

# Package: fgeo.tool (via r-universe)

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**Title** Import and Manipulate 'ForestGEO' Data

**Version** 1.2.8.9000

**Description** To help you access, transform, analyze, and visualize 'ForestGEO' data, we developed a collection of R packages (<<https://forestgeo.github.io/fgeo/>>). This package, in particular, helps you to easily import, filter, and modify 'ForestGEO' data. To learn more about 'ForestGEO' visit <<https://forestgeo.si.edu/>>.

**License** GPL-3

**URL** <https://forestgeo.github.io/fgeo.tool/>,  
<https://github.com/forestgeo/fgeo.tool>

**BugReports** <https://github.com/forestgeo/fgeo.tool/issues>

**Depends** R (>= 3.2)

**Imports** dplyr (>= 0.8.0.1), glue (>= 1.3.1), magrittr (>= 1.5), purrr (>= 0.3.2), readr (>= 1.3.1), rlang (>= 0.4.11), tibble (>= 2.1.1), tidyselect (>= 0.2.5)

**Suggests** covr (>= 3.2.1), fgeo.x (>= 1.1.3), knitr (>= 1.22), roxygen2 (>= 6.1.1), spelling (>= 2.1), stringr (>= 1.4.0), testthat (>= 2.1.1), tidyr (>= 0.8.3)

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add_status_tree	<i>Add column status_tree based on the status of all stems of each tree.</i>
-----------------	--

---

### Description

Add column status\_tree based on the status of all stems of each tree.

### Usage

```
add_status_tree(data, status_a = "A", status_d = "D")
```

### Arguments

data	A ForestGEO-like dataframe: A <i>ViewFullTable</i> , <i>tree</i> or <i>stem</i> table.
status_a, status_d	Sting to match alive and dead stems; it corresponds to the values of the variable status (in census tables) or Status (with capital "S" in ViewFull tables).

### Value

The input data set with the additional variable status\_tree.

### See Also

Other functions to add columns to dataframes: [add\\_subquad\(\)](#), [add\\_var\(\)](#)

Other functions for ForestGEO data: [add\\_subquad\(\)](#), [add\\_var\(\)](#)

Other functions for fgeo census: [add\\_var\(\)](#), [guess\\_plotdim\(\)](#), [pick\\_drop](#)

Other functions for fgeo vft: [add\\_subquad\(\)](#), [add\\_var\(\)](#), [guess\\_plotdim\(\)](#), [pick\\_drop](#)

**Examples**

```
# styler: off
stem <- tribble(
  ~CensusID, ~treeID, ~stemID, ~status,
    1,      1,      1,      "A",
    1,      1,      2,      "D",
    1,      2,      3,      "D",
    1,      2,      4,      "D",
    2,      1,      1,      "A",
    2,      1,      2,      "G",
    2,      2,      3,      "D",
    2,      2,      4,      "G"
)
# styler: on

add_status_tree(stem)
```

---

add\_subquad

*Add column subquadrat based on QX and QY coordinates.*


---

**Description**

Add column subquadrat based on QX and QY coordinates.

**Usage**

```
add_subquad(data, x_q, y_q = x_q, x_sq, y_sq = x_sq, subquad_offset = NULL)
```

**Arguments**

**data** A dataframe with quadrat coordinates QX and QY (e.g. a *ViewFullTable*).

**x\_q, y\_q** Size in meters of a quadrat's side. For ForestGEO sites, a common value is 20.

**x\_sq, y\_sq** Size in meters of a subquadrat's side. For ForestGEO sites, a common value is 5.

**subquad\_offset** Either -1 or 1, to rest or add one unit to the digit of each subquadrat that represents the column number.

First column is 0

First column is 1

-----  
04 14 24 34

-----  
14 24 34 44

03 13 23 33

13 23 33 43

02 12 22 32

12 22 32 42

01 11 21 31

11 21 31 41

**Value**

Returns data with the additional variable `subquadrat`.

**Author(s)**

Anudeep Singh and Mauro Lepore.

**See Also**

Other functions to add columns to dataframes: [add\\_status\\_tree\(\)](#), [add\\_var\(\)](#)

Other functions for ForestGEO data: [add\\_status\\_tree\(\)](#), [add\\_var\(\)](#)

Other functions for fgeo vft: [add\\_status\\_tree\(\)](#), [add\\_var\(\)](#), [guess\\_plotdim\(\)](#), [pick\\_drop](#)

**Examples**

```
# styler: off
vft <- tribble(
  ~QX, ~QY,
  17.9, 0,
  4.1, 15,
  6.1, 17.3,
  3.8, 5.9,
  4.5, 12.4,
  4.9, 9.3,
  9.8, 3.2,
  18.6, 1.1,
  17.3, 4.1,
  1.5, 16.3
)
# styler: on

add_subquad(vft, 20, 20, 5, 5)

add_subquad(vft, 20, 20, 5, 5, subquad_offset = -1)
```

---

<code>add_var</code>	<i>Add columns</i> <code>lx/ly</code> , <code>QX/QY</code> , <code>index</code> , <code>col/row</code> , <code>hectindex</code> , <code>quad</code> , <code>gx/gy</code> .
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---

**Description**

These functions add columns to position trees in a forest plot. They work with *ViewFullTable*, *tree* and *stem* tables. From the input table, most functions use only the `gx` and `gy` columns (or equivalent columns). The exception is the function `add_gxgy()` which inputs `quadrat` information. If your data lacks some important column, an error message will inform you which column is missing.

**Usage**

```

add_lxly(data, gridsize = 20, plotdim = NULL)

add_qxqy(data, gridsize = 20, plotdim = NULL)

add_index(data, gridsize = 20, plotdim = NULL)

add_col_row(data, gridsize = 20, plotdim = NULL)

add_hectindex(data, gridsize = 20, plotdim = NULL)

add_quad(data, gridsize = 20, plotdim = NULL, start = NULL, width = 2)

add_gxgy(data, gridsize = 20, start = 0)

```

**Arguments**

data	A ForestGEO-like dataframe: A <i>ViewFullTable</i> , <i>tree</i> or <i>stem</i> table.
gridsize	The gridsize of the census plot (commonly 20 m).
plotdim	The global dimensions of the census plot (i.e. the maximum possible values of gx and gy).
start	Defaults to label the first quadrat as "0101". Use 0 to label it as "0000" instead.
width	Number; width to pad the labels of plot-columns and -rows.

**Details**

These functions are adapted from the [CTFS R Package](#).

**Value**

For any given var, a function `add_var()` returns a modified version of the input dataframe, with the additional variable(s) var.

**See Also**

Other functions to add columns to dataframes: [add\\_status\\_tree\(\)](#), [add\\_subquad\(\)](#)  
 Other functions for ForestGEO data: [add\\_status\\_tree\(\)](#), [add\\_subquad\(\)](#)  
 Other functions for fgeo census: [add\\_status\\_tree\(\)](#), [guess\\_plotdim\(\)](#), [pick\\_drop](#)  
 Other functions for fgeo vft: [add\\_status\\_tree\(\)](#), [add\\_subquad\(\)](#), [guess\\_plotdim\(\)](#), [pick\\_drop](#)

**Examples**

```

# stycler: off
x <- tribble(
  ~gx,    ~gy,
    0,      0,
   50,    25,

```

```

    999.9, 499.95,
      1000,   500
  )
# styler: on

# `gridsize` has a common default; `plotdim` is guessed from the data
add_lxly(x)

gridsize <- 20
plotdim <- c(1000, 500)

add_qxqy(x, gridsize, plotdim)

add_index(x, gridsize, plotdim)

add_hectindex(x, gridsize, plotdim)

add_quad(x, gridsize, plotdim)

add_quad(x, gridsize, plotdim, start = 0)

# `width` gives the nuber of digits to pad the label of plot-rows and
# plot-columns, e.g. 3 pads plot-rows with three zeros and plot-columns with
# an extra thrree zeros, resulting in a total of 6 zeros.
add_quad(x, gridsize, plotdim, start = 0, width = 3)

add_col_row(x, gridsize, plotdim)

# From `quadrat` or `QuadratName` -----
# styler: off
x <- tribble(
  ~QuadratName,
    "0001",
    "0011",
    "0101",
    "1001"
)
# styler: on

# Output `gx` and `gy` -----

add_gxgy(x)

assert_is_installed("fgeo.x")
# Warning: The data may already have `gx` and `gy` columns
gxgy <- add_gxgy(fgeo.x::tree5)
select(gxgy, matches("gx|gy"))

# Output `col` and `row` -----

# Create columns `col` and `row` from `QuadratName` with `tidyr::separate()`
# The argument `sep` lets you separate `QuadratName` at any positon

```

```
## Not run:
tidyr_is_installed <- requireNamespace("tidyr", quietly = TRUE)
stringr_is_installed <- requireNamespace("stringr", quietly = TRUE)

if (tidyr_is_installed && stringr_is_installed) {
  library(tidyr)
  library(stringr)

  vft <- tibble(QuadratName = c("0001", "0011"))
  vft

  separate(
    vft,
    QuadratName,
    into = c("col", "row"),
    sep = 2
  )

  census <- select(fgeo.x::tree5, quadrat)
  census

  census$quadrat <- str_pad(census$quadrat, width = 4, pad = 0)

  separate(
    census,
    quadrat,
    into = c("col", "row"),
    sep = 2,
    remove = FALSE
  )
}

## End(Not run)
```

---

fgeo\_elevation      *Create elevation data.*

---

## Description

This function constructs an object of class "fgeo\_elevation". It standardizes the structure of elevation data to always output a dataframe with names `gx`, `gy` and `elev`.

## Usage

```
fgeo_elevation(elev)
```

**Arguments**

- `elev` One of these:
- A dataframe containing elevation data, with columns `gx`, `gy`, and `elev`, or `x`, `y`, and `elev` (e.g. `fgeo.x::elevation$col`).
  - A ForestGEO-like elevation list with elements `xdim` and `ydim` giving plot dimensions, and element `col` containing a dataframe as described in the previous item (e.g. `fgeo.x::elevation`).

**Value**

A dataframe with names `x/gx`, `y/gy` and `elev`.

**Acknowledgments**

This function was inspired by David Kenfack.

**Examples**

```
assert_is_installed("fgeo.x")

# Input: Elevation dataframe
elevation_df <- fgeo.x::elevation$col
fgeo_elevation(elevation_df)

class(elevation_df)
class(fgeo_elevation(elevation_df))

names(elevation_df)
names(fgeo_elevation(elevation_df))

# Input: Elevation list
elevation_ls <- fgeo.x::elevation
fgeo_elevation(elevation_ls)

class(elevation_ls)
class(fgeo_elevation(elevation_ls))

names(elevation_ls)
names(fgeo_elevation(elevation_ls))
```

---

`pick_drop`

*Pick and drop rows from ViewFullTable, tree, and stem tables.*

---

**Description**

These functions provide an expressive and convenient way to pick specific rows from ForestGEO datasets. They allow you to remove missing values (with `na.rm = TRUE`) but conservatively default to preserving them. This behavior is similar to `base::subset()` and unlike `dplyr::filter()`. This conservative default is important because you want to include missing trees in your analysis.



**Usage**

```
pick_dbh_min(data, value, na.rm = FALSE)

pick_dbh_max(data, value, na.rm = FALSE)

pick_dbh_under(data, value, na.rm = FALSE)

pick_dbh_over(data, value, na.rm = FALSE)

pick_status(data, value, na.rm = FALSE)

drop_status(data, value, na.rm = FALSE)
```

**Arguments**

data	A ForestGEO-like dataframe: A <i>ViewFullTable</i> , <i>tree</i> or <i>stem</i> table.
value	An atomic vector; a single value against to compare each value of the variable encoded in the function's name.
na.rm	Set to TRUE if you want to remove missing values from the variable encoded in the function's name.

**Value**

A dataframe similar to `.data` but including only the rows with matching conditions.

**See Also**

`dplyr::filter()`, `Extract (L)`.

Other functions for fgeo census and vft: [guess\\_plotdim\(\)](#)

Other functions for fgeo census: [add\\_status\\_tree\(\)](#), [add\\_var\(\)](#), [guess\\_plotdim\(\)](#)

Other functions for fgeo vft: [add\\_status\\_tree\(\)](#), [add\\_subquad\(\)](#), [add\\_var\(\)](#), [guess\\_plotdim\(\)](#)

Other functions to pick or drop rows of a ForestGEO dataframe: [pick\\_main\\_stem\(\)](#)

**Examples**

```
# styler: off
census <- tribble(
  ~dbh, ~status,
  0,     "A",
  50,    "A",
  100,   "A",
  150,   "A",
  NA,    "M",
  NA,    "D",
  NA,    NA
)
# styler: on
```

```
# <=
pick_dbh_max(census, 100)
pick_dbh_max(census, 100, na.rm = TRUE)

# >=
pick_dbh_min(census, 100)
pick_dbh_min(census, 100, na.rm = TRUE)

# <
pick_dbh_under(census, 100)
pick_dbh_under(census, 100, na.rm = TRUE)

# >
pick_dbh_over(census, 100)
pick_dbh_over(census, 100, na.rm = TRUE)
# Same, but `subset()` does not let you keep NAs.
subset(census, dbh > 100)

# ==
pick_status(census, "A")
pick_status(census, "A", na.rm = TRUE)

# !=
drop_status(census, "D")
drop_status(census, "D", na.rm = TRUE)

# Compose
pick_dbh_over(
  drop_status(census, "D", na.rm = TRUE),
  100
)

# More readable as a pipeline
census %>%
  drop_status("D", na.rm = TRUE) %>%
  pick_dbh_over(100)

# Also works with ViewFullTables
# styler: off
vft <- tribble(
  ~DBH, ~Status,
  0, "alive",
  50, "alive",
  100, "alive",
  150, "alive",
  NA, "missing",
  NA, "dead",
  NA, NA
)
# styler: on

pick_dbh_max(vft, 100)
```

```
pick_status(vft, "alive", na.rm = TRUE)
```

---

pick_main_stem	<i>Pick the main stem or main stemid(s) of each tree in each census.</i>
----------------	--

---

### Description

- `pick_main_stem()` picks a unique row for each treeID per census.
- `pick_main_stemid()` picks a unique row for each stemID per census. It is only useful when a single stem was measured twice in the same census, which sometimes happens to correct for the effect of large buttresses.

### Usage

```
pick_main_stem(data)
```

```
pick_main_stemid(data)
```

### Arguments

data                    A ForestGEO-like dataframe: A *ViewFullTable*, *tree* or *stem* table.

### Details

- `pick_main_stem()` picks the main stem of each tree in each census. It collapses data of multi-stem trees by picking a single stem per treeid per censusid. From this group, it picks the stem at the top of a list sorted first by descending order of hom and then by descending order of dbh. This this corrects the effect of buttresses and picks the main stem. It ignores groups of grouped data and rejects data with multiple plots.
- `pick_main_stemid()` does one step less than `pick_main_stem()`. It only picks the main stemid(s) of each tree in each census and keeps all stems per treeid. This is useful when calculating the total basal area of a tree, because you need to sum the basal area of each individual stem as well as sum only one of the potentially multiple measurements of each buttressed stem per census.

### Value

A dataframe with a single plotname, and one row per per treeid per censusid.

### Warning

These functions may be considerably slow. They are fastest if the data already has a single stem per treeid. They are slower with data containing multiple stems per treeid (per censusid), which is the main reason for using this function. The slowest scenario is when data also contains duplicated values of stemid per treeid (per censusid). This may happen if trees have buttresses, in which

case these functions check every stem for potential duplicates and pick the one with the largest hom value.

For example, in a windows computer with 32 GB of RAM, a dataset with 2 million rows with multiple stems and buttresses took about 3 minutes to run. And a dataset with 2 million rows made up entirely of main stems took about ten seconds to run.

### See Also

Other functions to pick or drop rows of a ForestGEO dataframe: [pick\\_drop](#)

### Examples

```
# One `treeID` with multiple stems.
# `stemID == 1.1` has two measurements (due to buttresses).
# `stemID == 1.2` has a single measurement.
# styler: off
census <- tribble(
  ~sp, ~treeID, ~stemID, ~hom, ~dbh, ~CensusID,
  "sp1", "1", "1.1", 140, 40, 1, # main stemID (max `hom`)
  "sp1", "1", "1.1", 130, 60, 1,
  "sp1", "1", "1.2", 130, 55, 1 # main stemID (only one)
)
#' # styler: on

# Picks a unique row per unique `treeID`
pick_main_stem(census)

# Picks a unique row per unique `stemID`
pick_main_stemid(census)
```

---

read\_vft

*Import ViewFullTable or ViewTaxonomy data from a .tsv or .csv file.*

---

### Description

[read\\_vft\(\)](#) and [read\\_taxa\(\)](#) help you to read *ViewFullTable* and *ViewTaxonomy* data from text files delivered by the ForestGEO database. These functions avoid common problems about column separators, missing values, column names, and column types.

### Usage

```
read_vft(file, delim = NULL, na = c("", "NA", "NULL"), ...)
```

```
read_taxa(file, delim = NULL, na = c("", "NA", "NULL"), ...)
```

**Arguments**

file	A path to a file.
delim	Single character used to separate fields within a record. The default (delim = NULL) is to guess between comma or tab (", " or "\t").
na	Character vector of strings to interpret as missing values. Set this option to character() to indicate no missing values.
...	Other arguments passed to <code>readr::read_delim()</code> .

**Value**

A [tibble](#).

**Acknowledgments**

Thanks to Shameema Jafferjee Esufali for inspiring the feature that automatically detects delim (issue 65).

**See Also**

[readr::read\\_delim\(\)](#), [type\\_vft\(\)](#), [type\\_taxa\(\)](#).

Other functions to read text files delivered by ForestGEO's database: [type\\_vft\(\)](#)

**Examples**

```
assert_is_installed("fgeo.x")
library(fgeo.x)

example_path()

file_vft <- example_path("view/vft_4quad.csv")
read_vft(file_vft)

file_taxa <- example_path("view/taxa.csv")
read_taxa(file_taxa)
```

---

sanitize\_vft

*Fix common problems in ViewFullTable and ViewTaxonomy data.*

---

**Description**

These functions fix common problems of *ViewFullTable* and *ViewTaxonomy* data:

- Ensure that each column has the correct type.
- Ensure that missing values are represented with NAs – not with the literal string "NULL".

**Usage**

```
sanitize_vft(.data, na = c("", "NA", "NULL"), ...)

sanitize_taxa(.data, na = c("", "NA", "NULL"), ...)
```

**Arguments**

.data	A dataframe; either a ForestGEO <i>ViewFullTable</i> ( <code>sanitize_vft()</code> ). or <i>View-Taxonomy</i> ( <code>sanitize_vft()</code> ).
na	Character vector of strings to interpret as missing values. Set this option to <code>character()</code> to indicate no missing values.
...	Arguments passed to <code>readr::type_convert()</code> .

**Value**

A dataframe.

**Acknowledgments**

Thanks to Shameema Jafferjee Esufali for motivating this functions.

**See Also**

[read\\_vft\(\)](#).

**Examples**

```
assert_is_installed("fgeo.x")

vft <- fgeo.x::vft_4quad

# Introduce problems to show how to fix them
# Bad column types
vft[] <- lapply(vft, as.character)
# Bad representation of missing values
vft$PlotName <- "NULL"

# "NULL" should be replaced by `NA` and `DBH` should be numeric
str(vft[c("PlotName", "DBH")])

# Fix
vft_sane <- sanitize_vft(vft)
str(vft_sane[c("PlotName", "DBH")])

taxa <- read.csv(fgeo.x::example_path("taxa.csv"))
# E.g. inserting bad column types
taxa[] <- lapply(taxa, as.character)
# E.g. inserting bad representation of missing values
taxa$SubspeciesID <- "NULL"
```

```
# "NULL" should be replaced by `NA` and `ViewID` should be integer
str(taxa[c("SubspeciesID", "ViewID")])

# Fix
taxa_sane <- sanitize_taxa(taxa)
str(taxa_sane[c("SubspeciesID", "ViewID")])
```

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