

Package ‘ForIT’

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Title Functions to Estimate Tree Volume and Phytomass in the Italian Forest Inventory 2005

Version 2.5.1

Description Tabacchi et al. (2011) published a very detailed study producing a uniform system of functions to estimate tree volume and phytomass components (stem, branches, stool). The estimates of the 2005 Italian forest inventory (<<https://www.inventarioforestale.org/it/>>) are based on these functions. The study documents the domain of applicability of each function and the equations to quantify estimates accuracies for individual estimates as well as for aggregated estimates. This package makes the functions available in the R environment. Version 2 exposes two distinct functions for individual and summary estimates. To facilitate access to the functions, tree species identification is now based on EPPO species codes (<<https://data.eppo.int/>>).

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

Imports magrittr, dplyr (>= 1.1.0), purrr, tibble, tidyr, RColorBrewer, metR, rlang, ggplot2, Matrix

Suggests testthat

URL <https://gitlab.com/NuoroForestrySchool/ForIT.git>,
<https://zenodo.org/records/5790157>

Depends R (>= 2.10)

NeedsCompilation no

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ForIT_DataBase	<i>'ForIT'-package Database - Ver.2</i>
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Description

The package exposes 5 tightly interconnected tibbles:
INFCspecies, INFCcatalog, Quantities, INFCparam, INFCf_domains

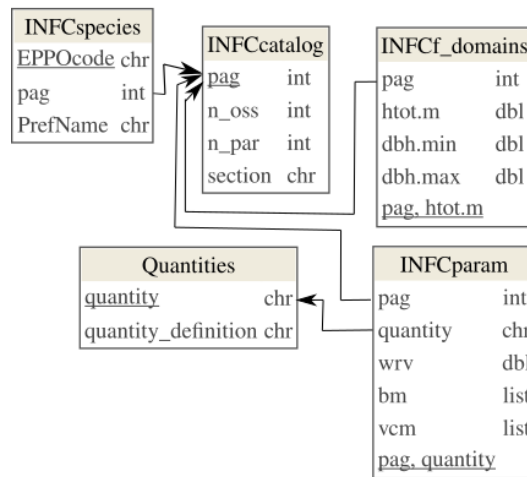
Usage

- INFCspecies
- INFCcatalog
- Quantities
- INFCparam
- INFCf_domains

Format

- An object of class tbl_df (inherits from tbl, data.frame) with 44 rows and 3 columns.
- An object of class tbl_df (inherits from tbl, data.frame) with 26 rows and 4 columns.
- An object of class tbl_df (inherits from tbl, data.frame) with 5 rows and 2 columns.
- An object of class tbl_df (inherits from tbl, data.frame) with 130 rows and 5 columns.
- An object of class tbl_df (inherits from tbl, data.frame) with 617 rows and 4 columns.

Details



Tables columns

INFCspecies

- EPPOcode [PK]: species code, adopting **EPPO** database
- pag: section page number in the original reference (Tabacchi et al., 2011a)
- PrefName: EPPO preferred name for the species

INFCcatalog

- pag [PK]: section page number in the original reference (Tabacchi et al., 2011a)
- n_oss: number of sample trees for the section
- n_par: number of parameters in the equations for the section
- section: section name (species or species group)

Quantities

- quantity [PK]: code of the estimated quantity
- quantity_definition: estimated quantity definition and measurement units

INFCparam

- pag [PK]: section page number in the original reference (Tabacchi et al., 2011a)
- quantity [PK]: code of the estimated quantity (see Quantities)
- wrv: weighted residual variance
- bm: functions coefficients (a list of arrays)
- vcm: variance-covariance matrices (a list of 'dspMatrix')

INFCf_domains

- pag [PK]: section page number in the original reference (Tabacchi et al., 2011a)

- `htot.m` [PK]: tree height class [m] (class width 1 m)
- `dbh.min`: minimum tree diameter class [cm] (class width 1 cm)
- `dbh.max`: maximum tree diameter class [cm] (class width 1 cm)

Columns `bm` and `vcm` are lists, the dimensions of the arrays and matrices they store vary depending on `n_par`.

Matrices in `vcm` are symmetric, stored as "dspMatrix" class objects.

Database schema is defined, verified and illustrated using package `dm`

```
library(dm)
ForIT_DB <- dm(INFCcatalog,
               INFCspecies,
               Quantities,
               INFCparam,
               INFCf_domains) %>%
dm_add_pk(INFCcatalog, pag, check = TRUE) %>%

dm_add_pk(INFCspecies, EPP0code, check = TRUE) %>%
dm_add_fk(INFCspecies, pag, INFCcatalog, check = TRUE) %>%

dm_add_pk(Quantities, quantity, check = TRUE) %>%

dm_add_pk(INFCparam, c(pag, quantity), check = TRUE) %>%
dm_add_fk(INFCparam, pag, INFCcatalog, check = TRUE) %>%
dm_add_fk(INFCparam, quantity, Quantities, check = TRUE) %>%

dm_add_pk(INFCf_domains, c(pag, htot.m), check = TRUE) %>%
dm_add_fk(INFCf_domains, pag, INFCcatalog, check = TRUE)

dm_examine_constraints(ForIT_DB)

dm_draw(ForIT_DB, rankdir = "BT", view_type = "all", column_types = T)
```

ForIT_test_data	<i>'ForIT'-package TEST-data - Ver.2</i>
-----------------	--

Description

A tiny test dataset including example data displayed in Tabacchi et al. (2011), the basic reference for ForIT package.

Usage

```
ForIT_test_data
```

Format

A data frame with 16 rows and 5 variables:

Details

The dataset is produced by the following code.

```
ForIT_test_data <- dplyr::tribble(
  ~UC, ~IdF, ~specie, ~d130, ~h_dendro,
  # UC: Plot Id (Unità Campionaria)
  # IdF: Stem ID (Identificativo Fusto)
  # specie: EPP0 species code (see https://gd.eppo.int/)
  # - ACRCA: Acer campestre
  # - ABIAL: Abies alba
  # - FAUSY: Fagus sylvatica
  # d130: trunk diameter at breast height [cm]
  # h_dendro: tree height [m]
  # Example data in Tabacchi et al. (2011) pag. 25
  "U1", "01", "ACRCA", 10, 7,
  "U1", "02", "ACRCA", 15, 9,
  "U1", "03", "ACRCA", 20, 12,
  "U1", "04", "ACRCA", 30, 20,
  "U1", "05", "ACRCA", 32, 21,
  "U1", "06", "ACRCA", 24, 18,
  "U1", "07", "ACRCA", 36, 21,
  "U1", "08", "ACRCA", 40, 22,
  "U1", "09", "ACRCA", 8, 8,
  "U1", "10", "ACRCA", 18, 12,

  # Example continuation, pag. 27
  "U2", "01", "ABIAL", 38, 21,
  "U2", "02", "ABIAL", 52, 28,
  "U2", "03", "FAUSY", 25, 16,
  "U2", "04", "FAUSY", 30, 18,
  "U2", "05", "FAUSY", 12, 10,

  # Extra lines, to test for 'out of domain'
  "U0", "01", "ACRCA", 22, 14, # pag. 24
  "U0", "02", "ACRCA", 30, 10
)
```

INFCdomain

The range of applicability of INFCvpe() function

Description

A data.frame containing the "range of applicability" (or "domain") of INFCvpe() function

Format

A data frame with 18563 observations on the following 2 variables.

key a character vector

in.range a factor with levels y

References

Tabacchi G., Di Cosmo L., Gasparini P., Morelli S., 2011a. *Stima del volume e della fitomassa delle principali specie forestali italiane. Equazioni di previsione, tavole del volume e tavole della fitomassa arborea epigea. Stima del volume e della fitomassa delle principali specie forestali italiane. Equazioni di previsione, tavole del volume e tavole della fitomassa arborea epigea.* 412 pp. [ITA, ita]

INFCtabulate

Reproduce the tables that Tabacchi et al. published in 2011

Description

The tables published in the work on which this package is based, convey a very relevant part of the information produced: printed numbers serve as reference to verify that coded functions return expected results and, more specifically, empty spaces in the printed tables signal function applicability domain. In other words, measurement data used to estimate function coefficients values, cover only the portion of the (dbh, htot) plane where numbers are printed.

Usage

```
INFCtabulate(
  EPP0code,
  quantity = "vol",
  dbh.by = 5,
  htot.by = 3,
  digits = 1,
  print_tab = T
)
```

Arguments

EPP0code	tree species code defined by the EPP0 database https://gd.eppo.int/search . Lookup 'INFCspecies' dataframe to retrieve recognized codes.
quantity	for each species (or species group) different quantities can be estimated. Quantity's definitions and Ids are exposed by the 'Quantities' dataframe. Default value is "vol", estimation of timber volume.
dbh.by	...
htot.by	increment value between rows (respectively columns) expressed in 'cm' (respectively 'm') for dbh (respectively total height, htot). Default 5 cm (respectively 1 m).

digits number of decimal digits to expose in the table. Default one decimal digit.
print_tab defaults to TRUE in order to produce a text output. If set to FALSE no printing
 will occur (see 'return')

Value

Function principal output is the printout of the volume or phytomass tables. If `print_tab = FALSE`, the function will only return a tibble with a list column containing the tabulation of the required estimation equation/s. Using default values, tables will be identical (or anyway similar) to the corresponding published tables, with white (NA) cells delimiting the domain of applicability of the equation.

Examples

```
## Not run:
  INFCTabulate(c("ABIAL", "ACRCA"),
               quantity = "vol",
               dbh.by = 5,
               htot.by = 3,
               digits = 1)

# Eppo code: ABIAL - pag = 33 - quantity = vol
#   htot.m
# dbh.cm   7    10    13    16    19    22    25    28    31
# 9  23.2  32.4   NA   NA   NA   NA   NA   NA   NA
# 14 NA  77.9 100.2   NA   NA   NA   NA   NA   NA
# 19 NA 142.3 183.3 224.3   NA   NA   NA   NA   NA
# 24 NA   NA 291.1 356.4 421.8 487.2   NA   NA   NA
# 29 NA   NA   NA 518.9 614.3 709.8 805.2   NA   NA
# 34 NA   NA   NA 711.6 842.8 974.0 1105.2 1236.4   NA
# 39 NA   NA   NA   NA 1107.2 1279.8 1452.5 1625.1 1797.7
# 44 NA   NA   NA   NA   NA 1627.2 1847.0 2066.7 2286.5
# 49 NA   NA   NA   NA   NA 2016.3 2288.8 2561.4 2833.9
# 54 NA   NA   NA   NA   NA   NA 2778.0 3109.0 3439.9
# 59 NA   NA   NA   NA   NA   NA 3314.4 3709.5 4104.6
# 64 NA   NA   NA   NA   NA   NA   NA 4363.1 4828.0

# ---
#   Eppo code: ACRCA - pag = 231 - quantity = vol
#   htot.m
# dbh.cm   7.5  10.5  13.5  16.5  19.5  22.5
# 9.5  26.8  36.8   NA   NA   NA   NA
# 14.5 NA  83.6 106.9   NA   NA   NA
# 19.5 NA 149.7 192.0 234.3 276.6   NA
# 24.5 NA   NA 302.2 369.0 435.7   NA
# 29.5 NA   NA   NA 534.2 631.0 727.8
# 34.5 NA   NA   NA 729.9 862.4 994.8
# 39.5 NA   NA   NA   NA 1129.9 1303.5
# ---

## End(Not run)
```

INFCvpe	<i>Estimate bole volume or tree phytomass for individual stems, with associated accuracy info</i>
---------	---

Description

Using the functions developed for INFC 2005 (the 2005 Italian national forest inventory), stem volume or tree compartment phytomass are estimated for each (EPP0code, dbh.cm, htot.m) input tuple. Accompanying the main value, accuracy estimates are returned, as attributes. The functions are documented in Tabacchi et al. (2011a)

Usage

```
INFCvpe(EPP0code, dbh.cm, htot.m, quantity = "vol")
```

Arguments

EPP0code	Character vector of tree species code, as defined in EPPO database, (See INFCspecies() and https://gd.eppo.int)
dbh.cm	Numeric vector of stem/s breast height diameter (in cm)
htot.m	Numeric vector of tree total height/s (in m). Length equal to dbh.cm vector or one. In this case same value will be replicated for all dbh.cm entries
quantity	(default = vol) Character vector specifying required quantity, one of c("vol", "dw1" : "dw4"). Use quantities() to retrieve codes definitions. Length equal to dbh.cm vector or one. In this case same value will be replicated for all dbh.cm entries

Details

Output value will have following added attributes with estimates accuracy evaluations for each stem:

1. pag - page number, referred to original source
2. wrv - weighted residual variance
3. Var_ea - variance for an estimated average
or variance for 'confidence interval' estimation, see `prediction.lm(..., interval = "confidence")`
4. Var_ie - variance for an individual estimate
or 'prediction variance', (see `prediction.lm(..., interval = "prediction")`) and Freese, 1964 - in:Tabacchi, 2011
5. InDomain - logical indicating whether the (dbh, htot) point lies out of the domain explored by the experimental data (see 'INFCtabulate()')

Value

The functions returns a Numeric vector of the same length of the dbh.cm argument, with accuracy info as attributes

See Also

[INFCvpe_summarise\(\)](#) and functions related to [INFCvpe_sum\(\)](#) to produce estimates of aggregates with better accuracy evaluation

Examples

```
# COMPARE WITH Tabacchi (2011a) page 25 ----
(v <- INFCvpe("ACRCA", dbh.cm = 22, htot.m = 14))
# [1] 252.9581
# attr(,"pag")
# [1] 231
# attr(,"wrv")
# [1] 2.271e-05
# attr(,"Var_ea")
# [1] 33.17182
# attr(,"Var_ie")
# [1] 1075.883
# attr(,"InDomain")
# [1] TRUE

# Standard Error of the Estimate
see <- sqrt(attr(v, "Var_ie"))
# Degrees of freedom
df <- INFCcatalog$n_oss[INFCcatalog$pag == attr(v, "pag")] -
  INFCcatalog$n_par[INFCcatalog$pag == attr(v, "pag")]
# confidence level
p <- 95/100
# Confidence Interval Half Width
cihw <- qt(1-(1-p)/2, df) * see
cat(" *** Volume confidence interval (p = ", p*100, "%) is [", round(v, 1),
    " +/- ", round(cihw, 1), "] dm^3\n", sep = " ")

# ESTIMATION OF PHYTOMASS ----
Quantities[5,] %>% as.data.frame()
#   quantity      quantity_definition
# 1      dw4 phytomass of the whole tree [kg]
tree_phy <- INFCvpe(c("ACRCA", "ALUCO"),
  dbh.cm = c(22, 15),
  htot.m = c(14, 16),
  quantity = "dw4")

tree_phy
# [1] 185.1291  87.7970
# attr(,"pag")
# [1] 231 245
# attr(,"wrv")
# [1] 3.142e-05 2.104e-05
# attr(,"Var_ea")
# [1] 45.89002  9.12407
# attr(,"Var_ie")
# [1] 1488.5135 281.8072
# attr(,"InDomain")
# [1] TRUE TRUE
```

```

# PROCESSING A TALLY DATA-FRAME ----
tst_vol <- ForIT_test_data %>%
  dplyr::mutate(vol = INFCvpe(specie, d130, h_dendro),
    OutOfDomain = !attr(vol, "InDomain"))
tst_vol %>%
  dplyr::filter(OutOfDomain)
tst_vol %>%
  dplyr::filter(UC == "U1")

# SUMS AND direct ACCUARACY AGGREGATION (instead of via ?INFCvpeSUM) ----
df <- function(pag) return(
  INFCcatalog %>%
    dplyr::right_join(tibble::tibble(pag = !!pag), by = "pag") %>%
    dplyr::transmute(df = n_oss - n_par) %>%
    purrr::pluck(1)
)
p <- 95/100
tst_vol %>%
  dplyr::mutate(cihw = qt(1-(1-p)/2,
    df(attr(vol, "pag")) *
    sqrt(attr(vol, "Var_ie")))
  ) %>%
  dplyr::filter(!OutOfDomain) %>%
  dplyr::group_by(specie) %>%
  dplyr::summarise(.groups = "drop",
    est = sum(vol),
    cihw = sqrt(sum(cihw^2)),
  ) %>%
  dplyr::left_join(INFCspecies %>% dplyr::select(EPP0code, pag),
    by = c("specie" = "EPP0code")) %>%
  dplyr::left_join(INFCcatalog %>% dplyr::select(pag, section),
    by = "pag") %>%
  dplyr::select(-c(specie, pag)) %>%
  dplyr::rename(specie = section) %>%
  dplyr::mutate(dplyr::across(c("est", "cihw"), ~round(.x, 1))) %>%
  dplyr::arrange(specie) %>%
  dplyr::select(specie, est, cihw) -> tab
tab[c(2,1,3),] %>%
  t()
rm(tst_vol, tab, df)

```

INFCvpeSUM

Estimate tree bole volume or phytomass for stems groups, with associated accuracy info

Description

Cumulative estimation of the volume or phytomass of groups of trees is just the summation of the values computed with INFCvpe(), but the computation of accuracy estimates is improved using

these summation functions.

Two approaches are available.

- Via INFCvpe_summarise() that processes and returns a data frame
- or by following aggregation functions within a standard summarise():
 - INFCvpe_sum()
 - INFCvpe_ConfInt()
 - INFCvpe_OutOfDomain()

Usage

```
INFCvpe_summarise(
  in.data,
  EPPOcode_C,
  dbh_C,
  h_tot_C,
  quantity = "vol",
  p = 0.95
)
```

```
INFCvpe_sum(EPPOcode, dbh, h_tot, quantity = "vol")
```

```
INFCvpe_ConfInt(EPPOcode, dbh, h_tot, quantity = "vol", p = 0.95)
```

```
INFCvpe_OutOfDomain(EPPOcode, dbh, h_tot)
```

Arguments

in.data	A dataframe (or tibble) containing tally data to be matched with "EPPOcode_C", "dbh_C" and "htot_C" arguments
EPPOcode_C	A string, the name of the column in in.data with the species EPPO codes
dbh_C	A string, the name of the column in in.data with the breast height diameter values
h_tot_C	A string, the name of the column in in.data with the tree total height values
quantity	(default = "vol") A character vector specifying required quantity/ies: c("vol", "dw1" : "dw4"). Use quantities() to decode definitions. • for INFCvpe_summarise(), if length(unique(quantity)) > 1, rows in in.data will be replicated for each value. • for INFCvpe_SUM functions, length(quantity) must be 1
p	(default p = 95%) probability used to compute cihw (with length = 1 or length = length(dbh)) OPZIONE 2 INFCvpe_SUM functions:
EPPOcode	A character vector with the species EPPO codes (with length = 1 or length = length(dbh))
dbh	A numeric vector with the breast height diameter values
h_tot	A numeric vector with the tree total height values (with length = 1 or length = length(dbh))

Details

Functions developed following Tabacchi et al. (2011), pages 23-26.

Value

- `INFCvpe_summarise()` returns a dataframe (tibble) with the grouping columns defined with `group_by()`, and the following columns:
 - `quantity`: as additional grouping column,
 - `n`: number of trees in the group,
 - `n_out`: the number of (`dbh`, `htot`) pairs that are 'out of the domain',
 - `est`: the estimated value,
 - `cihw`: confidence interval half width
 - `p`: probability used computing `cihw`
- `INFCvpe_SUM` - the functions of this family return a numeric vector, aggregating rows within the same group,
 - `INFCvpe_sum()` returns the sum of the estimated quantities,
 - `INFCvpe_ConfInt()` returns 'confidence interval half width',
 - `INFCvpe_OutOfDomain()` returns the number of 'out of domain' (`dbh`, `h_tot`) pairs included in the summation

See Also

[INFCvpe\(\)](#) to compute individual estimates, with detailed accuracy evaluation

Examples

```
## Not run:
Sezione <- function(EPP0codes){
  # retrieve 'Sezione' name, decoding EPP0 codes
  INFCspecies %>%
    dplyr::filter(EPP0code %in% EPP0codes) %>%
    dplyr::left_join(INFCcatalog, by = "pag") %>%
    dplyr::select(section) %>%
    purrr::pluck(1)
}

tst <- ForIT_test_data %>%
  dplyr::filter(UC != "U0")
# select Tabacchi et al. example data

tst %>%
  dplyr::group_by(specie) %>%
  INFCvpe_summarise("specie", "d130", "h_dendro") %>%
  dplyr::ungroup() %>%
  dplyr::mutate(specie = Sezione(specie),
                dplyr::across(c("est", "cihw"), ~round(.x, 1))
  ) %>%
  dplyr::select(specie, est, cihw) %>%
  dplyr::arrange(specie) %>%
```

```

dplyr::slice(2, 1, 3) %>%
t() %>%
  provideDimnames(base = list(dimnames(.)[[1]], ""), unique=FALSE)
# Compare ForIT (ver 2) output
## specie "Aceri" "Abete bianco" "Faggio"
## est "4623.0" "4044.2" "1079.4"
## cihw "567.5" "661.2" "275.4"
# with 'Tabella 2' in Tabacchi et al. (2011, pag. 27)
## specie "aceri" "abete bianco" "faggio"
## est "4623.0" "4044.2" "1079.4"
## cihw "567.4" "662.4" "279.2"

# Using 'INFCvpe_summarise()'

## Overall totals
tst %>%
  INFCvpe_summarise("specie", "d130", "h_dendro", quantity = c("vol", "dw4"))

## Group by dbh class ('cld')
tst %>%
  dplyr::mutate(cld = ceiling(d130/5)*5) %>%
  dplyr::group_by(UC, specie, cld) %>%
  INFCvpe_summarise("specie", "d130", "h_dendro")

## Group by sampling unit ('UC')
tst %>%
  dplyr::group_by(UC) %>%
  INFCvpe_summarise("specie", "d130", "h_dendro", quantity = "dw4")

# Using 'INFCvpeSUM' aggregation functions

## Estimate 'dw4' phytomass, by sampling unit ('UC')
tst %>%
  dplyr::group_by(UC) %>%
  dplyr::summarise(
    n_stems = dplyr::n(),
    OoD = INFCvpe_OutOfDomain(specie, d130, h_dendro),
    dw4 = INFCvpe_sum(specie, d130, h_dendro, quantity = "dw4"),
    dw4_ConfInt = INFCvpe_ConfInt(specie, d130, h_dendro, quantity = "dw4")
  )

## Estimate volume, by sampling unit ('UC')
tst %>%
  dplyr::group_by(UC) %>%
  dplyr::summarise(
    n_stems = dplyr::n(),
    OoD = INFCvpe_OutOfDomain(specie, d130, h_dendro),
    vol = INFCvpe_sum(specie, d130, h_dendro),
    vol_ConfInt = INFCvpe_ConfInt(specie, d130, h_dendro)
  )

rm(tst, Sezione)

```

```
## End(Not run)
```

INFC_CVgrid

'ForIT'-package Auxiliary pre-computed data - Ver.2

Description

A large dataset used by 'INFCaccuracyPlot0()' to speed the production of a fine resolution CV surface for the plots.

Usage

```
INFC_CVgrid
```

Format

A data frame with 167560 rows and 7 variables:

pag see 'INFCcatalog' primary key

quantity see 'Quantities'

dbh trunk diameter at breast height (dbh), in cm

h_tot tree height, in m

cv_ie coefficient of variation for an individual estimate

cv_ea coefficient of variation for the estimate of an average

est estimated value for the selected 'quantity'. See 'INFCvpe()' for more details

n_par number of parameters that the function requires

inD is the (dbh, htot) point within the function domain?

Details

The dataset is produced by the following code.

```
Populate_INFC_CVgrid <- function() {
  INFCcatalog %>%
    select(pag) %>%
    inner_join(INFCspecies %>%
      select(pag, EPP0code),
      by = "pag") %>%
    group_by(pag) %>%
    summarise(EPP0code = first(EPP0code),
      .groups = "drop") %>%
    inner_join(Quantities %>% select(quantity), by = character()) %>%
    mutate(grid.k = pmap(list(pag, EPP0code, quantity), compute_grid0)) %>%
    select(-EPP0code) %>%
    unnest(cols = c(grid.k)) %>%
    return()
}
```

PlottingINFCaccuracy	<i>Plotting the accuracy and reliability region (or 'domain') of the volume and phytomass estimation functions</i>
----------------------	--

Description

Volume and phytomass functions are tabulated in Tabacchi et al. (2011a). The tabulation covers a limited region of the dbh by h_tot rectangle. This region is the "domain" of the reliable estimates, based on the distribution of the sample trees used to calibrate the functions. The coefficient of variation ($CV = \text{standard_deviation} / \text{estimate}$) is computed and plotted (as 'filled contours') for the whole rectangular area, the limits of the region of reliable estimates (the "domain"), is superimposed as a light colored line. Function output is a ggplot object that can be used by its self or as a background on top of which the user can plot his/her data to verify eventual accuracy or reliability problems.

Two functions are available.

- `INFCaccuracyPlot()` - allows the plots to be fully customized but, beware, all values required for the 'fill' will be computed and, at finer resolution, the process can be slow.
- `INFCaccuracyPlot0()` - produces, much faster, the plots at the finest resolution, using pre-calculated values stored in a specific auxiliary data.frame (see [INFC_CVgrid](#)), necessarily leaving less customization freedom.

(** `compute_grid0()` - is an internal function exported for the sake of the `Populate_INFC_CVgrid()` function **)

Usage

```
INFCaccuracyPlot(
  EPP0cod,
  quantity = "vol",
  ie.Var = FALSE,
  cv.ul = 0.1,
  fixed = TRUE,
  plot.est = FALSE,
  dbh.step = 5,
  htot.step = dbh.step,
  dbh.buf = 1,
  htot.buf = dbh.buf
)
```

```
INFCaccuracyPlot0(
  EPP0cod,
  quantity = "vol",
  ie.Var = FALSE,
  cv.ul = 0.1,
  fixed = TRUE,
  plot.est = FALSE
)
```

```
)

compute_grid0(pag, EPP0cod, quantity)
```

Arguments

EPP0cod	A string, one of the EPPO tree species codes listed in INFCspecies table (Reference: https://gd.eppo.int)
quantity	(optional) A string specifying the quantity to be estimated, one of c("vol", "dw1" : "dw4"). Lookup Quantities table to retrieve codes definitions. Defaults to "vol".
ie.Var	(optional) Logical. Choose variance estimator: • TRUE = variance for an 'individual estimate' • FALSE = variance for the 'estimate of an average' value Default ie.Va = FALSE
cv.ul	(optional) Numeric. Cutoff CV level for the plot. Defaults to 0.1
fixed	(optional) Logical. Contour plot breaks: • TRUE = break levels are fixed • FALSE = breaks are tailored to the specific case (in order to split the values within the range of interest [0, cv.ul], into equally numerous bins) Default fixed = TRUE
plot.est	(optional) Logical. Add the 'estimated quantity' layer as contour lines. Default plot.est = FALSE
dbh.step	(optional) Numeric. Computation with smaller step produces a plot with better resolution but increases consistently computation time (see INFCaccuracyPlot0()). To reduce computation time, the step defaults to 5.
htot.step	(optional) Numeric. As for dbh.
dbh.buf	(optional) Numeric. Extra space in the plot beyond the 'domain'. Default: 1
htot.buf	(optional) Numeric. As for dbh.
pag	for the internal function compute_grid0()

Value

INFCaccuracyPlot The function returns a ggplot object.

Examples

```
## Not run:
INFCaccuracyPlot("FRXAN") # 'INFCaccuracyPlot()' can be slow because
#   it computes all the CV values needed to fill background plot,
#   hence default values are set to a coarser resolution.
\donttest{
  INFCaccuracyPlot("FRXAN",
                    dbh.step = 1,
                    htot.step = 1)
  # computing with high resolution is slow
```

```

}

INFCaccuracyPlot0("FRXAN")
# 'INFCaccuracyPlot0()' is quick, it uses stored values
INFCaccuracyPlot0("FRXAN", "dw4")
INFCaccuracyPlot0("FRXAN", "dw4", ie.Var = TRUE)
# default fixed break values are not always optimal
INFCaccuracyPlot0("FRXAN", "dw4", ie.Var = TRUE, fixed = FALSE, cv.ul=.9)
# tailoring can improve
INFCaccuracyPlot0("FRXAN", plot.est = TRUE)
# 'quantity' estimation iso-lines can be superimposed

background <- INFCaccuracyPlot0("ACROP", plot.est = TRUE)
foreground <- ForIT_test_data %>%
  dplyr::filter(specie == "ACROP") %>%
  dplyr::mutate(vol = INFCvpe(specie, d130, h_dendro)) %>%
  ggplot2::geom_point(map = ggplot2::aes(h_dendro, d130, size = vol))
background + foreground # Adding a custom foreground
rm(background, foreground)

INFCaccuracyPlot0("ABIAL")
# high resolution and quick, using pre-calculated background values
INFCaccuracyPlot("ABIAL")
# default values produce a coarser resolution

## End(Not run)

```

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