

Package ‘SticsRFiles’

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Title Read and Modify STICS Input/Output Files

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Description Manipulating input and output files of the 'STICS' crop model (Beaudouin et al. (2022) <[doi:10.35690/978-2-7592-3679-4](https://doi.org/10.35690/978-2-7592-3679-4)>). The package is based on the model software, which is accessible, as well as resources, on its web site <<https://stics.inrae.fr/eng/>>. Files are either 'JavaSTICS' XML files or text files used by the model 'fortran' executable. Most basic functionalities are reading or writing parameter names and values in both XML or text input files, and getting data from output files. Advanced functionalities include XML files generation from XML templates and/or spreadsheets, or text files generation from XML files by using 'xslt' transformation.

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URL <https://github.com/SticsRPacks/SticsRFiles>,
<https://doi.org/10.5281/zenodo.4443206>

BugReports <https://github.com/SticsRPacks/SticsRFiles/issues>

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'all_out_var.R' 'approx_vapour_pressure.R'
'attributes_list2matrix.R' 'check_choice_param.R'
'check_java_path.R' 'check_java_workspace.R'
'check_output_files.R' 'check_param_names.R'
'check_upgrade_versions.R' 'col_names_to_var.R'
'compute_date_from_day.R' 'compute_day_number.R'
'convert_xml2txt.R' 'convert_xml2txt_int.R' 'download_data.R'
'download_usm_xl.R' 'exist_param_xml.R'
'exists_javastics_pref.R' 'exists_param.R'
'expand_stics_names.R' 'extract.R' 'extract_workspace.R'
'global.R' 'file_document.R' 'find_names.R'
'force_param_values.R' 'gen_climate.R'
'gen_general_param_xml.R' 'gen_ini_doc.R' 'gen_ini_xml.R'
'gen_new_travail.R' 'gen_obs.R' 'gen_paramsti.R'
'gen_sol_xsl_file.R' 'gen_sols_xml.R' 'gen_sta_doc.R'
'gen_sta_xml.R' 'gen_tec_doc.R' 'gen_tec_xml.R'
'gen_usms_sols_doc.R' 'gen_usms_xml.R' 'gen_usms_xml2txt.R'
'gen_varmod.R' 'get_climate_txt.R' 'get_cores_nb.R'
'get_cultivars_list.R' 'get_cultivars_param.R'
'get_dev_stages.R' 'get_file.R' 'get_file_int.R'
'get_files_list.R' 'get_formalisms_xml.R'
'get_java_workspace.R' 'get_lai_forcing.R'
'get_name_value_file_value.R' 'get_obs.R'
'get_option_choice_param_values.R' 'get_options_choices.R'
'get_options_names.R' 'get_param_bounds.R'
'get_param_bounds_xml.R' 'get_param_formalisms.R'
'get_param_info_xml.R' 'get_param_names.R'
'get_param_names_xml.R' 'get_param_number.R' 'get_param_txt.R'
'get_param_type.R' 'get_param_value.R' 'get_param_xml.R'
'get_params_dict.R' 'get_params_from_doc.R'
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'get_params_from_table.R' 'get_plant_name.R' 'get_plants_nb.R'
'get_report_results.R' 'get_sim.R' 'get_soils_list.R'
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'get_xml_base_doc.R' 'get_xml_base_node.R'
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'set_param_xml.R' 'set_sols_param_xml.R' 'set_usms_param_xml.R'

'setup_parallelism.R' 'static_help.R' 'stics_environment.R'
 'stics_files_utils.R' 'upgrade_v10_v11.R' 'upgrade_v9_v10.R'
 'upgrade_xml_files.R' 'var_to_col_names.R' 'xml_document.R'
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approx_vapour_pressure

Approximate vapour pressure

Description

Approximates vapour pressure as the saturated vapour pressure at the daily mean air temperature using relative humidity. See section 9.3 of the STICS book, as well as M. Launay's explanations on the STICS forum ([link](#)).

Usage

```
approx_vapour_pressure(mean_temp, rel_humid)
```

Arguments

mean_temp	numeric vector of daily mean air temperature (in Celsius degrees)
rel_humid	numeric vector of relative humidity (in percentage)

Value

numeric vector

Author(s)

Timothee Flutre

Examples

```
approx_vapour_pressure(15, 60)
```

compute_date_from_day *Convert day number into date*

Description

Computes the date corresponding to a given day number (or vector of) with reference to a start year. Typically, the start year should be the year of a STICS simulation start, but not necessarily.

Usage

```
compute_date_from_day(day, start_year)
```

Arguments

day	day number(s) to be converted
start_year	year to be used as time reference (simulation start year).

Value

Date vector

Author(s)

Timothee Flutre

Examples

```
compute_date_from_day(day = 290, start_year = 1994)

compute_date_from_day(day = 700, start_year = 1994)

compute_date_from_day(day = 999, start_year = 1994)
```

compute_day_from_date *Convert date into day number*

Description

Computes the day number corresponding to a given date (or vector of) from the first day of a start year. Typically, the start year should be the year of a STICS simulation start. Leap years are properly handled.

Usage

```
compute_day_from_date(date, start_year = NULL)
```

Arguments

date	date(s) vector to be converted, in the character format ("YYYY-MM-DD") or Date format
start_year	year to be used as time reference (simulation start year). Optional.

Value

numeric vector

Author(s)

Timothee Flutre

Examples

```
compute_day_from_date(date = as.Date("2015-02-10"))
compute_day_from_date(date = "2015-02-10", start_year = 2014)

compute_day_from_date(date = as.Date("2009-02-10"), start_year = 2008)

dates <- c(as.Date("2008-02-10"), as.Date("2009-02-10"))
compute_day_from_date(date = dates, start_year = 2008)
```

convert_xml2txt*Transforming a STICS xml file into a text file*

Description

The input file according to his type (ini,plant,tec,station,soil,par) is converted to a text file readable by the STICS model (ficini.txt, ficplt1.txt,...)

Usage

```
convert_xml2txt(  
  file,  
  plant_id = 1,  
  soil_name = NULL,  
  out_dir = NULL,  
  save_as = NULL,  
  stics_version = "latest"  
)
```

Arguments

file	Path (including name) of the xml file to convert
plant_id	The plant identifier (main crop: 1 ; associated crop: 2)
soil_name	Soil name (optional, required for soil file)
out_dir	Path of the directory where to generate the file. Optional, set to the path of the input xml file by default
save_as	Name of the output file (optional, default: fixed name for STICS)
stics_version	the STICS files version to use (optional, default to latest).

Value

None

Examples

```
xml_path <- file.path(get_examples_path("xml"), "file_plt.xml")  
convert_xml2txt(file = xml_path)  
xml_path <- file.path(get_examples_path("xml"), "sols.xml")  
convert_xml2txt(file = xml_path, soil_name = "soil_rice")
```

download_data	<i>Download example USMs</i>
---------------	------------------------------

Description

Download locally the example data from the [data repository](#) in the SticsRPacks organization.

Usage

```
download_data(
  branch = NULL,
  out_dir = tempdir(),
  example_dirs = NULL,
  stics_version = "latest",
  raise_error = FALSE
)
```

Arguments

branch	Git branch name (optional)
out_dir	Path of the directory where to download the data (optional, default: tempdir())
example_dirs	List of use case directories names (optional)
stics_version	Name of the STICS version (optional) The default value is the latest version returned by get_stics_versions_compat().
raise_error	Logical, if TRUE, an error is raised instead of message when FALSE (default)

Value

The path of the folder data have been downloaded into or NULL if the download fails and raise_error is FALSE.

Examples

```
# Getting data for a given example : study_case_1 and a given STICS version
download_data(example_dirs = "study_case_1", stics_version = "V9.0")
# raising an error instead of a message
download_data(
  example_dirs = "study_case_1", stics_version = "V9.0",
  raise_error = TRUE
)
```

download_usm_csv	<i>Downloading a CSV usms data file example into a directory</i>
------------------	--

Description

The file is an example that can be used for generating JavaSTICS usms.xml input file from parameters values stored in a CSV file using the function [gen_usms_xml](#)

Usage

```
download_usm_csv(  
  file = NULL,  
  out_dir = tempdir(),  
  stics_version = "latest",  
  overwrite = FALSE,  
  verbose = FALSE  
)
```

Arguments

file	Name of a csv file (optional, not used for the moment)
out_dir	Directory path where to copy the csv file (default: tempdir())
stics_version	Name of the STICS version. Optional, by default the latest version returned by <code>get_stics_versions_compat()</code> is used.
overwrite	Optional logical, TRUE for overwriting files, FALSE otherwise (default)
verbose	Logical value for displaying information while running

Value

A vector of copied files path.

Examples

```
download_usm_csv()
```

download_usm_xl

*Downloading an Excel usms data file example into a directory***Description**

The file is an example that can be used for generating JavaSTICS input files from parameters values stored in Excel spreadsheet format (USMs, Ini, Soils, Tec, Station, ...). Each sheet contains parameters values to insert into XML files, with the help of these functions: [gen_usms_xml](#), [gen_sols_xml](#), [gen_tec_xml](#), [gen_sta_xml](#), [gen_usms_xml](#), [gen_ini_xml](#)

Usage

```
download_usm_xl(
  file = NULL,
  out_dir = tempdir(),
  stics_version = "latest",
  overwrite = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

file	Name of an Excel file (optional, not used for the moment)
out_dir	Directory path where to copy the Excel file (optional, default: tempdir())
stics_version	Name of the STICS version. Optional, by default the latest version returned by <code>get_stics_versions_compat()</code> is used.
overwrite	Optional logical, TRUE for overwriting files, FALSE otherwise (default)
verbose	Logical value for displaying information while running
...	Additional arguments to be passed

Value

A vector of copied files path.

Examples

```
download_usm_xl()
```

extract_workspace	<i>Extract an XML JavaSTICS workspace from a source workspace</i>
-------------------	---

Description

Extract an XML JavaSTICS workspace from a source workspace

Usage

```
extract_workspace(
    from_workspace,
    to_workspace,
    javastics,
    usm = NULL,
    use_mod_files = FALSE
)
```

Arguments

from_workspace	Source workspace path
to_workspace	Target workspace path
javastics	JavaSTICS directory path, needed for getting plant files which are stored in JavaSTICS plant directory, or general parameters files and *.mod files from the config directory
usm	vector of situation names (i.e. USMs to extract.)
use_mod_files	Logical: if TRUE, *.mod files are searched in the from_workspace and copied to the to_workspace if found. Default is FALSE.

Value

None

Examples

```
## Not run:
# Extract all usms from a source workspace to a target workspace
extract_workspace(
  "/path/to/source/workspace",
  "/path/to/target/workspace",
  "/path/to/javastics/dir"
)

# Extract only selected usms from a source workspace to a target workspace
extract_workspace("/path/to/source/workspace",
  "/path/to/target/workspace",
  "/path/to/javastics/dir",
  usm = c("SugarCane", "potato")
)
```

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

force_param_values	<i>Generates files to force parameters values in STICS simulations</i>
--------------------	--

Description

Generates a param.sti file and sets code optim in new_travail.usm to force parameters values in STICS simulations (this function is typically called before SticsOnR::run_stics())

Usage

```
force_param_values(workspace, values, javastics, force = FALSE)
```

Arguments

workspace	Path of the workspace containing the STICS (txt) input files.
values	named vector of parameter values to force. See Details for more information.
javastics	Path of JavaSTICS
force	Logical, if TRUE, unknown parameter names only trigger a warning and are still written to param.sti. If FALSE (default), unknown parameter names trigger an error.

Details

This function operates on STICS text input files. Do not use it before calling gen_usms_xml2txt(), otherwise param.sti and new_travail.usm files will be overwritten.

This function has been created to be called before SticsOnR::run_stics(). It can not work with SticsOnR::run_javastics(), that will overwrite param.sti and new_travail.usm files.

values can contain NA. In this case, the corresponding parameter(s) will not be forced (default value(s), i.e. read in STICS input files, will be used). If values==NA or values==NULL, not any parameter will be forced (all default values used).

Value

A logical status TRUE if successful, FALSE otherwise

See Also

SticsOnR::run_stics()

Examples

```
## Not run:
example_txt_dir <- get_examples_path(file_type = "txt")
force_param_values(example_txt_dir,
  setNames(object = c(220, 330), c("stlevamf", "stamflax")),
  javastics = "/path/to/javastics"
)

## End(Not run)
```

gen_general_param_xml *Generate STICS general parameters xml file(s) from a template file according to a STICS version*

Description

Generate STICS general parameters xml file(s) from a template file according to a STICS version

Usage

```
gen_general_param_xml(out_dir, stics_version = "latest", overwrite = FALSE)
```

Arguments

out_dir	Path of the directory where to generate the file(s).
stics_version	Name of the STICS version. Optional, the latest one is used as default
overwrite	Optional logical, TRUE for overwriting files, FALSE otherwise (default)

Details

Please see `get_stics_versions_compat()` for the full list of STICS versions that can be used for the argument `stics_version`.

Value

None

Examples

```
gen_general_param_xml(out_dir = tempdir())

gen_general_param_xml(
  out_dir = tempdir(),
  stics_version = "V10.0",
  overwrite = TRUE
)
```

gen_ini_xml

*Generate STICS ini xml file(s) from a template or an input file***Description**

Generate STICS ini xml file(s) from a template or an input file

Usage

```
gen_ini_xml(
  param_df,
  file = NULL,
  out_dir,
  crop_tag = "Crop",
  stics_version = "latest"
)
```

Arguments

param_df	A table (df, tibble) containing the values of the parameters to use (see details)
file	Path of an ini xml file to be used as a template. Optional, if not provided, the function will use a standard template depending on the STICS version (see stics_version argument)
out_dir	Path of the directory where to generate the file(s).
crop_tag	identifier for the crop parameters names related to the main crop, or the associated crop if any (example: Crop is used in the param_table example in the details section below)
stics_version	Name of the STICS version. Optional, used if the file argument is not provided. In this case the function uses a standard template associated to the STICS version.

Details

Please see `get_stics_versions_compat()` for the full list of STICS versions that can be used for the argument `stics_version`.

`param_df` is a `data.frame` with the following format:

Ini_name	nbplantes	stade0_Crop1	lai0_Crop1	masec0_Crop1
USM_2017_T1_ini.xml	1	snu	0	0
Vill09_ini.xml	1	snu	0	0
Vill10_ini.xml	1	snu	0	0
Vill11_ini.xml	1	snu	0	0
Vill12_ini.xml	1	snu	0	0
Vill13_ini.xml	1	snu	0	0
Vill14_ini.xml	1	snu	0	0

Standard_ini.xml	1	snu	0	0
------------------	---	-----	---	---

The first column gives the ini file name (to be generated), all following columns give the parameter value to put in the file, and each line denotes a separate ini file (for e.g. several USMs).

The first column name must contain the keyword ini or Ini or INI as a prefix to be detected (as shown in the table extract above).

If not given (the default, NULL), the function returns the template as is.

Value

None

Examples

```
library(readxl)

xl_path <- download_usm_xl(file = "inputs_stics_example.xlsx")

ini_param_df <- read_excel(xl_path, sheet = "Ini")
gen_ini_xml(
  out_dir = tempdir(),
  param_df = ini_param_df[1:2, ]
)
```

gen_obs	<i>Generating observation data files from a data.frame</i>
---------	--

Description

Generating observation data files from a data.frame

Usage

```
gen_obs(df, out_dir, usms_list = NULL)
```

Arguments

df	A data frame containing the values of the observations to use (see Details).
out_dir	Path of the directory where to generate the file(s).
usms_list	An optional list of usms names to be used for selecting which files to generate from the obs_table

Details

df is a data.frame with the following format:

usm_name	ian	mo	jo	jul	densite	lai(n)	masec(n)	azomes
USM_2017_T1_CI	2017	9	6	249	NA	NA	0.31	27.07395
USM_2017_T1_CI	2017	9	20	263	NA	NA	0.60	27.90000
USM_2018_T1	2017	10	20	293	NA	0.1	NA	NA
USM_2018_T1	2018	5	15	482	NA	1.2	NA	NA

- usm_name column contains usms names which are used as output .obs files names
- ian, mo, jo and jul are mandatory (year, month, day and julian date)
- Other columns one per variable contain observations values or NA

@seealso [get_var_info](#) for getting variable right syntax or searching a variable name.

Value

A return logical status indicating if any error when writing files (FALSE), TRUE when no errors.

Examples

```
xl_path <- download_usm_xl(file = "inputs_stics_example.xlsx")
obs_df <- read_params_table(file = xl_path, sheet_name = "Obs")
gen_obs(df = obs_df, out_dir = "/path/to/dest/dir")
```

gen_sols_xml

Generate STICS sols xml file from a template or an input file

Description

Generate STICS sols xml file from a template or an input file

Usage

```
gen_sols_xml(file, param_df, template = NULL, stics_version = "latest")
```

Arguments

file	Path (including name) of the sols file to generate.
param_df	A table (df, tibble) containing the values of the parameters to use (see details)
template	Path of a soil xml file to be used as a template. Optional, if not provided, the function will use a standard template depending on the STICS version.
stics_version	Name of the STICS version. Optional, used if the file argument is not provided. In this case the function uses a standard template associated to the STICS version.

Details

Please see `get_stics_versions_compat()` for the full list of STICS versions that can be used for the argument `stics_version`.

`param_df` is a `data.frame` with the following format:

Soil_name	argi	norg	calc	pH	albedo	q0	epc_1
USM_T1	20.35000	0.100	0.52	8.23	0.22	9.630	30
LF1	17.00000	1.900	0.00	6.70	0.22	9.360	30
LF2	17.00000	1.800	0.00	6.70	0.22	9.360	30
LAP	22.00000	2.000	0.00	6.50	0.22	9.760	25
LAS	24.05000	2.500	30.00	8.00	0.22	9.928	30
LA0	30.00675	2.300	0.50	7.50	0.22	10.400	30
LC0	22.38750	2.000	10.00	7.90	0.22	9.792	25
Vill09	25.00000	0.101	0.40	7.90	0.22	10.000	30
Vill10	14.30000	0.099	1.50	8.20	0.22	9.144	30
Vill11	11.80000	0.100	0.00	7.30	0.22	8.944	30
Vill12	14.30000	0.091	0.60	8.30	0.22	9.144	30
Vill13	16.80000	0.088	0.20	7.80	0.22	9.344	30
Vill14	15.10000	0.095	1.30	7.90	0.22	9.208	30

The first column gives the soil name, all following columns give the parameter values to put in the `sols.xml` file for each soil row.

The first column name must contain the keyword `Soil` or `soil` or `SOIL` as a prefix to be detected (as shown in the table extract above).

If not given (the default, `NULL`), the function returns the template as is.

Value

None

Examples

```
xl_path <- download_usm_xl(file = "inputs_stics_example.xlsx")

sols_param_df <- read_params_table(file = xl_path, sheet_name = "Soils")
gen_sols_xml(
  file = file.path(tempdir(), "sols.xml"),
  param_df = sols_param_df
)
```

gen_sta_xml

*Generate STICS sta xml file(s) from a template or an input file***Description**

Generate STICS sta xml file(s) from a template or an input file

Usage

```
gen_sta_xml(param_df, file = NULL, out_dir, stics_version = "latest")
```

Arguments

param_df	A table (df, tibble) containing the values of the parameters to use (see details)
file	Path of a sta xml file to be used as a template. Optional, if not provided, the function will use a standard template depending on the STICS version.
out_dir	Path of the directory where to generate the file(s).
stics_version	Name of the STICS version. Optional, used if the file argument is not provided. In this case the function uses a standard template associated to the STICS version.

Details

Please see `get_stics_versions_compat()` for the full list of STICS versions that can be used for the argument `stics_version`.

`param_df` is a `data.frame` with the following format:

Sta_name	zr	NH3ref	latitude	patm	aclim
climatex_sta.xml	2.5	0	49	1000	20
climatex2_sta.xml	2.8	0	49	1000	20
climatex3_sta.xml	2.2	0	49	1000	20

The first column gives the sta file name (to be generated), all following columns give the parameter value to put in the file, and each line denotes a separate sta file (for e.g. several USMs).

The first column name must contain the keyword `sta` or `Sta` or `STA` as a prefix to be detected (as shown in the table extract above).

If not given (the default, `NULL`), the function returns the template as is.

Value

None

Examples

```
xl_path <- download_usm_xl(file = "inputs_stics_example.xlsx")
sta_param_df <- read_params_table(file = xl_path, sheet_name = "Station")
gen_sta_xml(out_dir = tempdir(), param_df = sta_param_df)
```

gen_tec_xml	<i>Generate STICS tec xml file(s) from a template or an input file</i>
-------------	--

Description

Generate STICS tec xml file(s) from a template or an input file

Usage

```
gen_tec_xml(
  param_df,
  file_tmpl = NULL,
  out_dir,
  stics_version = "latest",
  na_values = NA
)
```

Arguments

param_df	A table (df, tibble) containing the values of the parameters to use (see details)
file_tmpl	Path of a tec xml file to be used as a template. Optional, if not provided, the function will use a standard template depending on the STICS version.
out_dir	Path of the directory where to generate the file(s).
stics_version	Name of the STICS version. Optional, used if the file_tmpl argument is not provided. In this case the function uses a standard template associated to the STICS version.
na_values	value to use as missing value in param_table (optional, default : NA)

Details

Please see `get_stics_versions_compat()` for the full list of STICS versions that can be used for the argument `stics_version`.

`param_df` is a `data.frame` with the following format:

Tec_name	julres_1	coderes_1
USM_2017_T1_CI_tec.xml	NA	1
BIN_CANPC_05_SEC_220-0-0_34K_CANPC05T3_Q_tec.xml	110	1
BIN_AGT_04_IRR_220-0-0_33K_AGT04T2_Q_tec.xml	73	1
AGA_ARB_13_IRR_220-0-0_37K_ARB13_C_tec.xml	82	1

AGA_ARB_13_SEC_220-0-0_37K_ARB13_C_tec.xml	82	1
FRA_ARB_11_SEC_220-0-0_38K_E_tec.xml	70	1
MAG_ARB_09_SEC_220-0-0_38K_E_tec.xml	81	1
MAG_ARV_12_IRR_220-0-0_36K_ARV12_C_tec.xml	100	1
MAG_ARV_12_SEC_220-0-0_36K_ARV12_C_tec.xml	100	1
FRA_ARB_12_SEC_220-0-0_31K_ARB12_C_tec.xml	92	1
FRA_ARB_13_SEC_220-0-0_37K_ARB13_C_tec.xml	82	1

The first column gives the tec file name (to be generated), all following columns give the parameter value to put in the file, and each line denotes a separate tec file (for e.g. several USMs).

The first column name must contain the keyword tec or Tec or TEC as a prefix to be detected (as shown in the table extract above).

If not given (the default, NULL), the function returns the template as is.

Value

None

Examples

```
xl_path <- download_usm_xl(file = "inputs_stics_example.xlsx")
tec_param_df <- read_params_table(file = xl_path, sheet_name = "Tec")
gen_tec_xml(out_dir = tempdir(), param_df = tec_param_df[1:2, ])
```

gen_usms_xml	<i>Generate STICS usms xml file from a template or an input file</i>
--------------	--

Description

Generate STICS usms xml file from a template or an input file

Usage

```
gen_usms_xml(file, param_df, template = NULL, stics_version = "latest")
```

Arguments

file	Path (including name) of the usms file to generate.
param_df	A table (df, tibble) containing the values of the parameters to use (see details)
template	Path of an USM xml file to be used as a template. Optional, if not provided, the function will use a standard template depending on the STICS version.
stics_version	Name of the STICS version. Optional, used if the file argument is not provided. In this case the function uses a standard template associated to the STICS version.

Details

Please see `get_stics_versions_compat()` for the full list of STICS versions that can be used for the argument `stics_version`.

`param_df` is a `data.frame` with the following format:

usm_name	datedebut	datefin	nomsol
USM_2017_T1_CI	199	263	USM_T1
USM_2018_T1	264	570	USM_T1
BIN_CANPC_05_SEC_220-0-0_34K_CANPC05T3_Q	199	263	LF1
BIN_AGT_04_IRR_220-0-0_33K_AGT04T2_Q	264	570	LF1
AGA_ARB_13_IRR_220-0-0_37K_ARB13_C	199	263	F1
AGA_ARB_13_SEC_220-0-0_37K_ARB13_C	264	570	LF1
FRA_ARB_11_SEC_220-0-0_38K_E	199	263	LF1
MAG_ARB_09_SEC_220-0-0_38K_E	264	570	LF1
MAG_ARV_12_IRR_220-0-0_36K_ARV12_C	199	263	LF1
MAG_ARV_12_SEC_220-0-0_36K_ARV12_C	264	570	LF1
FRA_ARB_12_SEC_220-0-0_31K_ARB12_C	199	263	LF1
FRA_ARB_13_SEC_220-0-0_37K_ARB13_C	264	570	LF1

The first column gives the usm name, all following columns give the parameter values to put in the `usms.xml` file for each usm row.

The first column name must contain the keyword `Usm` or `usm` or `USM` as a prefix to be detected (as shown in the table extract above).

If not given (the default, `NULL`), the function returns the template as is.

Value

an invisible `xml_document` object

Examples

```
xl_path <- download_usm_xl(file = "inputs_stics_example.xlsx")
usms_param_df <- read_params_table(file = xl_path, sheet_name = "USMs")
gen_usms_xml(
  file = file.path(tempdir(), "usms.xml"),
  param_df = usms_param_df
)
```

Description

The function creates sets of input files for one or multiple usms from usms data stored in a JavaSTICS workspace. For multiple usms, sets will be generated into individual folders named with usm names. Observations files will be also copied if they are named [usm_name].obs For one usm, files will be generated either in the workspace directory or in a subdirectory.

Usage

```
gen_usms_xml2txt(
  javastics = NULL,
  workspace = NULL,
  out_dir = NULL,
  usm = NULL,
  stics_version = "latest",
  verbose = TRUE,
  dir_per_usm_flag = TRUE,
  java_cmd = "java",
  java_converter = FALSE,
  parallel = FALSE,
  cores = NA
)
```

Arguments

javastics	Path of JavaSTICS. Optional (needed if the JavaSTICS converter is used, java_converter set to TRUE in inputs)
workspace	Path of a JavaSTICS workspace (i.e. containing the STICS XML input files). Optional, if not provided the current workspace stored in JavaSTICS preferences will be used.
out_dir	The path of the directory where to create usms directories (Optional), if not provided the JavaSTICS workspace will be used as root
usm	List of usms to generate (Optional). If not provided, all usms contained in workspace/usms.xml file will be generated.
stics_version	the STICS files version to use (optional, default to latest).
verbose	Logical value TRUE (default) for displaying information while running, FALSE otherwise
dir_per_usm_flag	logical, optional; TRUE (default) if one want to create one directory per USM, FALSE if USM files are generated in the out_dir (only useful for usm of size one)
java_cmd	For unix like systems, the java virtual machine command name or executable path. Useful only if the JavaSTICS command line is used for generating files. "java" is the default system command, but a full path to a java executable (other than the default one) may be given
java_converter	logical, optional; TRUE for using the JavaSTICS command (a JavaSTICS path must be set in the function inputs), FALSE otherwise (default)

parallel	Boolean. Is the computation to be done in parallel ?
cores	Number of cores to use for parallel computation.

Value

A list with named elements: usms_path : created directories paths (for storing STICS input files), files : generated files list (in JavaSTICS workspace origin), copy_status : logical value vector, indicating if all files have been generated for each usm obs_copy_status : logical value vector, indicating if observation files have been successfully copied in usms directories

Examples

```
## Not run:
javastics <- "/path/to/JavaSTICS/folder"
workspace <- "/path/to/workspace"

# For all usms
gen_usms_xml2txt(javastics, workspace)

# For an usms list
usm_list <- c("usm1", "usm2")
gen_usms_xml2txt(javastics, workspace, usms = usm_list)

## End(Not run)
```

gen_varmod	<i>Generating a var.mod type file</i>
------------	---------------------------------------

Description

Generating a daily variable list file from variables names

Usage

```
gen_varmod(
  workspace,
  var,
  append = FALSE,
  file_name = "var.mod",
  stics_version = "latest",
  force = FALSE,
  verbose = FALSE
)
```

Arguments

workspace	Path of the directory containing the STICS var.mod file to modify
var	vector of variables names (see details)
append	if TRUE, var data are appended to file_name
file_name	file name to generate (without path, default value: "var.mod")
stics_version	Name of the STICS version (used to check variable names)
force	Force variables writing even if they are not a STICS variable (default: FALSE).
verbose	if TRUE displaying warning, FALSE otherwise (default)

Details

Variable names can be found using `get_var_info()`. They are checked before writing. If any variable name does not exist, it will not be written by default, but the function will still write the variables that exist. `force= TRUE` may however be used to write variables that do not exist. Variables already present in a var.mod file can be listed using `get_varmod()`.

Value

None

Examples

```
# generate a new file
gen_varmod(tempdir(), c("lai(n)", "hauteur"))
# Add a variable to the others
# var.mod will contain now "lai(n)", "hauteur" and "masec(n)"
gen_varmod(tempdir(), "masec(n)", append = TRUE)
```

get_climate_txt	<i>Read STICS input meteorology file</i>
-----------------	--

Description

Read the meteorology input for STICS ("climat.txt")

Usage

```
get_climate_txt(workspace, file_name = "climat.txt", preserve = TRUE)
```

Arguments

workspace	Path of the workspace containing the STICS climate file to read
file_name	The meteorology file name (default to climat.txt).
preserve	Logical, TRUE`` for keeping the STICS columns related to date calculation (year, month, da

Value

A data.frame of the input meteorological variables used as input for the STICS model.

Note

The time-related variables are summarized into one POSIXct column named date.

Examples

```
path <- get_examples_path(file_type = "txt")
meteo_data <- get_climate_txt(path)
```

get_cultivars_list	<i>Get the cultivar names for an xml plant file (*_plt.xml)</i>
--------------------	---

Description

Extracts the cultivar names from a plant file

Usage

```
get_cultivars_list(file)
```

Arguments

file	The path of a plant file.
------	---------------------------

Value

A vector of cultivar names

Examples

```
path <- get_examples_path(file_type = "xml")

# Read from a plant file (all cultivars available in a plant file)
cv_list <- get_cultivars_list(file = file.path(path, "file_plt.xml"))
```

get_cultivars_param	<i>Get the values of cultivar-specific parameters from an xml plant file (*_plt.xml)</i>
---------------------	--

Description

Extracts the values of cultivar-specific parameters from a plant file

Usage

```
get_cultivars_param(file)
```

Arguments

file	The path of a plant file.
------	---------------------------

Value

A data.frame with one row per cultivar and one column per parameter

Examples

```
path <- get_examples_path(file_type = "xml")

# Read from a plant file (all cultivars available in a plant file)
cv_param_df <- get_cultivars_param(file = file.path(path, "file_plt.xml"))
```

get_dev_stages	<i>Get developmental stages from simulations</i>
----------------	--

Description

Extracts the values of developmental stages from simulations

Usage

```
get_dev_stages(
  sim,
  dev_vars = c("iplts", "imbs", "ilets", "igers", "idebdorms", "ifindorms", "ilevs",
    "iamfs", "ilaxs", "ilats", "iflos", "idrps", "inous", "idebdess", "imats", "irecs"),
  usm = NULL
)
```

Arguments

sim	A list, where each element is a data.frame of simulation results for the given usm. The list is named after the USM name.
dev_vars	Vector of output variables corresponding to developmental stages.
usm	Vector of USM names. Optional, if not provided, the function returns the results for all USMs.

Value

List of data.frame, one per USM, with one row per developmental stage.

Author(s)

Timothee Flutre

See Also

[get_sim](#)

Examples

```
## Not run:
simulations <- get_sim(workspace)
get_dev_stages(simulations, "iplts")

## End(Not run)
```

get_examples_path	<i>Getting examples files path attached to a STICS version for a given file type</i>
-------------------	--

Description

Getting examples files path attached to a STICS version for a given file type

Usage

```
get_examples_path(file_type, stics_version = "latest", overwrite = FALSE)
```

Arguments

file_type	A file type string among files types or a vector of ("csv", "obs", "sti", "txt", "xml")
stics_version	Name of the STICS version. Optional, by default the latest version returned by get_stics_versions_compat() is used.
overwrite	TRUE for overwriting directory; FALSE otherwise

Value

A directory path for examples files for given file type and STICS version or a vector of (for unknown file types "" is returned as path)

Examples

```
get_examples_path(file_type = "csv")

get_examples_path(file_type = c("csv", "sti"))

get_examples_path(file_type = "csv", stics_version = "V8.5")
```

get_files_list	<i>Getting existing xml files path list per usm from an usms.xml file</i>
----------------	---

Description

Getting existing xml files path list per usm from an usms.xml file

Usage

```
get_files_list(
  workspace,
  usm = NULL,
  usms_file = "usms.xml",
  file_type = NULL,
  only_existing = TRUE,
  javastics = NULL,
  use_mod_files = FALSE
)
```

Arguments

workspace	Path of a JavaSTICS workspace (i.e. containing the STICS XML input files)
usm	Vector of usms names (optional)
usms_file	Path (including name) of a USM XML file (default: usms.xml).
file_type	Vector of file(s) type to get (optional; if not given, all types are returned, see details)
only_existing	logical, optional; if TRUE (default) only existing files list is returned, FALSE otherwise for all files
javastics	Path of JavaSTICS (optional), only needed when the plant files, general parameter files or .mod files are not in the workspace but included in the JavaSTICS distribution
use_mod_files	logical, optional; if TRUE adding the .mod files to the list FALSE otherwise (default)

Details

The possible values for file_type are: "fplt", "finit", "fclim1", "fclim2", "fstation", "ftec", "sols", "pargen", "parnew", "usms", "mod"

Value

A named list (usms names) with files path in paths field and a logical vector in exist field indicating if the file exists or not.

See Also

See get_soils_list() to get all soils in a usm file, and get_usms_list() to get the list of usms.

Examples

```
## Not run:

get_files_list(
  workspace = "/path/to/workspace",
  javastics = "/path/to/JavaSTICS/folder"
)

get_files_list(
  workspace = "/path/to/workspace",
  javastics = "/path/to/JavaSTICS/folder",
  usm = c("usm1", "usm3")
)

get_files_list(
  workspace = "/path/to/workspace",
  file_type = c("finit", "ftec")
)

get_files_list(
  workspace = "/path/to/workspace",
  use_mod_files = TRUE,
  javastics = "/path/to/JavaSTICS/folder"
)

## End(Not run)
```

get_lai_forcing

Getting LAI forcing for each usm

Description

Is LAI forced for usms in usms.xml

Usage

```
get_lai_forcing(usm_file_path, usms_list = c())
```

Arguments

```
usm_file_path  Path to usms.xml file
usms_list      Usm(s) name(s) (optional, see details)
```

Details

Use `get_usms_list()` to get the list of the usm names for an usms.xml file.

Value

A named numeric vector with a Boolean value (TRUE = forced) for each usm

Examples

```
# Xml case
xml_usms <- file.path(get_examples_path(file_type = "xml"), "usms.xml")
get_lai_forcing(xml_usms)
get_lai_forcing(xml_usms, "wheat")
get_lai_forcing(xml_usms, c("wheat", "intercrop_pea_barley"))
```

get_obs

Read STICS observation files (.obs)*

Description

Read STICS observation files from a JavaSTICS workspace and store data into a list per usm

Usage

```
get_obs(
  workspace,
  usm = NULL,
  var = NULL,
  dates = NULL,
  usms_file = NULL,
  javastics = NULL,
  verbose = TRUE,
  parallel = FALSE,
  cores = NA
)
```

Arguments

workspace	Vector of path(s) of directory(ies) containing the STICS observation files to read (*.obs file) or path of a single directory containing one sub-folder per USM (named as the USM names), each of them containing the corresponding files to read. In the second case, the argument usm must also be provided.
usm	Vector of USM names. Optional, if not provided, the function returns the results for all USMs.
var	Vector of variable names for which results have to be provided. Optional, all variables considered by default. See get_var_info() to get the list of STICS variables names.
dates	list of dates to filter (POSIX date)
usms_file	Path of a USM xml file. Optional, if provided, the plant names are added in the Plant column (see details).
javastics	Path of JavaSTICS. Optional, should be provided in addition to usms_file to get the plant codes if the plant files used are not in the workspace but in the JavaSTICS distribution (see Details).
verbose	Logical value for displaying or not information while running
parallel	Boolean. Is the computation to be done in parallel ?
cores	Number of cores to use for parallel computation.

Details

The .obs files names must match USMs names, *e.g.* for a usm called "banana", the .obs file should be named banana.obs. For intercrops, the name should be suffixed by "p" for the principal and "a" for the associated plant.

If usm is not specified (or equal to NULL), the function reads the files from all usms in the workspace(s).

If usms_file is provided and if the associated plant file is found, the plant names in the "Plant" column of the generated data.frame are either the plant code (as specified in the plant file) or the name of the plant file, if the plant file is not found.

If usms_file is not specified, the plants are named "plant_1" by default (+ "plant_2" for intercrops).

Value

A list, where each element is a data.frame of observations for the given usm. The list is named after the USM name.

Intercrops are returned in a single data.frame, and are identified using either the "Plant" or "Dominance" columns.

See Details section for more information about the "Plant" column.

Examples

```
path <- file.path(get_examples_path(file_type = "obs"), "mixed")

# Get observations for all usms, but only banana has observations:
Meas <- get_obs(path)
```

```
# Get observations only for banana:
Meas_banana <- get_obs(path, "banana")

## Not run:
# Get observations with real plant names when plant
# folder is not in the workspace:
get_obs(path, "banana", javastics = "/path/to/JavaSTICS/folder")

## End(Not run)
```

get_param_info

Finding parameters information using partial search words

Description

Helper function that returns names and descriptions of STICS input parameters from a partial name and/or descriptive keywords.

Usage

```
get_param_info(param = NULL, keyword = NULL, stics_version = "latest")
```

Arguments

param	Vector of parameter names (or partial names). Optional, if not provided, the function returns information for all parameters
keyword	Optional, strings or a vector of to be used for searching in parameters names and definition
stics_version	Name of the STICS version. Optional, can be used to search parameters information relative to a specific STICS version. By default the latest version returned by <code>get_stics_versions_compat()</code> is used.

Details

The function understand [regex](#) as input.

Value

A data.frame with information about parameter(s) with columns name, file, min, max, definition, unit and cultivar

Examples

```
# Find by parameter name (fuzzy search):
SticsRFiles::get_param_info("alb")
SticsRFiles::get_param_info("alb[e]?")

# Find by keyword (fuzzy search in parameter name and description):
SticsRFiles::get_param_info(keyword = "bdil")

# Find for a particular version:
SticsRFiles::get_param_info("alb", stics_version = "V9.0")

get_param_info()
```

get_param_txt	<i>Read STICS input parameters from text files</i>
---------------	--

Description

Read STICS model input parameters from a usm in text format (STICS input) Generally used after calling building a usm with JavaSTICS.

Read a specific STICS model input parameter file. Users would generally use the wrapper get_param_txt() instead.

Usage

```
get_param_txt(
  workspace,
  param = NULL,
  plant_id = NULL,
  variety = NULL,
  value_id = NULL,
  exact = FALSE,
  stics_version = "latest",
  ...
)

get_ini_txt(file = "ficini.txt", stics_version, workspace = NULL)

get_general_txt(file = "tempopar.sti", workspace = NULL)

get_tmp_txt(file = "tempoparv6.sti", workspace = NULL)

get_plant_txt(file = "ficplt1.txt", variety = NULL, workspace = NULL)

get_tec_txt(
  file = "fictec1.txt",
```

```

    stics_version = "latest",
    several_fert = NULL,
    several_thin = NULL,
    is_pasture = NULL,
    workspace = NULL,
    ...
)

get_soil_txt(file = "param.sol", stics_version, workspace = NULL)

get_station_txt(file = "station.txt", workspace = NULL)

get_usm_txt(file = "new_travail.usm", plant_id = NULL, workspace = NULL)

```

Arguments

workspace	Path of the workspace containing the STICS (txt) input files.
param	Vector of parameter names. Optional, if not provided, the function returns an object with all parameters.
plant_id	plant index (1, 2), default(NULL) calculated from from plant number in STICS initialization file
variety	Integer. The plant variety to get the parameter from.
value_id	index of technical interventions to be used to retrieve parameter values, or layer index for soil parameters
exact	Boolean indicating if the function must return results only for exact match.
stics_version	An optional version name as listed in get_stics_versions_compat() return
...	Further arguments to pass (for future-proofing only)
file	File path
several_fert	Is there several fertilization in the USM ? See details.
several_thin	Is there several thinning in the USM ? See details.
is_pasture	Is the plant a pasture ? See details.

Details

If the variety is not given and a param is asked, the function will return the values for the variety that is simulated in the USM by checking the variete parameter in the technical file. If param is not provided by the user, the values from all varieties will be returned unless the user ask for a given variety.

several_fert, several_thin and is_pasture are read from the tmp file (tempoparv6.sti). get_param_txt() does it automatically. If you absolutely need to use directly get_tec_txt, please see example.

Value

A list of parameters value(s), or if param = NULL a list of all parameters:

ini	Initialization parameters
general	General parameters
tec	Technical parameters
plant	Plant parameters
soil	Soil parameters
station	Station parameters

A list of parameters, depending on the file/function:

ini	Initialization parameters
general	General parameters
tec	Technical parameters
plant	Plant parameters
soil	Soil parameters
station	Station parameters
tmp	Temporary parameters

Note

Users would generally use get_param_txt to identify parameters names and values and pass them to other functions.

The functions are compatible with intercrops. Users generally only use get_param_txt(), which is a wrapper for all these functions.

See Also

gen_varmod(),
get_param_txt().

Examples

```
path <- get_examples_path(file_type = "txt")

# Getting the interrow distance parameter value
get_param_txt(path, param = "interrang")

# Getting varietal parameters values
# Get the leaf lifespan of the variety used in the usm:
get_param_txt(workspace = path, param = "durvieF")
# Get the leaf lifespan of another variety available in the plant file:
get_param_txt(workspace = path, param = "durvieF", variety = "Furio")
# To get the values for several (or all) varieties, either put all varieties:
varieties <- c("Pactol", "Cherif", "Furio", "Dunia", "Volga", "Cecilia")
get_param_txt(workspace = path, param = "durvieF", variety = varieties)
```

```

# Or get it from the output of the function returning all parameters:
get_param_txt(workspace = path)$plant$plant1$durvieF

# Get parameters for a specific plant
get_param_txt(workspace = path, plant_id = 1)
get_param_txt(workspace = path, param = "durvieF", plant_id = 1)
get_param_txt(
  workspace = path, param = "durvieF", plant_id = 1,
  variety = varieties
)

# Get parameters for specific interventions or soil layers
get_param_txt(workspace = path, param = "amount", value_id = c(1, 3))
get_param_txt(workspace = path, param = "Hinitf", value_id = c(1, 3))
get_param_txt(workspace = path, param = "epc", value_id = c(1, 3))

## Not run:
# Read the initialization file (ficini.txt):
library(SticsRFiles)
path <- file.path(get_examples_path(file_type = "txt"), "ficini.txt")
get_ini_txt(path)

# Read the tec file directly:

# First, get the parameters from the tmp file:
tmp <- get_tmp_txt(
  workspace = get_examples_path(file_type = "txt")
)
several_fert <- tmp$option_engrais_multiple == 1
several_thin <- tmp$option_thinning == 1
is_pasture <- tmp$option_pature == 1

# Then, get the technical parameters:
get_tec_txt(
  workspace = get_examples_path(file_type = "txt"),
  file = "fictec1.txt",
  several_fert = several_fert, several_thin = several_thin,
  is_pasture = is_pasture
)

## End(Not run)

```

get_param_xml

Getting parameter values from xml files

Description

Extracting parameter values for a list of xml files and parameters

Usage

```
get_param_xml(
  file,
  param = NULL,
  select = NULL,
  select_value = NULL,
  value_id = NULL,
  ...
)
```

Arguments

file	Vector of the xml file paths from which parameters values must be extracted
param	Vector of parameter names. Optional, if not provided, the function returns information for all parameters.
select	node name or attribute name to use for selection (optional, default to no selection)
select_value	Vector of values used for select (see examples). Optional, should be provided only if select is provided.
value_id	Vector of ids of the parameters values to be retrieved from the parameter values vector
...	Pass further arguments to get_param_value()

Value

A list of parameter values for each file (a list of list)

Examples

```
# Soil file
file <- file.path(get_examples_path(file_type = "xml"), "sols.xml")

# For all soils
get_param_xml(file)
get_param_xml(file, c("argi", "norg"))

# With soil selection
# scalar parameters per soil
get_param_xml(file, c("argi", "norg"),
  select = "sol", select_value = c("solcanne", "solbanane")
)

# Crop management file
file <- file.path(get_examples_path(file_type = "xml"), "file_tec.xml")

# Getting parameters for irrigation (date and quantity)
get_param_xml(file, c("julapI_or_sum_upvt", "amount"))
```

get_plants_nb	<i>Getting plants number per usm for all usms or selected from a usm name vector</i>
---------------	--

Description

Extracting plant number from usms.xml or new_travail.usm file data

Usage

```
get_plants_nb(usms_file, usms_list = c())
```

Arguments

usms_file	Path (including name) of a USM xml file or of a new_travail.usm file
usms_list	Usm(s) name(s) (optional, see details)

Details

Use get_usms_list() to get the list of the usm names for an usms.xml file.

Value

A named numeric vector of plants number per usm

Examples

```
# Xml case
xml_usms <- file.path(get_examples_path(file_type = "xml"), "usms.xml")
get_plants_nb(xml_usms)
get_plants_nb(xml_usms, "wheat")
get_plants_nb(xml_usms, c("wheat", "intercrop_pea_barley"))

# Txt case
txt_usm <- file.path(get_examples_path(file_type = "txt"), "new_travail.usm")
get_plants_nb(txt_usm)
```

get_report_results	<i>Extracting data from the STICS report file</i>
--------------------	---

Description

Extracting data from the STICS report file

Usage

```
get_report_results(  
  workspace,  
  file_name = "mod_rapport.sti",  
  usm = NULL,  
  var_list = NULL  
)
```

Arguments

workspace	Path of the directory containing the STICS report file to read.
file_name	A report file name among "mod_rapport.sti" (default), "mod_rapportA.sti", "mod_rapportP.sti"
usm	Vector of USM names. Optional, if not provided, the function returns the results for all USMs.
var_list	vector of output variables names to filter (optional, see get_var_info() to get the names of the variables)

Details

The data may be filtered using usm_name vector of usm names and and/or var_list vector of variables names. In the returned data.frame, variables names respect the same syntax as in the get_sim output.

Value

A data.frame

Examples

```
path <- get_examples_path(file_type = "sti")  
get_report_results(workspace = path)  
  
get_report_results(workspace = path, usm = c("DurumWheat", "grass"))  
  
get_report_results(workspace = path, var_list = c("masec(n)", "QNplante"))  
  
get_report_results(workspace = path, usm = c("DurumWheat", "grass"))  
  
get_report_results(workspace = path)
```

```
get_report_results(workspace = path, file_name = "mod_rapportA.sti")
```

get_sim

Load and format STICS daily output file(s)

Description

Reads and format daily output file(s) (mod_s*.sti) for usm(s) with possible selection on variable names, cumulative DOY and dates

Usage

```
get_sim(
  workspace,
  usm = NULL,
  var = NULL,
  dates = NULL,
  usms_file = NULL,
  javastics = NULL,
  verbose = TRUE,
  parallel = FALSE,
  cores = NA
)
```

Arguments

workspace	Vector of path(s) of directory(ies) containing the STICS output files to read (mod_s*.sti file) or path of a single directory containing one sub-folder per USM (named as the USM names), each of them containing the corresponding STICS output file to read. In the second case, the argument usm must also be provided.
usm	Vector of USM names. Optional, if not provided, the function returns the results for all USMs.
var	Vector of variable names for which results have to be provided. Optional, all variables considered by default. See get_var_info() to get the list of STICS variables names.
dates	list of dates to filter (POSIX date)
usms_file	Path of a USM xml file. Optional, if provided, the plant names are added in the Plant column (see details).
javastics	Path of JavaSTICS Optional, should be provided in addition to usms_file to get the plant codes if the plant files used are not in the workspace but in the JavaSTICS distribution (see Details).
verbose	Logical value for displaying or not information while running
parallel	Boolean. Is the computation to be done in parallel ?
cores	Number of cores to use for parallel computation.

Details

If usm is not specified (or equal to NULL), the function reads the files from all usms in the workspace(s).

If usms_file is provided and if the associated plant file is found, the plant names in the "Plant" column of the generated data.frame are either the plant code (as specified in the plant file) or the name of the plant file, if the plant file is not found.

If usms_file is not specified, the plants are named "plant_1" by default (+ "plant_2" for intercrops).

Value

A list, where each element is a data.frame of simulation results for the given usm. The list is named after the USM name.

Intercrops are returned in a single data.frame, and are identified using either the "Plant" or "Dominance" columns.

See Details section for more information about the "Plant" column.

Examples

```
path <- get_examples_path(file_type = "sti")
sim_data <- get_sim(path, "banana")
```

get_soils_list

Get the soil names for an usms.xml or sols.xml file

Description

Extracts the soil names from a USMs file, or from a soil file

Usage

```
get_soils_list(file, soil = NULL)
```

Arguments

file	Either the path of an usm file or of a soil file.
soil	Vector of soil names (or partial names). Optional, if not provided, the function returns the names of all the soils included in the given file.

Details

The file given as the file_path is either a "usms" file type to get all the soils used in a particular USM, or a soil file type ("sols") to get all soil types available in a soil file.

Value

A vector of soil names

Examples

```

path <- get_examples_path(file_type = "xml")

# Read from a usms file (soils used in a USM):
soil_list <- get_soils_list(file = file.path(path, "usms.xml"))

# Read from a soil file (all soil types available in a soil file)
soil_list <- get_soils_list(file = file.path(path, "sols.xml"))

soil_list <- get_soils_list(
  file = file.path(path, "usms.xml"),
  soil = c("solcanne", "sole")
)

```

```
get_stics_versions_compat
```

Get the compatible STICS versions

Description

Get the versions of STICS that are fully compatible with this package.

Usage

```
get_stics_versions_compat(version_index = NULL)
```

Arguments

`version_index` Absolute positive index, or negative relative index from latest version

Value

A named list with the STICS versions compatible with this package (`$versions_list`), and the latest version in use (`$latest_version`) or an existing version selected using `version_index`.

Examples

```

# Getting the complete versions list
get_stics_versions_compat()

# Getting the first version
get_stics_versions_compat(1)

# Getting the previous version of the latest one
get_stics_versions_compat(-1)

```

`get_usms_list`*Getting usms names list for an usms.xml file*

Description

Extracting a usm names list from an usms.xml file

Usage

```
get_usms_list(file, usm = NULL)
```

Arguments

<code>file</code>	Path (including name) of the USM xml file
<code>usm</code>	Vector of USM names (or partial names). Optional, if not provided, the function returns the names of all the USMs included in the given file.

Value

A vector of usm names

Examples

```
path <- get_examples_path(file_type = "xml")

usms_list <- get_usms_list(file = file.path(path, "usms.xml"))

usms_list <- get_usms_list(
  file = file.path(path, "usms.xml"),
  usm = c("usm1", "usm2")
)
```

`get_varmod`*Get desired STICS outputs*

Description

Get the STICS output variables (from var.mod file)

Usage

```
get_varmod(workspace, file_name = "var.mod")
```

Arguments

workspace	Path of the directory containing the STICS var.mod file
file_name	file name to read (without path, default value: "var.mod")

Details

A var.mod file can be created or modified using `gen_varmod()`.

Value

The variables that will be returned by STICS

See Also

`gen_varmod`

Examples

```
get_varmod(get_examples_path(file_type = "txt"))
```

get_var_info

Find STICS output variable names and description

Description

Helper function that returns names and descriptions of STICS output variables from a partial name and/or descriptive keywords.

Usage

```
get_var_info(var = NULL, keyword = NULL, stics_version = "latest")
```

Arguments

var	Vector of variable names (or partial names). Optional, if not provided, the function returns information for all variables.
keyword	Search by keyword instead of variable name (search in the name and description field)
stics_version	Name of the STICS version. Optional, can be used to search parameters information relative to a specific STICS version. By default the latest version returned by <code>get_stics_versions_compat()</code> is used.

Details

The function understand [regex](#) as input.

Value

A data.frame with information about variable(s) with columns name, definition, unit, type

Examples

```
# Find by variable name (fuzzy search):
SticsRFiles::get_var_info("lai")

# Find by keyword (fuzzy search in variable name and description):
SticsRFiles::get_var_info(keyword = "lai")

# Find for a particular version:
SticsRFiles::get_var_info("lai", stics_version = "V9.0")

get_var_info()
```

```
get_xml_files_param_df
```

Extracting a data.frame of parameters values for an xml file or a set of (whatever the xml file kind)

Description

Extracting a data.frame of parameters values for an xml file or a set of (whatever the xml file kind)

Usage

```
get_xml_files_param_df(file_path, param_names = NULL, wide_shape = FALSE)
```

Arguments

file_path	A file path or a vector of STICS XML files
param_names	vector of parameters names (optional)
wide_shape	Optional logical for keeping the long data.frame format FALSE, default) or converting it to a wider format one (TRUE), with parameters as columns

Details

An extract of returned data.frames with the 2 formats from an usms.xml file as input

- Default data.frame long format

name	type	param	id	value
SugarCane	usms	datedebut	NA	286
SugarCane	usms	datefin	NA	650

SugarCane	usms	finit	NA	canne_ini.xml
SugarCane	usms	nomsol	NA	solcanne
SugarCane	usms	fstation	NA	climcanj_sta.xml
...	...	...	...	...
...	...	...	...	...
param_gen.xml	fichierpar	Qmulchdec	17	0
param_gen.xml	fichierpar	Qmulchdec	18	0
param_gen.xml	fichierpar	Qmulchdec	19	0
param_gen.xml	fichierpar	Qmulchdec	20	0
param_gen.xml	fichierpar	Qmulchdec	21	0

name: a file name or an usm or soil name type: type of file param: param name id: NA for scalar, integer id for vectors parameters value: parameter value

- wide data.frame format

name	type	datedebut	datefin	finit	nomsol
SugarCane	usms	286	650	canne_ini.xml	solcanne
potato	usms	91	250	patate_ini.xml	solpatate
banana	usms	30	300	banane_ini.xml	solbanane
sorghum	usms	112	360	sorgho_ini.xml	solsorgho
barley	usms	88	196	orge_ini.xml	solorge

name: a file name or an usm or soil name type: type of file all other columns names correspond to parameter names, with indices as suffix for multiple values (as in _tec.xml files)

Value

A single long data.frame with name, type, param, id and value columns, value is of type character. or a wide a data.frame with name, type, and all other columns correspond to parameter names, with indices as suffix for multiple values (as in _tec.xml files for water supply, N supply, ...)

Examples

```
## Not run:
dir_path <- get_examples_path("xml")

get_xml_files_param_df(
  file_path = file.path(dir_path, "sols.xml")
)

files_list <- file.path(dir_path, c("sols.xml", "usms.xml", "param_gen.xml"))
# long format (default)
get_xml_files_param_df(file_path = files_list)

# wide format
get_xml_files_param_df(file_path = files_list, wide_shape = TRUE)
```

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

is_mac

Evaluating if the OS is a Mac OS type

Description

Evaluating if the OS is a Mac OS type

Usage

```
is_mac()
```

Value

TRUE/FALSE

Examples

```
is_mac()
```

is_stics_param

Search if a STICS parameter exist

Description

Tells if one or more parameter names are valid STICS input parameters.

Usage

```
is_stics_param(param, stics_version = "latest")
```

Arguments

param	A vector of parameter names
stics_version	Name of the STICS version. Optional, can be used to search parameters information relative to a specific STICS version. By default the latest version returned by <code>get_stics_versions_compat()</code> is used.

Value

A boolean vector: TRUE if the parameter exist, FALSE otherwise

See Also

`get_param_info()` for interactive use.

Examples

```
is_stics_param(c("adil", "adilmax", "unknown"))
```

is_stics_var	<i>Search if a STICS variable exist</i>
--------------	---

Description

Tells if one or more variable names are valid STICS output variables.

Usage

```
is_stics_var(var, stics_version = "latest", verbose = FALSE)
```

Arguments

var	A vector of variable names
stics_version	Name of the STICS version. Optional, can be used to search parameters information relative to a specific STICS version. By default the latest version returned by <code>get_stics_versions_compat()</code> is used.
verbose	if TRUE displaying warning, FALSE otherwise (default)

Value

A boolean vector: TRUE if the variable exist, FALSE otherwise

See Also

`get_var_info()` for interactive use.

Examples

```
is_stics_var(c("lai(n)", "masec(n)", "unknown"))
```

`is_unix`*Evaluating if the OS is a unix like type*

Description

Evaluating if the OS is a unix like type

Usage

```
is_unix()
```

Value

TRUE/FALSE

Examples

```
is_unix()
```

`is_windows`*Evaluating if the OS is a windows type*

Description

Evaluating if the OS is a windows type

Usage

```
is_windows()
```

Value

TRUE/FALSE

Examples

```
is_windows()
```

read_params_table	<i>Getting parameters data from tables files (Excel sheet, csv)</i>
-------------------	---

Description

Getting parameters data from tables files (Excel sheet, csv)

Usage

```
read_params_table(file_path, sheet_name = NULL, num_na = "NA", char_na = "NA")
```

Arguments

file_path	Excel or csv file path (including name of the file)
sheet_name	Name of an Excel sheet (useless for csv files)
num_na	Replacement value for numerical NA values (default: NA)
char_na	Replacement value for character NA values (default: "")

Details

After data are loaded, numerical and string NA values are replaced respectively with num_na or char_na

Value

A tibble of parameters

Examples

```
usm_xl_file <- download_usm_xl(  
  file_name = "inputs_stics_example.xlsx",  
  verbose = FALSE  
)  
read_params_table(usm_xl_file, sheet = "USMs")  
usm_csv_file <- download_usm_csv(  
  file = "inputs_stics_example_USMs.csv",  
  stics_version = "V9.2"  
)  
read_params_table(file_path = usm_csv_file)
```

set_param_txt	<i>Set (replace) STICS input file parameters</i>
---------------	--

Description

Replace or set an input parameter from an existing STICS input file.

Usage

```

set_param_txt(
    workspace,
    param,
    value,
    append = FALSE,
    plant_id = 1,
    variety = NULL,
    value_id = NULL,
    stics_version = "latest"
)

set_usm_txt(file = "new_travail.usm", param, value, append = FALSE)

set_station_txt(file = "station.txt", param, value, append = FALSE)

set_ini_txt(
    file = "ficini.txt",
    param,
    value,
    append = FALSE,
    plant_id = 1,
    value_id = NULL,
    stics_version = "latest"
)

set_general_txt(file = "tempopar.sti", param, value, append = FALSE)

set_tmp_txt(file = "tempoparv6.sti", param, value, append = FALSE)

set_plant_txt(
    file = "ficplt1.txt",
    param,
    value,
    append = FALSE,
    variety = NULL
)

set_tec_txt(

```

```

    file = "fictec1.txt",
    param,
    value,
    append = FALSE,
    value_id = NULL
)

set_soil_txt(
  file = "param.sol",
  param,
  value,
  value_id = NULL,
  stics_version = "latest"
)

```

Arguments

workspace	Path of the workspace containing the STICS (txt) input files.
param	Vector of parameter names.
value	New parameter value
append	Boolean. Append input to existing file
plant_id	The plant identifier (main crop: 1 ; associated crop: 2). Only used for plant, technical or initialization parameters (default = 1).
variety	The plant variety to set the parameter value, either the variety name (codevar in the plant file) or the index (variete in the technical file).
value_id	The soil layers id or technical interventions id
stics_version	An optional version name as listed in <code>get_stics_versions_compat()</code> return
file	Path (including name) of the file to modify

Details

The plant parameter can be either equal to 1, 2 for the associated plant in the case of intercrop, or c(1, 2) for both Principal and associated plants. [get_var_info](#) is a helper function that returns all possible output variables. If the variety is not given and if param is a varietal parameter, the function will modify the value of param for the simulated variety, as given in the technical file.

Value

None

Note

gen_varmod is not used by set_param_txt. To replace the output variables required from STICS, please directly call gen_varmod.

Examples

```
# Getting example data path
path <- get_examples_path(file_type = "txt")

# Change the value of durvieF for the current variety:
set_param_txt(workspace = path, param = "durvieF", value = 245)

# Change the value of durvieF for another variety:
set_param_txt(
  workspace = path, param = "durvieF",
  variety = "Nefer", value = 178
)
# Change the value of soil parameter "cailloux" for all layers
# or a specific one
set_param_txt(workspace = path, param = "cailloux", value = 1)
set_param_txt(workspace = path, param = "cailloux", value_id = 2, value = 2)

# Change the value of parameter "amount" for all water supply interventions
# or a specific one
set_param_txt(workspace = path, param = "amount", value = 50)
set_param_txt(workspace = path, param = "amount", value_id = 2, value = 40)
```

set_param_xml

*Setting parameter values into xml files***Description**

Setting parameter values for a parameter or a vector of and with a parameters values vector

Usage

```
set_param_xml(
  file,
  param,
  values,
  save_as = NULL,
  select = NULL,
  select_value = NULL,
  value_id = NULL,
  overwrite = FALSE,
  ...
)
```

Arguments

file	Path (including name) of the xml file to modify
param	Vector of parameter names.

values	A vector or a list of parameter(s) values (see details).
save_as	Path (including name) of the xml file to generate. Optional, if NULL file is overwritten.
select	node name or attribute name to use for selection (optional, default to no selection)
select_value	Vector of values used for select (see examples). Optional, should be provided only if select is provided.
value_id	Vector of ids of the parameters values to be retrieved from the parameter values vector
overwrite	Logical TRUE for overwriting the output file, FALSE otherwise (default)
...	Pass further arguments to set_param_value().

Details

It is possible to give several values for a parameter by passing a vector of values. For example, for two parameters with two values each: `value= list(c(1,2), c(2.3,4.5))`

Value

A logical value TRUE for operation success, FALSE otherwise

Examples

```
ex_path <- get_examples_path(file_type = "xml")

# Soil file

sol_path <- file.path(ex_path, "sols.xml")

# For scalar parameters per soil
# Setting all soils "argi" values to 50
set_param_xml(sol_path, "argi", 50, overwrite = TRUE)
# Getting changed values
# get_param_xml(sol_path, "argi")

# Setting a specific value to "argi" for "solcanne" soil
set_param_xml(
  file = sol_path, param = "argi", values = 56,
  select = "sol", select_value = "solcanne", overwrite = TRUE
)
# Getting changed values
# get_param_xml(sol_path, "argi",
#   select = "sol", select_value = "solcanne"
# )

# Setting a specific values to 2 parameters "argi" and
# "norg" for "solcanne" soil
set_param_xml(sol_path, c("argi", "norg"), list(100, 150),
  select = "sol", select_value = "solcanne", overwrite = TRUE
```

```

)
# Getting changed values
# get_param_xml(sol_path, c("argi", "norg"),
#   select = "sol", select_value = "solcanne"
# )

# For vector parameters per soil (5 values, one per soil layer)
set_param_xml(sol_path, c("epc", "HCCF"),
  select = "sol",
  select_value = c("solcanne", "solbanane"),
  values = list(c(20:24, 10:14), c(50:54, 40:44)),
  overwrite = TRUE
)

# Getting changed values
# get_param_xml(sol_path, c("epc", "HCCF"),
#   select = "sol",
#   select_value = c("solcanne", "solbanane")
# )

# For specific values of vector parameters
set_param_xml(sol_path, "HCCF",
  select = "sol",
  select_value = "solcanne",
  values = c(46.8, 48.5, 50.1),
  value_id = c(1, 3, 5),
  overwrite = TRUE
)

# Getting changed values
# get_param_xml(sol_path, "HCCF",
#   select = "sol",
#   select_value = "solcanne",
#   value_id = c(1,3,5)
# )

# Crop management file

tec_path <- file.path(ex_path, "file_tec.xml")

# Modifying irrigations parameters
set_param_xml(tec_path, c("julapI_or_sum_upvt", "amount"),
  values = list(200:215, 20:35), overwrite = TRUE
)
# Getting changed values
# get_param_xml(tec_path, c("julapI_or_sum_upvt", "amount"))

```

Description

Upgrade _ini.xml file(s) to a next major version

Usage

```
upgrade_ini_xml(file, out_dir, param_gen_file, overwrite = FALSE)
```

Arguments

file	xml plant file path or a vector of
out_dir	Output directory path
param_gen_file	Path of the param_gen.xml file corresponding to the initial version
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)

Value

None

Examples

```
dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_ini_xml(
  file = file.path(dir_path, "file_ini.xml"),
  out_dir = tempdir(),
  param_gen_file = file.path(dir_path, "param_gen.xml")
)
```

upgrade_param_gen_xml *Upgrade a param_gen.xml file to a next major version*

Description

Upgrade a param_gen.xml file to a next major version

Usage

```
upgrade_param_gen_xml(file, out_dir, ..., overwrite = FALSE)
```

Arguments

file	xml param_gen file path or a vector of
out_dir	Output directory path
...	additional argument(s) to pass to called functions
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)

Value

None

Examples

```

dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_param_gen_xml(
  file = file.path(dir_path, "param_gen.xml"),
  out_dir = tempdir()
)

```

```
upgrade_param_newform_xml
```

Upgrade a param_newform.xml file to a next major version

Description

Upgrade a param_newform.xml file to a next major version

Usage

```

upgrade_param_newform_xml(
  file,
  out_dir,
  param_gen_file,
  ...,
  overwrite = FALSE
)

```

Arguments

file	xml param_newform file path or a vector of
out_dir	Output directory path
param_gen_file	Path of the param_gen.xml file corresponding to the file version
...	additional argument(s) to pass to called functions
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)

Value

None

Examples

```

dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_param_newform_xml(
  file = file.path(dir_path, "param_newform.xml"),
  out_dir = tempdir(),
  param_gen_file = file.path(dir_path, "param_gen.xml")
)

```

upgrade_plt_xml	<i>Upgrade _plt.xml file(s) to a next major version</i>
-----------------	---

Description

Upgrade _plt.xml file(s) to a next major version

Usage

```

upgrade_plt_xml(
  file,
  out_dir,
  param_gen_file,
  param_newform_file,
  ...,
  overwrite = FALSE,
  warning = TRUE
)

```

Arguments

file	xml plant file path or a vector of
out_dir	Output directory path
param_gen_file	Path of the param_gen.xml file corresponding to the initial version
param_newform_file	Path of the param_newform.xml file corresponding to the file version
...	additional argument(s) to pass to called functions
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)
warning	Logical for rising warnings, FALSE otherwise

Value

None

Examples

```

dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_plt_xml(
  file = file.path(dir_path, "file_plt.xml"),
  out_dir = tempdir(),
  param_gen_file = file.path(dir_path, "param_gen.xml"),
  param_newform_file = file.path(dir_path, "param_newform.xml")
)

```

upgrade_sols_xml	<i>Upgrade a sols.xml file to a next major version</i>
------------------	--

Description

Upgrade a sols.xml file to a next major version

Usage

```
upgrade_sols_xml(file, out_dir, param_gen_file, overwrite = FALSE)
```

Arguments

file	xml sols file path
out_dir	Output directory path
param_gen_file	Path of the param_gen.xml file corresponding to the file version
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)

Value

None

Examples

```

dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_sols_xml(
  file = file.path(dir_path, "sols.xml"),
  out_dir = tempdir(),
  param_gen_file = file.path(dir_path, "param_gen.xml")
)

```

upgrade_sta_xml	<i>Upgrade _sta.xml file(s) to a next major version</i>
-----------------	---

Description

Upgrade _sta.xml file(s) to a next major version

Usage

```
upgrade_sta_xml(file, out_dir, param_gen_file, overwrite = FALSE)
```

Arguments

- file xml plant file path or a vector of
- out_dir Output directory path
- param_gen_file Path of the param_gen.xml file corresponding to the initial version
- overwrite Logical TRUE for overwriting files, FALSE otherwise (default)

Value

None

Examples

```
dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_sta_xml(
  file = file.path(dir_path, "file_sta.xml"),
  out_dir = tempdir(),
  param_gen_file = file.path(dir_path, "param_gen.xml")
)
```

upgrade_tec_xml	<i>Upgrade _tec.xml file(s) to a next major version</i>
-----------------	---

Description

Upgrade _tec.xml file(s) to a next major version

Usage

```
upgrade_tec_xml(
  file,
  out_dir,
  param_gen_file,
  param_newform_file,
  ...,
  overwrite = FALSE
)
```

Arguments

file	xml technical file path or a vector of
out_dir	Output directory path
param_gen_file	Path of the param_gen.xml file corresponding to the initial version
param_newform_file	Path of the param_newform.xml file corresponding to the file version
...	additional argument(s) to pass to called functions
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)

Value

None

Examples

```
dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_tec_xml(
  file = file.path(dir_path, "file_tec.xml"),
  out_dir = tempdir(),
  param_gen_file = file.path(dir_path, "param_gen.xml"),
  param_newform_file = file.path(dir_path, "param_newform.xml")
)
```

upgrade_usms_xml	<i>Upgrade a usms.xml file to a next major version</i>
------------------	--

Description

Upgrade a usms.xml file to a next major version

Usage

```
upgrade_usms_xml(file, out_dir, param_gen_file, overwrite = FALSE)
```

Arguments

file	xml usms file path
out_dir	Output directory path
param_gen_file	Path of the param_gen.xml file corresponding to the file version
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)

Value

None

Examples

```
dir_path <- get_examples_path(file_type = "xml", stics_version = "V10.0")

upgrade_usms_xml(
  file = file.path(dir_path, "usms.xml"),
  out_dir = tempdir(),
  param_gen_file = file.path(dir_path, "param_gen.xml")
)
```

upgrade_workspace_xml *Upgrade a Javastics STICS xml workspace directory to a next major version*

Description

Upgrade a Javastics STICS xml workspace directory to a next major version

Usage

```
upgrade_workspace_xml(
  workspace,
  out_dir,
  ...,
  javastics = NULL,
  overwrite = FALSE,
  verbose = FALSE
)
```

Arguments

workspace	JavaStics xml workspace path
out_dir	Output directory path
...	additional argument(s) to pass to called functions

javastics	Path of JavaSTICS containing the STICS version corresponding to the version of the files to be converted (optional)
overwrite	Logical TRUE for overwriting files, FALSE otherwise (default)
verbose	logical, TRUE for displaying a copy message FALSE otherwise (default)

Value

None

Examples

```
## Not run:
upgrade_workspace_xml(
  workspace = "/path/to/JavaSTICS/workspace",
  out_dir = "/path/to/an/output/directory",
  javastics = "/path/to/JavaSTICS/folder"
)

## End(Not run)
```

[.cropr_simulation *[method for cropr_simulation*

Description

This method ensure keeping the cropr_simulation attribute when subsetting a cropr_simulation list.

Usage

```
## S3 method for class 'cropr_simulation'
x[...]
```

Arguments

x	A cropr_simulation list
...	An index

Value

A subset of a cropr_simulation, keeping its attribute

Examples

```
path <- file.path(get_examples_path("sti"), "workspace1")
sim <- SticsRFiles::get_sim(workspace = path)
# sim returns a `cropr_simulation` list
```

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