# Elaborazioni dendrometriche - cubatura con tavole INFC

Accesso al DB costruito nelle lezioni precedenti

```
library(tidyverse)
```

```
## -- Attaching packages ----------------------------------- tidyverse 1.2.1 --
```

```
## v ggplot2 2.2.1     v purrr   0.2.4
## v tibble  1.4.1     v dplyr   0.7.4
## v tidyr   0.7.2     v stringr 1.2.0
## v readr   1.1.1     v forcats 0.2.0
```

```
## -- Conflicts -------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(magrittr)
```

```
##
## Attaching package: 'magrittr'
```

```
## The following object is masked from 'package:purrr':
##
##     set_names
```

```
## The following object is masked from 'package:tidyr':
##
##     extract
```

```
library(RSQLite)
```

```
## Warning: package 'RSQLite' was built under R version 3.4.4
```

```
DBname <- "RilieviDendrometria_v03.sqlite"
DBconn <- dbConnect(RSQLite::SQLite(), DBname)
DBI::dbListTables(DBconn)
```

```
##  [1] "AdS_Rilevat"       "Altezze"           "Boschi"
##  [4] "Cav_specie"        "Cavallettamento"   "Diradamento"
##  [7] "Rilevatori"        "Rilievi"           "Specie"
## [10] "V_Altezze"         "V_Cavallettamento" "prova"
## [13] "prova2"            "sqlite_sequence"
```

Prima prova di elaborazione

Sintesi base

```
# Partiamo dalla vista preparata nel DB
dbGetQuery(DBconn, 'select * from V_Cavallettamento') %>%
  group_by(Cod_bosco, AdS, cod_specie) %>%
  count()
```

| Cod_bosco <chr> | AdS <chr> | cod_specie <chr> | n <int> |
|---|---|---|---|
| ANE1 | 1 | CEDRUS | 158 |
| ANE1 | 2 | CEDRUS | 154 |
| ANE1 | 3 | CEDRUS | 153 |
| ANE1 | 4 | CEDRUS | 170 |
| SOLO | 1 | QUEILE | 62 |

5 rows

```
v_cav <- dbGetQuery(DBconn, 'select * from V_Cavallettamento')
v_cav %>%
  group_by(Cod_bosco, AdS, cod_specie) %>%
  summarise(n= n(), dg = sqrt(mean(d130^2))) %>%
  mutate(G = n * dg^2 * pi/40000)
```

| Cod_bosco <chr> | AdS <chr> | cod_specie <chr> | n <int> | dg <dbl> | G <dbl> |
|---|---|---|---|---|---|
| ANE1 | 1 | CEDRUS | 158 | 18.43583 | 4.217667 |
| ANE1 | 2 | CEDRUS | 154 | 17.77292 | 3.820569 |
| ANE1 | 3 | CEDRUS | 153 | 17.49995 | 3.680062 |
| ANE1 | 4 | CEDRUS | 170 | 20.63791 | 5.686832 |
| SOLO | 1 | QUEILE | 62 | 28.84441 | 4.051398 |

5 rows

Cubatura con tavole INFC

```
# Funzione che converte un fattore nel vettore dei corrispondenti livelli
#  (quindi in un vettore di stringhe 'chr', "character")
factor2chr <- function(x) levels(x)[x]


library(ForIT)
#Elenco delle SPECIE e dei corrispondenti codici
INFCstats %$%
  unique(data.frame(spg = factor2chr(spg), specie = factor2chr(specie))) %>%
  mutate(rownames = NULL)
```

| spg <fctr> | specie <fctr> |
|---|---|

| spg<br><fctr> | specie<br><fctr> |
|---|---|
| Abal | Abies alba |
| Acca | Acer campestre |
| Acmo | Acer monspessulanum |
| Acop | Acer opalus |
| Acps | Acer pseudoplatanus |
| Alco | Alnus cordata |
| Algl | Alnus glutinosa |
| Cabe | Carpinus betulus |
| Casa | Castanea sativa |
| Cuar | Cupressus arizonica |

1-10 of 44 rows Previous **1** 2 3 4 5 Next

```
# a list of different species
species <- rep(c('Abal','Piab'),2)
dbh <- c(10,41,20,30)
heigths <- c(12,14,13,15)
frequences <- c(2,6,5,4)
data.frame(species, dbh, heigths, frequences)
```

| species<br><fctr> | dbh<br><dbl> | heigths<br><dbl> | frequences<br><dbl> |
|---|---|---|---|
| Abal | 10 | 12 | 2 |
| Piab | 41 | 14 | 6 |
| Abal | 20 | 13 | 5 |
| Piab | 30 | 15 | 4 |

4 rows

```
# single-tree estimates
INFCvpe(species, dbh, heigths, mod='v', frequences, aggr=FALSE)
```

```
## Warning in (D_0[1, ] %*% mvc %*% t(t(D_0[1, ]))) + (sa2 * d2h^2): Recycling array of lengt
h 1 in array-vector arithmetic is deprecated.
##   Use c() or as.vector() instead.

## Warning in (D_0[1, ] %*% mvc %*% t(t(D_0[1, ]))) + (sa2 * d2h^2): Recycling array of lengt
h 1 in array-vector arithmetic is deprecated.
##   Use c() or as.vector() instead.
```

```
## $mainData
##          key  spg d130 h_tot freq mod    T_0        SEE dof in.range
## 1 Abal-10-12 Abal   10    12    2   v   93.0   9.485077  43        y
## 2 Abal-20-13 Abal   20    13    5   v  989.9 101.642677  43        y
## 3 Piab-30-15 Piab   30    15    4   v 1917.5 258.225578  90        y
## 4 Piab-41-14 Piab   41    14    6   v 4974.1 630.554678  90        n
##
## $out.of.range
##          key  spg d130 h_tot freq mod    T_0      SEE dof in.range
## 4 Piab-41-14 Piab   41    14    6   v 4974.1 630.5547  90        n
```

```
# estimates aggregated at species level
INFCvpe(species, dbh, heigths, mod='v', frequences, aggr=TRUE)
```

```
## $mainData
##    spg mod    T_0  N      SEE dof
## 1 Abal   v 1082.8  7 104.1568  43
## 2 Piab   v 6891.6 10 679.9029  90
##
## $out.of.range
##          key  spg d130 h_tot frequency in.range
## 4 Piab-41-14 Piab   41    14         6        n
```