    18    34  0.84 6
##  7 kings    A         0      4   0.2  12.1   1.4  23.7    43    55     3  0.5  7
##  8 kings    Bt1       4     13   0.6  12.1   7    18      36    49    15  0.75 8
##  9 kings    Bt2      13     40   0.8  17.7   4.4  20      27    45    27  0.67 9
## 10 mariposa A         0      3   0.6  28.3   5.8  29.3    42    26    32  0.25 1
## # … with 20 more rows
```

{aqp} Methods (extract)

[i,]

```
sp4[1:2,] # i-index: first two profiles
```

```
## SoilProfileCollection with 2 profiles and 6 horizons
## profile ID: id  |  horizon ID: hzID
## Depth range: 34 - 42 cm
##
## ----- Horizons (6 / 6 rows  |  10 / 13 columns) -----
## # A tibble: 6 x 10
##   id     hzID    top bottom name      K    Mg    Ca CEC_7  sand
##   <chr>  <chr> <int>  <int> <chr> <dbl> <dbl> <dbl> <dbl> <int>
## 1 colusa 1         0      3 A       0.3  25.7   9    23      46
## 2 colusa 2         3      8 ABt     0.2  23.7   5.6  21.4    42
## 3 colusa 3         8     30 Bt1     0.1  23.2   1.9  23.7    40
## 4 colusa 4        30     42 Bt2     0.1  44.3   0.3  43      27
## 5 glenn  5         0      9 A       0.2  21.9   4.4  18.8    54
## 6 glenn  6         9     34 Bt      0.3  18.9   4.5  27.5    49
##
## ----- Sites (2 / 2 rows  |  1 / 1 columns) -----
## # A tibble: 2 x 1
##   id
##   <chr>
```

{aqp} Methods (extract)

[i,]

```
sp4[1:2,] # i-index: first two profiles
```

[,j]

```
sp4[,1:2] # j-index: first two horizons (of each profile!)
```

```
## SoilProfileCollection with 10 profiles and 20 horizons
## profile ID: id  |  horizon ID: hzID
## Depth range: 5 - 40 cm
##
## ----- Horizons (6 / 20 rows  |  10 / 13 columns) -----
## # A tibble: 6 x 10
##   id     hzID    top bottom name      K    Mg    Ca CEC_7  sand
##   <chr>  <chr> <int>  <int> <chr> <dbl> <dbl> <dbl> <dbl> <int>
## 1 colusa 1         0      3 A       0.3  25.7   9    23       46
## 2 colusa 2         3      8 ABt     0.2  23.7   5.6  21.4     42
## 3 glenn  5         0      9 A       0.2  21.9   4.4  18.8     54
```

{aqp} Methods (accessors)

$

```
sp4$clay       # get clay data
```

```
##  [1] 21 27 32 55 25 34  3 15 27 32 25 31 33 13 21 23 15 17 12 19 14 14 22 25 40
```

{aqp} Methods (accessors)

$

```
sp4$clay       # get clay data
```

```
##  [1] 21 27 32 55 25 34  3 15 27 32 25 31 33 13 21 23 15 17 12 19 14 14 22 25 40
```

[[

```
sp4[["clay"]]  # using expression for name, not symbol
```

```
##  [1] 21 27 32 55 25 34  3 15 27 32 25 31 33 13 21 23 15 17 12 19 14 14 22 25 40
```

{aqp} Methods (setters)

$← and [[←

Calculate Ca:Mg ratio

```
sp4$ex_Ca_to_Mg      ← sp4$Ca / sp4$Mg
sp4[["ex_Ca_to_Mg"]] ← sp4$Ca / sp4$Mg
```

{aqp} Methods (setters)

$← and [[←

Calculate Ca:Mg ratio

```
sp4$ex_Ca_to_Mg      ← sp4$Ca / sp4$Mg

sp4[["ex_Ca_to_Mg"]] ← sp4$Ca / sp4$Mg
```

Initialize a new column with a single value

```
site(sp4)$new_var ← 2
horizons(sp4)$new_hz_var ← 3
```

{aqp} Methods (setters)

$← and [[←

Calculate Ca:Mg ratio

```
sp4$ex_Ca_to_Mg      ← sp4$Ca / sp4$Mg

sp4[["ex_Ca_to_Mg"]] ← sp4$Ca / sp4$Mg
```

Initialize a new column with a single value

```
site(sp4)$new_var ← 2
horizons(sp4)$new_hz_var ← 3
```

```
length(sp4$new_var) # 10 sites, 10 values
length(sp4$new_hz_var) # 30 horizons, 30 values
sp4$new_var ← NULL # remove a column
```

{aqp} Methods (subset)

`subset` is the {aqp} method for extracting profiles that meet certain logical criteria at the site or horizon level.

```
# site property filtering, using base
sub.sp4 ← subset(sp4, id %in% c("colusa","mariposa","shasta"))
```

{aqp} Methods (subset)

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```
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sub.sp4 ← subset(sp4, id %in% c("colusa","mariposa","shasta"))
```

```
#   or dplyr-like syntax: filter
sub.sp4 ← filter(sp4, id %in% c("colusa","mariposa","shasta"))
```

{aqp} Methods (subset)

`subset` is the {aqp} method for extracting profiles that meet certain logical criteria at the site or horizon level.

```
# site property filtering, using base
sub.sp4 ← subset(sp4, id %in% c("colusa","mariposa","shasta"))
```

```
#   or dplyr-like syntax: filter
sub.sp4 ← filter(sp4, id %in% c("colusa","mariposa","shasta"))
```

```
sub.sp4
```

```
## SoilProfileCollection with 3 profiles and 10 horizons
## profile ID: id  |  horizon ID: hzID
## Depth range: 40 - 49 cm
##
## ----- Horizons (6 / 10 rows  |  10 / 15 columns) -----
## # A tibble: 6 x 10
##   id       hzID    top bottom name      K    Mg    Ca CEC_7  sand
##   <chr>    <chr> <int>  <int> <chr> <dbl> <dbl> <dbl> <dbl> <int>
## 1 colusa   1         0      3 A       0.3  25.7   9    23       46
## 2 colusa   2         3      8 ABt     0.2  23.7   5.6  21.4     42
## 3 colusa   3         8     30 Bt1     0.1  23.2   1.9  23.7     40
## 4 colusa   4        30     43 Bt2     0.1  44.2   0.3  43       27
```

{aqp} Methods (subset)

```
# horizon properties (two simultaneous logical expressions)
sub.sp4 ← subset(sp4, clay > 30, ex_Ca_to_Mg < 0.05)
sub.sp4
```

```
## SoilProfileCollection with 2 profiles and 9 horizons
## profile ID: id  |  horizon ID: hzID
## Depth range: 40 - 42 cm
##
## ----- Horizons (6 / 9 rows  |  10 / 15 columns) -----
## # A tibble: 6 x 10
##   id             hzID    top bottom name      K    Mg    Ca CEC_7  sand
##   <chr>          <chr> <int>  <int> <chr> <dbl> <dbl> <dbl> <dbl> <int>
## 1 colusa         1         0      3 A       0.3  25.7   9    23      46
## 2 colusa         2         3      8 ABt     0.2  23.7   5.6  21.4    42
## 3 colusa         3         8     30 Bt1     0.1  23.2   1.9  23.7    40
## 4 colusa         4        30     42 Bt2     0.1  44.3   0.3  43      27
## 5 shasta-trinity 23        0      2 A1      0.2  18.8   6.6  23      34
## 6 shasta-trinity 24        2      5 A2      0.2  25.5   4.1  21.5    33
## [ ... more horizons ... ]
##
## ----- Sites (2 / 2 rows  |  2 / 2 columns) -----
## # A tibble: 2 x 2
##   id             new_var
##   <chr>            <dbl>
## 1 colusa               2
```

{aqp} Methods (split SPC -> list)

If you need to operate on groups, splitting into `list` is a good option.

```
a.list ← split(sp4, f = idname(sp4))
```

```
str(a.list, max.level = 1)
```

```
## List of 10
##  $ colusa         :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ glenn          :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ kings          :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ mariposa       :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ mendocino      :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ napa           :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ san benito     :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ shasta         :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ shasta-trinity:Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
##  $ tehama         :Formal class 'SoilProfileCollection' [package "aqp"] with 9 sl
```

{aqp} Methods (split SPC -> list)

If you need to operate on groups, splitting into `list` is a good option.

```
a.list ← split(sp4, f = idname(sp4))
```

```
str(a.list, max.level = 1)
```

```
a.list[[1]]
```

```
## SoilProfileCollection with 1 profiles and 4 horizons
## profile ID: id  |  horizon ID: hzID
## Depth range: 42 - 42 cm
##
## ----- Horizons (4 / 4 rows  |  10 / 15 columns) -----
## # A tibble: 4 x 10
##   id     hzID    top bottom name      K    Mg    Ca CEC_7  sand
##   <chr>  <chr> <int>  <int> <chr> <dbl> <dbl> <dbl> <dbl> <int>
## 1 colusa 1         0      3 A       0.3  25.7   9    23       46
## 2 colusa 2         3      8 ABt     0.2  23.7   5.6  21.4     42
## 3 colusa 3         8     30 Bt1     0.1  23.2   1.9  23.7     40
## 4 colusa 4        30     42 Bt2     0.1  44.3   0.3  43       27
##
## ----- Sites (1 / 1 rows  |  2 / 2 columns) -----
## # A tibble: 1 x 2
##   id     new_var
##   <chr>    <dbl>
```

{aqp} Methods (iteration)

```
sub.sp4$soil_depth ← profileApply(sub.sp4, estimateSoilDepth)
sub.sp4$soil_depth
```

```
##          colusa shasta-trinity
##              42              40
```

{aqp} Methods (iteration)

```
sub.sp4$soil_depth ← profileApply(sub.sp4, estimateSoilDepth)
sub.sp4$soil_depth
```

```
##         colusa shasta-trinity
##             42             40
```

```
profileApply(sp4, frameify = TRUE,
    function(p) {
      data.frame(id = profile_id(p),
                 soil_depth = estimateSoilDepth(p))
    })
```

```
## # A tibble: 10 x 2
##    id             soil_depth
##    <chr>               <int>
##  1 colusa                 42
##  2 glenn                  34
##  3 kings                  40
##  4 mariposa               49
##  5 mendocino              30
##  6 napa                   20
##  7 san benito             20
##  8 shasta                 40
##  9 shasta-trinity         40
```

{aqp} Methods (combine; list -> SPC)

Recombine list elements into "original" SoilProfileCollection with `combine`

```
combine(a.list)
```

```
## SoilProfileCollection with 10 profiles and 30 horizons
## profile ID: id  |  horizon ID: hzID
## Depth range: 16 - 49 cm
##
## ----- Horizons (6 / 30 rows  |  10 / 15 columns) -----
## # A tibble: 6 x 10
##   id     hzID    top bottom name      K    Mg    Ca CEC_7  sand
##   <chr>  <chr> <int>  <int> <chr> <dbl> <dbl> <dbl> <dbl> <int>
## 1 colusa 1         0      3 A       0.3  25.7   9    23      46
## 2 colusa 2         3      8 ABt     0.2  23.7   5.6  21.4    42
## 3 colusa 3         8     30 Bt1     0.1  23.2   1.9  23.7    40
## 4 colusa 4        30     42 Bt2     0.1  44.3   0.3  43      27
## 5 glenn  5         0      9 A       0.2  21.9   4.4  18.8    54
## 6 glenn  6         9     34 Bt      0.3  18.9   4.5  27.5    49
## [ ... more horizons ... ]
##
## ----- Sites (6 / 10 rows  |  2 / 2 columns) -----
## # A tibble: 6 x 2
##   id        new_var
```

{aqp} %>% (pipes)

Use {magrittr} "pipes" (`%>%` infix operator) to chain operations.

```
f(x, y) == x %>% f(y)
```

{aqp} %>% (pipes)

Use {magrittr} "pipes" (`%>%` infix operator) to chain operations.

```
f(x, y) == x %>% f(y)
```

```
your.data2 ← operation1(your.data, argument1, argument2)
result ← operation1(your.data2, argument3, argument4)
```

becomes...

```
result ← your.data %>%
           operation1(argument1, argument2) %>%
           operation2(argument3, argument4)
```

{aqp} %>% (pipes)

1. Truncate all profiles to 0 - 15 cm interval
2. Calculate NH4OAc (pH 7) Ca (0 - 15 cm depth-weighted average cmol/kg)
3. Plot horizon-level values, in order of increasing site-level average

{aqp} %>% (pipes)

1. Truncate all profiles to 0 - 15 cm interval
2. Calculate NH4OAc (pH 7) Ca (0 - 15 cm depth-weighted average cmol/kg)
3. Plot horizon-level values, in order of increasing site-level average

```
sp4 %>%
  trunc(0, 15) %>%
  mutate_profile(dwt = bottom - top / sum(bottom - top),
                 dwt_Ca = sum(Ca * dwt)) %>%
  plot(plot.order = order(.$dwt_Ca), color = "Ca", cex.names = 1)
```

{aqp} %>% (pipes)

1. Truncate all profiles to 0 - 15 cm interval
2. Calculate NH4OAc (pH 7) Ca (0 - 15 cm depth-weighted average cmol/kg)
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sp4 %>%
  trunc(0, 15) %>%
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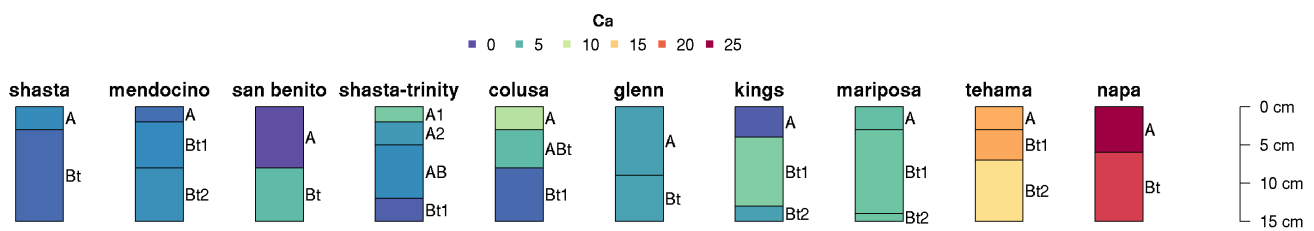
                 dwt_Ca = sum(Ca * dwt)) %>%
  plot(plot.order = order(.$dwt_Ca), color = "Ca", cex.names = 1)
```



{aqp} Methods (left joins)

site←

```
site(sp4) ← data.frame(id = c("mariposa","mendocino"),
                       site_grp = "ingroup")
```

```
head(site(sp4), 5)
```

```
## # A tibble: 5 x 3
##   id        new_var site_grp
##   <chr>       <dbl> <chr>
## 1 colusa          2 <NA>
## 2 glenn           2 <NA>
## 3 kings           2 <NA>
## 4 mariposa        2 ingroup
## 5 mendocino       2 ingroup
```

{aqp} Methods (left joins)

horizons←

```
horizons(sp4) ← data.frame(id = c("mariposa","mendocino"), hz_grp = "grou
h ← horizons(sp4)
```

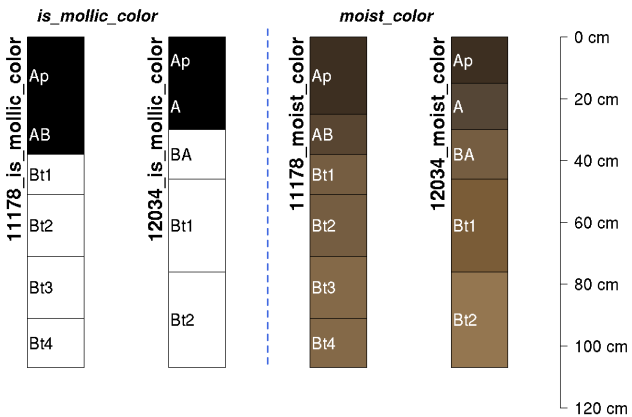
```
h[5:14,c(idname(sp4),"hz_grp")]
```

```
## # A tibble: 10 x 2
##    id        hz_grp
##    <chr>     <chr>
##  1 glenn     <NA>
##  2 glenn     <NA>
##  3 kings     <NA>
##  4 kings     <NA>
##  5 kings     <NA>
##  6 mariposa  group
##  7 mariposa  group
##  8 mariposa  group
##  9 mariposa  group
## 10 mendocino group
```

```
table(h$hz_grp, useNA = "ifany")
```

```
##
## group  <NA>
##     7    23
```

{aqp} Soil Color



{aqp} has methods for soil data in Munsell, sRGB and CIELAB.

`aggregateColor`, `colorContrast`, `colorQuantiles`, `contrastChart`, `contrastClass`, `getClosestMunsellChip`, `hasDarkColors`, `horizonColorIndices`, `huePosition`, `rgb2munsell`, `munsell2rgb`, `munsell2spc`, `parseMunsell`, `previewColors`, `soilColorSignature`, `soilPalette`

{aqp} Soil Color Opinions

```
n ← 8
hues ← c('10YR','7.5YR','2.5Y')
# hue
hh ← sample(hues, size = n,
            replace = TRUE,
            prob = c(0.7,0.2,0.1))
# value
vv ← sample(3:6, size = n,
            replace = TRUE)

# chroma
cc ← sample(c(3,4,6), size = n,
            replace = TRUE)
```

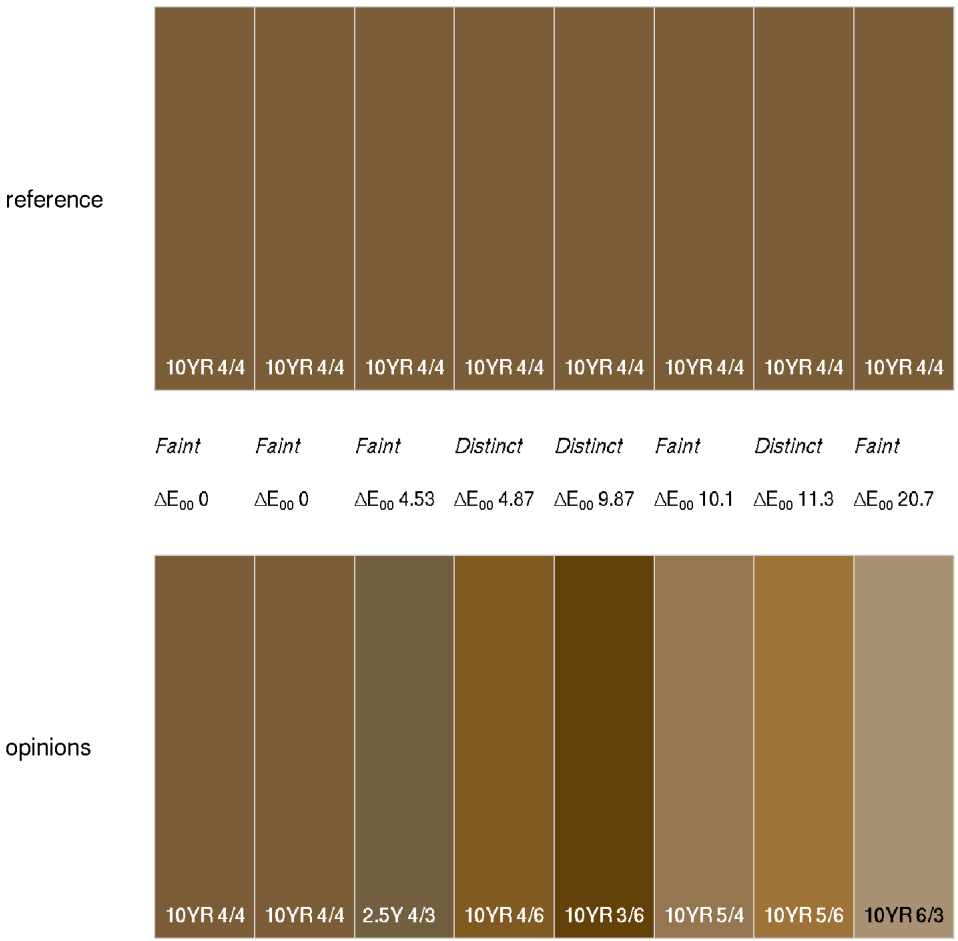
```
# reference soil color
m1 ← rep('10YR 4/4',
         times = n)

# opinions of soil color
m2 ← sprintf('%s %s/%s',
             hh, vv, cc)

# color contrast via dE00
cc ← colorContrast(m1, m2)

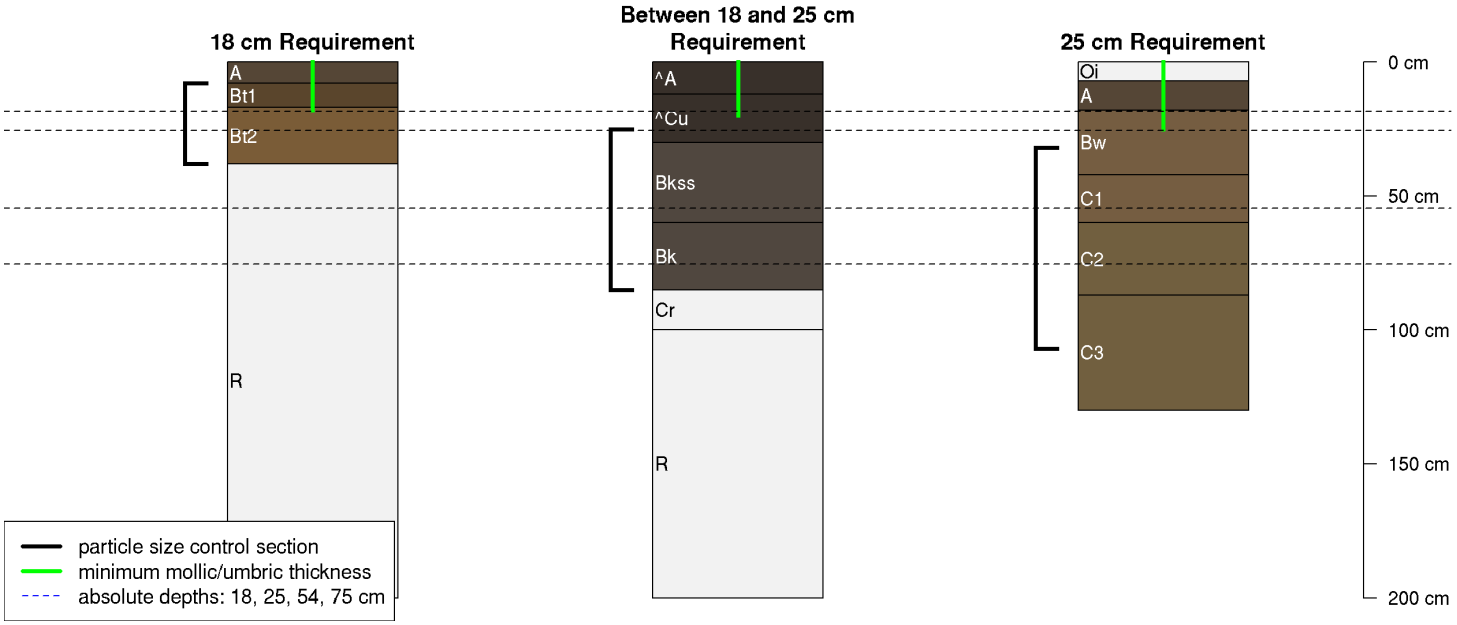
# re-order opinions
o ← order(cc$dE00)
m2 ← m2[o]
```

```
colorContrastPlot(m1, m2,
                  labels = c('reference', 'opinions'),
                  d.cex = 0.8, col.cex = 0.8)
```



{aqp} Soil Taxonomy & Classification

{aqp} has many functions that employ heuristics about horizon designations, geometry, and key diagnostic properties.



Thank you for your attention!

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