



United States Department of Agriculture

Expanding the 'Toolkit for Soil Scientists'

The aqp R package.

SSSA 2020 -- Big Data with Soil
Survey, Capacity Building

A close-up photograph of a dark, moist, crumbly soil sample, likely a compost or organic matter, being held by a person's hand.

Natural
Resources
Conservation
Service

Andrew G. Brown

 andrew.g.brown@usda.gov

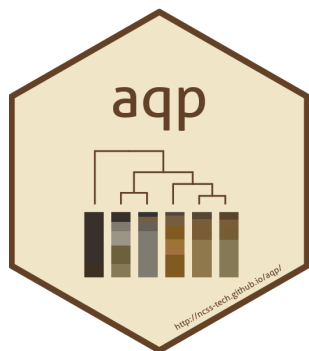
Dr. Dylan E. Beaudette

 dylan.beaudette@usda.gov

Natural
Resources
Conservation
Service

nrcs.usda.gov/

The {aqp} R package



The {aqp} **R** package provides functions that support data-driven tasks such as visualization, aggregation, and classification of soil profiles.

Project Homepage:

- <http://ncss-tech.github.io/AQP/>

{aqp} on CRAN (*stable*):

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

{aqp} on GitHub (*development*):

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



{soilDB} soil data inputs

The {soilDB} R package provides several handy ways to import soil data. It uses {aqp} for the *SoilProfileCollection* object.

- `fetchSDA`, `fetchSDA_spatial`, `SDA_query` & `SDA_spatialQuery` for **SSURGO** tabular or spatial data via **Soil Data Access** (SDA)
- `fetchKSSL` for querying data from a snapshot of the **Kellogg Soil Survey Laboratory database**
- `fetchOSD` for getting profile information from series type locations and narrative descriptions parsed from **Official Series Descriptions** (OSDs)
- `fetchNASIS` for accessing **NASIS** pedons and components via local database connection



{aqp} SoilProfileCollection

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



{aqp} SoilProfileCollection

```
library(aqp) # load aqp package

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

sp4

##		id	name	top	bottom	K	Mg	Ca	CEC_7	ex_Ca_to_Mg	sand	silt	clay
## 1		colusa	A	0	3	0.3	25.7	9.0	23.0	0.35	46	33	21
## 2		colusa	ABt	3	8	0.2	23.7	5.6	21.4	0.23	42	31	27
## 3		colusa	Bt1	8	30	0.1	23.2	1.9	23.7	0.08	40	28	32
## 4		colusa	Bt2	30	42	0.1	44.3	0.3	43.0	0.01	27	18	55
## 5		glenn	A	0	9	0.2	21.9	4.4	18.8	0.20	54	20	25
## 6		glenn	Bt	9	34	0.3	18.9	4.5	27.5	0.20	49	18	34
## 7		kings	A	0	4	0.2	12.1	1.4	23.7	0.58	43	55	3
## 8		kings	Bt1	4	13	0.6	12.1	7.0	18.0	0.51	36	49	15
## 9		kings	Bt2	13	40	0.8	17.7	4.4	20.0	0.25	27	45	27
## 10		napa	A	0	6	0.4	16.4	24.1	31.1	1.47	43	42	15
## 11		napa	Bt	6	20	0.1	16.2	21.5	27.9	1.32	54	29	17
## 12	san	benito	A	0	8	NA	3.0	0.7	3.1	0.24	80	8	12
## 13	san	benito	Bt	8	20	0.0	0.1	5.6	5.6	0.11	74	7	19
## 14		shasta	A	0	3	0.3	9.7	3.5	13.2	0.36	37	49	14
## 15		shasta	Bt	3	40	0.2	10.1	2.0	12.2	0.20	39	46	14



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 12
##   id      name    top bottom    K    Mg    Ca CEC_7  sand  silt  clay  CF
##   <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
## 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    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
```



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

```
class(sp4)
```

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



"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
```



"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"
```



"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"

profile_id(sp4) # view profile IDs

## [1] "colusa"      "glenn"      "kings"      "mariposa"   "mendocino"
## [8] "shasta"     "shasta-trinity" "tehama"

```



{aqp} S4 methods (basics)

site, SoilProfileCollection-method

```
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} S4 methods (basics)

site, SoilProfileCollection-method

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

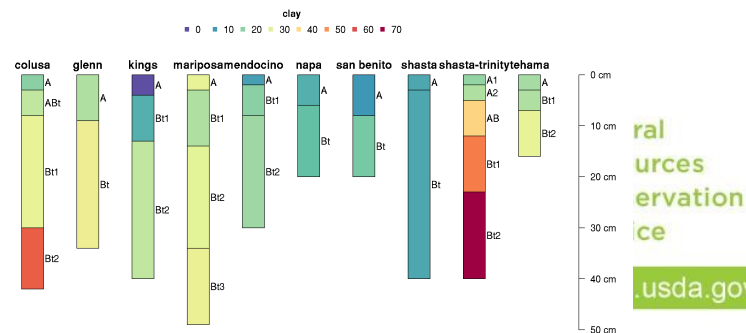
```
## # A tibble: 10 x 1
##   id
##   <chr>
## 1 colusa
## 2 glenn
## 3 kings
## 4 mariposa
## 5 mendocino
## 6 napa
## 7 san benito
## 8 shasta
## 9 shasta-trinity
## 10 tehama
```

horizons, SoilProfileCollection-method

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

plot, SoilProfileCollection-method

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



{aqp} S4 methods (extract)

[,SoilProfileCollection-method

```
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>
## 1 colusa
```



{aqp} S4 methods (extract)

[,SoilProfileCollection-method

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

```
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
## 4 glenn  6         9     34 Bt     0.3  18.9    4.5  27.5   49
## 5 kings  7         0      4 A      0.2  12.1    1.4  23.7   43
## 6 kings  8         4     13 Bt1    0.6  12.1    7    18    36
## [ ... more horizons ... ]
##
## ----- Sites (6 / 10 rows | 1 / 1 columns) -----
```



{aqp} S4 methods (accessors)

\$ and [[,SoilProfileCollection-methods

```
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} S4 methods (accessors)

\$ and [[,SoilProfileCollection-methods

```
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} S4 methods (setters)

`$←` and `[[←`, `SoilProfileCollection`-methods

```
## 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 singleton

```
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
```

Remove a column

```
sp4$new_var ← NULL
```



{aqp} S4 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  
subsp4 ← subset(sp4, id %in% c("colusa", "mariposa", "shasta"))
```



{aqp} S4 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  
subsp4 ← subset(sp4, id %in% c("colusa", "mariposa", "shasta"))
```

```
# or dplyr-like syntax: filter  
subsp4 ← filter(sp4, id %in% c("colusa", "mariposa", "shasta"))
```



{aqp} S4 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
subsp4 ← subset(sp4, id %in% c("colusa", "mariposa", "shasta"))
```

```
# or dplyr-like syntax: filter
subsp4 ← filter(sp4, id %in% c("colusa", "mariposa", "shasta"))
```

subsp4

```
## 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        20     42 Bt2    0.1   23.2    0.2    42     27
```



{aqp} S4 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 | 1 / 1 columns) -----
## # A tibble: 2 x 1
##   id
##   <chr>
## 1 colusa
```

Natural
Resources
Conservation
Service

nrcs.usda.gov/



{aqp} iteration



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

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



{aqp} iteration



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

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

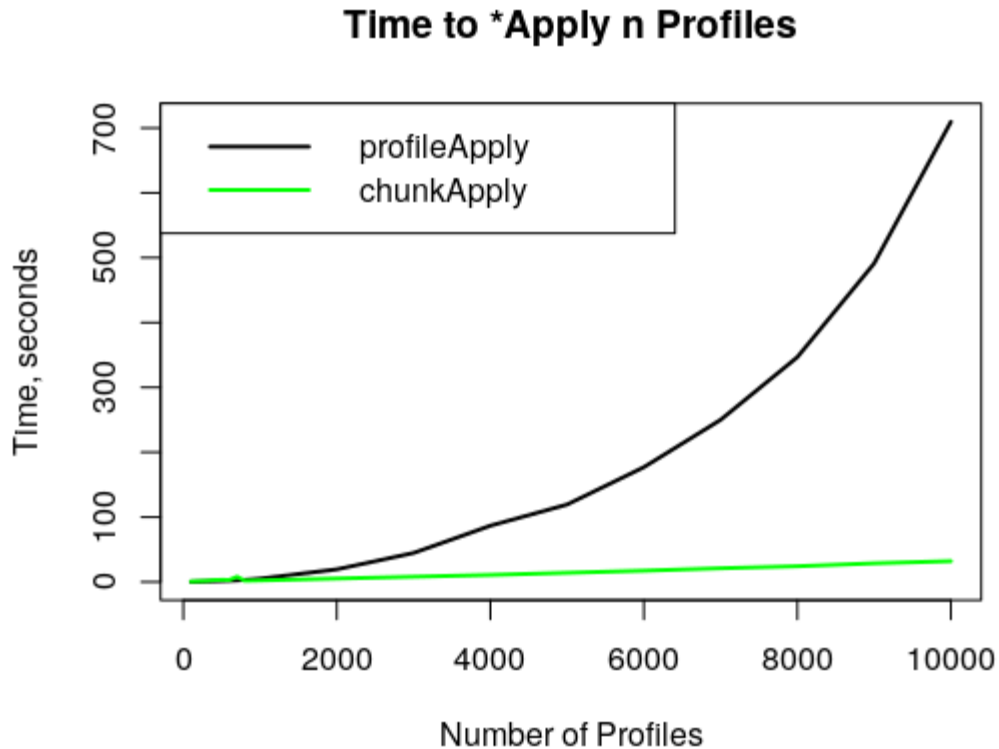
```
profileApply(sp4, frameify = TRUE,  
  function(p) {  
    data.frame(id = profile_id(p),  
              soil_depth = estimateSoilDepth(p))  
  })
```

```
## # 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} iteration

With recent internal optimizations, `profileApply` now scales to larger collections.



{aqp} split (SPC -> list)

If you need to operate on other types of (more complex) grouping, splitting into list is a good option.

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



{aqp} split (SPC -> list)

If you need to operate on other types of (more complex) grouping, 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
```

Natural
Resources
Conservation
Service

nrcs.usda.gov/



{aqp} split (SPC -> list)

If you need to operate on other types of (more complex) grouping, 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
```

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

```
## SoilProfileCollection with 1 profiles and 4 horizons
```

{aqp} combine (list -> SPC)

Re-combine list elements into "original" SoilProfileCollection with combine

```
sp4 ← combine(a.list)
```



{aqp} combine (list -> SPC)

Re-combine list elements into "original" SoilProfileCollection with `combine`

```
sp4 ← combine(a.list)
```

```
sp4
```

```
## 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 | 1 / 1 columns) -----
## # A tibble: 6 x 1
```



{aqp} %>% (pipes)



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

Use {magrittr} "pipes" (%>% infix operator) to decrease development time and improve readability.

```
library(magrittr)
```



{aqp} %>% (pipes)



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

Use {magrittr} "pipes" (%>% infix operator) to decrease development time and improve readability.

```
library(magrittr)
```

```
# NH4OAc (pH 7) extractable Ca (0-15cm depth-weighted average cmol/kg)
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)
```



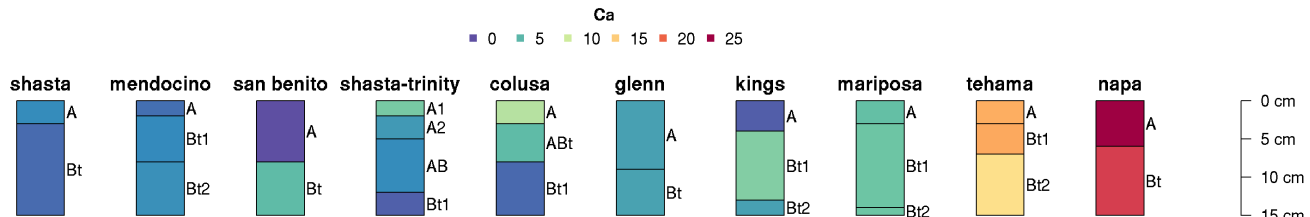
{aqp} %>% (pipes)

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

Use {magrittr} "pipes" (%>% infix operator) to decrease development time and improve readability.

```
library(magrittr)
```

```
# NH4OAc (pH 7) extractable Ca (0-15cm depth-weighted average cmol/kg)
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} S4 methods (left joins)

site←,SoilProfileCollection-method

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

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

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

```
table(site(sp4)$site_grp, useNA = "ifany")
```

```
##  
## ingroup    <NA>  
##         2      8
```



{aqp} S4 methods (left joins)

horizons ← **SoilProfileCollection-method**

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

```
head(horizons(sp4), 5)
```

```
## # A tibble: 5 x 16
##   id      name    top bottom      K      Mg      Ca CEC_7  sand  silt  clay  CF ex_C
##   <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
## 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    27    18    55  0.16
## 5 glenn  A         0      9  0.2  21.9    4.4  18.8    54    20    25  0.55
```

```
table(horizons(sp4)$hz_grp, useNA = "ifany")
```

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



{aqp} Soil Color

**{aqp} has methods for soil data in
Munsell, RGB and CIELAB color space.**

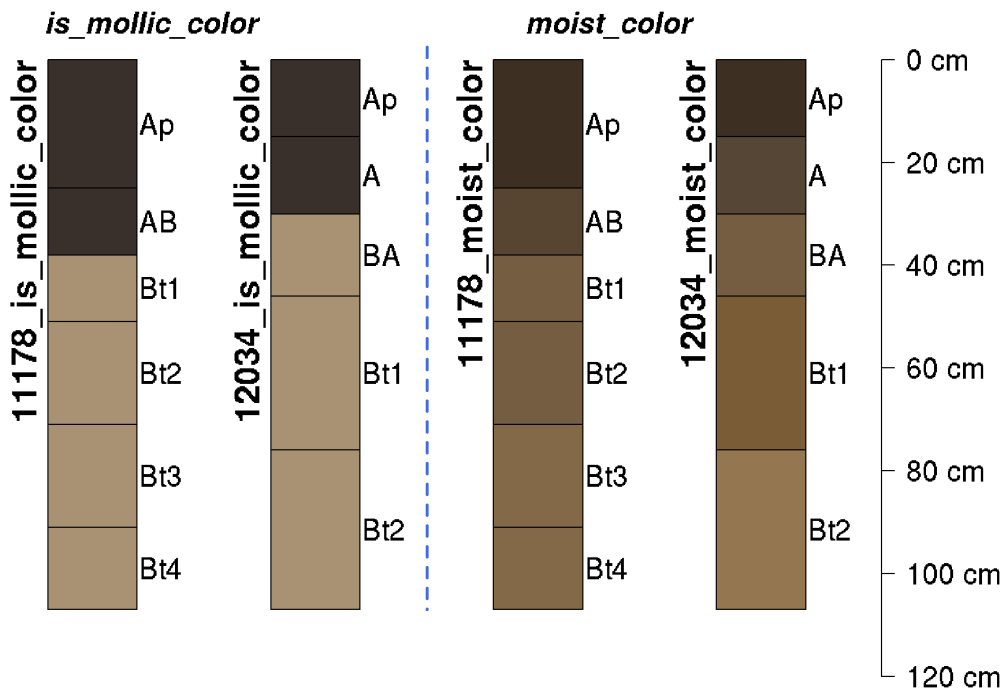
```
aggregateColor  
colorContrast  
colorQuantiles  
contrastChart  
contrastClass  
getClosestMunsellChip  
hasDarkColors  
horizonColorIndices  
huePosition  
rgb2munsell  
munsell2rgb  
munsell2spc  
parseMunsell  
previewColors  
soilColorSignature  
soilPalette
```



{aqp} Soil Color

{aqp} has methods for soil data in
Munsell, RGB and CIELAB color space.

```
aggregateColor
colorContrast
colorQuantiles
contrastChart
contrastClass
getClosestMunsellCh
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(3:6, 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)

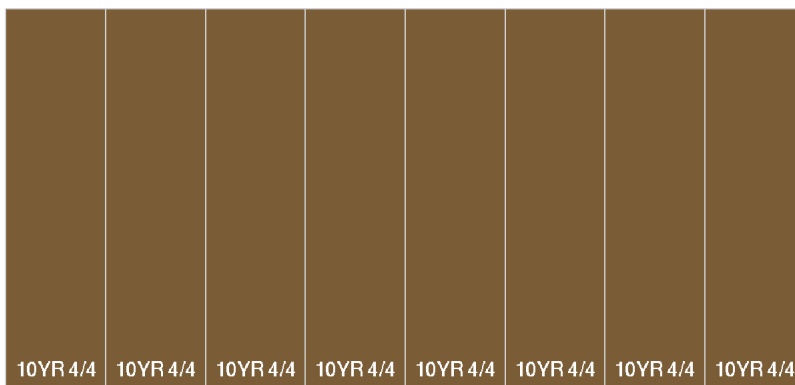
# re-order opinions
o ← order(cc$dE00)
m2 ← m2[o]
```





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

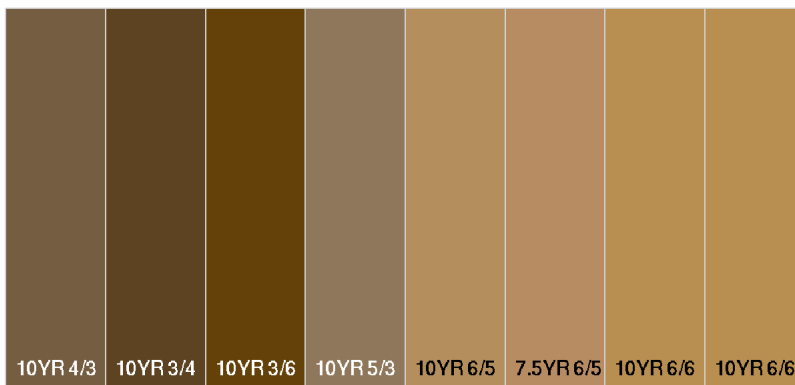
reference



Faint Faint Distinct Faint Faint Distinct Distinct Distinct

ΔE_{00} 3.11 ΔE_{00} 8.78 ΔE_{00} 9.87 ΔE_{00} 10.7 ΔE_{00} 20.5 ΔE_{00} 20.6 ΔE_{00} 21 ΔE_{00} 21

opinions



Natural
Resources
Conservation
Service

nrcs.usda.gov/



{aqp} Soil Taxonomy & Classification

Employ heuristics about horizon designations, geometry and key diagnostic properties.

- `estimateSoilDepth, estimatePSCS, getArgillicBounds, getCambicBounds, getMineralSoilSurfaceDepth, getPlowLayerDepth, getSoilDepthClass, getSurfaceHorizonDepth, hasDarkColors`
- `mollic.thickness.requirement, get.increase.matrix, get.ml.hz, brierScore, confusionIndex, shannonEntropy`



Thank you for your attention!



Andrew G. Brown, Soil Scientist, MLRA Soil Survey Office, Sonora, CA

✉ andrew.g.brown@usda.gov
 🔗 [brownag](#)
 🐦 [@humus_rocks](#)



Dr. Dylan E. Beaudette, Soil Scientist, National Soil Survey Center (duty station: Sonora, CA)

✉ dylan.beaudette@usda.gov
 🔗 [dylanbeaudette](#)
 🐦 [@dylanbeaudette](#)

USDA is an equal opportunity provider and employer.

Natural
Resources
Conservation
Service

nrcs.usda.gov/

