

Package: PSPclean (via r-universe)

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Type Package

Title Sources and standardizes permanent sample plot data

Version 1.0.0.9007

Depends R (>= 4.2)

Description Converts all data into two keyed tables. One is for tree measurements, and the other is for plot data. Some arguments exist for handling disturbance agents.

Encoding UTF-8

Language en-CA

LazyData true

License GPL-3

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Contents

assessTreeNumberConsistency	2
classify_tree_status	3

dataPurification_ABPSP	4
dataPurification_BCPSP	5
dataPurification_NBPSP	6
dataPurification_NFIPSP	6
dataPurification_ONPSP	7
dataPurification_QCPSP	8
dataPurification_SKPSP	9
dataPurification_SKTSP_Mistik	10
detect_dbh_outliers	10
geoCleanPSP	11
getPSP	11
prepInputsAlbertaPSP	12
prepInputsBCPSP	13
prepInputsNBPSP	13
prepInputsNFIPSP	14
prepInputsOntarioPSP	14
prepInputsQCPSP	15
prepInputsSaskatchewanPSP	15
prepInputsSaskatchewanTSP	16
prepPSP_climateNA	16
process_dbh_issues	17
standardizeSpeciesNames	17
treenum_to_multiplePSP	18

Index 19

assessTreeNumberConsistency

Analyze Regeneration Proportion and Tree DBH Growth

Description

1. Identifies plots where all trees identified, and their subsequent measurements. These are of interest as the stand age is unlikely to be correct
2. calculates elapsed time between successive measurements and flags trees with biologically implausible DBH growth based on the max_assumed_growth_rate param

Usage

```
assessTreeNumberConsistency(plots, max_assumed_growth_rate = 1)
```

Arguments

plots	A list containing at least a data frame PSPmeasure with tree measurements and PSPplot with measurement years.
max_assumed_growth_rate	Maximum plausible DBH growth per year for regenerating trees (cm/year, default = 1).

Value

A list with:

problematicMeasurements MeasurementIDs with 100% regen at some point in plot history. If the problematic measurement is the last measurement, then prior measurements are not included. If the problematic measurement is NOT the first, then all measurements are included.

problematic trees trees with problematic DBH (ie growing faster than max_assumed_growth_rate) and other variables: elapsedTime (years between measurements), DBHdiffFromMax (the difference between the actual growth rate and the expected maximum growth rate), and DBHdiffFromMax_perYear (the latter divided by the former).

classify_tree_status	<i>Classify Tree Status Based on Measurement History</i>
----------------------	--

Description

Assigns status to each tree based on its observation history. Detects new regeneration, lost trees, and survivors.

Usage

```
classify_tree_status(Trees)
```

Arguments

Trees A data.table of tree records across multiple measurement years.

Value

A list containing:

Trees The full dataset with status classification.

Regeneration Trees first appearing after plot monitoring began.

Last_Measurement Trees last measured before monitoring ended.

Alive Trees present consistently or throughout.

OrigPlotID1s Unique OrigPlotID1 identifiers.

dataPurification_ABPSP

Standardize and Treat the Alberta PSP Data

Description

This function cleans and standardizes the Alberta PSP data, including tree measurements and plot information. Species names can be standardized using a species equivalency table.

Usage

```
dataPurification_ABPSP(
  treeMeasure,
  plotMeasure,
  tree,
  plot,
  codesToExclude = 3,
  excludeAllObs = TRUE,
  areaDiffThresh = 0.95,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full"
)
```

Arguments

treeMeasure	A data.frame or data.table containing tree measurement data.
plotMeasure	A data.frame or data.table containing plot measurement data.
tree	A data.frame or data.table containing tree information.
plot	A data.frame or data.table containing plot information.
codesToExclude	Character vector of damage agent codes used to filter tree data (see GOA PSP Manual). Measurements with these codes will be removed.
excludeAllObs	Logical. If TRUE, all prior and future observations of trees with codes in codesToExclude are removed.
areaDiffThresh	Numeric. Threshold for plot size discrepancy below which plots are assigned a new ID. Expressed as $\min(\text{PlotSize})/\max(\text{PlotSize})$.
sppEquiv	A table providing species name equivalencies between the original PSP species names and the final standardized naming format. Default is LandR::sppEquivalencies_CA.
sppEquivCol	Character string. The column in sppEquiv that contains the standardized species' names. Default is "Latin_full".

Value

A list containing standardized plotData and treeData as data.tables.

```
dataPurification_BCPSP
```

```
#' Standardize and Treat the BC PSP Data
```

Description

This function cleans and standardizes the British Columbia PSP data, including tree measurements and plot header information. Species names can be standardized using a species equivalency table.

Usage

```
dataPurification_BCPSP(
  treeDataRow,
  plotHeaderDataRow,
  damageAgentCodes,
  codesToExclude = "IBM",
  excludeAllObs = TRUE,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full"
)
```

Arguments

<code>treeDataRow</code>	A <code>data.frame</code> or <code>data.table</code> containing the raw tree measurement data.
<code>plotHeaderDataRow</code>	A <code>data.frame</code> or <code>data.table</code> containing the raw plot header data.
<code>damageAgentCodes</code>	A character vector of damage agent codes present in the data.
<code>codesToExclude</code>	A character vector of damage agent codes to exclude from measurements.
<code>excludeAllObs</code>	Logical. If <code>TRUE</code> , all prior and future observations of a tree with a damage code in <code>codesToExclude</code> are removed. Default is <code>TRUE</code> .
<code>sppEquiv</code>	A table providing species name equivalencies between the original PSP species names and the final standardized naming format. Default is <code>LandR::sppEquivalencies_CA</code> .
<code>sppEquivCol</code>	Character string. The column in <code>sppEquiv</code> that contains the standardized species' names. Default is <code>"Latin_full"</code> .

Value

A list containing standardized `plotData` and `treeData` as `data.tables`.

dataPurification_NBPSP

Standardize and Treat the New Brunswick PSP Data

Description

This function cleans and standardizes New Brunswick PSP data, including tree and plot data. Species names can be standardized using a species equivalency table.

Usage

```
dataPurification_NBPSP(
  NB_PSP_Data,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full"
)
```

Arguments

NB_PSP_Data	A list of <code>data.tables</code> resulting from <code>prepInputsNBPSP</code> , containing raw PSP data.
sppEquiv	A table providing species name equivalencies between the original PSP species names and the final standardized naming format. Default is <code>LandR::sppEquivalencies_CA</code> .
sppEquivCol	Character string. The column in <code>sppEquiv</code> that contains the standardized species names. Default is <code>"Latin_full"</code> .

Value

A list containing standardized `plotData` and `treeData` as `data.tables`.

dataPurification_NFIPSP

Standardize and Treat the NFI PSP Data

Description

This function cleans and standardizes NFI PSP data, including tree, plot, and location data. Species names can be standardized using a species equivalency table.

Usage

```
dataPurification_NFIPSP(
  NFIdata,
  codesToExclude = "IB",
  excludeAllObs = TRUE,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full"
)
```

Arguments

NFIdata	A list containing NFI tree, plot, and location data.tables.
codesToExclude	Vector of damage agent codes. Measurements with these codes will be removed.
excludeAllObs	Logical. If TRUE, removing observations of individual trees due to damage codes will also remove all prior and future observations of that tree.
sppEquiv	A table providing species name equivalencies between the original PSP species names and the final standardized naming format. Default is LandR::sppEquivalencies_CA.
sppEquivCol	Character string. The column in sppEquiv that contains the standardized species names. Default is "Latin_full".

Value

A list containing standardized plotData and treeData as data.tables.

```
dataPurification_ONPSP
```

```
#' Standardize and Treat the Ontario PSP Data
```

Description

This function cleans and standardizes Ontario PSP data, including tree and plot data. Species names can be standardized using a species equivalency table.

Usage

```
dataPurification_ONPSP(
  ONPSPlist,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full"
)
```

Arguments

ONPSPlist	A list of relevant PSP plots and associated data.tables.
sppEquiv	A table providing species name equivalencies between the original PSP species names and the final standardized naming format. Default is LandR::sppEquivalencies_CA. Must include columns 'Latin' and 'PSP'.
sppEquivCol	Character string. The column in sppEquiv that contains the standardized species names. Default is "Latin_full".

Value

A list containing standardized plotData and treeData as data.tables.

dataPurification_QCPSP

Standardize and Treat the Quebec PSP Data

Description

This function cleans and standardizes the Quebec PSP data, including tree and plot data. Species names can be standardized using a species equivalency table.

Usage

```
dataPurification_QCPSP(
  QuebecPSP,
  codesToExclude = NULL,
  excludeAllObs = TRUE,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full"
)
```

Arguments

QuebecPSP	A list of data.tables containing raw PSP data obtained via prepInputsQCPSP.
codesToExclude	Character vector of damage or pest disturbance codes to exclude from measurements. Currently placeholder, update if applicable.
excludeAllObs	Logical. If TRUE and codesToExclude is not NULL, all prior and future observations of trees with these codes will be removed.
sppEquiv	A table providing species name equivalencies between the original PSP species names and the final standardized naming format. Default is LandR::sppEquivalencies_CA.
sppEquivCol	Character string. The column in sppEquiv that contains the standardized species names. Default is "Latin_full".

Value

A list containing standardized plotData and treeData as data.tables.

dataPurification_SKPSP

Standardize and Treat the Saskatchewan PSP Data

Description

This function cleans and standardizes the Saskatchewan PSP data, including tree measurements, plot headers, and measurement headers. Species names can be standardized using a species equivalency table.

Usage

```
dataPurification_SKPSP(
  SADataRaw,
  plotHeaderRaw,
  measureHeaderRaw,
  treeDataRaw,
  codesToExclude = NULL,
  excludeAllObs = TRUE,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full"
)
```

Arguments

SADataRaw	A data.frame or data.table containing raw tree measurement data.
plotHeaderRaw	A data.frame or data.table containing raw plot header data.
measureHeaderRaw	A data.frame or data.table containing raw measurement header data.
treeDataRaw	A data.frame or data.table containing tree data.
codesToExclude	Character vector of damage agent codes used to filter tree data. Codes: Natural or Undetermined = 1, Disease = 2, Insect = 3, Human = 4, Wind = 5, Snow = 6, Other Trees = 7, Hail or Ice Storm = 8. Measurements with these codes will be removed.
excludeAllObs	Logical. If TRUE, all prior and future observations of trees with codes in codesToExclude are removed.
sppEquiv	A table providing species name equivalencies between the original PSP species names and the final standardized naming format. Default is LandR::sppEquivalencies_CA.
sppEquivCol	Character string. The column in sppEquiv that contains the standardized species names. Default is "Latin_full".

Value

A list containing standardized plotData and treeData as data.tables.

```
dataPurification_SKTSP_Mistik
```

standardize and treat the Saskatchewan Mistik temporary sample plot data This function will be deprecated

Description

standardize and treat the Saskatchewan Mistik temporary sample plot data This function will be deprecated

Usage

```
dataPurification_SKTSP_Mistik(compiledPlotData, compiledTreeData)
```

Arguments

```
compiledPlotData
    the plot header data
compiledTreeData
    the tree data
```

Value

a list of plot and tree data.tables

```
detect_dbh_outliers
```

Detect and flag DBH outliers using z-scores by plot

Description

Flags statistically implausible DBH values based on the z-score method #' (using mean and standard deviation) within each plot group. This can help identify data entry or measurement errors in repeated tree measurements.

Usage

```
detect_dbh_outliers(
  Trees,
  dbh_col = "DBH",
  plot_col = "OrigPlotID1",
  z_thresh = 7
)
```

Arguments

<code>Trees</code>	A <code>data.table</code> or <code>data.frame</code> containing DBH and plot columns.
<code>dbh_col</code>	Character. Name of the DBH column. Default is "DBH".
<code>plot_col</code>	Character. Name of the plot/grouping column. Default is "OrigPlotID1".
<code>z_thresh</code>	Numeric. Z-score threshold for identifying outliers. Default is 7.

Value

A list with:

Trees The modified `data.table` with added columns: `meanDBH`, `sdDBH`, `zscore`, `is_outlier_z`

plotIDs Unique plot/group IDs used in analysis

<code>geoCleanPSP</code>	<i>convert plot location data to long/lat and output in a sf object</i>
--------------------------	---

Description

convert plot location data to long/lat and output in a sf object

Usage

```
geoCleanPSP(Locations)
```

Arguments

<code>Locations</code>	the compiled plot data
------------------------	------------------------

Value

an sf object with `OrigPlotID1` column

<code>getPSP</code>	<i>return a merged PSP object from a vector of data sources</i>
---------------------	---

Description

return a merged PSP object from a vector of data sources

Usage

```
getPSP(
  PSPdataTypes,
  destinationPath,
  forGMCS = FALSE,
  sppEquiv = LandR::sppEquivalencies_CA,
  sppEquivCol = "Latin_full",
  codesToExclude = NULL
)
```

Arguments

PSPdataTypes	character vector of PSP data sources - e.g. <code>c("BC", "SK")</code> Use "all" to get all available sources, and "dummy" for freely available data
destinationPath	destination folder for downloaded objects
forGMCS	if TRUE, will pre-filter plots with insect mortality to avoid attributing insect mortality with climate
sppEquiv	species equivalencies table.
sppEquivCol	Character string. The column in sppEquiv that contains the standardized name of each species. The default is "Latin_full". It is recommended not to change this as there must be a one-to-one or one-to-many (e.g. variants, hybrids) relationship for each column in sppEquiv that is used internally in the different standardization functions (e.g. AB_forestry)
codesToExclude	named list of damage agent codes, by source ("BC", "AB", "SK", "NFI"): every measurement of a tree recorded with one of them (for "SK", a tree that died of one of these causes) is removed. A source not named takes the forGMCS default (its insect codes if TRUE, none otherwise).

Value

a list of standardized plot and tree data.tables

prepInputsAlbertaPSP *source the Alberta PSP data*

Description

source the Alberta PSP data

Usage

```
prepInputsAlbertaPSP(dPath)
```

Arguments

dPath passed to prepInputs destinationPath

Value

a list of Alberta PSP data.tables

prepInputsBCPSP	<i>Source the BC PSP data</i>
-----------------	-------------------------------

Description

Source the BC PSP data

Usage

```
prepInputsBCPSP(dPath)
```

Arguments

dPath passed to destinationPath in prepInputs()

Value

a list of BC PSP objects

prepInputsNBPSP	<i>retrieve the New Brunswick PSP raw data</i>
-----------------	--

Description

retrieve the New Brunswick PSP raw data

Usage

```
prepInputsNBPSP(dPath)
```

Arguments

dPath data directory for raw data

Value

a list of plot, tree, measurement, and location data.tables after exporting mdb to csv txt

```
prepInputsNFIPSP      source the NFI PSP data
```

Description

source the NFI PSP data

Usage

```
prepInputsNFIPSP(dPath)
```

Arguments

dPath passed to prepInputs destinationPath

Value

a list of NFI PSP data.tables

```
prepInputsOntarioPSP  retrieve preprocessed Ontario PSP and PGP data
```

Description

retrieve preprocessed Ontario PSP and PGP data

Usage

```
prepInputsOntarioPSP(dPath, ...)
```

Arguments

dPath the Access database for PSP and PGP plots
 ... additional args passed to prepInputs

Value

a list of plot and tree data.tables

prepInputsQCPSP	<i>retrieve the Quebec PSP raw data</i>
-----------------	---

Description

retrieve the Quebec PSP raw data

Usage

prepInputsQCPSP(dPath)

Arguments

dPath	data directory for raw data
-------	-----------------------------

Value

a list of plot, tree, measurement, and location data.tables after exporting mdb to csv txt

prepInputsSaskatchewanPSP	<i>source the Saskatchewan PSP data</i>
---------------------------	---

Description

source the Saskatchewan PSP data

Usage

prepInputsSaskatchewanPSP(dPath)

Arguments

dPath	passed to prepInputs destinationPath
-------	--------------------------------------

Value

a list of Saskatchewan PSP data.tables

prepInputsSaskatchewanTSP	<i>source the Saskatchewan PSP data</i>
---------------------------	---

Description

source the Saskatchewan PSP data

Usage

prepInputsSaskatchewanTSP(dPath)

Arguments

dPath passed to prepInputs destinationPath

Value

a list of Saskatchewan PSP data.tables

prepPSP_climateNA	<i>standardize and treat the BC PSP data</i>
-------------------	--

Description

standardize and treat the BC PSP data

Usage

prepPSP_climateNA(dPath, filename2, PSPplot, PSPgis)

Arguments

dPath directory to download elevation data
filename2 the full filename of the output file
PSPplot the standardized PSP plot attribute data
PSPgis the standardized plot location sf object

Value

a text file

process_dbh_issues	<i>Process Implausible DBH Changes Across Measurement Years</i>
--------------------	---

Description

Detects and manages inconsistencies in tree DBH (Diameter at Breast Height) measurements across years within PSP. Flags implausible negative growth, cleans the dataset accordingly, and excludes OrigPlotID1s with high anomaly rates.

Usage

```
process_dbh_issues(Trees)
```

Arguments

Trees	A data.table of tree measurements over time within PSP.
-------	---

Value

A list containing:

Trees Cleaned dataset with problematic entries removed.

dbh_check Subset of detected DBH inconsistencies.

negative_growth_summary Summary of negative growth by OrigPlotID1.

OrigPlotID1s List of retained OrigPlotID1 identifiers.

standardizeSpeciesNames	<i>standardize the species names in a given PSP measurement data.table</i>
-------------------------	--

Description

standardize the species names in a given PSP measurement data.table

Usage

```
standardizeSpeciesNames(speciesTable, forestInventorySource)
```

Arguments

speciesTable	the tree measurement csv
forestInventorySource	one of MBTSP, ABPSP, BCPSP, SKPSP, NWTSP, NFIPSP.

Value

the species table with standardized species names

`treenum_to_multiplePSP`*Identify Tree Numbers Linked to Multiple Species Within a Plot*

Description

Ensures consistent Species and Tree numbering within a plot (OrigPlotID1)

Usage

```
treenum_to_multiplePSP(Trees)
```

Arguments

Trees	A data.table of tree observations containing OrigPlotID1, Species, PSP, MeasureYear and TreeNumber columns.
-------	---

Value

A list containing:

Trees_corrected Cleaned tree dataset.

Index

`assessTreeNumberConsistency`, [2](#)

`classify_tree_status`, [3](#)

`dataPurification_ABPSP`, [4](#)
`dataPurification_BCPSP`, [5](#)
`dataPurification_NBPSP`, [6](#)
`dataPurification_NFIPSP`, [6](#)
`dataPurification_ONPSP`, [7](#)
`dataPurification_QCPSP`, [8](#)
`dataPurification_SKPSP`, [9](#)
`dataPurification_SKTSP_Mistik`, [10](#)
`detect_dbh_outliers`, [10](#)

`geoCleanPSP`, [11](#)
`getPSP`, [11](#)

`prepInputsAlbertaPSP`, [12](#)
`prepInputsBCPSP`, [13](#)
`prepInputsNBPSP`, [13](#)
`prepInputsNFIPSP`, [14](#)
`prepInputsOntarioPSP`, [14](#)
`prepInputsQCPSP`, [15](#)
`prepInputsSaskatchewanPSP`, [15](#)
`prepInputsSaskatchewanTSP`, [16](#)
`prepPSP_climateNA`, [16](#)
`process_dbh_issues`, [17](#)

`standardizeSpeciesNames`, [17](#)

`treenum_to_multiplePSP`, [18](#)