Package ‘apsimx’

October 12, 2022

Title Inspect, Read, Edit and Run ‘APSIM’ ‘Next Generation’ and ‘APSIM’ Classic

Version 2.3.1

Description The functions in this package inspect, read, edit and run files for ‘APSIM’ ‘Next Generation’ (‘JSON’) and ‘APSIM’ ‘Classic’ (‘XML’). The files with an ‘apsim’ extension correspond to ‘APSIM’ Classic (7.x) - Windows only - and the ones with an ‘apsimx’ extension correspond to ‘APSIM’ ‘Next Generation’. For more information about ‘APSIM’ see (https://www.apsim.info/) and for ‘APSIM’ next generation (https://apsimnextgeneration.netlify.app/).

Depends R (>= 3.5.0)

License GPL-3

Encoding UTF-8

VignetteBuilder knitr

BugReports https://github.com/femiguez/apsimx/issues

Imports DBI, jsonlite, knitr, RSQLite, tools, utils, xml2

Suggests BayesianTools, chirps, datasets, daymetr, FedData, ggplot2, GSODR, listviewer, maps, mvtnorm, nasapower, nloptr, reactR, markdown, sensitivity, soilDB, sp, spData, sf, ucminf

LazyData true

RoxygenNote 7.1.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-01-04 18:00:02 UTC
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### add_column_apsim_met

Add a column to an object of class ‘met’

#### Description

The usual way of adding a column to a data frame might not work for an object of class ‘met’, so this method is recommended.
**Usage**

```r
add_column_apsim_met(met, value, name, units)
## S3 replacement method for class 'met'
x$name <- value
```

```r
remove_column_apsim_met(met, name)
```

**Arguments**

- `met` object of class ‘met’
- `value` value for the data.frame. It could be an integer, double or vector of length equal to the number of rows in `x`.
- `name` name of the variable to be removed
- `units` units for the new column (required)
- `x` object of class ‘met’

**Value**

- an object of class ‘met’ with the additional column
- an object of class ‘met’ without the variable (column) in ‘name’

**Examples**

```r
extd.dir <- system.file("extdata", package = "apsimx")
ames <- read_apsim_met("Ames.met", src.dir = extd.dir)

## The recommended method is
val <- abs(rnorm(nrow(ames), 10))
ames <- add_column_apsim_met(ames, value = val, name = "vp", units = "(hPa)"

## This is also possible
vp <- data.frame(vp = abs(rnorm(nrow(ames), 10)))
attr(vp, "units") <- "(hPa)"
ames$vp <- vp

## This is needed to ensure that units and related attributes are also removed
ames <- remove_column_apsim_met(ames, "vp")
## However, ames$vp <- NULL will also work
```
Run an APSIM (7.x) ‘Classic’ Simulation

Description

Run apsim from R. It's for Windows only. It uses ‘shell’.

Usage

apsim(
  file = "",
  src.dir = ".",
  silent = FALSE,
  value = c("report", "all", "none"),
  cleanup = FALSE,
  simplify = TRUE
)

Arguments

file file name to be run (the extension .apsim is optional)
src.dir directory containing the .apsim file to be run (defaults to the current directory)
silent whether to print messages from apsim simulation
value how much output to return:
  option ‘report’ returns only the ‘main’ report component; option ‘all’ returns all components of the simulation;
  option ‘none’ runs simulation but does not return a data frame.
cleanup logical. Whether to delete the .out and .sum files generated by APSIM. Default is FALSE.
simplify whether to return a single data frame when multiple simulations are present. If FALSE it will return a list.

Details

Run an APSIM (7.x) ‘Classic’ Simulation

A valid apsim file can be run from within R. The main goal is to make running APSIM-X simple, especially for large scale simulations or parameter optimization

Value

This function returns a data frame with APSIM output, but it depends on the argument ‘value’ above.
Examples

```r
## See function 'apsim_example'
```

---

### apsim.options

**Environment which stores APSIM options**

**Description**

Environment which can store the path to the executable and where examples are located. Creating an environment avoids the use of global variables or other similar practices which would have possible undesirable consequences.

**Usage**

```r
apsim.options
```

**Format**

An object of class `environment` of length 3.

**Details**

Environment which stores APSIM options

**Value**

This is an environment, so nothing to return.

**Examples**

```r
## Not run:
names(apsim.options)
apsim_options(exe.path = "some-new-path-to-executable")
apsim.options$exe.path

## End(Not run)
```
Run an APSIM-X simulation

Description
Run apsimx from R. It uses ‘system’ (unix) or ‘shell’ (windows) and it attempts to be platform independent.

Usage
apsimx(
    file = "",  
    src.dir = ".",  
    silent = FALSE,  
    value = "report",  
    cleanup = FALSE,  
    simplify = TRUE,  
    xargs
)

Arguments

file    file name to be run (the extension .apsimx is optional)
src.dir directory containing the .apsimx file to be run (defaults to the current directory)
silent  whether to print messages from apsim simulation
value   how much output to return:
        option ‘report’ returns only the ‘main’ report component;
        option ‘all’ returns all components of the simulation;
        option ‘none’ does not create a data.frame but it generates the databases option
        ‘user-defined’ should be the name of a specific table
cleanup logical. Whether to delete the .db file generated by APSIM-X. Default is FALSE
simplify whether to return a single data frame when multiple reports are present. If
            FALSE it will return a list.
xargs    extra arguments to be passed to the APSIM-X run. Use function xargs_apsimx.

Details
Run an APSIM-X Simulation
A valid apsimx file can be run from within R. The main goal is to make running APSIM-X simple, especially for large scale simulations or parameter optimization

Value
a data frame with the ‘Report’ from the APSIM-X simulation. The return value depends on the argument ‘value’ above.
Examples

## See function 'apsimx_example' and vignette 'apsimx'

---

apseimx.options

Environment which stores APSIM-X options

---

Description

Environment which can store the path to the executable, warning settings and where examples are located. Creating an environment avoids the use of global variables or other similar practices which would have possible undesirable consequences.

Usage

apseimx.options

Format

An object of class environment of length 7.

Details

Environment which stores APSIM-X options

Value

This is an environment, not a function, so nothing is returned.

Examples

names(apseimx.options)
apseimx_options(exe.path = "some-new-path-to-executable")
apseimx.options$exe.path
**apsimx_example**

---

**Access Example APSIM-X Simulations**

### Description

simple function to run some of the built-in APSIM-X examples

### Usage

```r
apsimx_example(example = "Wheat", silent = FALSE)
```

### Arguments

- **example**
  - run an example from built-in APSIM-X. Options are all of the ones included with the APSIM-X distribution, except ‘Graph’.
- **silent**
  - whether to print standard output from the APSIM-X execution

### Details

This function creates a temporary copy of the example file distributed with APSIM-X to avoid writing a .db file to the directory where the ‘Examples’ are located. It is not a good practice and there is no guarantee that the user has read/write permissions in that directory.

### Value

It returns a data frame

### Note

This function creates a new column ‘Date’ which is in the R ‘Date’ format which is convenient for graphics.

### Examples

```r
## Not run:
wheat <- apsimx_example("Wheat")
maize <- apsimx_example("Maize")
barley <- apsimx_example("Barley")
## The 'Date' column is created by this function, based on apsim output.
require(ggplot2)
ggplot(data = wheat , aes(x = Date, y = Yield)) +
  geom_point()
## End(Not run)
```
apsimx_filetype 

Test file format for .apsimx files

Description

Test whether an .apsimx file is XML or json

Usage

```r
apsimx_filetype(file = "", src.dir = ".")
```

Arguments

- `file`: file ending in .apsimx to be tested
- `src.dir`: directory containing the .apsimx file to be tested; defaults to the current working directory

Value

'xml', 'json' or 'unknown'

Note

Minimal function which reads only the first line in a file and tries to guess whether it is an 'xml' or 'json' file type.

Examples

```r
extd.dir <- system.file("extdata", package = "apsimx")
apsimx_filetype("Wheat.apsimx", src.dir = extd.dir)
```

apsimx_options

Setting some options for the package

Description

Set the path to the APSIM-X executable, examples and warning suppression.
Usage

```r
apsimx_options(
  exe.path = NA,
  dotnet = FALSE,
  mono = FALSE,
  examples.path = NA,
  warn.versions = TRUE,
  warn.find.apsimx = TRUE
)
```

Arguments

- `exe.path`: path to apsim executable. White spaces are not allowed.
- `dotnet`: logical indicating if APSIM should be run through the dotnet command
- `mono`: logical indicating if the mono command should be used when running APSIM. This is for versions for Mac/Linux older than Sept 2021.
- `examples.path`: path to apsim examples
- `warn.versions`: logical. warning if multiple versions of APSIM-X are detected.
- `warn.find.apsimx`: logical. By default a warning will be thrown if APSIM-X is not found. If ‘exe.path’ is ‘NA’ an error will be thrown instead.

Details

Set apsimx options

Value

as a side effect it modifies the ‘apsimx.options’ environment.

Note

It is possible that APSIM-X is installed in some alternative location other than the defaults ones. Guessing this can be difficult and then the auto_detect functions might fail. Also, if multiple versions of APSIM-X are installed apsimx will choose the newest one but it will issue a warning. Suppress the warning by setting `warn.versions = FALSE`.

Examples

```r
names(apsimx.options)
apsimx_options(exe.path = "some-new-path-to-executable")
apsimx.options$exe.path
```
Create APSIM-X Soil Profiles

Description

Generates a soil profile that can then replace the existing one in an `.apsim` or `.apsim` simulation file.

plotting function for a soil profile, it requires `ggplot2`

cHECKING an apsimx soil profile for reasonable values

Usage

```r
apsimx_soil_profile(
  nlayers = 10,
  Depth = NULL,
  Thickness = NULL,
  BD = NULL,
  AirDry = NULL,
  LL15 = NULL,
  DUL = NULL,
  SAT = NULL,
  KS = NULL,
  crop.LL = NULL,
  crop.KL = NULL,
  crop.XF = NULL,
  Carbon = NULL,
  SoilCNRatio = NULL,
  FOM = NULL,
  FOM.CN = NULL,
  FBiom = NULL,
  FInert = NULL,
  NO3N = NULL,
  NH4N = NULL,
  PH = NULL,
  ParticleSizeClay = NULL,
  ParticleSizeSilt = NULL,
  ParticleSizeSand = NULL,
  soil.bottom = 150,
  water.table = 200,
  soil.type = 0,
  crops = c("Maize", "Soybean", "Wheat"),
  metadata = NULL,
  soilwat = NA,
  swim = NA,
  soilorganicmatter = NA,
  dist parms = list(a = 0, b = 0.2)
)```
## S3 method for class 'soil_profile'
plot(
  x,
  ..., 
)

check_apsimx_soil_profile(x)

**Arguments**

- `nlayers` Number of soil layers (default = 10)
- `Depth` specific depths for each soil layer (cm)
- `Thickness` thickness for each soil layer (mm)
- `BD` bulk density for each soil layer (g/cc) – 'cc' is cubic cm
- `AirDry` air dry for each soil layer (mm/mm)
- `LL15` lower limit (15 bar) for each soil layer (mm/mm)
- `DUL` drainage upper limit (0.33 bar) for each soil layer (mm/mm)
- `SAT` saturation (0 bar) for each soil layer (mm/mm)
- `KS` saturated hydraulic conductivity (mm/day)
- `crop.LL` lower limit for a specific crop
- `crop.KL` root ability to extract water for a specific crop
- `crop.XF` soil root exploration for a specific crop
- `Carbon` organic carbon (percent)
- `SoilCNRatio` organic carbon C:N ratio
- `FOM` fresh organic matter (kg/ha)
- `FOM.CN` fresh organic matter C:N ratio
- `FBiom` Fraction of microbial biomass (0-1)
- `FInert` Fraction of inert carbon (0-1)
- `NO3N` nitrate nitrogen (Chemical) (ppm)
- `NH4N` ammonium nitrogen (Chemical) (ppm)
- `PH` soil pH
- `ParticleSizeClay` particle size clay (in percent)
- `ParticleSizeSilt` particle size silt (in percent)
- `ParticleSizeSand` particle size sand (in percent)
- `soil.bottom` bottom of the soil profile (cm)
**Details**

Soil Profiles

Real soils might have discontinuities, but for APSIM it might be beneficial to be able to create a soil profile with an arbitrary number of layers and have flexibility in the distribution of soil physical and chemical properties. Steps:

1. `apsimx_soil_profile` is a function which can create a soil matrix with many layers
2. It allows for creating a smooth distribution for Physical (or Water), Chemical, InitialWater, Analysis, InitialN, Organic or SoilOrganicMatter
3. The distribution can be specified with the ‘a’ and ‘c’ parameter of an exponential decay function, using a list. E.g. DUL = list(0.35, 0, -0.1). This means that the top value for DUL will be 0.35 and it will decay with a rate of -0.1.
4. If an increase and then a decay is needed the Ricker function can be used. See ‘SSricker’ in the ‘nlraa’ package.

**Value**

a soil profile with class ‘soil_profile’ with elements ‘soil’, ‘crops’, ‘metadata’, ‘soilwat’ and ‘swim’.

It produces a plot

It does not produce output unless potential issues are found. Only warnings are produced and it returns an object of class ‘soil_profile’.
Examples

```r
sp <- apsimx_soil_profile()
require(ggplot2)
plot(sp)
```

Description

simple function to run some of the built-in APSIM examples

Usage

```r
apsim_example(example = "Millet", silent = FALSE, tmp.dir = NULL)
```

Arguments

- `example` run an example from built-in APSIM. Options are all of the ones included with the APSIM distribution, except ‘Graph’.
- `silent` whether to print standard output from the APSIM execution
- `tmp.dir` temporary directory where to write files

Details

This function creates a temporary copy of the example file distributed with APSIM to avoid writing a .out file to the directory where the ‘Examples’ are located. It is not a good practice and there is no guarantee that the user has read/write permissions in that directory.

Value

This function returns a data frame with APSIM output

Note

This function creates a new column ‘Date’ which is in the R ‘Date’ format which is convenient for graphics.
Examples

```r
## Not run:
## Only run these if you have APSIM 'Classic' installed (Windows only)
millet <- apsim_example("Millet")
potato <- apsim_example("Potato")
sugar <- apsim_example("Sugar")
## The 'Date' column is created by this function, based on apsim output.
require(ggplot2)
ggplot(data = millet, aes(x = Date, y = millet_biomass)) +
  geom_line()
## End(Not run)
```

### Description

Set the path to the APSIM executable, examples and warning suppression.

### Usage

```r
apsim_options(exe.path = NA, examples.path = NA, warn.versions = TRUE)
```

### Arguments

- `exe.path`: path to apsim executable
- `examples.path`: path to apsim examples
- `warn.versions`: logical. warning if multiple versions of APSIM are detected.

### Details

Set apsim options

### Value

It modifies the ‘apsim.options’ environment as a side effect.

### Note

It is possible that APSIM 7.x ‘Classic’ is installed in some alternative location other than the defaults ones. Guessing this can be difficult and then the auto_detect functions might fail. Also, if multiple versions of APSIM are installed apsim will choose the newest one but it will issue a warning. Suppress the warning by setting `warn.versions = FALSE`. 
### apsim_version

Display available APSIM ‘Classic’ and APSIM-X versions

#### Description

Display available APSIM ‘Classic’ and APSIM-X versions

#### Usage

```r
apsim_version(which = c("all", "inuse"), verbose = TRUE)
```

#### Arguments

- `which`: either ‘all’ or ‘inuse’
- `verbose`: whether to print the information to standard output

#### Value

- a data frame (all) or a vector (inuse) with APSIM-X and/or APSIM versions

#### Examples

```r
## Not run:
## Check which apsim version are available
ava <- apsim_version(verbos = TRUE)

## End(Not run)
```
Conversion from data frame to met object

Description

It makes minimum assumptions about the data so it is recommended to change defaults

Usage

```r
as_apsim_met(
  x,
  filename = "noname.met",
  site = "nosite",
  latitude = 0,
  longitude = 0,
  tav = NA,
  amp = NA,
  colnames = c("year", "day", "radn", "maxt", "mint", "rain"),
  units = c("()", "()", "(MJ/m2/day)", "(oC)", "(oC)", "(mm)"),
  constants = NA,
  comments = NA,
  check = TRUE
)
```

Arguments

- `x` object of class ‘data frame’
- `filename` default ‘noname.met’
- `site` default ‘nosite’
- `latitude` default is zero (0)
- `longitude` default is zero (0)
- `tav` average temperature (calculated if not supplied)
- `amp` temperature amplitude (calculated if not supplied)
- `colnames` default are “year”, “day”, “radn”, “maxt”, “mint”, “rain”
- `units` default are “()”, “()”, “(MJ/m2/day)”, “(oC)”, “(oC)”, “(mm)”
- `constants` default is “NA”
- `comments` default is “NA”
- `check` whether to check the resulting met file using `check_apsim_met`. default is TRUE.

Details

Simple utility for converting a data frame to an object of class met
auto_detect_apsimx_examples

Value
it returns an object of class ‘met’.

Description
simple function to detect where APSIM-X examples are located

Usage
auto_detect_apsimx_examples()

Details
Auto detect where apsimx examples are located

Value
will create a directory (character string) pointing to APSIM-X distributed examples

Examples
## Not run:
ex.dir <- auto_detect_apsimx_examples()
## End(Not run)

auto_detect_apsim_examples

Description
simple function to detect where APSIM ‘Classic’ examples are located

Usage
auto_detect_apsim_examples()

Details
Auto detect where APSIM (7.x) ‘Classic’ examples are located
Value

will create a directory pointing to APSIM ‘Classic’ distributed examples

Examples

```r
## Not run:
ex.dir <- auto_detect_apsim_examples()

## End(Not run)
```

carbon_stocks  Calculate soil carbon stocks

Description

Calculation of carbon stocks based on an object of class ‘soil_profile’

Usage

```r
carbon_stocks(
  x, 
  depth, 
  area = c("m2", "ha"), 
  method = c("linear", "constant"), 
  ...
)
```

Arguments

- `x`: object of class ‘soil_profile’
- `depth`: soil depth (in meters). If missing then the whole soil profile is used.
- `area`: either ‘m2’ meter squared or ‘ha’.
- `...`: additional arguments passed to internal functions (none used at the moment).

Details

Function to calculate carbon stocks. The output units depend on the choice of area. If ‘m2’ is used, then the output units will be ‘kg/m2’. If the ‘area’ is ‘ha’, then the output units will be ‘Mg/ha’.

Value

returns a value with attribute ‘units’ and ‘depth’
Examples

```r
## Not run:
sp <- apsimx_soil_profile()
carbon_stocks(sp)
carbon_stocks(sp, depth = 0.1)
carbon_stocks(sp, depth = 0.2)
carbon_stocks(sp, depth = 0.3)
carbon_stocks(sp, depth = 0.4)

## End(Not run)
```

Description

Takes in an object of class ‘met’ and checks for missing/valid/reasonable values

Usage

```r
check_apsim_met(met)
```

Arguments

| met          | object of class ‘met’ |

Details

It will only check for missing values and reasonable (within range) values for: ‘year’: range (1500 to 3000);
‘day’: range (1 to 366);
‘maxt’: range (-60 to 60) – units (C);
‘mint’: range (-60 to 40) – units (C);
‘radn’: range (0 to 40) – units (MJ/m2/day);
‘rain’: range (0 to 100) – units (mm/day)

Value

does not return anything unless possible errors are found
compare_apsim  

Compare two or more apsim output objects

Description

Function which allows for a simple comparison between APSIM output objects

print method for ‘out_mrg’

plotting function for compare_apsim, it requires ggplot2

Usage

compare_apsim(..., variable, index = "Date", by, labels, verbose = FALSE)

## S3 method for class 'out_mrg'
print(x, ..., digits = 2)

## S3 method for class 'out_mrg'
plot(
  x,
  ..., plot.type = c("vs", "diff", "ts", "density"),
  pairs = c(1, 2),
  cumulative = FALSE,
  variable,
  id,
  by,
  facet = FALSE,
  span = 0.75
)

Arguments

...  
data frames with APSIM output or observed data.

variable  
variable to plot

index  
index for merging objects. Default is ‘Date’

by  
variable in ‘index’ used for plotting

labels  
labels for plotting and identification of objects.

verbose  
whether to print indexes to console (default is FALSE).

x  
object of class ‘out_mrg’

digits  
digits to print (default is 2)

plot.type  
either ‘vs’, ‘diff’, ‘ts’ - for time series or ‘density’

pairs  
pair of objects to compare, defaults to 1 and 2 but others are possible

cumulative  
whether to plot cumulative values (default FALSE)
compare_apsim

<table>
<thead>
<tr>
<th>id</th>
<th>identification (not implemented yet)</th>
</tr>
</thead>
<tbody>
<tr>
<td>facet</td>
<td>whether to facet or use color for the by variable (default is FALSE, meaning ‘color’)</td>
</tr>
<tr>
<td>span</td>
<td>argument passed to ‘geom_smooth’</td>
</tr>
</tbody>
</table>

Details

Plotting function for weather data

Value

object of class ‘out_mrg’, which can be used for further plotting

it prints the index.table data.frame

it produces a plot

Note

‘Con Corr’ is the concordance correlation coefficient (https://en.wikipedia.org/wiki/Concordance_correlation_coefficient);
‘ME’ is the model efficiency (https://en.wikipedia.org/wiki/Nash

Examples

```r
## Directory with files
extd.dir <- system.file("extdata", package = "apsimx")
## Comparing observed and simulated for Wheat
data(obsWheat)
sim.opt <- read.csv(file.path(extd.dir, "wheat-sim-opt.csv"))
sim.opt$Date <- as.Date(sim.opt$Date)
cap <- compare_apsim(obsWheat, sim.opt, labels = c("obs", "sim"))
plot(cap)
plot(cap, plot.type = "diff")
plot(cap, plot.type = "ts")
plot(cap, variable = "AboveGround")
plot(cap, variable = "AboveGround", plot.type = "diff")
plot(cap, variable = "AboveGround", plot.type = "ts")
```
compare_apsim_met  

Compare two or more metfiles

Description

Helper function which allows for a simple comparison among 'met' objects

print method for 'met_mrg'

plotting function for compare_apsim_met, it requires ggplot2

Usage

```r
compare_apsim_met(
  ...,  
  met.var = c("all", "radn", "maxt", "mint", "rain", "rh", "wind_speed", "vp"), 
  labels, 
  check = FALSE, 
  verbose = FALSE 
)
```

```r
## S3 method for class '/quotesingle.Var
met_mrg'/quotesingle.Var
print(x, ..., digits = 2)
```

```r
## S3 method for class '/quotesingle.Var
met_mrg'/quotesingle.Var
plot(
  x,  
  ...,  
  plot.type = c("vs", "diff", "ts", "density"), 
  pairs = c(1, 2), 
  cumulative = FALSE, 
  met.var = c("radn", "maxt", "mint", "rain"), 
  id, 
  span = 0.75 
)
```

Arguments

```r
...  
met.file  
met.var  
labels  
check  
verbose  
x  
digits  
plot.type
```

- `...`: met file objects. Should be of class ‘met’
- `met.var`: meteorological variable to plot
- `labels`: labels for plotting and identification of ‘met’ objects.
- `check`: whether to check ‘met’ objects using ‘check_apsim_met’.
- `verbose`: whether to print agreement stats to console (default is FALSE).
- `x`: object of class ‘met_mrg’
- `digits`: digits to print (default is 2)
- `plot.type`: either ‘vs’, ‘diff’, ‘ts’ - for time series or ‘density’
**Value**

object of class `met_mrg`, which can be used for further plotting

it prints the index.table data.frame

it produces a plot

**Note**

I have only tested this for 2 or 3 objects. The code is set up to be able to compare more, but I’m not sure that would be all that useful.

**Examples**

```r
## Not run:
require(nasapower)
## Specify the location
lonlat <- c(-93, 42)
## dates
dts <- c("2017-01-01","2017-12-31")
## Get pwr
pwr <- get_power_apsim_met(lonlat = lonlat, dates = dts)
## Get data from IEM
iem <- get_iem_apsim_met(lonlat = lonlat, dates = dts)
## Compare them
cmet <- compare_apsim_met(pwr[,1:6], iem, labels = c("pwr","iem"))
## Visualize radiation
plot(cmet, met.var = "radn")
plot(cmet, plot.type = "diff")
plot(cmet, plot.type = "ts")
## Visualize maxt
plot(cmet, met.var = "maxt")
plot(cmet, met.var = "maxt", plot.type = "diff")
plot(cmet, met.var = "maxt", plot.type = "ts")
## Cumulative rain
plot(cmet, met.var = "rain", plot.type = "ts", cumulative = TRUE)
## End(Not run)
```
compare_apsim_soil_profile

Compare two or more soil profiles

Description

Helper function which allows for a simple comparison among soil_profile objects

print method for 'soil_profile_mrg'

plotting function for compare_apsim_soil_profile, it requires ggplot2

Usage

```
compare_apsim_soil_profile(
  ..., 
  soil.var = c("all", "Thickness", "BD", "AirDry", "LL15", "DUL", "SAT", "KS", 
  "Carbon", "SoilCNRatio", "FOM", "FOM.CN", "FBiom", "FINert", "NO3N", "NH4N", "PH"), 
  labels, 
  check = FALSE, 
  verbose = FALSE
)
```

```
## S3 method for class 'soil_profile_mrg'
print(x, ..., digits = 2)
```

```
## S3 method for class 'soil_profile_mrg'
plot(
  x, 
  ..., 
  plot.type = c("depth", "vs", "diff", "density"), 
  pairs = c(1, 2), 
  soil.var = c("all", "Thickness", "BD", "AirDry", "LL15", "DUL", "SAT", "KS", 
  "Carbon", "SoilCNRatio", "FOM", "FOM.CN", "FBiom", "FINert", "NO3N", "NH4N", "PH"), 
  span = 0.75
)
```

Arguments

- `...`: 'soil_profile' objects. Should be of class 'soil_profile'
- `soil.var`: soil variable to plot
- `labels`: labels for plotting and identification of 'soil_profile' objects.
- `check`: whether to check 'soil_profile' objects using 'check_apsimx_soil_profile'.
- `verbose`: whether to print agreement values (default is FALSE).
- `x`: object of class 'soil_profile_mrg'
- `digits`: number of digits to print (default is 2)
**doy2date**

Converts from doy to date

**Description**

Given a day of the year as julian (1-366) it converts to ‘Date’

- Given a ‘Date’ it converts to julian day (1-366) or day of the year

**Usage**

- `doy2date(x, year = 2001, inverse = FALSE)`
- `date2doy(x, year = 2001, inverse = FALSE)`

**doy2date**

- `plot.type` either ‘depth’, ‘vs’, ‘diff’ or ‘density’
- `pairs` pair of objects to compare, defaults to 1 and 2 but others are possible
- `span` argument to be passed to ‘geom_smooth’

**Value**

- object of class ‘soil_profile_mrg’, which can be used for further plotting
- a table with indexes for the soil profiles
- it produces a plot

**Note**

- I have only tested this for 2 or 3 objects. The code is set up to be able to compare more, but I’m not sure that would be all that useful.

**Examples**

```r
## Not run:
require(soilDB)
require(sp)
require(sf)
require(spData)
# Get two soil profiles
sp1 <- get_ssurgo_soil_profile(lonlat = c(-93, 42))
sp2 <- get_ssurgo_soil_profile(lonlat = c(-92, 41))
# Compare them
cmp <- compare_apsim_soil_profile(sp1[[1]], sp2[[1]], labels = c("sp1", "sp2"))
# Plot the variables
plot(cmp)
## End(Not run)
```

---

**doy2date**

Converts from doy to date

**Description**

Given a day of the year as julian (1-366) it converts to ‘Date’

- Given a ‘Date’ it converts to julian day (1-366) or day of the year

**Usage**

- `doy2date(x, year = 2001, inverse = FALSE)`
- `date2doy(x, year = 2001, inverse = FALSE)`

**doy2date**

- `plot.type` either ‘depth’, ‘vs’, ‘diff’ or ‘density’
- `pairs` pair of objects to compare, defaults to 1 and 2 but others are possible
- `span` argument to be passed to ‘geom_smooth’

**Value**

- object of class ‘soil_profile_mrg’, which can be used for further plotting
- a table with indexes for the soil profiles
- it produces a plot

**Note**

- I have only tested this for 2 or 3 objects. The code is set up to be able to compare more, but I’m not sure that would be all that useful.

**Examples**

```r
## Not run:
require(soilDB)
require(sp)
require(sf)
require(spData)
# Get two soil profiles
sp1 <- get_ssurgo_soil_profile(lonlat = c(-93, 42))
sp2 <- get_ssurgo_soil_profile(lonlat = c(-92, 41))
# Compare them
cmp <- compare_apsim_soil_profile(sp1[[1]], sp2[[1]], labels = c("sp1", "sp2"))
# Plot the variables
plot(cmp)
## End(Not run)
```
Arguments

x either an integer 1-366 or a ‘Date’
year year
inverse if TRUE it goes from doy to ‘Date’

Value

an object of class ‘Date’ or a numeric if inverse equals TRUE.
an numeric or an object of class ‘Date’ if inverse equals TRUE.

Examples

doy2date(120)
date2doy("04-30")

edit_apsim Edit an APSIM (Classic) Simulation

Description

This function allows editing of an APSIM (Classic) simulation file.

Usage

```
edit_apsim(
  file,
  src.dir = ".",
  wrt.dir = NULL,
            "Manager", "Outputfile", "Other"),
                 "Analysis", "InitialWater", "Sample", "SWIM"),
  manager.child = NULL,
  parm = NULL,
  value = NULL,
  overwrite = FALSE,
  edit.tag = "-edited",
  parm.path = NULL,
  root,
  verbose = TRUE,
  check.length = TRUE
)
```
Arguments

- **file**: file ending in .apsim to be edited
- **src.dir**: directory containing the .apsim file to be edited; defaults to the current working directory
- **wrt.dir**: should be used if the destination directory is different from the src.dir
- **soil.child**: specific soil component to be edited
- **manager.child**: specific manager component to be edited (not implemented yet)
- **parm**: parameter to be edited
- **value**: new values for the parameter to be edited
- **overwrite**: logical; if TRUE the old file is overwritten, a new file is written otherwise
- **edit.tag**: if the file is edited a different tag from the default ‘-edited’ can be used.
- **parm.path**: path to the attribute to edit when node is ‘Other’
- **root**: supply the node position in the case of multiple simulations such as factorials.
- **verbose**: whether to print information about successful edit
- **check.length**: check whether vectors are of the correct length

Details

The variables specified by **parm** within the .apsim file specified by **file** in the source directory **src.dir** are edited. The old values are replaced with **value**, which is a list that has the same number of elements as the length of the vector **parm**. The current .apsim file will be overwritten if **overwrite** is set to TRUE; otherwise the file ‘file’ *.edited.apsim* will be created. If (verbose = TRUE) then the name of the written file is returned.

When node equals Outputfile, the editing allows to add variables, but not to remove them at the moment.

Value

(when verbose=TRUE) complete file path to edited .apsimx file is returned as a character string. As a side effect this function creates a new (XML) .apsimx file.

Note

The components that can be edited are restricted because this is better in preventing errors of editing unintended parts of the file. The disadvantage is that there is less flexibility compared to the similar function in the `apsimr` package.

Examples

```r
## This example will read one of the examples distributed with APSIM
## but write to a temporary directory
```
tmp.dir <- tempdir()

extd.dir <- system.file("extdata", package = "apsimx")
edit_apsim("Millet", src.dir = extd.dir, wrt.dir = tmp.dir,
    node = "Clock",
    parm = "start_date", value = "01/02/1940")

## Editing all of the KL values for Millet
pp.KL <- inspect_apsim_xml("Millet.apsim", src.dir = extd.dir,
    parm = "SoilCrop[8]/KL")

kls <- seq(0.08, 0.2, length.out = 11)
edit_apsim("Millet.apsim",
    src.dir = extd.dir,
    wrt.dir = tmp.dir,
    node = "Other",
    parm.path = pp.KL,
    value = kls)

## Check that it was properly edited
inspect_apsim("Millet-edited.apsim",
    src.dir = tmp.dir,
    node = "Soil",
    soil.child = "Water",
    parm = "KL")

edit_apsimx  

Edit an APSIM-X (JSON) Simulation

Description

This function allows editing of an APSIM-X (JSON) simulation file.

Usage

edit_apsimx(
    file,
    src.dir = ".",
    wrt.dir = NULL,
        "Manager", "Report", "Other"),
        "Chemical", "InitialWater", "Sample"),
    ## Editing all of the KL values for Millet
    pp.KL <- inspect_apsim_xml("Millet.apsim", src.dir = extd.dir,
        parm = "SoilCrop[8]/KL")
    kls <- seq(0.08, 0.2, length.out = 11)
edit_apsim("Millet.apsim",
    src.dir = extd.dir,
    wrt.dir = tmp.dir,
    node = "Other",
    parm.path = pp.KL,
    value = kls)

## Check that it was properly edited
inspect_apsim("Millet-edited.apsim",
    src.dir = tmp.dir,
    node = "Soil",
    soil.child = "Water",
    parm = "KL")

edit_apsimx  

Edit an APSIM-X (JSON) Simulation

Description

This function allows editing of an APSIM-X (JSON) simulation file.

Usage

edit_apsimx(
    file,
    src.dir = ".",
    wrt.dir = NULL,
        "Manager", "Report", "Other"),
        "Chemical", "InitialWater", "Sample"),
    ## Editing all of the KL values for Millet
    pp.KL <- inspect_apsim_xml("Millet.apsim", src.dir = extd.dir,
        parm = "SoilCrop[8]/KL")
    kls <- seq(0.08, 0.2, length.out = 11)
edit_apsim("Millet.apsim",
    src.dir = extd.dir,
    wrt.dir = tmp.dir,
    node = "Other",
    parm.path = pp.KL,
    value = kls)

## Check that it was properly edited
inspect_apsim("Millet-edited.apsim",
    src.dir = tmp.dir,
    node = "Soil",
    soil.child = "Water",
    parm = "KL")
**Arguments**

- `file`: file ending in .apsimx to be edited (JSON)
- `src.dir`: directory containing the .apsimx file to be edited; defaults to the current working directory
- `wrt.dir`: should be used if the destination directory is different from the src.dir
- `soil.child`: specific soil component to be edited
- `manager.child`: specific manager component to be edited
- `parm`: parameter to be edited
- `value`: new values for the parameter to be edited
- `overwrite`: logical; if TRUE the old file is overwritten, a new file is written otherwise
- `edit.tag`: if the file is edited a different tag from the default ‘-edited’ can be used.
- `parm.path`: path to the attribute to edit when node is ‘Other’
- `root`: supply the node position in the case of multiple simulations such as factorials.
- `verbose`: whether to print information about successful edit

**Details**

The variables specified by `parm` within the .apsimx file specified by `file` in the source directory `src.dir` are edited. The old values are replaced with `value`, which is a list that has the same number of elements as the length of the vector `parm`. The current .apsimx file will be overwritten if `overwrite` is set to TRUE; otherwise the file ‘file’ - `edit.apsimx` will be created. If (verbose = TRUE) then the name of the written file is returned.

When node equals Report, the editing allows to add variables, but not to remove them at the moment.

**Value**

(when verbose=TRUE) complete file path to edited .apsimx file is returned as a character string. As a side effect this function creates a new (JSON) .apsimx file.
Examples

```r
## This example will read one of the examples distributed with APSIM-X
## but write to a temporary directory
tmp.dir <- tempdir()

## Edit Bulk density
extd.dir <- system.file("extdata", package = "apsimx")
bds <- c(1.02, 1.03, 1.09, 1.16, 1.18, 1.19, 1.20)
edt_apsim("Wheat.apsim", src.dir = extd.dir,
           wrt.dir = tmp.dir,
           node = "Soil",
           soil.child = "Water",
           parm = "BD", value = bds,
           verbose = FALSE)

## Inspect file
inspect_apsim("Wheat-edited.apsim", src.dir = tmp.dir,
              node = "Soil", soil.child = "Water")

## To delete the file...
file.remove(file.path(tmp.dir, "Wheat-edited.apsim"))

## Edit the fertilizer amount in 'Maize.apsimx'
edit_apsim("Maize.apsimx", src.dir = extd.dir,
           wrt.dir = tmp.dir, node = "Manager",
           manager.child = "SowingFertiliser",
           parm = "Amount", value = 200, verbose = TRUE)

## Make sure it worked
inspect_apsim("Maize-edited.apsim", src.dir = tmp.dir, node = "Manager")

## Remove the file
file.remove(file.path(tmp.dir, "Maize-edited.apsimx"))
```

edit_apsimx_batch

### Edit an APSIM-X (JSON) Simulation in Batch mode

#### Description

This function allows editing of an APSIM-X (JSON) simulation file in batch mode.

#### Usage

```r
edit_apsimx_batch(
  file,  
  src.dir = ".",  
  wrt.dir = NULL,  
  parms = NULL,
```
Arguments

- **file**: file ending in .apsimx to be edited (JSON)
- **src.dir**: directory containing the .apsimx file to be edited; defaults to the current working directory
- **wrt.dir**: should be used if the destination directory is different from the src.dir
- **parms**: parameter to be edited in the form ‘key = value’
- **silent**: controls the output of running APSIM at the command line
- **verbose**: whether to print information about successful edit

Details

from hol430

This allows the user to specify an .apsimx file and a config file when running Models.exe. The .apsimx file will not be run but instead, the changes listed in the config file will be applied to the .apsimx file, which will then be written to disk under the same filename.

The config file should contain lines of the form ‘path = value’

e.g.

```
[Clock].StartDate = 2019-1-20
.Simulations.Sim1.Name = SimulationVariant35
.Simulations.Sim2.Enabled = false
```

Command line arguments should look like: Models.exe file.apsimx /Edit /path/to/config/file.conf

Relative paths will be resolved to the first match. i.e. [Clock].StartDate will match the first clock found in the file.

Dates can be specified as yyyy-mm-dd or mm/dd/yyyy.

Strings should not be quoted

Array indices will be interpreted as 1-indexed (mad face). So the first element in the array should have index 1 in the config file.

The file will be upgraded to the latest file version as part of this process.

Value

(when verbose=TRUE) complete file path to edited .apsimx file is returned as a character string. As a side effect this function creates a new (JSON) .apsimx file.

Examples

```r
## This example will read one of the examples distributed with APSIM-X
## but write to a temporary directory

tmp.dir <- tempdir()
```
## Edit InitialResidueMass

```
extd.dir <- system.file("extdata", package = "apsimx")
edit_apsimx_batch("Wheat.apsimx", src.dir = extd.dir, wrt.dir = tmp.dir, parms = parms)
```

### edit_apsimx_replacement

**Edit a replacement component in an .apsim (JSON) file**

**Description**

edit the replacement component of an JSON apsimx file. It does not replace the GUI, but it can save time by quickly editing parameters and values.

**Usage**

```
edit_apsimx_replacement(
  file = "",
  src.dir = ".",
  wrt.dir = ".",
  node = NULL,
  node.child = NULL,
  node.subchild = NULL,
  node.subsubchild = NULL,
  node.sub3child = NULL,
  node.sub4child = NULL,
  node.sub5child = NULL,
  node.string = NULL,
  root = list("Models.Core.Replacements", NA),
  parm = NULL,
  value = NULL,
  overwrite = FALSE,
  edit.tag = "-edited",
  verbose = TRUE,
  grep.options
)
```

**Arguments**

- `file` file ending in .apsimx to edit (JSON)
- `src.dir` directory containing the .apsimx file; defaults to the current working directory
- `wrt.dir` should be used if the destination directory is different from the src.dir
- `node` specific node to edit
node.child specific node child component to edit.
node.subchild specific node sub-child to edit.
node.subsubchild specific node sub-subchild to edit.
node.sub3child specific node sub-sub-subchild to edit.
node.sub4child specific node sub-sub-sub-subchild to edit.
node.sub5child specific node sub-sub-sub-sub-subchild to edit.
node.string passing of a string instead of the node hierarchy. It can either start with a dot or not. However, the ‘best’ form is not to start with a dot as it should be a more convenient form of passing the nodes and their children and not a real ‘jsonp path’.
root ‘root’ node to explore (default = “Models.Core.Replacements”)
parm specific parameter to edit
value new values for the parameter
overwrite logical; if TRUE the old file is overwritten, a new file is written otherwise
edit.tag if the file is edited a different tag from the default ‘-edited’ can be used.
verbose whether to print information about successful edit
grep.options Additional options for grep. To be passed as a list.

Details
This is simply a script that prints the relevant parameters which are likely to need editing. It does not print all information from an .apsimx file.

Value
(when verbose=TRUE) complete file path to edited .apsimx file is returned as a character string. As a side effect this function creates a new (JSON) .apsimx file.

Note
The components that can be edited are restricted because this is better in preventing errors of editing unintended parts of the file.

Examples

extd.dir <- system.file("extdata", package = "apsimx")
## Writing to a temp directory, but change as needed
tmp.dir <- tempdir()

## Inspect original values
inspect_apsimx_replacement("MaizeSoybean.apsimx",
                           src.dir = extd.dir,
                           node = "Maize",
                           node.child = "Phenology",
                           node.subchild = "ThermalTime",
                           node.subsubchild = "ThermalTime",
                           node.sub3child = "ThermalTime",
                           node.sub4child = "ThermalTime",
                           node.sub5child = "ThermalTime",
                           node.string = "ThermalTime",
                           root = "Models.Core.Replacements",
                           parm = "Phenology",
                           value = "New Value",
                           overwrite = TRUE,
                           edit.tag = "CustomTag",
                           verbose = TRUE,
                           grep.options = "-e 'Phenology'"
edit_apsimx_replace_soil_profile

Edit APSIM-X file with a replaced soil profile

Description

Edits an APSIM-X simulation by replacing the soil profile.
Usage

```r
edit_apsimx_replace_soil_profile(
  file = "",
  src.dir = ".",
  wrt.dir = NULL,
  soil.profile = NULL,
  edit.tag = "-edited",
  overwrite = FALSE,
  verbose = TRUE,
  root
)
```

Arguments

- `file` (name of the .apsimx file to be edited)
- `src.dir` (source directory)
- `wrt.dir` (writing directory)
- `soil.profile` (a soil profile object with class ‘soil_profile’)
- `edit.tag` (default edit tag ‘-edited’)
- `overwrite` (default FALSE)
- `verbose` (default TRUE and it will print messages to console)
- `root` (supply the node position in the case of multiple simulations such as factorials)

Details

This function is designed to batch replace the whole soil in an APSIM simulation file.

Value

writes a file to disk with the supplied soil profile

Note

There is no such thing as a default soil, carefully build the profile for each simulation.

Examples

```r
sp <- apsimx_soil_profile()
extd.dir <- system.file("extdata", package = "apsimx")

## I write to a temp directory but replace as needed
tmp.dir <- tempfile()

edit_apsimx_replace_soil_profile("Maize.apsimx", soil.profile = sp,
  src.dir = extd.dir, wrt.dir = tmp.dir)
inspect_apsimx("Maize-edited.apsimx", src.dir = tmp.dir,
  node = "Soil")
```
Edit APSIM ‘Classic’ file with a replaced soil profile

Description
Edits an APSIM Classic simulation by replacing the soil profile

Usage
edit_apsim_replace_soil_profile(
  file = "", 
  src.dir = ".", 
  wrt.dir = NULL, 
  soil.profile = NULL, 
  swim = NULL, 
  soilwat = NULL, 
  edit.tag = "-edited", 
  overwrite = FALSE, 
  verbose = TRUE
)

Arguments

file name of the .apsim file to be edited
src.dir source directory
wrt.dir writing directory
soil.profile a soil profile object with class ‘soil_profile’
swim list with SWIM specific parameters
soilwat list with SoilWat specific parameters
edit.tag default edit tag ‘-edited’
overwrite default FALSE
verbose default TRUE. Will print messages indicating what was done.

Details
This function is designed to batch replace the whole soil in an APSIM simulation.

Value
writes an APSIM file to disk with the supplied soil profile
Note

There is no such thing as a default soil, carefully build the profile for each simulation. This function replaces values and it can grow an XML node, but it cannot edit a property which is not present in the original file.

Examples

```r
sp <- apsim_soil_profile(nlayers = 20,
  crops = c("Barley", "Chickpea", "Lucerne",
            "Maize", "Perennial Grass", "Sorghum",
            "Wheat", "Millet"))

extd.dir <- system.file("extdata", package = "apsimx")

## Writing to a temp directory
tmp.dir <- tempdir()
edit_apsim_replace_soil_profile("Millet.apsim", soil.profile = sp,
  edit.tag = "-newsoil",
  src.dir = extd.dir,
  wrt.dir = tmp.dir)

inspect_apsim("Millet-newsoil.apsim", src.dir = tmp.dir,
  node = "Soil", soil.child = "Water")
```

edit_apsim_xml

Edit an APSIM (Classic) Simulation auxiliary xml file

Description

This function allows editing of an APSIM (Classic) simulation xml file.

Usage

```r
edit_apsim_xml(
  file,
  src.dir = ".",
  wrt.dir = NULL,
  parm.path = NULL,
  value = NULL,
  overwrite = FALSE,
  edit.tag = "-edited",
  verbose = TRUE
)
```
**_edit_apsim_xml_**

**Arguments**

- **file**: file ending in .xml to be edited
- **src.dir**: directory containing the .xml file to be edited; defaults to the current working directory
- **wrt.dir**: should be used if the destination directory is different from the src.dir
- **parm.path**: parameter path to be edited (see example)
- **value**: new values for the parameter to be edited
- **overwrite**: logical; if TRUE the old file is overwritten, a new file is written otherwise
- **edit.tag**: if the file is edited a different tag from the default ‘-edited’ can be used.
- **verbose**: whether to print information about successful edit

**Details**

The variables specified by parm within the .apsim file specified by file in the source directory src.dir are edited. The old values are replaced with value, which is a list that has the same number of elements as the length of the vector parm. The current .xml file will be overwritten if overwrite is set to TRUE; otherwise the file ‘file’-edited.xml will be created. If (verbose = TRUE) then the name of the written file is returned. The function is similar to the edit_sim_file function in the ‘apsimr’ package, but with the difference that here the xml2 package is used instead.

**Value**

(when verbose=TRUE) complete file path to edited .xml file is returned as a character string. As a side effect this function creates a new XML file.

**Note**

This function cannot check whether replacement is of the correct length. Also, there is an inspect equivalent. It is more flexible than ‘edit_apsim’ and (perhaps) similar to ‘apsimr::edit_sim_file’.

**Examples**

```r
## This example changes the RUE values
extd.dir <- system.file("extdata", package = "apsimx")
values <- paste(rep(1.7, 12), collapse = " ")
## Writing to a temp directory, but replace as needed
tmp.dir <- tempdir()
edit_apsim_xml("Maize75.xml",
  src.dir = extd.dir,
  wrt.dir = tmp.dir,
  parm.path = ".//Model/rue",
  value = values)
```
**extract_values_apsimx**  
*Extract values from a parameter path*

**Description**

Extract initial values from a parameter path

**Usage**

```r
extract_values_apsimx(file, src.dir, parm.path)
```

**Arguments**

- `file`  
  file name to be run (the extension .apsimx is optional)
- `src.dir`  
  directory containing the .apsimx file to be run (defaults to the current directory)
- `parm.path`  
  parameter path either use inspect_apsimx or see example below

**Value**

a vector with extracted parameter values from an APSIM file.

**Examples**

```r
## Find examples
extd.dir <- system.file("extdata", package = "apsimx")
## Extract parameter path
pp <- inspect_apsimx("Maize.apsimx", src.dir = extd.dir,
                     node = "Manager", parm = list("Fert", 1))
ppa <- paste0(pp, ".Amount")
## Extract value
extract_values_apsimx("Maize.apsimx", src.dir = extd.dir, parm.path = ppa)
```

---

**get_apsimx_json**  
*fetched the json file for a specific model from APSIMX github*

**Description**

Retreives the json replacement file for a specific model

**Usage**

```r
get_apsimx_json(model = "Wheat", wrt.dir = ".", cleanup = FALSE)
```
Arguments

- model: a model (e.g. ‘Wheat’ or ‘Maize’)
- wrt.dir: directory to save the JSON file (default is the current directory)
- cleanup: whether to delete the JSON file

Details

Get APSIM-X Model Replacement from github

Value

a list read through the jsonlite package

See Also

insert_replacement_node

Examples

tmp.dir <- tempdir()
wheat <- get_apsimx_json(model = "Wheat", wrt.dir = tmp.dir)

get_chirps_apsim_met

Get CHIRPS data for an APSIM met file

Description

Uses get_chirps from the chirps package to download data to create an APSIM met file.

Usage

getchirps_apsim_met(
    lonlat,  # longitude and latitude
    dates,   # dates for which data is needed
    wrt.dir = ".",  # directory to save the JSON file
    filename = NULL,  # filename for the JSON file
    fillin.radn = TRUE,  # fill in missing data
    silent = FALSE  # whether to print the progress
)
get_daymet2_apsim_met

Arguments

lonlat Longitude and latitude vector
dates date ranges
wrt.dir write directory
filename file name for writing out to disk
fillin.radn whether to fill in radiation data using the nasapower package. Default is TRUE. default is FALSE. Changing it will not do anything at the moment. A future feature.

Details

This function requires the chirps package
If the filename is not provided it will not write the file to disk, but it will return an object of class ‘met’. This is useful in case manipulation is required before writing to disk.

Value

returns an object of class ‘met’ and writes a file to disk when filename is supplied.

Examples

## Not run:
require(chirps)
## This will not write a file to disk
chrp <- get_chirps_apsim_met(lonlat = c(-93,42), dates = c("2012-01-01","2012-12-31"))
## End(Not run)

get_daymet2_apsim_met  Get DAYMET data for an APSIM met file

Description

Uses download_daymet from the daymetr package to download data to create an APSIM met file.

Usage

get_daymet2_apsim_met(lonlat, years, wrt.dir = ".", filename, silent = FALSE)

Arguments

lonlat Longitude and latitude vector
years a numeric vector of years to extract (c(start, end)). For example, if you need 2012 through 2015, use c(2012, 2015).
wrt.dir write directory (default is the current directory)
filename file name for writing out to disk
silent argument passed to download_daymet
get_daymet_apsim_met

Details

This function requires the daymet package. This function should replace the get_daymet_apsim_met function.

If the filename is not provided it will not write the file to disk, but it will return an object of class ‘met’. This is useful in case manipulation is required before writing to disk. The variable ‘srad’ as downloaded from daymet is average solar radiation, so it is converted to total. Daily total radiation (MJ/m2/day) can be calculated as follows: ((srad (W/m2) * dayl (s/day)) / 1,000,000)

Vapor Pressure Deficit (vp) should be in hecto Pascals

Value

It returns an object of class ‘met’ and writes a file to disk when filename is supplied.

Source

The data is retrieved using the daymet package. For the original source see: https://daymet.ornl.gov/

Examples

```r
## Not run:
require(daymet)
## I write to a temp directory but replace as needed
dmet12 <- get_daymet2_apsim_met(lonlat = c(-93,42), years = 2012)
summary(dmet12)
## Check for reasonable ranges
cHECK_apsim_met(dmet12)
## End(Not run)
```

get_daymet_apsim_met  Get DAYMET data for an APSIM met file

Description

Uses download_daymet from the daymet package to download data to create an APSIM met file.

Usage

```r
get_daymet_apsim_met(lonlat, years, wrt.dir = ".", filename, silent = FALSE)
```

Arguments

- `lonlat`: Longitude and latitude vector
- `years`: a numeric vector of years to extract (c(start, end)). For example, if you need 2012 through 2015, use c(2012, 2015).
- `wrt.dir`: write directory (default is the current directory)
- `filename`: file name for writing out to disk
- `silent`: argument passed to download_daymet
get_gsod_apsim_met

Details

This function requires the daymetr package. This function should replace the get_daymet_apsim_met function.

If the filename is not provided it will not write the file to disk, but it will return an object of class ‘met’. This is useful in case manipulation is required before writing to disk. The variable ‘srad’ as downloaded from daymet is average solar radiation, so it is converted to total. Daily total radiation (MJ/m2/day) can be calculated as follows: ((srad (W/m2) * dayl (s/day)) / 1,000,000)

Vapor Pressure Deficit (vp) should be in hecto Pascals

Value

It returns an object of class ‘met’ and writes a file to disk when filename is supplied.

Source

The data is retrieved using the daymetr package. For the original source see: https://daymet.ornl.gov/

Examples

```r
## Not run:
require(daymetr)
## I write to a temp directory but replace as needed
dmet12 <- get_daymet_apsim_met(lonlat = c(-93,42), years = 2012)
summary(dmet12)
## Check for reasonable ranges
check_apsim_met(dmet12)
## End(Not run)
```

---

get_gsod_apsim_met  Get GSOD data for an APSIM met file

Description

Uses get_GSOD from the GSODR package to download data to create an APSIM met file.

Usage

```r
get_gsod_apsim_met(
  lonlat,
  dates,
  wrt.dir = ".",
  filename = NULL,
  distance = 100,
  fillin.radn = FALSE
)
```
get_iemre_apsim_met

**Arguments**

- **lonlat**: Longitude and latitude vector
- **dates**: date ranges
- **wrt.dir**: write directory
- **filename**: file name for writing out to disk
- **distance**: distance in kilometers for the nearest station
- **fillin.radn**: whether to fill in radiation data using the nasapower package. Default is FALSE.

**Details**

This function requires the **GSODR** package.

If the filename is not provided it will not write the file to disk, but it will return an object of class ‘met’. This is useful in case manipulation is required before writing to disk.

**Value**

returns an object of class ‘met’ and writes a file to disk when filename is supplied.

**Note**

This source of data does not provide solar radiation. If ‘fillin.radn’ is TRUE it fill in radiation data using the nasapower package.

**Examples**

```r
## Not run:
require(GSODR)
## This will not write a file to disk
gsd <- get_gSODR_apsim_met(lonlat = c(-93,42), dates = c("2012-01-01","2012-12-31"),
                           fillin.radn = TRUE)
summary(gsd)
# Check for reasonable ranges
check_apsim_met(gsd)
```

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

---

**get_iemre_apsim_met**  
*Get weather data from Iowa Environmental Mesonet Reanalysis*

**Description**

Retrieves weather data from Iowa Environmental Mesonet Reanalysis into an APSIM met file
get_iemre_apsim_met

Usage

get_iemre_apsim_met(
  lonlat,
  dates,
  wrt.dir = ".",
  filename = NULL,
  fillin.radn = FALSE
)

Arguments

lonlat Longitude and latitude vector
dates date ranges
wrt.dir write directory
filename file name for writing out to disk
fillin.radn whether to fill in radiation data using the nasapower package. Default is FALSE.

Details

The original data can be obtained from: https://mesonet.agron.iastate.edu/iemre/

If the filename is not provided it will not write the file to disk, but it will return an object of class ‘met’. This is useful in case manipulation is required before writing to disk.

Value

returns an object of class ‘met’ and writes a file to disk when filename is supplied.

Note

Multi-year query is not supported for this product.

Examples

## Not run:
## This will not write a file to disk
iemre <- get_iemre_apsim_met(lonlat = c(-93,42), dates = c("2012-01-01","2012-12-31"))
## Note that solar radiation is not available, but can be filled in
## using the nasapower package
iemre2 <- get_iemre_apsim_met(lonlat = c(-93,42),
  dates = c("2012-01-01","2012-12-31"),
  fillin.radn = TRUE)
summary(iemre)
summary(iemre2)

## Still it is important to check this object
check_apsim_met(iemre2)

## End(Not run)
**get_iem_apsim_met**  
*Get weather data from Iowa Environmental Ag Weather Stations*

**Description**
Retrieves weather data from Iowa Environmental Mesonet (AgWeather) into an APSIM met file.

**Usage**
```
get_iem_apsim_met(lonlat, dates, wrt.dir = ".", state, station, filename)
```

**Arguments**
- `lonlat`: Longitude and latitude vector (optional)
- `dates`: date ranges
- `wrt.dir`: write directory
- `state`: state which you choose climate data from
- `station`: station which you choose climate data from
- `filename`: file name for writing out to disk

**Details**
The original data can be obtained from: https://mesonet.agron.iastate.edu/request/coop/fe.phtml
If the filename is not provided it will not write the file to disk, but it will return an object of class `met`. This is useful in case manipulation is required before writing to disk. For this function either provide the longitude and latitude or the state and station, but not both. In fact, `state` and `station` will be ignored if `lonlat` is supplied.

**Value**
returns an object of class `met` and writes a file to disk when `filename` is supplied.

**Examples**
```r
## Not run:
## This will not write a file to disk
iem.met <- get_iem_apsim_met(  
  state = "IA",  
  station = "IA0200",  
  dates = c("2012-01-01","2012-12-31"))
summary(iem.met)

## Alternatively, coordinates can be used
## This should be equivalent to the previous request
iem.met2 <- get_iem_apsim_met(  
  lonlat = c(-93.77, 42.02),  
  dates = c("2012-01-01","2012-12-31"))
```
get_isric_soil_profile

Generate a synthetic APSIM soil profile from the ISRIC soil database

Description
Retrieves soil data from the ISRIC global database and converts it to an APSIM soil_profile object.

Usage
get_isric_soil_profile(
  lonlat,
  statistic = c("mean", "Q0.5"),
  soil.profile,
  find.location.name = TRUE
)

Arguments
- lonlat: Longitude and latitude vector (e.g. c(-93, 42)).
- statistic: default is the mean.
- soil.profile: a soil profile to fill in in case the default one is not appropriate.
- find.location.name: default is TRUE. Use either maps package or photon API to find Country/State. If you are running this function many times it might be better to set this to FALSE.

Details
Source: https://www.isric.org/
Details: https://www.isric.org/explore/soilgrids/faq-soilgrids


TODO: need to look into how this is done in APSIM NG https://github.com/APSIMInitiative/ApsimX/pull/3994/files

NOTE: Eric Zurcher provided help by sending me an R file originally written by Andrew Moore. It provides a bit of context for how some of the decisions were made for constructing the synthetic soil profiles in APSIM. (email from June 3 2021).
Variable which are directly retrieved and a simple unit conversion is performed:
  * Bulk density - bdod
  * Carbon - soc
  * Clay - clay
  * Sand - sand
  * PH - phh2o
  * Nitrogen - nitrogen

Variables which are estimated using pedotransfer functions:
LL15, DUL, SAT, KS, AirDry

TO-DO:
What do I do with nitrogen?
Can I use CEC?
How can I have a guess at FBiom and Finert?
FBiom does not depend on any soil property at the moment, should it?

Value

it generates an object of class ‘soil_profile’.

Author(s)

Fernando E. Miguez, Eric Zurcher (CSIRO) and Andrew Moore (CSIRO)

See Also

apsimx_soil_profile, edit_apsim_replace_soil_profile, edit_apsimx_replace_soil_profile.

Examples

```r
## Not run:
## Get soil profile properties for a single point
sp1 <- get_isric_soil_profile(lonlat = c(-93, 42))

## Visualize
plot(sp1)
plot(sp1, property = "water")

## End(Not run)
```

get_power_apsim_met

Get NASA-POWER data for an APSIM met file

Description

Uses `get_power` from the `nasapower` package to download data to create an APSIM met file.
get_ssurgo_soil_profile

Usage

get_power_apsim_met(lonlat, dates, wrt.dir = ".", filename = NULL)

Arguments

lonlat Longitude and latitude vector
dates date ranges
wrt.dir write directory
filename file name for writing out to disk

Details

This function requires the `nasapower` package version 4.0.0.

If the filename is not provided it will not write the file to disk, but it will return an object of class `met`. This is useful in case manipulation is required before writing to disk.

Value

returns an object of class `met` and writes a file to disk when filename is supplied.

Examples

## Not run:
require(nasapower)
## This will not write a file to disk
pwr <- get_power_apsim_met(lonlat = c(-93,42), dates = c("2012-01-01","2012-12-31"))
## Let's insert a missing value
pwr[100, "radn"] <- NA
summary(pwr)
## Check the met file
check_apsim_met(pwr)
## Impute using linear interpolation
pwr.imptd <- impute_apsim_met(pwr, verbose = TRUE)
summary(pwr.imptd)
check_apsim_met(pwr.imptd)

## End(Not run)

get_ssurgo_soil_profile

Retrieves soil profile data and converts it to an object of class `soil_profile`

Description

Generate a synthetic soil profile based on the information in SSURGO database.
get_ssurgo_soil_profile

Usage

get_ssurgo_soil_profile(
  lonlat,
  shift = -1,
  nmapunit = 1,
  nsoil = 1,
  xout = NULL,
  soil.bottom = 200,
  method = c("constant", "linear"),
  nlayers = 10,
  verbose = FALSE
)

Arguments

lonlat Longitude and latitude vector (e.g. c(-93, 42))
shift simple mechanism for creating an area of interest by displacing the point indicated in lonlat by some amount of distance (e.g. 300 - in meters)
nmapunit number of mapunits to select (see ssurgo2sp)
nsoil number of soils to select (see ssurgo2sp)
xout see ssurgo2sp
soil.bottom see ssurgo2sp
method interpolation method see ssurgo2sp
nlayers number for layer for the new soil profile
verbose default FALSE. Whether to print messages.

Details

Data source is USDA-NRCS Soil Data Access. See package soilDB for more details

Value

this function will always return a list. Each element of the list will be an object of class ‘soil_profile’

Examples

## Not run:
require(soilDB)
require(sp)
require(sf)
require(spData)
## Soil information for a single point
sp <- get_ssurgo_soil_profile(lonlat = c(-93, 42))
plot(sp[[1]])
plot(sp[[1]], property = "water")

## End(Not run)
get_ssurgo_tables

Retrieve soil profile data and return a table with data

Description

This function does partially what get_ssurgo_soil_profile does, but it returns a list with tables for mapunit, component, chorizon and mapunit.shp (object of class sf)

Usage

get_ssurgo_tables(lonlat, shift = -1, aoi, verbose = FALSE)

Arguments

lonlat Longitude and latitude vector (e.g. c(-93, 42))
shift simple mechanism for creating an area of interest by displacing the point indicated in lonlat by some amount of distance (e.g. 300 - in meters)
aoi area of interest, if supplied the lonlat and shift arguments will be ignored. Should be of class ‘sp::SpatialPolygons’.
verbose whether to print messages and warnings to the console default FALSE

Details

Data source is USDA-NRCS Soil Data Access. See package soilDB for more details
* If a point is requested then an object of class ‘sf’ is returned (for mapunit.shp) with the MUKEY and AREASYMBOL with GEOMETRY type: POINT.
* If a the request is for a spatial polygon, then an object of class ‘sf’ is returned with gid, mukey and area_ac with GEOMETRY type: POLYGON.

Value

a list with elements: mapunit, component, chorizon and mapunit.shp

Examples

```r
## Not run:
require(soilDB)
require(sp)
require(sf)
require(spData)
## retrieve data from lon -93, lat = 42
stbls <- get_ssurgo_tables(lonlat = c(-93, 42))

stbls2 <- get_ssurgo_tables(lonlat = c(-93, 42), shift = 200)
```
## grep_json_list

grep but for json list

### Description

recursive grep adapted for a json list

### Usage

grep_json_list(pattern, x, ignore.case = FALSE, search.depth = 10)

### Arguments

- **pattern**: as in grep
- **x**: object (a list)
- **ignore.case**: as in grep
- **search.depth**: search depth for the list (to prevent endless search)

### Value

It returns a list with the found object, the json path and the positions in the list.

---

## impute_apsim_met

Perform imputation for missing data in a met file

### Description

Takes in an object of class 'met' and imputes values

### Usage

impute_apsim_met(
    met,
    method = c("approx", "spline", "mean"),
    verbose = FALSE,
    ...
  )
**insert_replacement_node**

*Inserts a replacement node in a simple apsimx simulation file*

**Description**

Inserts a replacement node in a simple apsimx simulation file

**Usage**

```r
insert_replacement_node(
  file, 
  src.dir, 
  wrt.dir, 
  rep.node, 
  rep.node.position = 1, 
  new.core.position = rep.node.position + 1, 
  edit.tag = "-edited", 
  overwrite = FALSE, 
  verbose = TRUE, 
  root
)
```

**Arguments**

- **file**: file ending in `.apsimx` to be edited (JSON)
- **src.dir**: directory containing the `.apsimx` file to be edited; defaults to the current working directory
- **wrt.dir**: should be used if the destination directory is different from the src.dir
- **rep.node**: replacement node as obtained by the `get_apsimx_json` function
- **rep.node.position**: position where the replacement node will be inserted, default is 1
inspect_apsim

Inspect an .apsim (XML) file

Description

inspect an XML apsim file. It does not replace the GUI, but it can save time by quickly checking parameters and values.

Usage

inspect_apsim(
  file = "",
  src.dir = ".",
            "Outputfile", "Other"),
                 "InitialWater", "Sample", "SWIM"),
  parm = NULL,
  digits = 3,
  print.path = FALSE,
  root
)

Examples

## Not run:
tmp.dir <- tempdir()
wheat <- get_apsimx_json(model = "Wheat", wrt.dir = tmp.dir)
extd.dir <- system.file("extdata", package = "apsimx")
insert_replacement_node("Wheat.apsimx", 
  src.dir = extd.dir, wrt.dir = tmp.dir, 
  rep.node = wheat)
**inspect_apsim**

**Arguments**

- **file**: file ending in .apsim (Classic) to be inspected (XML)
- **src.dir**: directory containing the .apsim file to be inspected; defaults to the current working directory
- **soil.child**: specific soil component to be inspected
- **parm**: parameter to inspect when node = ‘Crop’, ‘Manager’, ‘Outputfile’ or ‘Other’
- **digits**: number of decimals to print (default 3)
- **print.path**: whether to print the parameter path (default = FALSE)
- **root**: root node label. In simulation structures such as factorials there will be multiple possible nodes. This can be specified by supplying an appropriate character.

**Details**

This is simply a script that prints the relevant parameters which are likely to need editing. It does not print all information from an .apsim file. For ‘Crop’, ‘Manager’ and ‘Other’, ‘parm’ should be indicated with a first element to look for and a second with the relative position in case there are multiple results.

**Value**

It returns the parameter path (when print.path equals TRUE) and table with inspected parameters and values.

**Note**

When multiple folders are present as it is the case when there are factorials. Inspect will find the instance in the first folder unless ‘root’ is supplied. By providing the name of the folder to root (or a regular expression), the appropriate node can be selected. In this case the printed path will be absolute instead of relative.

**Examples**

```r
extd.dir <- system.file("extdata", package = "apsimx")
## Testing using 'Millet'
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Clock")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Weather")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil", soil.child = "Metadata")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil", soil.child = "OrganicMatter")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil", soil.child = "Analysis")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil", soil.child = "InitialWater")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil", soil.child = "Sample")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "SurfaceOrganicMatter")
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Crop", parm = list("sow",NA))
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Crop", parm = list("sow",7))
```
# when soil.child = "Water" there are potentially many crops to chose from
# This selects LL, KL and XF for Barley
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "Water", parm = "Barley")

# This selects LL for all the crops
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "Water", parm = "LL")

# To print the parm.path the selection needs to be unique
# but still there will be multiple soil layers
# 'parm' can be a list or a character vector of length equal to two
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "Water", parm = list("Barley", "LL"),
    print.path = TRUE)

# Inspect outputfile
inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Outputfile",
    parm = "filename")

inspect_apsim("Millet.apsim", src.dir = extd.dir, node = "Outputfile",
    parm = "variables")

# Testing with maize-soybean-rotation.apsim
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Clock")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Weather")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "Metadata")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "OrganicMatter")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "Analysis")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "InitialWater")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Soil",
    soil.child = "Sample")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir,
    node = "SurfaceOrganicMatter")
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir, node = "Crop")

# This has many options and a complex structure
# It is possible to select unique managements, but not non-unique ones
# The first element in parm can be a regular expression
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir,
    node = "Manager", parm = list("rotat",NA))
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir,
    node = "Manager",
    parm = list("sow on a fixed date - maize",NA))

# Select an individual row by position
inspect_apsim("maize-soybean-rotation.apsim", src.dir = extd.dir,
    node = "Manager",
    parm = list("sow on a fixed date - maize",7))

# Illustrating the 'print.path' feature.
inspect_apsim("Millet.apsim", src.dir = extd.dir,
    node = "Soil", soil.child = "Water",
    print.path = TRUE)
Inspect an .apsimx (JSON) file

### Description

inspect a JSON apsimx file. It does not replace the GUI, but it can save time by quickly checking parameters and values.

### Usage

```r
inspect_apsimx(
  file = "", 
  src.dir = ".", 
  parm = NULL, 
  digits = 3, 
  print.path = FALSE, 
  root 
)
```

### Arguments

- `file`: file ending in .apsimx to be inspected (JSON)
- `src.dir`: directory containing the .apsimx file to be inspected; defaults to the current working directory
**inspect_apsimx**

- **node** specific node to be inspected either ‘Clock’, ‘Weather’, ‘Soil’, ‘SurfaceOrganicMatter’, ‘MicroClimate’, ‘Crop’, ‘Manager’ or ‘Other’
- **soil.child** specific soil component to be inspected. The options vary depending on what is available (see details)
- **parm** parameter to refine the inspection of the ‘manager’ list(‘parm’, ‘position’), use ‘NA’ for all the positions. ‘parm’ can be a regular expression for partial matching.
- **digits** number of decimals to print (default 3). Not used now because everything is a character.
- **print.path** whether to print the path to the specific parameter. Useful to give the later editing. (Also returned as ‘invisible’)
- **root** root node label. In simulation structures such as factorials there will be multiple possible nodes. This can be specified by supplying an appropriate character.

**Details**

In general, this function is used to edit one parameter at a time. There are some exceptions.

- For the Clock, both the ‘Start’ and ‘End’ can be edited in one call.

This is simply a script that prints the relevant parameters which are likely to need editing. It does not print all information from an .apsimx file. To investigate the available ‘soil.childs’ specify ‘Soil’ for ‘node’ and do not specify the ‘soil.child’.

**Value**

prints a table with inspected parameters and values (and ‘parm path’ when ‘print.path’ = TRUE).

**Examples**

```r
extd.dir <- system.file("extdata", package = "apsimx")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Clock")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Weather")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Soil", soil.child = "Metadata")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Soil", soil.child = "Physical")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Soil", soil.child = "SoilWater")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Soil", soil.child = "Organic")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Soil", soil.child = "Chemical")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Soil", soil.child = "InitialWater")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Soil", soil.child = "InitialN")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "SurfaceOrganicMatter")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "MicroClimate")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Crop")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Manager")
inspect_apsimx("Wheat.apsimx", src.dir = extd.dir, node = "Report")
```

## Manager folder present

```r
extd.dir <- system.file("extdata", package = "apsimx")
inspect_apsimx("maize-manager-folder.apsimx", node = "Other", src.dir = extd.dir,
```
inspect_apsimx_json

parm = list("Manager", "Fertiliser", "Amount")

inspect_apsimx_json       
Inspect an .apsimx or .json (JSON) file

Description

inspect an .apsimx or .json (JSON) file. It does not replace the GUI, but it can save time by quickly checking parameters and values.

Usage

inspect_apsimx_json(
  file = "",
  src.dir = ".",
  parm,
  search.depth = 15,
  print.path = FALSE,
  verbose = FALSE
)

Arguments

file file ending in .apsimx or .json to be inspected (JSON)
src.dir directory containing the .apsimx or .json file to be inspected; defaults to the current working directory
parm string or regular expression for partial matching.
search.depth default is 15. How deep should the algorithm explore the structure of the list.
print.path whether to print the parameter path (default is FALSE)
verbose whether to print additional information (mostly used for debugging)

Details

This function is a work in progress. There are many instances for which it will not work. It will probably only find the first instance that matches.
A future feature will be to search for a jspath instead of simply a regular expression

Value

prints a table with inspected parameters and values (and the path when ‘print.path’ = TRUE).
Examples

```r
extd.dir <- system.file("extdata", package = "apsimx")
# It seems to work for simple search
inspect_apsimx_json("Wheat.apsimx", src.dir = extd.dir, parm = "Version")
inspect_apsimx_json("Wheat.apsimx", src.dir = extd.dir, parm = "Simulations")
inspect_apsimx_json("Wheat.apsimx", src.dir = extd.dir, parm = "Clock")
inspect_apsimx_json("Wheat.apsimx", src.dir = extd.dir, parm = "Weather")
# Does return soil components
inspect_apsimx_json("Wheat.apsimx", src.dir = extd.dir, parm = "DUL")
# Or cultivar
inspect_apsimx_json("Wheat.apsimx", src.dir = extd.dir, parm = "Hartog")
```

inspect_apsimx_replacement

*Inspect a replacement component in an .apsimx (JSON) file*

Description

inspect the replacement component of an JSON apsimx file. It does not replace the GUI, but it can save time by quickly checking parameters and values.

Usage

```r
inspect_apsimx_replacement(
  file = "", 
  src.dir = ".", 
  node = NULL, 
  node.child = NULL, 
  node.subchild = NULL, 
  node.subsubchild = NULL, 
  node.sub3child = NULL, 
  node.sub4child = NULL, 
  node.sub5child = NULL, 
  node.string = NULL, 
  root = list("Models.Core.Replacements", NA), 
  parm = NULL, 
  display.available = FALSE, 
  digits = 3, 
  print.path = FALSE, 
  verbose = TRUE, 
  grep.options
)
```
Arguments

file  
file ending in .apsimx to be inspected (JSON)

src.dir  
directory containing the .apsimx file to be inspected; defaults to the current working directory

node  
specific node to be inspected

node.child  
specific node child component to be inspected.

node.subchild  
specific node sub-child to be inspected.

node.subsubchild  
specific node sub-subchild to be inspected.

node.sub3child  
specific node sub3child to be inspected.

node.sub4child  
specific node sub4child to be inspected.

node.sub5child  
specific node sub5child to be inspected.

node.string  
passing of a string instead of the node hierarchy. Do not use this and also the other node arguments. This argument will overwrite the other node specifications.

root  
‘root’ for the inspection of a replacement file (it gives flexibility to inspect other types of files).

cparm  
specific parameter to display

display.available  
logical. Whether to display available components to be inspected (default = FALSE)

digits  
number of decimals to print (default 3)

print.path  
print the path to the inspected parameter (default FALSE)

verbose  
whether to print additional information, default: TRUE

grep.options  
Additional options for grep. To be passed as a list.

Details

This is simply a script that prints the relevant parameters which are likely to need editing. It does not print all information from an .apsimx file.

Value

table with inspected parameters and values (and ‘parm path’ when ‘print.path’ = TRUE).

Note

I need to make some changes in order to be able to handle multiple parameters. At this point, it might work but it will generate warnings.
Examples

extd.dir <- system.file("extdata", package = "apsimx")
inspect_apsimx_replacement("MaizeSoybean.apsimx", src.dir = extd.dir,
    node = "Maize", node.child = "Phenology",
    node.subchild = "ThermalTime",
    node.subsubchild = "BaseThermalTime",
    node.sub3child = "Response")

## For Wheat
## getting down to 'XYPairs'
inspect_apsimx_replacement("WheatRye.apsimx",
    src.dir = extd.dir,
    node = "Wheat",
    node.child = "Structure",
    node.subchild = "BranchingRate",
    node.subsubchild = "PotentialBranchingRate",
    node.sub3child = "Vegetative",
    node.sub4child = "PotentialBranchingRate",
    node.sub5child = "XYPairs")

---

**inspect_apsim_xml**

*Inspect an APSIM Classic auxiliary (XML) file*

Description

inspect an auxiliary XML apsim file.

Usage

```r
inspect_apsim_xml(
    file = "",
    src.dir = ".",
    parm,
    verbose = TRUE,
    print.path = TRUE
)
```

Arguments

- **file**
  - file ending in .xml to be inspected.
- **src.dir**
  - directory containing the .xml file to be inspected; defaults to the current working directory
- **parm**
  - parameter to inspect.
- **verbose**
  - Whether to print to standard output
- **print.path**
  - Whether to print the parameter path
**mcmc.apsim.env**

**Value**

it returns an absolute parameter path(s)

**Note**

the behavior has changed from previous versions (earlier than 1.977). Before, if more than match was found it would return an error. Now it returns a list with all possible matches. This can be useful when trying to find a parameter.

**Examples**

```r
extd.dir <- system.file("extdata", package = "apsimx")

inspect_apsim_xml("Maize75.xml", src.dir = extd.dir,
                  parm = "leaf_no_rate_change")

pp <- inspect_apsim_xml("Maize75.xml", src.dir = extd.dir,
                        parm = "leaf_no_rate_change",
                        verbose = FALSE,
                        print.path = FALSE)
```

---

**mcmc.apsim.env**

Environment to store data for apsim MCMC

**Description**

Environment which stores data for MCMC

**Usage**

mcmc.apsim.env

**Format**

An object of class environment of length 0.

**Details**

Create an apsim environment for MCMC

**Value**

This is an environment, so nothing to return.
napad_apsim_met

mcmc.apsimx.env

Environment to store data for apsimx MCMC

Description

Environment which stores data for MCMC

Usage

mcmc.apsimx.env

Format

An object of class environment of length 0.

Details

Create an apsimx environment for MCMC

Value

This is an environment, so nothing to return.

napad_apsim_met

Pad a met file with NAs when there are date discontinuities

Description

It will fill in or ‘pad’ a met object with NAs

Usage

napad_apsim_met(met)

Arguments

met object of class ‘met’

Details

Fill in with missing data date discontinuities in a met file

Value

It returns an object of class ‘met’ with padded NAs.

Note

The purpose of this function is to allow for imputation using impute_apsim_met
obsWheat

*Observed wheat phenology, LAI and biomass*

**Description**

Artificial observed data for Wheat

**Usage**

obsWheat

**Format**

A data frame with 10 rows and 4 variables:

- **Date** - date starting Oct 1 2016 and ending June 6 2017
- **Wheat.Phenology.Stage** - numeric - phenology stage of wheat
- **Wheat.Leaf.LAI** - numeric - Leaf Area Index
- **Wheat.AboveGround.Wt** - numeric - above ground biomass (g/m2)

**Details**

A dataset containing the Date, phenology stage, LAI and above ground biomass for Wheat

**Source**

These are simulated data. For details see the APSIM documentation

---

optim_apsim

*Optimize parameters in an APSIM simulation*

**Description**

It is a wrapper for running APSIM and optimizing parameters using `optim`

- Friendly printing of `optim_apsim`
- Variance-Covariance for an `optim_apsim` object
- Parameter estimates for an `optim_apsim` object
- Confidence intervals for parameter estimates for an `optim_apsim` object
Usage

```r
optim_apsim(
    file,
    src.dir = ".",
    crop.file,
    parm.paths,
    data,
    type = c("optim", "nloptr", "mcmc", "ucminf"),
    weights,
    index = "Date",
    parm.vector.index,
    xml.parm,
    ...
)
```

### S3 method for class 'optim_apsim'
print(x, ..., digits = 3, level = 0.95)

### S3 method for class 'optim_apsim'
v cov(object, ..., scaled = TRUE)

### S3 method for class 'optim_apsim'
coef(object, ..., scaled = FALSE)

### S3 method for class 'optim_apsim'
confint(object, parm, level = 0.95, ...)

Arguments

- **file**
  - file name to be run (the extension .apsim is optional)
- **src.dir**
  - directory containing the .apsim file to be run (defaults to the current directory)
- **crop.file**
  - name of auxiliary xml file where parameters are stored. If this is missing, it is assumed that the parameters to be edited are in the main simulation file.
- **parm.paths**
  - absolute paths of the coefficients to be optimized. It is recommended that you use `inspect_apsim` or `inspect_apsim_xml` for this.
- **data**
  - data frame with the observed data. By default assumes there is a 'Date' column for the index.
- **type**
  - Type of optimization. For now, `optim` and, if available, `nloptr` or `mcmc` through `runMCMC`. Option ‘ucminf’ uses the `ucminf` function.
- **weights**
  - Weighting method or values for computing the residual sum of squares (see Note).
- **index**
  - Index for filtering APSIM output. ‘Date’ is currently used. (I have not tested how well it works using anything other than Date).
- **parm.vector.index**
  - Index to optimize a specific element of a parameter vector. At the moment it is possible to only edit one element at a time. This is because there is a
conflict when generating multiple elements in the candidate vector for the same parameter.

xml.parm
optional logical vector used when optimizing parameters which are both in the .apsim file and in the `crop.file`. If `crop.file` is missing it is assumed that the parameters to be optimized are in the .apsim file. If `crop.file` is not missing it is assumed that they are in the `crop.file`. If the parameters are in both, this needs to be specified in this argument.

... additional arguments (none used at the moment)

x
object of class `optim_apsim`

digits
number of digits to round up the output

level
confidence level (default is 0.95)

object
object of class `optim_apsim`

scaled
whether to return the scaled or unscaled estimates (TRUE in the optimized scale, FALSE in the original scale)

parm
parameter to select (it can be a regular expression)

Details

Simple optimization for APSIM Classic

* This function assumes that you want to optimize parameters which are stored in an auxiliary XML file. These are typically crop or cultivar specific parameters. However, it is possible to optimize parameters present in the main simulation file.

* Only one observation per day is allowed in the data.

* Given how APSIM Classic works, this can only be run when the main simulation file is in the current directory and the crop file (or XML) should be in the same directory as the main simulation.

* The initial values for the optimization should be the ones in the stored crop parameter file.

* It is suggested that you keep a backup of the original file. This function will edit and overwrite the file during the optimization.

* When you use the parm.vector.index you cannot edit two separate elements of a vector at the same time. This should be used to target a single element of a vector only.

* Internally, the optimization is done around the scaled value of the initial parameter values. A value of 1 would correspond to the initial value of the parameter. The `lower` and `upper` (or `ub` and `lb`) are also scaled to the initial values of the parameters. So, for example, if your initial value is 20 and you provide an upper bound of 5, it means that the actual upper value that you are allowing for is 100.

Value

object of class `optim_apsim`, but really just a list with results from optim and additional information.

prints to console

it returns the variance-covariance matrix for an object of class `optim_apsim`.

a numeric vector with the value of the parameter estimates.

a matrix with lower and upper limits and the point estimate (coef)
Note

When computing the objective function (residual sum-of-squares) different variables are combined. It is common to weight them since they are in different units. If the argument weights is not supplied no weighting is applied. It can be ‘mean’, ‘var’ or a numeric vector of appropriate length. This in the scale of the optimized parameters which are scaled to be around 1.

\[
\text{optim_apsimx} \quad \text{Optimize parameters in an APSIM Next Generation simulation}
\]

Description

It is a wrapper for running APSIM-X and optimizing parameters using \texttt{optim}

Usage

\[
\text{optim_apsimx}( \\
\text{file, } \\
\text{src.dir = ".", } \\
\text{parm.paths, } \\
\text{data, } \\
\text{type = c("optim", "nloptr", "mcmc", "ucminf"), } \\
\text{weights, } \\
\text{index = "Date", } \\
\text{parm.vector.index, } \\
\text{replacement, } \\
\text{root, } \\
\text{initial.values, } \\
\text{...})
\]

Arguments

- \textit{file} file name to be run (the extension .apsimx is optional)
- \textit{src.dir} directory containing the .apsimx file to be run (defaults to the current directory)
- \textit{parm.paths} absolute or relative paths of the coefficients to be optimized. It is recommended that you use \texttt{inspect_apsimx} for this
- \textit{data} data frame with the observed data. By default is assumes there is a 'Date' column for the index.
- \textit{type} Type of optimization. For now, \texttt{optim}, and, if available, \texttt{nloptr} or 'mcmc' through \texttt{runMCMC}. Option 'ucminf' uses the \texttt{ucminf} function.
- \textit{weights} Weighting method or values for computing the residual sum of squares.
- \textit{index} Index for filtering APSIM output. Typically, “Date”, but it can be c("report", “Date”) for multiple simulations
parm.vector.index

Index to optimize a specific element of a parameter vector. At the moment it is possible to only edit one element at a time. This is because there is a conflict when generating multiple elements in the candidate vector for the same parameter.

replacement

TRUE or FALSE for each parameter. Indicating whether it is part of the ‘replacement’ component. Its length should be equal to the length of ‘parm.paths’.

root

root argument for edit_apsimx_replacement

initial.values

(required) supply the initial values of the parameters. (Working on fixing this...). If the parameters to be optimized correspond to a single value, then a simple numeric vector can be supplied. If one or more of the parameters represent a vector in APSIM, then the initial values should be passed as a list. At the moment, it is not possible to check if these are appropriate (correct name and length).

... additional arguments to be passed to the optimization algorithm. See optim

Details

Simple optimization for APSIM Next Generation

* At the moment it is required to provide starting values for the parameters of interest.

* It is suggested that you keep a backup of the original file. This function will edit and overwrite the file during the optimization.

* When you use the parm.vector.index you cannot edit two separate elements of a vector at the same time. This should be used to target a single element of a vector only. (I can add this feature in the future if it is justified.)

* Internally, the optimization is done around the scaled value of the initial parameter values. A value of 1 would correspond to the initial value of the parameter. The ‘lower’ and ‘upper’ (or ‘ub’ and ‘lb’) are also scaled to the initial values of the parameters. So, for example, if your initial value is 20 and you provide an upper bound of 5, it means that the actual upper value that you are allowing for is 100.

* I have tested other optimizers and packages, but I think these are enough for most purposes. I tried function stats::nlm (but it does not support bounds and it can fail), package ‘optimx’ is a bit messy and it does not provide sufficient additional functionality. Package ‘ucminf’ seems like a good alternative, but it did not perform better than the other ones.

Value

object of class ‘optim_apsim’, but really just a list with results from optim and additional information.

Note

When computing the objective function (residual sum-of-squares) different variables are combined. It is common to weight them since they are in different units. If the argument weights is not supplied no weighting is applied. It can be ’mean’, ’variance’ or a numeric vector of appropriate length.
Examples

```r
## See the vignette for examples
```
print.met

Examples

## Read in and plot a met file
extd.dir <- system.file("extdata", package = "apsimx")
ames <- read_apsim_met("Ames.met", src.dir = extd.dir)
plot(ames, years = 2012:2015)
## Perhaps more informative
plot(ames, years = 2012:2015, cumulative = TRUE)
## for rain
plot(ames, met.var = "rain", years = 2012:2015, cumulative = TRUE)
## It is possible to add ggplot elements
library(ggplot2)
p1 <- plot(ames, met.var = "rain", years = 2012:2015, cumulative = TRUE)
p1 + ggtitle("Cumulative rain for 2012-2015")

print.met

Printer-friendly version of a metfile

Description

Print a met file in a friendly way

Usage

## S3 method for class 'met'
print(x, ...)

Arguments

x an R object of class ‘met’
...
additional printing arguments

Value

It prints to console. Not used to return an R object.
**Description**

read ‘output’ databases created by APSIM runs (.out and .sim). One file at a time.

**Usage**

```r
read_apsim(
  file = "", 
  src.dir = ".", 
  value = c("report", "all"),
  date.format = "%d/%m/%Y"
)
```

**Arguments**

- `file` file name
- `src.dir` source directory where file is located
- `value` either ‘report’ (data.frame) or ‘all’ (list)
- `date.format` format for adding ‘Date’ column

**Details**

Read APSIM generated .out files

**Value**

This function returns a data frame with APSIM output or a list if value equals ‘all’

**Examples**

```r
## Not run:
extd.dir <- system.file("extdata", package = "apsimx")
maize.out <- read_apsim("Maize", src.dir = extd.dir, value = "report")
millet.out <- read_apsim("Millet", src.dir = extd.dir, value = "report")

## End(Not run)
```
**read_apsimx**

*Read APSIM-X generated .db files*

**Description**

Read SQLite databases created by APSIM-X runs. One file at a time.

**Usage**

```r
read_apsimx(file = "", src.dir = ".", value = "report", simplify = TRUE)
```

**Arguments**

- `file` file name
- `src.dir` source directory where file is located
- `value` either ‘report’, ‘all’ (list) or user-defined for a specific report
- `simplify` if TRUE will attempt to simplify multiple reports into a single data.frame. If FALSE it will return a list.

**Details**

Read APSIM-X generated .db files

**Value**

normally it returns a data frame, but it depends on the argument ‘value’ above

**Note**

if there is one single report it will return a data.frame. If there are multiple reports, it will attempt to merge them into a data frame. If not possible it will return a list with names corresponding to the table report names. It is also possible to select a specific report from several available by selecting ‘value = ReportName’, where ‘ReportName’ is the name of the specific report that should be returned. If you select ‘all’ it will return all the components in the data base also as a list.

---

**read_apsimx_all**

*Read all APSIM-X generated .db files in a directory*

**Description**

Like `read_apsimx`, but it reads all .db files in a directory.

**Usage**

```r
read_apsimx_all(src.dir = ".", value = "report")
```
Arguments

src.dir  source directory where files are located
value either ‘report’ or ‘all’ (only ‘report’ implemented at the moment)

Details

Read all APSIM-X generated .db files in a directory

Value

it returns a data frame or a list if ‘value’ equals ‘all’.

Note

Warning: very simple function at the moment, not optimized for memory or speed.

read_apsim_all  Read all APSIM generated .out files in a directory

Description

Like read_apsim, but it reads all .out files in a directory.

Usage

read_apsim_all(
filenames,
src.dir = ".",
value = c("report", "all"),
date.format = "%d/%m/%Y",
simplify = TRUE
)

Arguments

filenames  names of files to be read
src.dir  source directory where files are located
value either ‘report’ or ‘all’ (only ‘report’ implemented at the moment)
date.format  format for adding ‘Date’ column
simplify  whether to return a single data frame or a list.

Details

Read all APSIM generated .out files in a directory
Value

returns a data frame or a list depending on the argument 'simplify' above.

Note

Warning: very simple function at the moment, not optimized for memory or speed.

---

**read_apsim_met**

*Read in an APSIM met file*

---

**Description**

Read into R a met file and return an object of class ‘met’

**Usage**

```
read_apsim_met(file, src.dir = ".", verbose = TRUE)
```

**Arguments**

- **file**: path to met file
- **src.dir**: optional source directory
- **verbose**: whether to suppress all messages and warnings

**Details**

Read a met file into R

This function uses S3 classes and stores the additional information as attributes
I use a more strict format than APSIM and reading and writing will not
preserve all the details. For example, at this moment comments are lost through
the process of read and write unless they are added back in manually.
Also, empty lines are ignored so these will be lost as well in the read and write process.

**Value**

an object of class ‘met’ with attributes

**Examples**

```
extd.dir <- system.file("extdata", package = "apsimx")
ames.met <- read_apsim_met("Ames.met", src.dir = extd.dir)
ames.met
```
Description

It is a wrapper for running APSIM and evaluating different parameters values

Usage

sens_apsim(
file,
src.dir = ".",
crop.file,
parm.paths,
parm.vector.index,
xm.parm,
grid,
summary = c("mean", "max", "var", "sd", "none"),
root,
verbose = TRUE,
...
)

Arguments

file file name to be run (with extension .apsim)
src.dir directory containing the .apsim file to be run (defaults to the current directory)
crop.file name of auxiliary xml file where parameters are stored. If this is missing, it is assumed that the parameters to be edited are in the main simulation file.
parm.paths absolute or relative paths of the coefficients to be evaluated. It is recommended that you use inspect_apsim for this
parm.vector.index Index to evaluate a specific element of a parameter vector. At the moment it is possible to only edit one element at a time. This is because there is a conflict when generating multiple elements in the candidate vector for the same parameter.
xm.parm TRUE or FALSE for each parameter. Indicating whether it is part of an xml file. Its length should be equal to the length of ‘parm.paths’.
grid grid of parameter values for the evaluation. It can be a data.frame.
summary function name to use to summarize the output to be a single row (default is the mean).
root root argument for edit_apsim
verbose whether to print progress in percent and elapsed time.
... additional arguments (none used at the moment).
Value

object of class `sens_apsim`, but really just a list with results from the evaluations.

Note

The summary function is stored as an attribute of the data frame `grid.sims`.

Examples

```r
## See the vignette for examples
```

---

**sens_apsim**  
_Sensitivity Analysis for APSIM Next Generation simulation_

Description

It is a wrapper for running APSIM-X and evaluating different parameters values.  
Summary computes variance-based sensitivity indexes from an object of class `sens_apsim`.

Usage

```r
sens_apsimx(
  file,  
src.dir = ":.",  
parm.paths,  
convert,  
replacement,  
grid,  
summary = c("mean", "max", "var", "sd", "none"),  
root,  
verbose = TRUE,  
...  
)
```

```r
## S3 method for class 'sens_apsim'
summary(object, ..., scale = FALSE, select = "all")
```

Arguments

- `file` file name to be run (the extension .apsimx is optional)
- `src.dir` directory containing the .apsimx file to be run (defaults to the current directory)
- `parm.paths` absolute or relative paths of the coefficients to be evaluated. It is recommended that you use `inspect_apsimx` for this
convert (logical) This argument is needed if there is a need to pass a vector instead of a single value. The vector can be passed as a character string (separated by spaces) and it will be converted to a numeric vector. It should be either TRUE or FALSE for each parameter.

replacement TRUE or FALSE for each parameter. Indicating whether it is part of the ‘replacement’ component. Its length should be equal to the length of ‘parm.paths’.

grid grid of parameter values for the evaluation. It can be a data.frame.

summary function name to use to summarize the output to be a single row (default is the mean).

root root argument for `edit_apsim_replacement`

verbose whether to print progress in percent and elapsed time.

... additional arguments (none used at the moment)

object object of class ‘sens_apsim’

scale if all inputs are numeric it is better to scale them. The default is FALSE as some inputs might be characters or factors. In this case all inputs will be treated as factors in the sum of squares decomposition.

select option for selecting specific variables in the APSIM output. It will be treated as a regular expression

Details

Suggested reading on the topic of sensitivity analysis:


Saltelli et al. . Global Sensitivity Analysis.

Value

object of class ‘sens_apsim’, but really just a list with results from the evaluations.

prints to console

Note

The summary function is stored as an attribute of the data frame ‘grid.sims’.

Examples

```r
## See the vignette for examples
```
soilorganicmatter_parms

*Helper function to supply additional Soil Organic Matter parameters*

**Description**

Creates a list with specific components for the Soil Organic Matter module

**Usage**

```r
soilorganicmatter_parms(
  RootCN = NA,
  RootWt = NA,
  EnrACoeff = NA,
  EnrBCoeff = NA,
  OCUnits = NA
)
```

**Arguments**

- **RootCN**: Root Carbon:Nitrogen ratio (see APSIM documentation)
- **RootWt**: Root weight (see APSIM documentation)
- **EnrACoeff**: (see APSIM documentation)
- **EnrBCoeff**: (see APSIM documentation)
- **OCUnits**: Organic Carbon Units

soilwat_parms

*Helper function to supply SoilWat parameters*

**Description**

Creates a list with specific components for the SoilWat model

**Usage**

```r
soilwat_parms(
  SummerCona = NA,
  SummerU = NA,
  SummerDate = NA,
  WinterCona = NA,
  WinterU = NA,
  WinterDate = NA,
  DiffusConst = NA,
  DiffusSlope = NA,
)
```
soilwat_parms

Salb = NA,
CN2Bare = NA,
CNRed = NA,
CNCov = NA,
Slope = NA,
DischargeWidth = NA,
CatchmentArea = NA,
MaxPond = NA,
SWCON = NA,
Thickness = NA
)

Arguments

SummerCona see APSIM documentation
SummerU see APSIM documentation
SummerDate see APSIM documentation
WinterCona see APSIM documentation
WinterU see APSIM documentation
WinterDate see APSIM documentation
DiffusConst see APSIM documentation
DiffusSlope see APSIM documentation
Salb soil albedo (see APSIM documentation)
CN2Bare see APSIM documentation
CNRed see APSIM documentation
CNCov see APSIM documentation
Slope see APSIM documentation
DischargeWidth see APSIM documentation
CatchmentArea see APSIM documentation
MaxPond see APSIM documentation
SWCON see APSIM documentation
Thickness provide the corresponding thickness layer

Details

current documentation for APSIM 7.10 https://www.apsim.info/documentation/model-documentation/
soil-modules-documentation/soilwat/

Value

a ‘list’ with class ‘soilwat_parms’
ssurgo2sp

Take in SSURGO csv files and create a soil profile

Description
Utility function to convert SSURGO data to soil profile

Usage
ssurgo2sp(
  mapunit = NULL,
  component = NULL,
  chorizon = NULL,
  mapunit.shp = NULL,
  nmapunit = 1,
  nsoil = 1,
  xout = NULL,
  soil.bottom = 200,
  method = c("constant", "linear"),
  nlayers = 10,
  verbose = FALSE
)

Arguments

mapunit mapunit SSURGO file
component component SSURGO file
chorizon chorizon SSURGO file
mapunit.shp mapunit shapefile for creating metadata
nmapunit number of mapunits to select
nsoil number of soil components (within a mapunit) to consider
xout vector for interpolation and extrapolation
soil.bottom bottom of the soil profile
method method used for interpolation (see approx)
nlayers number of soil layers to generate
verbose whether to print details of the process

Details

Download the data from SSURGO using the ‘FedData’ package
This will generate csv files ‘chorizon’, ‘component’ and ‘mapunit’, but also many other files which are not needed for creating a soil profile.
**Value**

a list with soil profile matrices with length equal to nsoil

**Examples**

```r
require(ggplot2)
require(sf)
extd.dir <- system.file("extdata", package = "apsimx")

chorizon <- read.csv(paste0(extd.dir,"/ISUAG/SSURGO/ISUAG_SSURGO_chorizon.csv"))
component <- read.csv(paste0(extd.dir,"/ISUAG/SSURGO/ISUAG_SSURGO_component.csv"))
mapunit <- read.csv(paste0(extd.dir,"/ISUAG/SSURGO/ISUAG_SSURGO_mapunit.csv"))
mapunit.shp <- st_read(paste0(extd.dir,"/ISUAG/SSURGO/ISUAG_SSURGO_Mapunits.shp"), quiet = TRUE)

## Using default 'constant' method
sp.c <- ssurgo2sp(mapunit = mapunit,
                   component = component,
                   chorizon = chorizon,
                   mapunit.shp = mapunit.shp)

sp.c <- sp.c[[1]]

ggplot(data = sp.c, aes(y = -Depth, x = Carbon)) +
geom_point() +
geom_path() +
  ylab("Soil Depth (cm)") + xlab("Organic Matter (percent)") +
  ggtitle("method = constant")

## Using 'linear' method
sp.l <- ssurgo2sp(mapunit = mapunit,
                   component = component,
                   chorizon = chorizon,
                   mapunit.shp = mapunit.shp,
                   method = "linear")

sp.l <- sp.l[[1]]

ggplot(data = sp.l, aes(y = -Depth, x = Carbon)) +
geom_point() +
geom_path() +
  ylab("Soil Depth (cm)") + xlab("Organic Matter (percent)") +
  ggtitle("Method linear")

## Not run:
## Method using get_ssurgo_tables

require(soilDB)
require(sp)
require(sf)
```
require(spData)
## retrieve data from lon -93, lat = 42
stbls <- get_ssurgo_tables(lonlat = c(-93, 42))

sp2.c <- ssurgo2sp(mapunit = stbls$mapunit,
                   component = stbls$component,
                   chorizon = stbls$chorizon,
                   mapunit.shp = stbls$mapunit.shp)

names(sp2.c)

metadata <- attributes(sp2.c[[1]])
metadata$names <- NULL; metadata$class <- NULL; metadata$row.names <- NULL

## Convert to an APSIM soil profile
asp2.c <- apsimx_soil_profile(nlayers = 10,
                              Thickness = sp2.c[[1]]$Thickness * 10,
                              BD = sp2.c[[1]]$BD,
                              AirDry = sp2.c[[1]]$AirDry,
                              LL15 = sp2.c[[1]]$LL15,
                              DUL = sp2.c[[1]]$DUL,
                              SAT = sp2.c[[1]]$SAT,
                              KS = sp2.c[[1]]$KS,
                              Carbon = sp2.c[[1]]$Carbon,
                              PH = sp2.c[[1]]$PH,
                              ParticleSizeClay = sp2.c[[1]]$ParticleSizeClay,
                              ParticleSizeSilt = sp2.c[[1]]$ParticleSizeSilt,
                              ParticleSizeSand = sp2.c[[1]]$ParticleSizeSand,
                              metadata = metadata)

plot(asp2.c)
plot(asp2.c, property = "water")

## End(Not run)
days,
julian.days,
compute.frost = FALSE,
frost.temperature = 0,
check = FALSE,
verbose = FALSE,
na.rm = FALSE,
digits = 2)

Arguments

object object of class ‘met’
...
optional argument (none used at the momemt)
years optional argument to subset years
months optional argument to subset by months. If an integer, it should be between 1 and 12. If a character, it can be in the format, for example, ‘jan’ or ‘Jan’.
days optional argument to subset by days. It should be an integer between 1 and 31.
julian.days optional argument to subset by julian days. It should be a vector of integers between 1 and 365. Either use ‘days’ or ‘julian.days’ but not both.
compute.frost logical (default FALSE). Whether to compute frost statistics.
frost.temperature value to use for the calculation of the frost period (default is zero).
check logical (default FALSE). Whether to ‘check’ the ‘met’ object.
verbose whether to print additional information to the console
na.rm whether to remove missing values. Passed to ‘aggregate’
digits digits for rounding (default is 2).

Details

The frost free period is computed by first splitting each year (or year interval) in two halves. The first and last frosts in the first and second period are found. For the Northern hemisphere calendar days are used (1-365). For the Southern hemisphere the year is split in two halves, but the second half of the year is used as the first part of the growing season. If not frost is found a zero is returned.

Value

an object of class ‘data.frame’ with attributes

Examples

extd.dir <- system.file("extdata", package = "apsimx")
ames <- read_apsim_met("Ames.met", src.dir = extd.dir)

summary(ames, years = 2014:2016)
**swim parms**

*Helper function to supply SWIM parameters*

---

**Description**

Creates a list with specific components for the SWIM model

**Usage**

```r
swim_parms(
  Salb = NA,
  CN2Bare = NA,
  CNRed = NA,
  CNCov = NA,
  KDul = NA,
  PSIDul = NA,
  VC = NA,
  DTmin = NA,
  DTmax = NA,
  MaxWaterIncrement = NA,
  SpaceWeightingFactor = NA,
  SoluteSpaceWeightingFactor = NA,
  Diagnostics = NA,
  SwimWaterTable_WaterTableDepth = NA,
  SwimSubsurfaceDrain_DrainDepth = NA,
  SwimSubsurfaceDrain_DrainSpacing = NA,
  SwimSubsurfaceDrain_DrainRadius = NA,
  SwimSubsurfaceDrain_Klat = NA,
  SwimSubsurfaceDrain_ImpermDepth = NA
)
```

**Arguments**

- **Salb** see APSIM documentation
- **CN2Bare** see APSIM documentation
- **CNRed** see APSIM documentation
- **CNCov** see APSIM documentation
- **KDul** see APSIM documentation
- **PSIDul** see APSIM documentation
- **VC** see APSIM documentation
- **DTmin** see APSIM documentation
- **DTmax** see APSIM documentation
- **MaxWaterIncrement** see APSIM documentation
tt_apsim_met

Calculates Thermal Time taking a ‘met’ object

Description

Calculates Thermal Time using the ‘Classic’ formula, Heat Stress, Crop Heat Unit and other methods

Usage

```r
tt_apsim_met(
  met,
  dates,
  method = c("Classic_TT", "HeatStress_TT", "CropHeatUnit_TT", "APSIM_TT", "CERES_TT", "all"),
  x_temp = c(0, 26, 34),
  y_tt = c(0, 26, 0),
  base_temp = 0,
  max_temp = 30,
  dates.format = c("%d-%m")
)
```
**Arguments**

- **met**: object of class ‘met’
- **dates**: when the calculation starts and when it ends. At the moment it needs to be a character vector (e.g. c('01-05', '10-10')). It will use the same dates every year for multiple years.
- **method**: one of ‘Classic_TT’, ‘HeatStress_TT’, ‘ASPIM_TT’, ‘CERES_TT’ and ‘all’
- **x_temp**: cardinal temperatures (base, optimal and maximum)
- **y_tt**: thermal time accumulation for cardinal temperatures
- **base_temp**: base temperature for Classic TT calculation
- **max_temp**: maximum temperature for Classic TT calculation
- **dates.format**: default is ‘%d-%m’ which means day and month

**Details**

Calculating Thermal Time using a variety of methods. The function will fail if the method is not selected. Also, it does not work if each year does not have at least 365 days.

**Value**

It returns an object of class ‘met’ with additional columns ‘Date’ and the corresponding TT calculation.

**References**


**Examples**

```r
## Not run:
require(nasapower)
require(ggplot2)
pwr <- get_power_apsim_met(lonlat = c(-93,42), dates = c("2012-01-01","2015-12-31"))
check_apsim_met(pwr)
pwr <- impute_apsim_met(pwr)
pwr2 <- tt_apsim_met(pwr, dates = c("01-05", "30-10"), method = c("Classic", "Heat"))
ggplot(data = pwr2, aes(x = Date, y = Classic_TT)) + geom_point()
ggplot(data = pwr2, aes(x = Date, y = HeatStress_TT)) + geom_point()

## End(Not run)
```
Description

This function is slowly getting better. Adding more unit conversions as I need them.

Usage

unit_conv(x, from, to, ...)

Arguments

x
input variable

from
original units

to
target units

... additional arguments passed to specific conversions

Details

Function which performs common unit conversions

At the moment possible conversions are:

- ‘g/m2’ to ‘kg/ha’
- ‘kg/ha’ to ‘g/m2’
- ‘lb’ to ‘kg’
- ‘kg’ to ‘lb’
- ‘maize bu’ to ‘kg’
- ‘kg’ to ‘maize bu’
- ‘soy bu’ to ‘kg’
- ‘kg’ to ‘soy bu’
- ‘maize bu/ac’ to ‘kg/ha’
- ‘maize bu/ac’ to ‘g/m2’
- ‘kg/ha’ to ‘maize bu/ac’
- ‘g/m2’ to ‘maize bu/ac’
- ‘soy bu/ac’ to ‘kg/ha’
- ‘soy bu/ac’ to ‘g/m2’
- ‘kg/ha’ to ‘soy bu/ac’
- ‘g/m2’ to ‘soy bu/ac’
- ‘mm’ to ‘inches’
- ‘inches’ to ‘mm’
• ‘lb/ac’ to ‘kg/ha’
• ‘kg/ha’ to ‘lb/ac’
• ‘lb/ac’ to ‘g/m2’
• ‘g/m2’ to ‘lb/ac’
• ‘decimal’ to ‘degrees’
• ‘degrees’ to ‘decimal’

This is for metric and Imperial conversions Source: https://www.extension.iastate.edu/agdm/wholefarm/html/c6-80.html

Value

value of the input variable with new units

Examples

grain.yield.gm2 <- 600
grain.yield.kgha <- unit_conv(grain.yield.gm2, from = “g/m2”, to = “kg/ha”)
grain.yield.kgha
## Converting coordinates
require(sp)
unit_conv("42d 0’ 0"\ N", from = “degrees”, to = “decimal”)
unit_conv(42, from = “decimal”, to = “degrees”) ## EW by default
unit_conv(42, from = “decimal”, to = “degrees”, NS = TRUE)

view_apsim

Viewing an APSIM Classic file interactively

Description

Generate an interactive viewer for an APSIM file

Usage

view_apsim(file, src.dir, viewer = c("json", "react"), ...)

Arguments

file a file ending in .apsim to be inspected (XML)
src.dir directory containing the .apsim file to be inspected; defaults to the current working directory
viewer either “json” or “react”.
... additional arguments passed to either ‘jsonedit’ or ‘reactjson’. These are functions in package listviewer.
Value

a display with the APSIM file structure.

Note

I do not know how to edit an APSIM file using this method yet.

Examples

```r
extd.dir <- system.file("extdata", package = "apsimx")
## View the structure of the APSIM-X simulation file
view_apsim("Millet.apsim", src.dir = extd.dir)
```

Description

Generate an interactive viewer for an APSIM-X file

Usage

```r
view_apsimx(file, src.dir, viewer = c("json", "react"), ...)
```

Arguments

- `file` a file ending in .apsimx to be inspected (JSON)
- `src.dir` directory containing the .apsimx file to be inspected; defaults to the current working directory
- `viewer` either “json” or “react”.
- `...` additional arguments passed to either `jsonedit` or `reactjson`. These are functions in package `listviewer`.

Value

a display with the APSIM file structure.

Note

I do not know how to edit an APSIM-X file using this method yet.
Examples

```r
extd.dir <- system.file("extdata", package = "apsimx")
## View the structure of the APSIM-X simulation file
view_apsimx("Wheat.apsimx", src.dir = extd.dir)
```

---

**view_apsim_xml**  
View an APSIM Classic auxiliary (XML) file

**Description**

View an auxiliary XML apsim file.

**Usage**

```r
view_apsim_xml(file, src.dir, viewer = c("json", "react"), ...)
```

**Arguments**

- `file`  
  file ending in .xml to be viewed.

- `src.dir`  
  directory containing the .xml file to be viewed; defaults to the current working directory

- `viewer`  
  either “json” or “react”.

- `...`  
  additional arguments passed to either ‘jsonedit’ or ‘reactjson’.

**Details**

View APSIM XML file

**Value**

It does not return an object but it produces a tree display of the APSIM file.

**Examples**

```r
extd.dir <- system.file("extdata", package = "apsimx")
view_apsim_xml("Maize75.xml", src.dir = extd.dir)
```
**wop**

*Wheat example optimization results*

**Description**

Results from Wheat optimization example

**Usage**

`wop`

**Format**

An object of class `optim_apsim`

`wop` wheat optimization results

**Source**

Result of running the examples in Parameter Optimization vignette

**wop.h**

*Wheat example optimization results plus Hessian*

**Description**

Results from Wheat optimization example plus the Hessian

**Usage**

`wop.h`

**Format**

An object of class `optim_apsim`

`wop.h` wheat optimization results plus Hessian

**Source**

Result of running the examples in Parameter Optimization vignette with the added Hessian
write_apsim_met

Write an APSIM met file

Description

Write an object of class ‘met’ to disk

Usage

write_apsim_met(met, wrt.dir = NULL, filename = NULL)

Arguments

met object of class ‘met’

wrt.dir directory where the file will be written

filename optional alternative filename

Details

Write a met file to disk. It takes an object of class ‘met’
at the moment the read-write cycle will strip comments

Value

does not create an R object, it only writes to disk

Examples

extd.dir <- system.file("extdata", package = "apsimx")
ames.met <- read_apsim_met("Ames.met", src.dir = extd.dir)
ames.met
tmp.dir <- tempdir()
write_apsim_met(ames.met, wrt.dir = tmp.dir, filename = "Ames.met")
## Here I write to a temporary directory, but change this to where
## you want to write to
xargs_apsimx

Provide extra arguments for APSIM-X

Description
This provides additional command line arguments when running the model

Usage

```r
xargs_apsimx(
  verbose = FALSE,
  csv = FALSE,
  merge.db.files = FALSE,
  list.simulations = FALSE,
  list.referenced.filenames = FALSE,
  single.threaded = FALSE,
  cpu.count = -1L,
  simulation.names = FALSE,
  dotnet = FALSE,
  mono = FALSE,
  exe.path = NA
)
```

Arguments

- `verbose` Write detailed messages to stdout when a simulation starts/finishes.
- `csv` Export all reports to .csv files.
- `merge.db.files` Merge multiple .db files into a single .db file.
- `list.simulations` List simulation names without running them.
- `list.referenced.filenames` List all files that are referenced by an .apsimx file(s).
- `single.threaded` Run all simulations sequentially on a single thread.
- `cpu.count` (Default: -1) Maximum number of threads/processes to spawn for running simulations.
- `simulation.names` Only run simulations if their names match this regular expression.
- `dotnet` Logical. There is a global option for this argument, but this will override it. This can be useful if the goal is to compare an old version of Next Gen (before Sept 2021) with a more recent version in the same script. This might be needed if you have your own compiled version of APSIM Next Gen.
- `mono` Logical. Should be set to TRUE if running a version of APSIM Next Gen from Aug 2021 or older on Mac or Linux.
exe.path executable path. This can be useful for having both a global option through 'apsimx.options' and a local option that will override that. This option will take precedence.

Details

Extra arguments for running APSIM-X

Value

it returns a character vector with the extra arguments.
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