

# Package ‘pmml’

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**Type** Package

**Title** Generate PMML for Various Models

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**Imports** methods, stats, utils, stringr

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**Description** The Predictive Model Markup Language (PMML) is an XML-based language which provides a way for applications to define machine learning, statistical and data mining models and to share models between PMML compliant applications. More information about the PMML industry standard and the Data Mining Group can be found at <<http://www.dmg.org>>. The generated PMML can be imported into any PMML consuming application, such as Zementis Predictive Analytics products, which integrate with web services, relational database systems and deploy natively on Hadoop in conjunction with Hive, Spark or Storm, as well as allow predictive analytics to be executed for IBM z Systems mainframe applications and real-time, streaming analytics platforms. The package isofor (used for anomaly detection) can be installed with devtools::install\_github("Zelazny7/isofor").

**URL** <https://www.softwareag.com/zementis>

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---

*add\_attributes*      *Add attribute values to an existing element in a given PMML file.*

---

**Description**

Add attribute values to an existing element in a given PMML file.

**Usage**

```
add_attributes(xml_model = NULL, xpath = NULL, attributes = NULL,  
              namespace = "4_3", ...)
```

**Arguments**

<code>xml_model</code>	The PMML model in a XML node format. If the model is a text file, it should be converted to an XML node, for example, using the <code>file_to_xml_node</code> function.
<code>xpath</code>	The XPath to the element to which the attributes are to be added.
<code>attributes</code>	The attributes to be added to the data fields. The user should make sure that the attributes being added are allowed in the PMML schema.
<code>namespace</code>	The namespace of the PMML model. This is frequently also the PMML version of the model.
<code>...</code>	Further arguments passed to or from other methods.

**Details**

Add attributes to an arbitrary XML element. This is an experimental function designed to be more general than the `'add_mining_field_attributes'` and `'add_data_field_attributes'` functions.

The attribute information can be provided as a vector. Multiple attribute names and values can be passes as vector elements to enable inserting multiple attributes. However, this function overwrites any pre-existing attribute values, so it must be used with care. This behavior is by design as this feature is meant to help an user add new defined attribute values at different times. The XPath has to include the namespace as shown in the examples.

**Value**

An object of class `XMLNode` as that defined by the **XML** package. This represents the top level, or root node, of the XML document and is of type `PMML`. It can be written to file with `saveXML`.

**Author(s)**

Tridivesh Jena

## Examples

```

# Make a sample model:
model0 <- lm(Sepal.Length ~ ., data = iris[, -5])
model <- pmml(model0)

# The resulting PMML:
# <PMML version="4.3" ... xmlns="http://www.dmg.org/PMML-4_3">
# <Header ... description="Linear Regression Model"/>
# <DataDictionary numberOfFields="4">
# .
# .
# </DataDictionary>
# <RegressionModel modelName="Linear_Regression_Model"
#   functionName="regression"
#   algorithmName="least squares">
# <MiningSchema>
# .
# .
# </MiningSchema>
# .
# .
# <RegressionTable intercept="1.85599749291755">
# <NumericPredictor name="Sepal.Width" exponent="1"
#   coefficient="0.650837159313218"/>
# <NumericPredictor name="Petal.Length" exponent="1"
#   coefficient="0.709131959136729"/>
# <NumericPredictor name="Petal.Width" exponent="1"
#   coefficient="-0.556482660167024"/>
# </RegressionTable>
# </RegressionModel>
# </PMML>

# Add arbitrary attributes to the 1st 'NumericPredictor' element. The
# attributes are for demonstration only (they are not allowed under
# the PMML schema). The command assumes the default namespace.
add_attributes(model, "/p:PMML/descendant::p:NumericPredictor[1]",
  attributes = c(a = 1, b = "b"))
)

# Add attributes to the NumericPredictor element which has
# 'Petal.Length' as the 'name' attribute:
add_attributes(model,
  "/p:PMML/descendant::p:NumericPredictor[@name='Petal.Length']",
  attributes = c(a = 1, b = "b"))
)

# 3 NumericElements exist which have '1' as the 'exponent' attribute.
# Add new attributes to the 3rd one:
add_attributes(model,
  "/p:PMML/descendant::p:NumericPredictor[@exponent='1'][3]",
  attributes = c(a = 1, b = "b"))
)

```

```
# Add attributes to the 1st element whose 'name' attribute contains
# 'Length':
add_attributes(model,
  "/p:PMML/descendant::p:NumericPredictor[contains(@name,'Length')]",
  attributes = c(a = 1, b = "b")
)
```

---

add\_data\_field\_attributes

*Add attribute values to an existing DataField element in a given PMML file*

---

### Description

Add attribute values to an existing DataField element in a given PMML file

### Usage

```
add_data_field_attributes(xml_model = NULL, attributes = NULL,
  field = NULL, namespace = "4_3", ...)
```

### Arguments

xml_model	The PMML model in a XML node format. If the model is a text file, it should be converted to an XML node, for example, using the file_to_xml_node function.
attributes	The attributes to be added to the data fields. The user should make sure that the attributes being added are allowed in the PMML schema.
field	The field to which the attributes are to be added. This is used when the attributes are a vector of name-value pairs, intended for this one field.
namespace	The namespace of the PMML model. This is frequently also the PMML version of the model.
...	Further arguments passed to or from other methods.

### Details

The PMML format allows a DataField element to have various attributes, which, although useful, may not always be present in a PMML model. This function allows one to take an existing PMML file and add these attributes to the DataFields.

The attribute information can be provided as a dataframe or a vector. Each row of the data frame corresponds to an attribute name and each column corresponding to a variable name. This way one can add as many attributes to as many variables as one wants in one step. A more convenient method to add multiple attributes to one field might be to give the attribute name and values as a vector. This function may be used multiple times to add new attribute values step-by-step. However this function overwrites any pre-existing attribute values, so it must be used with care. This behavior is by design as this feature is meant to help an user add new defined attribute values at different times. For example, one may use this to modify the display name of a field at different times.

**Value**

An object of class XMLNode as that defined by the **XML** package. This represents the top level, or root node, of the XML document and is of type PMML. It can be written to file with saveXML.

**Author(s)**

Tridivesh Jena

**Examples**

```
# Make a sample model:
model0 <- lm(Sepal.Length ~ ., data = iris[, -5])
model <- pmml(model0)

# The resulting model has mining fields with no information besides
# fieldName, dataType and optype. This object is already an xml
# node (not an external text file), so there is no need to convert
# it to an xml node object.

# Create data frame with attribute information:

attributes <- data.frame(c("FlowerWidth", 1), c("FlowerLength", 0),
  stringAsFactors = FALSE
)
rownames(attributes) <- c("displayName", "isCyclic")
colnames(attributes) <- c("Sepal.Width", "Petal.Length")

# Although not needed in this first try, necessary to easily add
# new values later. Removes values as factors so that new values
# added later are not evaluated as factor values and thus rejected
# as invalid.
attributes[] <- lapply(attributes, as.character)

add_data_field_attributes(model, attributes, namespace = "4_3")

# Alternative method to add attributes to a single field,
# "Sepal.Width":
add_data_field_attributes(
  model, c(displayName = "FlowerWidth", isCyclic = 1),
  "Sepal.Width"
)

mi <- make_intervals(
  list("openClosed", "closedClosed", "closedOpen"),
  list(NULL, 1, 2), list(1, 2, NULL)
)
mv <- make_values(
  list("A", "B", "C"), list(NULL, NULL, NULL),
  list("valid", NULL, "invalid")
)
add_data_field_children(model, field = "Sepal.Length", interval = mi, values = mv)
```

---

`add_data_field_children`

*Add 'Interval' and 'Value' child elements to a given DataField element in a given PMML file.*

---

### Description

Add 'Interval' and 'Value' child elements to a given DataField element in a given PMML file.

### Usage

```
add_data_field_children(xml_model = NULL, field = NULL,  
  intervals = NULL, values = NULL, namespace = "4_3", ...)
```

### Arguments

<code>xml_model</code>	The PMML model in a XML node format. If the model is a text file, it should be converted to an XML node, for example, using the <code>file_to_xml_node</code> function.
<code>field</code>	The field to which the attributes are to be added. This is used when the attributes are a vector of name-value pairs, intended for this one field.
<code>intervals</code>	The 'Interval' elements given as a list
<code>values</code>	The 'Value' elements given as a list.
<code>namespace</code>	The namespace of the PMML model. This is frequently also the PMML version of the model.
<code>...</code>	Further arguments passed to or from other methods.

### Details

The PMML format allows a DataField element to have 'Interval' and 'Value' child elements which although useful, may not always be present in a PMML model. This function allows one to take an existing PMML file and add these elements to the DataFields.

The 'Interval' elements or the 'Value' elements can be typed in, but more conveniently created by using the helper functions 'make\_intervals' and 'MakeValues'. This function can then add these extra information to the PMML.

### Value

An object of class XMLNode as that defined by the **XML** package. This represents the top level, or root node, of the XML document and is of type PMML. It can be written to file with `saveXML`.

### Author(s)

Tridivesh Jena

**Examples**

```

# Make a sample model:
model0 <- lm(Sepal.Length ~ ., data = iris[, -5])
model <- pmml(model0)

# The resulting model has data fields but with no 'Interval' or 'Value'
# elements. This object is already an xml node (not an external text
# file), so there is no need to convert it to an xml node object.

# Add an 'Interval' element node by typing it in
add_data_field_children(model,
  field = "Sepal.Length",
  intervals = list(newXMLNode("Interval",
    attrs = c(closure = "openClosed", rightMargin = 3)
  ))
)

# Use helper functions to create list of 'Interval' and 'Value'
# elements. We define the 3 Intervals as ,1] (1,2) and [2,
mi <- make_intervals(
  list("openClosed", "openOpen", "closedOpen"),
  list(NULL, 1, 2), list(1, 2, NULL)
)

# Define 3 values, none with a 'displayValue' attribute and 1 value
# defined as 'invalid'. The 2nd one is 'valid' by default.
mv <- make_values(
  list(1.1, 2.2, 3.3), list(NULL, NULL, NULL),
  list("valid", NULL, "invalid")
)

# As an example, apply these to the Sepal.Length field:
add_data_field_children(model, field = "Sepal.Length", intervals = mi, values = mv)

# Only defined 'Interval's:
add_data_field_children(model, field = "Sepal.Length", intervals = mi)

```

---

add\_mining\_field\_attributes

*Add attribute values to an existing MiningField element in a given PMML file.*

---

**Description**

Add attribute values to an existing MiningField element in a given PMML file.

**Usage**

```
add_mining_field_attributes(xml_model = NULL, attributes = NULL,
  namespace = "4_3", ...)
```



**Arguments**

xml_model	The PMML model in a XML node format. If the model is a text file, it should be converted to an XML node, for example, using the file_to_xml_node function.
attributes	The attributes to be added to the mining fields. The user should make sure that the attributes being added are allowed in the PMML schema.
namespace	The namespace of the PMML model. This is frequently also the PMML version of the model.
...	Further arguments passed to or from other methods.

**Details**

The PMML format allows a MiningField element to have attributes 'usageType', 'missingValueReplacement' and 'invalidValueTreatment' which although useful, may not always be present in a PMML model. This function allows one to take an existing PMML file and add these attributes to the MiningFields.

The attribute information should be provided as a dataframe; each row corresponding to an attribute name and each column corresponding to a variable name. This way one can add as many attributes to as many variables as one wants in one step. On the other extreme, a one-by-one data frame may be used to add one new attribute to one variable. This function may be used multiple times to add new attribute values step-by-step. This function overwrites any pre-existing attribute values, so it must be used with care. However, this is by design as this feature is meant to help an user defined new attribute values at different times. For example, one may use this to impute missing values in a model at different times.

**Value**

An object of class XMLNode as that defined by the **XML** package. This represents the top level, or root node, of the XML document and is of type PMML. It can be written to file with saveXML.

**Author(s)**

Tridivesh Jena

**Examples**

```
# Make a sample model
model0 <- lm(Sepal.Length ~ ., data = iris[, -5])
model <- pmml(model0)

# The resulting model has mining fields with no information
# besides fieldName, dataType and optype. This object is
# already an xml node (not an external text file), so there
# is no need to convert it to an xml node object.

# Create data frame with attribute information:
attributes <- data.frame(
  c("active", 1.1, "asIs"),
  c("active", 2.2, "asIs"),
  c("active", NA, "asMissing")
```

```

)
rownames(attributes) <- c(
  "usageType", "missingValueReplacement",
  "invalidValueTreatment"
)
colnames(attributes) <- c(
  "Sepal.Width", "Petal.Length",
  "Petal.Width"
)

# Although not needed in this first try, necessary to easily
# add new values later:
for (k in 1:ncol(attributes)) {
  attributes[[k]] <- as.character(attributes[[k]])
}

add_mining_field_attributes(model, attributes, namespace = "4_3")

```

---

add\_output\_field      *Add Output nodes to a PMML object.*

---

### Description

Add Output nodes to a PMML object.

### Usage

```

add_output_field(xml_model = NULL, outputNodes = NULL, at = "End",
  xformText = NULL, nodeName = NULL, attributes = NULL,
  whichOutput = 1, namespace = "4_3")

```

### Arguments

xml_model	The PMML model to which the OutputField elements are to be added
outputNodes	The Output nodes to be added. These may be created using the 'make_output_nodes' helper function
at	Given an Output element, the 1 based index after which the given Output child element should be inserted at
xformText	Post-processing information to be included in the OutputField element. This expression will be processed by the function_to_pmml function
nodeName	The name of the element to be added
attributes	The attributes to be added
whichOutput	The index of the Output element
namespace	The namespace of the PMML model

## Details

This function is meant to add any post-processing information to an existing model via the OutputField element. One can also use this to tell the PMML model to output other values not automatically added to the model output. The first method is to use the 'make\_output\_nodes' helper function to make a list of output elements to be added. 'whichOutput' lets the function know which of the Output elements we want to work with; there may be more than one in a multiple model file. One can then add those elements there, at the desired index given by the 'at' parameter; the elements are inserted after the OutputField element at the 'at' index. In other words, find the 'whichOutput' Output element, add the 'outputNodes' child elements (which should be OutputField nodes) at the 'at' position in the child nodes. This function can also be used with the 'nodeName' and 'attributes' to add the list of attributes to an OutputField element with name 'nodeName' element using the 'xml\_model', 'outputNodes' and 'at' parameters. Finally, one can use this to add the transformation expression given by the 'xformText' parameter to the node with name 'nodeName'. The string given via 'xformText' is converted to an XML expression similarly to the function\_to\_pmml function. In other words, find the OutputField node with the name 'nodeName' and add the list of attributes given with 'attributes' and also, add the child transformations given in the 'xformText' parameter.

## Value

Output node with the OutputField elements inserted.

## Author(s)

Tridivesh Jena

## Examples

```
# Load the standard iris dataset
data(iris)

# Create a linear model and convert it to PMML
mod <- lm(Sepal.Length ~ ., iris)
pmod <- pmml(mod)

# Create additional output nodes
onodes0 <- make_output_nodes(
  name = list("OutputField", "OutputField"),
  attributes = list(list(
    name = "dbl",
    optype = "continuous"
  )), NULL,
  expression = list("ln(x)", "ln(x/(1-x))")
)
onodes2 <- make_output_nodes(
  name = list("OutputField", "OutputField"),
  attributes = list(
    list(
      name = "F1",
      dataType = "double", optype = "continuous"
    )
  )
)
```

```

    ),
    list(name = "F2")
  )
)

# Create new pmml objects with the output nodes appended
add_output_field(
  xml_model = pmod, outputNodes = onodes2, at = "End",
  xformText = NULL, nodeName = NULL, attributes = NULL,
  whichOutput = 1
)
pmod2 <- add_output_field(
  xml_model = pmod, outputNodes = onodes0, at = "End",
  xformText = NULL, nodeName = NULL,
  attributes = NULL, whichOutput = 1
)

# Create nodes with attributes and transformations
add_output_field(xml_model = pmod2, outputNodes = onodes2, at = 2)
add_output_field(
  xml_model = pmod2, xformText = list("exp(x) && !x"),
  nodeName = "Predicted_Sepal.Length"
)

att <- list(datype = "dbl", optpe = "dsc")
add_output_field(
  xml_model = pmod2, nodeName = "Predicted_Sepal.Length",
  attributes = att
)

```

---

 audit

*Audit: artificially constructed dataset*


---

### Description

This is an artificial dataset consisting of fictional clients who have been audited, perhaps for tax refund compliance. For each case an outcome is recorded (whether the taxpayer's claims had to be adjusted or not) and any amount of adjustment that resulted is also recorded.

### Format

A data frame containing:

Age	Numeric
Employment	Categorical string with 7 levels
Education	Categorical string with 16 levels
Marital	Categorical string with 6 levels
Occupation	Categorical string with 14 levels
Income	Numeric

Sex	Categorical string with 2 levels
Deductions	Numeric
Hours	Numeric
Accounts	Categorical string with 32 levels
Adjustment	Numeric
Adjusted	Numeric value 0 or 1

## References

- Togaware rattle package : *Audit dataset*
- [DMG description of the Audit dataset](#)

## Examples

```
data(audit, package = "pmml")
```

---

file\_to\_xml\_node      *Read in a file and parse it into an object of type XMLNode.*

---

## Description

Read in a file and parse it into an object of type XMLNode.

## Usage

```
file_to_xml_node(file)
```

## Arguments

`file`      The external file to be read in. This file can be any file in PMML format, regardless of the source or model type.

## Details

Read in an external file and convert it into an XMLNode to be used subsequently by other R functions.

This format is the one that will be obtained when a model is constructed in R and output in PMML format.

This function is mainly meant to be used to read in external files instead of depending on models saved in R. As an example, the pmml package requires as input an object of type XMLNode before its functions can be applied. Function 'file\_to\_xml\_node' can be used to read in an existing PMML file, convert it to an XML node and then make it available for use by any of the pmml functions.

**Value**

An object of class XMLNode as that defined by the **XML** package. This represents the top level, or root node, of the XML document and is of type PMML. It can be written to file with saveXML.

**Author(s)**

Tridivesh Jena

**Examples**

```
## Not run:
# Define some transformations:
iris_box <- xform_wrap(iris)
iris_box <- xform_z_score(iris_box, xform_info = "column1->d1")
iris_box <- xform_z_score(iris_box, xform_info = "column2->d2")

# Make a LocalTransformations element and save it to an external file:
pmml_trans <- pmml(NULL, transforms = iris_box)
write(toString(pmml_trans), file = "xform_iris.pmml")

# Later, we may need to read in the PMML model into R
# 'lt' below is now a XML Node, as opposed to a string:
lt <- file_to_xml_node("xform_iris.pmml")

## End(Not run)
```

---

function\_to\_pmml

---

*Convert an R expression to PMML.*


---

**Description**

Convert an R expression to PMML.

**Usage**

```
function_to_pmml(expr)
```

**Arguments**

expr            An R expression enclosed in quotes.

**Details**

As long as the expression passed to the function is a valid R expression (e.g., no unbalanced parenthesis), it can contain arbitrary function names not defined in R. Variables in the expression passed to ‘xform\_function’ are always assumed to be fields, and not substituted. That is, even if ‘x’ has a value in the R environment, the resulting expression will still use ‘x’.

An expression such as 'foo(x)' is treated as a function 'foo' with argument 'x'. Consequently, passing in an R vector 'c(1,2,3)' to 'function\_to\_pmml()' will produce PMML where 'c' is a function and '1,2,3' are the arguments.

An expression starting with '-' or '+' (for example, "-3" or "-(a+b)") will be treated as if there is a 0 before the initial '-' or '+' sign. This makes it possible to represent expressions that start with a sign, since PMML's '-' and '+' functions require two arguments. The resulting PMML node will have a constant 0 as a child.

## Value

PMML version of the input expression

## Author(s)

Dmitriy Bolotov

## Examples

```
# Operator precedence and parenthesis
function_to_pmml("1 + 3/5 - (4 * 2)")

# Nested arbitrary functions
function_to_pmml("foo(bar(x)) - bar(foo(y-z))")

# If-else expression
function_to_pmml("if (x==3) { 3 } else { 0 }")

# If-else with boolean output
function_to_pmml("if (x==3) { TRUE } else { FALSE }")

# Function with string argument types
function_to_pmml("colors('red', 'green', 'blue')")

# Sign in front of expression
function_to_pmml("-(x/y)")
```

---

houseVotes84

*Modified 1984 United States Congressional Voting Records Database*

---

## Description

This data set includes votes for each of the U.S. House of Representatives Congressmen on the 16 key votes identified by the CQA. The CQA lists nine different types of votes: voted for, paired for, and announced for (these three simplified to yea), voted against, paired against, and announced against (these three simplified to nay), voted present, voted present to avoid conflict of interest, and did not vote or otherwise make a position known (these three simplified to an unknown disposition). Originally containing a binomial variable "class" and 16 other binary variables, those 16 variables have been renamed to simply "V1", "V2", ..., "V16".

**Format**

A data frame containing:

Class	Boolean variable
V1	Boolean variable
V2	Boolean variable
V3	Boolean variable
V4	Boolean variable
V5	Boolean variable
V6	Boolean variable
V7	Boolean variable
V8	Boolean variable
V9	Boolean variable
V10	Boolean variable
V11	Boolean variable
V12	Boolean variable
V13	Boolean variable
V14	Boolean variable
V15	Boolean variable
V16	Boolean variable

**References**

[UCI Machine Learning Repository](#)

**Examples**

```
data(houseVotes84, package = "pmm1")
```

---

make_intervals	<i>Create Interval elements, most likely to add to a DataDictionary element.</i>
----------------	--

---

**Description**

Create Interval elements, most likely to add to a DataDictionary element.

**Usage**

```
make_intervals(closure = NULL, leftMargin = NULL, rightMargin = NULL,
              namespace = "4_3")
```



**Arguments**

closure	The 'closure' attribute of each 'Interval' element to be created in order.
leftMargin	The 'leftMargin' attribute of each 'Interval' element to be created in order.
rightMargin	The 'rightMargin' attribute of each 'Interval' element to be created in order.
namespace	The namespace of the PMML model

**Details**

The 'Interval' element allows 3 attributes, all of which may be defined in the 'make\_intervals' function. The value of these attributes should be provided as a list. Thus the elements of the 'leftMargin' for example define the value of that attribute for each 'Interval' element in order.

**Value**

PMML Intervals elements.

**Author(s)**

Tridivesh Jena

**See Also**

[make\\_values](#) to make Values child elements, [add\\_data\\_field\\_children](#) to add these xml fragments to the DataDictionary PMML element.

**Examples**

```
# make 3 Interval elements
# we define the 3 Intervals as ,1] (1,2) and [2,
mi <- make_intervals(
  list("openClosed", "openOpen", "closedOpen"),
  list(NULL, 1, 2), list(1, 2, NULL)
)
```

---

make\_output\_nodes      *Add Output nodes to a PMML object.*

---

**Description**

Add Output nodes to a PMML object.

**Usage**

```
make_output_nodes(name = "OutputField", attributes = NULL,
  expression = NULL, namespace = "4_3")
```

**Arguments**

name	The name of the element to be created
attributes	The node attributes to be added
expression	Post-processing information to be included in the element. This expression will be processed by the function_to_pmml function
namespace	The namespace of the PMML model

**Details**

This function will create a list of nodes with names 'name', attributes 'attributes' and child elements 'expression'. 'expression' is a string converted to XML similar to the function\_to\_pmml function. Meant to create OutputField elements, 'expressions' allows one to include post-processing transformations to a model. To create multiple such nodes, all the parameters must be given as lists of equal length.

**Value**

List of nodes

**Author(s)**

Tridivesh Jena

**Examples**

```
# Make two nodes, one with attributes
TwoNodes <- make_output_nodes(
  name = list("OutputField", "OutputField"),
  attributes = list(list(name = "dbl", optype = "continuous"), NULL),
  expression = list("ln(x)", "ln(x/(1-x))")
)
```

---

make\_values

*Create Values element, most likely to add to a DataDictionary element.*

---

**Description**

Create Values element, most likely to add to a DataDictionary element.

**Usage**

```
make_values(value = NULL, displayValue = NULL, property = NULL,
  namespace = "4_3")
```

**Arguments**

value	The 'value' attribute of each 'Value' element to be created in order.
displayValue	The 'displayValue' attribute of each 'Value' element to be created in order.
property	The 'property' attribute of each 'Value' element to be created in order.
namespace	The namespace of the PMML model

**Details**

This function is used the same way as the `make_intervals` function. If certain attributes for an element should not be included, they should be input in the list as `NULL`.

**Value**

PMML Values elements.

**Author(s)**

Tridivesh Jena

**See Also**

[make\\_intervals](#) to make Interval child elements, [add\\_data\\_field\\_children](#) to add these xml fragments to the DataDictionary PMML element.

**Examples**

```
# define 3 values, none with a 'displayValue' attribute and 1 value
# defined as 'invalid'. The 2nd one is 'valid' by default.
mv <- make_values(
  list(1.1, 2.2, 3.3), list(NULL, NULL, NULL),
  list("valid", NULL, "invalid")
)
```

---

pmml

*Generate the PMML representation for R objects.*

---

**Description**

`pmml` is a generic function implementing S3 methods used to produce the PMML (Predictive Model Markup Language) representation of an R model. The resulting PMML file can then be imported into other systems that accept PMML.

**Usage**

```
pmml(model = NULL, model_name = "R_Model",
      app_name = "SoftwareAG PMML Generator", description = NULL,
      copyright = NULL, transforms = NULL, ...)
```

## Arguments

<code>model</code>	An object to be converted to PMML.
<code>model_name</code>	A name to be given to the PMML model.
<code>app_name</code>	The name of the application that generated the PMML.
<code>description</code>	A descriptive text for the Header element of the PMML.
<code>copyright</code>	The copyright notice for the model.
<code>transforms</code>	Data transformations.
<code>...</code>	Further arguments passed to or from other methods.

## Details

The data transformation functions previously available in the separate `pmmlTransformations` package have been merged into `pmml` starting with version 2.0.0.

This function can also be used to output variable transformations in PMML format. In particular, it can be used as a transformations generator. Various transformation operations can be implemented in R and those transformations can then be output in PMML format by calling the function with a `NULL` value for the model input and a data transformation object as the `transforms` input. Please see the documentation for `xform_wrap` for more information on how to create a data transformation object.

In addition, the `pmml` function can also be called using a pre-existing PMML model as the first input and a data transformation object as the `transforms` input. The result is a new PMML model with the transformation inserted as a "LocalTransformations" element in the original model. If the original model already had a "LocalTransformations" element, the new information will be appended to that element. If the model variables are derived directly from a chain of transformations defined in the `transforms` input, the field names in the model are replaced with the original field names with the correct data types to make a consistent model. The covered cases include model fields derived from an original field, model fields derived from a chain of transformations starting from an original field and multiple fields derived from the same original field.

This package converts models to PMML version 4.3.

Please note that package **XML\_3.95-0.1** or later is required to perform the full and correct functionality of **pmml**.

If data used for an R model contains features of type character, these must be converted to factors before the model is trained and converted with `pmml`.

A list of all the supported models and packages is available in the vignette:

```
vignette("packages_and_functions", package="pmml").
```

## Value

An object of class `XMLNode` as that defined by the **XML** package. This represents the top level, or root node, of the XML document and is of type `PMML`. It can be written to file with `saveXML`.

## Author(s)

Graham Williams

## References

- [PMML home page](#)
- [PMML transformations](#)

## See Also

[pmml.ada](#), [pmml.rules](#), [pmml.coxph](#), [pmml.cv.glmnet](#), [pmml.glm](#), [pmml.hclust](#), [pmml.kmeans](#), [pmml.ksvm](#), [pmml.lm](#), [pmml.multinom](#), [pmml.naiveBayes](#), [pmml.neighbor](#), [pmml.nnet](#), [pmml.randomForest](#), [pmml.rfsrc](#), [pmml.rpart](#), [pmml.svm](#), [pmml.xgb.Booster](#)

## Examples

```
# Build an lm model
iris_lm <- lm(Sepal.Length ~ ., data = iris)

# Convert to pmml
pmml(iris_lm)

# Create a data transformation object
iris_trans <- xform_wrap(iris)

# Transform the 'Sepal.Length' variable
iris_trans <- xform_min_max(iris_trans, xform_info = "column1->d_sl")

# Output the tranformation in PMML format
pmml(NULL, transforms = iris_trans)
```

---

pmml.ada

*Generate the PMML representation for an ada object from the package **ada**.*

---

## Description

Generate the PMML representation for an ada object from the package **ada**.

## Usage

```
## S3 method for class 'ada'
pmml(model, model_name = "AdaBoost_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "AdaBoost Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL, ...)
```

**Arguments**

model	An ada object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
...	Further arguments passed to or from other methods.

**Details**

Export the ada model in the PMML MiningModel (multiple models) format. The MiningModel element consists of a list of TreeModel elements, one in each model segment.

This function implements the discrete adaboost algorithm only. Note that each segment tree is a classification model, returning either -1 or 1. However the MiningModel (ada algorithm) is doing a weighted sum of the returned value, -1 or 1. So the value of attribute functionName of element MiningModel is set to "regression"; the value of attribute functionName of each segment tree is also set to "regression" (they have to be the same as the parent MiningModel per PMML schema). Although each segment/tree is being named a "regression" tree, the actual returned score can only be -1 or 1, which practically turns each segment into a classification tree.

The model in PMML format has 5 different outputs. The "rawValue" output is the value of the model expressed as a tree model. The boosted tree model uses a transformation of this value, this is the "boostValue" output. The last 3 outputs are the predicted class and the probabilities of each of the 2 classes (The ada package Boosted Tree models can only handle binary classification models).

**Author(s)**

Wen Lin

**References**

[ada: an R package for stochastic boosting \(on CRAN\)](#)

**Examples**

```
library(ada)
data(audit)

fit <- ada(Adjusted ~ Employment + Education + Hours + Income, iter = 3, audit)
pmml_fit <- pmml(fit)
```

---

pmml.coxph	<i>Generate the PMML representation for a coxph object from the package <b>survival</b>.</i>
------------	--

---

## Description

Generate the PMML representation for a coxph object from the package **survival**.

## Usage

```
## S3 method for class 'coxph'  
pmml(model,  
      model_name = "CoxPH_Survival_Regression_Model",  
      app_name = "SoftwareAG PMML Generator",  
      description = "CoxPH Survival Regression Model", copyright = NULL,  
      transforms = NULL, missing_value_replacement = NULL, ...)
```

## Arguments

model	A coxph object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
...	Further arguments passed to or from other methods.

## Details

A coxph object is the result of fitting a proportional hazards regression model, using the coxph function from the package **survival**. Although the **survival** package supports special terms "cluster", "tt" and "strata", only the special term "strata" is supported by the **pmml** package. Note that special term "strata" cannot be a multiplicative variable and only numeric risk regression is supported.

## Author(s)

Graham Williams

## References

[coxph: Survival Analysis](#)

---

pmml.cv.glmnet	<i>Generate the PMML representation for a cv.glmnet object from the package <b>glmnet</b>.</i>
----------------	--

---

## Description

Generate the PMML representation for a cv.glmnet object from the package **glmnet**.

## Usage

```
## S3 method for class 'cv.glmnet'
pmml(model, model_name = "Elasticnet_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Generalized Linear Regression Model",
      copyright = NULL, transforms = NULL,
      missing_value_replacement = NULL, dataset = NULL, s = NULL, ...)
```

## Arguments

model	A cv.glmnet object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
dataset	Data used to train the cv.glmnet model.
s	'lambda' parameter at which to output the model. If not given, the lambda.1se parameter from the model is used instead.
...	Further arguments passed to or from other methods.

## Details

The glmnet package expects the input and predicted values in a matrix format - not as arrays or data frames. As of now, it will also accept numerical values only. As such, any string variables must be converted to numerical ones. One possible way to do so is to use data transformation functions from this package. However, the result is a data frame. In all cases, lists, arrays and data frames can be converted to a matrix format using the data.matrix function from the base package. Given a data frame df, a matrix m can thus be created by using `m <- data.matrix(df)`.

The PMML language requires variable names which will be read in as the column names of the input matrix. If the matrix does not have variable names, they will be given the default values of "X1", "X2", ...

Currently, only gaussian and poisson family types are supported.



**Value**

PMML representation of the cv.glmnet object.

**Author(s)**

Tridivesh Jena

**References**

[glmnet: Lasso and elastic-net regularized generalized linear models \(on CRAN\)](#)

**Examples**

```
library(glmnet)

# Create a simple predictor (x) and response(y) matrices:
x <- matrix(rnorm(100 * 20), 100, 20)
y <- rnorm(100)

# Build a simple gaussian model:
model1 <- cv.glmnet(x, y)

# Output the model in PMML format:
pmml(model1)

# Shift y between 0 and 1 to create a poisson response:
y <- y - min(y)

# Give the predictor variables names (default values are V1,V2,...):
name <- NULL
for (i in 1:20) {
  name <- c(name, paste("variable", i, sep = ""))
}
colnames(x) <- name

# Create a simple poisson model:
model2 <- cv.glmnet(x, y, family = "poisson")

# Output the regression model in PMML format at the lambda
# parameter = 0.006:
pmml(model2, s = 0.006)
```

---

pmml.gbm

*Generate the PMML representation for a gbm object from the package **gbm**.*

---

**Description**

Generate the PMML representation for a gbm object from the package **gbm**.

## Usage

```
## S3 method for class 'gbm'  
pmml(model, model_name = "GBM_Model",  
      app_name = "SoftwareAG PMML Generator",  
      description = "Generalized Boosted Tree Model", copyright = NULL,  
      transforms = NULL, missing_value_replacement = NULL, ...)
```

## Arguments

model	A gbm object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
...	Further arguments passed to or from other methods.

## Details

The 'gbm' function uses various distribution types to fit a model; currently only the "bernoulli", "poisson" and "multinomial" distribution types are supported.

For all cases, the model output includes the gbm prediction type "link" and "response".

## Value

PMML representation of the gbm object.

## Author(s)

Tridivesh Jena

## References

[gbm: Generalized Boosted Regression Models \(on CRAN\)](#)

## Examples

```
library(gbm)  
data(audit)  
  
mod <- gbm(Adjusted ~ .,  
          data = audit[, -c(1, 4, 6, 9, 10, 11, 12)],  
          n.trees = 3, interaction.depth = 4  
          )
```

```

pmml(mod)

# Classification example:
mod2 <- gbm(Species ~ .,
  data = iris, n.trees = 2,
  interaction.depth = 3, distribution = "multinomial"
)

# The PMML will include a regression model to read the gbm object outputs
# and convert to a "response" prediction type.
pmml(mod2)

```

---

pmml.glm	<i>Generate the PMML representation for a glm object from the package <b>stats</b>.</i>
----------	---

---

## Description

Generate the PMML representation for a glm object from the package **stats**.

## Usage

```

## S3 method for class 'glm'
pmml(model, model_name = "General_Regression_Model",
  app_name = "SoftwareAG PMML Generator",
  description = "Generalized Linear Regression Model",
  copyright = NULL, transforms = NULL,
  missing_value_replacement = NULL, weights = NULL, ...)

```

## Arguments

model	A glm object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
weights	The weights used for building the model.
...	Further arguments passed to or from other methods.

## Details

The function exports the glm model in the PMML GeneralRegressionModel format.

Note on glm models for 2-class problems: a dataset where the target categorical variable has more than 2 classes may be turned into a 2-class problem by creating a new target variable that is TRUE for a particular class and FALSE for all other classes. While the R formula function allows such a transformation to be passed directly to it, this may cause issues when the model is converted to PMML. Therefore, it is advised to create a new 2-class separately, and then pass that variable to glm(). This is shown in an example below.

## Value

PMML representation of the glm object.

## References

[R project: Fitting Generalized Linear Models](#)

## Examples

```
data(iris)
mod <- glm(Sepal.Length ~ ., data = iris, family = "gaussian")
mod_pmml <- pmml(mod)
rm(mod, mod_pmml)

data(audit)
mod <- glm(Adjusted ~ Age + Employment + Education + Income, data = audit, family = binomial(logit))
mod_pmml <- pmml(mod)
rm(mod, mod_pmml)

# Create a new 2-class target from a 3-class variable:
data(iris)
dat <- iris[, 1:4]
# Add a new 2-class target "Species_setosa" before passing it to glm():
dat$Species_setosa <- iris$Species == "setosa"
mod <- glm(Species_setosa ~ ., data = dat, family = binomial(logit))
mod_pmml <- pmml(mod)
rm(dat, mod, mod_pmml)
```

---

pmml.hclust

*Generate the PMML representation for a hclust object from the package **amap**.*

---

## Description

Generate the PMML representation for a hclust object from the package **amap**.

**Usage**

```
## S3 method for class 'hclust'
pmml(model, model_name = "HClust_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Hierarchical Cluster Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL, centers, ...)
```

**Arguments**

model	A hclust object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
centers	A list of means to represent the clusters.
...	Further arguments passed to or from other methods.

**Details**

This function converts a hclust object created by the `hclusterpar` function from the **amap** package. A hclust object is a cluster model created hierarchically. The data is divided recursively until a criteria is met. This function then takes the final model and represents it as a standard k-means cluster model. This is possible since while the method of constructing the model is different, the final model can be represented in the same way.

To use this `pmml` function, therefore, one must pick the number of clusters desired and the coordinate values at those cluster centers. This can be done using the `hclusterpar` and `centers.hclust` functions from the **amap** and **rattle** packages respectively.

The hclust object will be approximated by k centroids and is converted into a PMML representation for kmeans clusters.

**Value**

PMML representation of the hclust object.

**Author(s)**

Graham Williams

**References**

[R project: Hierarchical Clustering](#)

## Examples

```
## Not run:

# Cluster the 4 numeric variables of the iris dataset.
library(ama)
library(rattle)

model <- hclusterpar(iris[, -5])

# Get the information about the cluster centers. The last
# parameter of the function used is the number of clusters
# desired.
centerInfo <- centers.hclust(iris[, -5], model, 3)

# Convert to pmml
pmml(model, centers = centerInfo)

## End(Not run)
```

---

pmml.iForest

*Generate PMML for an iForest object from the **isofor** package.*

---

## Description

Generate PMML for an iForest object from the **isofor** package.

## Usage

```
## S3 method for class 'iForest'
pmml(model, model_name = "isolationForest_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Isolation Forest Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL,
      anomalyThreshold = 0.6,
      parent_invalid_value_treatment = "returnInvalid",
      child_invalid_value_treatment = "asIs", ...)
```

## Arguments

model	An iForest object from package <b>isofor</b> .
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.

missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all MiningFields.
anomalyThreshold	Double between 0 and 1. Predicted values greater than this are classified as anomalies.
parent_invalid_value_treatment	Invalid value treatment at the top MiningField level.
child_invalid_value_treatment	Invalid value treatment at the model segment MiningField level.
...	Further arguments passed to or from other methods.

### Details

This function converts the iForest model object to the PMML format. The PMML outputs the anomaly score as well as a boolean value indicating whether the input is an anomaly or not. This is done by simply comparing the anomaly score with `anomalyThreshold`, a parameter in the `pmml` function. The iForest function automatically adds an extra level to all categorical variables, labelled "."; this is kept in the PMML representation even though the use of this extra factor in the predict function is unclear.

Isolation forest anomaly detection models are not yet supported by DMG PMML schema version 4.3. The PMML produced by this exporter uses an extended schema, and can be consumed by Zementis products. The extended schema is a superset of 4.3, and contains enhancements that will be part of the upcoming PMML 4.4 release.

### Value

PMML representation of the iForest object.

### Author(s)

Tridivesh Jena

### References

[iso4or package on GitHub](#)

### See Also

[pmml](#)

### Examples

```
## Not run:  
  
# Build iForest model using iris dataset. Create an isolation  
# forest with 10 trees. Sample 30 data points at a time from  
# the iris dataset to fit the trees.  
library(iso4or)  
data(iris)
```

```

mod <- iForest(iris, nt = 10, phi = 30)

# Convert to PMML:
pm <- pmml(mod)

## End(Not run)

```

---

pmml.kmeans	<i>Generate the PMML representation for a kmeans object from the package <b>stats</b>.</i>
-------------	--

---

### Description

The kmeans object (a cluster described by k centroids) is converted into a PMML representation.

### Usage

```

## S3 method for class 'kmeans'
pmml(model, model_name = "KMeans_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "KMeans cluster model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL,
      algorithm.name = "KMeans: Hartigan and Wong", ...)

```

### Arguments

model	A kmeans object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
algorithm.name	The variety of kmeans used.
...	Further arguments passed to or from other methods.

### Details

A kmeans object is obtained by applying the kmeans function from the stats package. This method typically requires the user to normalize all the variables; these operations can be done using transforms so that the normalization information is included in PMML.



**Author(s)**

Graham Williams

**References**[R project: K-Means Clustering](#)**Examples**

```
ds <- rbind(
  matrix(rnorm(100, sd = 0.3), ncol = 2),
  matrix(rnorm(100, mean = 1, sd = 0.3), ncol = 2)
)
colnames(ds) <- c("Dimension1", "Dimension2")
cl <- kmeans(ds, 2)
pmml(cl)
```

pmml.ksvm

---

*Generate the PMML representation for a ksvm object from the package **kernlab**.*

---

**Description**

Generate the PMML representation for a ksvm object from the package **kernlab**.

**Usage**

```
## S3 method for class 'ksvm'
pmml(model, model_name = "SVM_model",
      app_name = "SoftwareAG PMML Generator",
      description = "Support Vector Machine Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL,
      dataset = NULL, ...)
```

**Arguments**

model	A ksvm object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.

dataset            Data used to train the ksvm model.  
 ...                Further arguments passed to or from other methods.

### Details

Both classification (multi-class and binary) as well as regression cases are supported.

The following ksvm kernels are currently supported: rbfdot, polydot, vanilladot, tanhdot.

The argument dataset is required since the ksvm object does not contain information about the used categorical variable.

### Value

PMML representation of the ksvm object.

### References

[kernlab: Kernel-based Machine Learning Lab \(on CRAN\)](#)

### Examples

```
# Train a support vector machine to perform classification.
library(kernlab)

model <- ksvm(Species ~ ., data = iris)

p <- pmml(model, dataset = iris)
```

---

pmml.lm	<i>Generate the PMML representation for an lm object from the package stats.</i>
---------	--

---

### Description

Generate the PMML representation for an lm object from the package **stats**.

### Usage

```
## S3 method for class 'lm'
pmml(model, model_name = "lm_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Linear Regression Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL,
      weights = NULL, ...)
```

**Arguments**

<code>model</code>	An lm object.
<code>model_name</code>	A name to be given to the PMML model.
<code>app_name</code>	The name of the application that generated the PMML.
<code>description</code>	A descriptive text for the Header element of the PMML.
<code>copyright</code>	The copyright notice for the model.
<code>transforms</code>	Data transformations.
<code>missing_value_replacement</code>	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
<code>weights</code>	The weights used for building the model.
<code>...</code>	Further arguments passed to or from other methods.

**Details**

The resulting PMML representation will not encode interaction terms. Currently, only numeric regression is supported.

**Value**

PMML representation of the lm object.

**Author(s)**

Rajarshi Guha

**References**

[R project: Fitting Linear Models](#)

**Examples**

```
fit <- lm(Sepal.Length ~ ., data = iris)
pmml(fit)

rm(fit)
```

---

pmml.multinom	<i>Generate the PMML representation for a multinom object from package <b>nnet</b>.</i>
---------------	---

---

### Description

Generate the multinomial logistic model in the PMML RegressionModel format. The function implements the use of numerical, categorical and multiplicative terms involving both numerical and categorical variables.

### Usage

```
## S3 method for class 'multinom'
pmml(model, model_name = "multinom_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Multinomial Logistic Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL, ...)
```

### Arguments

model	A multinom object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
...	Further arguments passed to or from other methods.

### Value

PMML representation of the multinom object.

### Author(s)

Tridivesh Jena

### References

[nnet: Feed-forward Neural Networks and Multinomial Log-Linear Models \(on CRAN\)](#)

---

pmml.naiveBayes	<i>Generate the PMML representation for a naiveBayes object from the package <b>e1071</b>.</i>
-----------------	--

---

## Description

Generate the PMML representation for a naiveBayes object from the package **e1071**.

## Usage

```
## S3 method for class 'naiveBayes'
pmml(model, model_name = "naiveBayes_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "NaiveBayes Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL, predicted_field,
      ...)
```

## Arguments

model	A naiveBayes object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
predicted_field	Required parameter; the name of the predicted field.
...	Further arguments passed to or from other methods.

## Details

The PMML representation of the NaiveBayes model implements the definition as specified by the Data Mining Group: intermediate probability values which are less than the threshold value are replaced by the threshold value. This is different from the prediction function of the **e1071** in which only probability values of 0 and standard deviations of continuous variables of with the value 0 are replaced by the threshold value. The two values will therefore not match exactly for cases involving very small probabilities.

## Value

PMML representation of the naiveBayes object.

**Author(s)**

Tridivesh Jena

**References**

- [e1071: Misc Functions of the Department of Statistics, Probability Theory Group \(Formerly: E1071\), TU Wien \(on CRAN\)](#)
- A. Guazzelli, T. Jena, W. Lin, M. Zeller (2013). Extending the Naive Bayes Model Element in PMML: Adding Support for Continuous Input Variables. In *Proceedings of the 19th ACM SIGKDD Conference on Knowledge Discovery and Data Mining*.

**Examples**

```
library(e1071)

data(houseVotes84)
house <- na.omit(houseVotes84)

model <- naiveBayes(Class ~ V1 + V2 + V3, data = house, threshold = 0.003)

pmml(model, dataset = house, predicted_field = "Class")
```

---

pmml.neighbor

---

*Generate PMML for a neighbor object from the **neighbor** package.*


---

**Description**

Generate PMML for a neighbor object from the **neighbor** package.

**Usage**

```
## S3 method for class 'neighbor'
pmml(model, model_name = "kNN_model",
      app_name = "SoftwareAG PMML Generator",
      description = "K Nearest Neighbors Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL, ...)
```

**Arguments**

model	A neighbor object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.

```
missing_value_replacement
    Value to be used as the 'missingValueReplacement' attribute for all Mining-
    Fields.
...
    Further arguments passed to or from other methods.
```

### Details

The model is represented in the PMML NearestNeighborModel format.

The current version of this converter does not support transformations (transforms must be left as NULL), sets categoricalScoringMethod to "majorityVote", sets continuousScoringMethod to "average", and isTransoformed to "false".

### Value

PMML representation of the neighbr object.

### See Also

[pmml](#), [PMML KNN specification](#)

### Examples

```
## Not run:

# Continuous features with continuous target, categorical target,
# and neighbor ranking:

library(neighbr)
data(iris)

# Add an ID column to the data for neighbor ranking:
iris$ID <- c(1:150)

# Train set contains all predicted variables, features, and ID column:
train_set <- iris[1:140, ]

# Omit predicted variables or ID column from test set:
test_set <- iris[141:150, -c(4, 5, 6)]

fit <- knn(
  train_set = train_set, test_set = test_set,
  k = 3,
  categorical_target = "Species",
  continuous_target = "Petal.Width",
  comparison_measure = "squared_euclidean",
  return_ranked_neighbors = 3,
  id = "ID"
)

pmml(fit)
```

```

# Logical features with categorical target and neighbor ranking:

library(neighbr)
data("houseVotes84")

# Remove any rows with N/A elements:
dat <- houseVotes84[complete.cases(houseVotes84), ]

# Change all {yes,no} factors to {0,1}:
feature_names <- names(dat)[!names(dat) %in% c("Class", "ID")]
for (n in feature_names) {
  levels(dat[, n])[levels(dat[, n]) == "n"] <- 0
  levels(dat[, n])[levels(dat[, n]) == "y"] <- 1
}

# Change factors to numeric:
for (n in feature_names) {
  dat[, n] <- as.numeric(levels(dat[, n]))[dat[, n]]
}

# Add an ID column for neighbor ranking:
dat$ID <- c(1:nrow(dat))

# Train set contains features, predicted variable, and ID:
train_set <- dat[1:225, ]

# Test set contains features only:
test_set <- dat[226:232, !names(dat) %in% c("Class", "ID")]

fit <- knn(
  train_set = train_set, test_set = test_set,
  k = 5,
  categorical_target = "Class",
  comparison_measure = "jaccard",
  return_ranked_neighbors = 3,
  id = "ID"
)

pmml(fit)

## End(Not run)

```

---

pmml.nnet

---

*Generate the PMML representation for a nnet object from package  
nnet.*

---

### Description

Generate the PMML representation for a nnet object from package **nnet**.



**Usage**

```
## S3 method for class 'nnet'  
pmml(model, model_name = "NeuralNet_model",  
      app_name = "SoftwareAG PMML Generator",  
      description = "Neural Network Model", copyright = NULL,  
      transforms = NULL, missing_value_replacement = NULL, ...)
```

**Arguments**

model	A nnet object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
...	Further arguments passed to or from other methods.

**Details**

This function supports both regression and classification neural network models. The model is represented in the PMML NeuralNetwork format.

**Value**

PMML representation of the nnet object.

**Author(s)**

Tridivesh Jena

**References**

[nnet: Feed-forward Neural Networks and Multinomial Log-Linear Models \(on CRAN\)](#)

**Examples**

```
library(nnet)  
fit <- nnet(Species ~ ., data = iris, size = 4)  
pmml(fit)  
  
rm(fit)
```

---

pmml.randomForest	<i>Generate the PMML representation for a randomForest object from the package <b>randomForest</b>.</i>
-------------------	---

---

### Description

Generate the PMML representation for a randomForest object from the package **randomForest**.

### Usage

```
## S3 method for class 'randomForest'
pmml(model, model_name = "randomForest_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Random Forest Tree Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL,
      parent_invalid_value_treatment = "returnInvalid",
      child_invalid_value_treatment = "asIs", ...)
```

### Arguments

model	A randomForest object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all MiningFields.
parent_invalid_value_treatment	Invalid value treatment at the top MiningField level.
child_invalid_value_treatment	Invalid value treatment at the model segment MiningField level.
...	Further arguments passed to or from other methods.

### Details

This function outputs a Random Forest in PMML format.

### Value

PMML representation of the randomForest object.

### Author(s)

Tridivesh Jena

## References

[randomForest: Breiman and Cutler's random forests for classification and regression](#)

## Examples

```
# Build a randomForest model
library(randomForest)
iris.rf <- randomForest(Species ~ ., data = iris, ntree = 20)

# Convert to pmml
pmml(iris.rf)

rm(iris.rf)
```

---

pmml.rfsrc	<i>Generate the PMML representation for an rfsrc object from the package <b>randomForestSRC</b>.</i>
------------	--

---

## Description

Generate the PMML representation for an rfsrc object from the package **randomForestSRC**.

## Usage

```
## S3 method for class 'rfsrc'
pmml(model, model_name = "rsf_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Random Survival Forest Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL, ...)
```

## Arguments

model	An rfsrc object returned by the function <code>rfsrc</code> with the parameter <code>forest=TRUE</code> .
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
...	Further arguments passed to or from other methods.

## Details

This function is used to export the geometry of the forest to other PMML compliant applications, including graphics packages that are capable of printing binary trees.

The **pmml** package supports randomSurvivalForest up to version 2.5.0.

## Value

PMML representation of the rfsrc object.

## Author(s)

Tridivesh Jena

## References

- H. Ishwaran, U.B. Kogalur, E.H. Blackstone, M.S. Lauer (2008), RANDOM SURVIVAL FORESTS. *The Annals of Applied Statistics, Vol. 2, No. 3, 841-860.*
- H. Ishwaran and Udaya B. Kogalur (2006). Random Survival Forests. *Cleveland Clinic Technical Report.*

## Examples

```
## Not run:
library(randomForestSRC)

data(veteran)

veteran_mod <- rfsrc(Surv(time, status) ~ .,
  data = veteran,
  ntree = 5, forest = TRUE,
  membership = TRUE
)

pmml(veteran_mod)

## End(Not run)
```

---

pmml.rpart

*Generate the PMML representation for an rpart object from the package **rpart**.*

---

## Description

Generate the PMML representation for an rpart object from the package **rpart**.

**Usage**

```
## S3 method for class 'rpart'  
pmml(model, model_name = "RPart_Model",  
      app_name = "SoftwareAG PMML Generator",  
      description = "RPart Decision Tree Model", copyright = NULL,  
      transforms = NULL, missing_value_replacement = NULL,  
      dataset = NULL, ...)
```

**Arguments**

model	An rpart object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
dataset	Data used to train the rpart model.
...	Further arguments passed to or from other methods.

**Details**

Supports regression tree as well as classification. The object is represented in the PMML TreeModel format.

**Value**

PMML representation of the rpart object.

**Author(s)**

Graham Williams

**References**

[rpart: Recursive Partitioning \(on CRAN\)](#)

**Examples**

```
library(rpart)  
  
fit <- rpart(Species ~ ., data = iris)  
  
pmml(fit)
```

---

pmml.rules	<i>Generate the PMML representation for a rules or an itemset object from package <b>arules</b>.</i>
------------	--

---

### Description

Generate the PMML representation for a rules or an itemset object from package **arules**.

### Usage

```
## S3 method for class 'rules'
pmml(model, model_name = "arules_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Association Rules Model", copyright = NULL,
      transforms = NULL, ...)
```

### Arguments

model	A rules or itemsets object.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
...	Further arguments passed to or from other methods.

### Details

The model is represented in the PMML AssociationModel format.

### Value

PMML representation of the rules or itemsets object.

### Author(s)

Graham Williams, Michael Hahsler

### References

[arules: Mining Association Rules and Frequent Itemsets](#)

---

pmml.svm	<i>Generate the PMML representation of an svm object from the <b>e1071</b> package.</i>
----------	---

---

## Description

Generate the PMML representation of an svm object from the **e1071** package.

## Usage

```
## S3 method for class 'svm'
pmml(model, model_name = "LIBSVM_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Support Vector Machine Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL,
      dataset = NULL, ...)
```

## Arguments

model	An svm object from package <b>e1071</b> .
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.
dataset	Required for one-classification only; data used to train the one-class SVM model.
...	Further arguments passed to or from other methods.

## Details

The model is represented in the PMML SupportVectorMachineModel format.

Note that the sign of the coefficient of each support vector flips between the R object and the exported PMML file for classification and regression models. This is due to the minor difference in the training/scoring formula between the LIBSVM algorithm and the DMG specification. Hence the output value of each support vector machine has a sign flip between the DMG definition and the svm prediction function.

In a classification model, even though the output of the support vector machine has a sign flip, it does not affect the final predicted category. This is because in the DMG definition, the winning category is defined as the left side of threshold 0 while the LIBSVM defines the winning category as the right side of threshold 0.

For a regression model, the exported PMML code has two OutputField elements. The OutputField predictedValue shows the support vector machine output per DMG definition. The OutputField svm\_predict\_function gives the value corresponding to the R predict function for the svm model. This output should be used when making model predictions.

For a one-classification svm (OCSVM) model, the PMML has three OutputField elements. The OutputField anomaly is a boolean value that conforms to the DMG definition of an anomaly detection model; this value is TRUE when an anomaly is detected. This value is the opposite of the prediction by the e1071 object, which predicts FALSE when an anomaly is detected; that is, the R svm model predicts whether an input is an inlier. The OutputField anomalyScore is the signed distance to the separating boundary; anomalyScore corresponds to the decision.values attribute of the output of the svm predict function in R.

For example, say that for an input of observations, the R OCSVM model predicts a positive decision value of 0.4 and label of TRUE. According to the R object, this means that the observation is an inlier. The PMML export of this model will give the following for the same input: anomalyScore = 0.4, anomaly = "false". According to the PMML, the observation is not an anomaly. Note that there is no sign flip between R and PMML for OCSVM models.

To export a OCSVM model, an additional argument, dataset, is required by the function. This argument expects a dataframe with data that was used to train the model. This is necessary because for one-class svm, the R svm object does not contain information about the data types of the features used to train the model. The exporter does not yet support the formula interface for one-classification models, so the default S3 method must be used to train the SVM. The data used to train the one-class SVM must be numeric and not of integer class.

SVM anomaly detection models are not yet supported by DMG PMML schema version 4.3. The PMML produced by this exporter uses an extended schema, and can be consumed by Zementis products. The extended schema is a superset of 4.3, and contains enhancements that will be part of the upcoming PMML 4.4 release.

## Value

PMML representation of the svm object.

## References

\* R project CRAN package: *e1071: Misc Functions of the Department of Statistics, Probability Theory Group (Formerly: E1071), TU Wien* <https://CRAN.R-project.org/package=e1071>

\* Chang, Chih-Chung and Lin, Chih-Jen, *LIBSVM: a library for Support Vector Machines* <http://www.csie.ntu.edu.tw/~cjlin/libsvm>

## See Also

[pmml](#), [PMML SVM specification](#)

## Examples

```
## Not run:  
library(e1071)  
data(iris)
```



```

# Classification with a polynomial kernel
fit <- svm(Species ~ ., data = iris, kernel = "polynomial")
pmml(fit)

# Regression
fit <- svm(Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width, data = iris)
pmml(fit)

# Anomaly detection with one-classification
fit <- svm(iris[, 1:4], y = NULL, type = "one-classification")
pmml(fit, dataset = iris[, 1:4])

## End(Not run)

```

---

pmml.xgb.Booster

*Generate PMML for a xgb.Booster object from the package **xgboost**.*


---

## Description

Generate PMML for a xgb.Booster object from the package **xgboost**.

## Usage

```

## S3 method for class 'xgb.Booster'
pmml(model, model_name = "xboost_Model",
      app_name = "SoftwareAG PMML Generator",
      description = "Extreme Gradient Boosting Model", copyright = NULL,
      transforms = NULL, missing_value_replacement = NULL,
      input_feature_names = NULL, output_label_name = NULL,
      output_categories = NULL, xgb_dump_file = NULL,
      parent_invalid_value_treatment = "returnInvalid",
      child_invalid_value_treatment = "asIs", ...)

```

## Arguments

model	An object created by the 'xgboost' function.
model_name	A name to be given to the PMML model.
app_name	The name of the application that generated the PMML.
description	A descriptive text for the Header element of the PMML.
copyright	The copyright notice for the model.
transforms	Data transformations.
missing_value_replacement	Value to be used as the 'missingValueReplacement' attribute for all Mining-Fields.

<code>input_feature_names</code>	Input variable names used in training the model.
<code>output_label_name</code>	Name of the predicted field.
<code>output_categories</code>	Possible values of the predicted field, for classification models.
<code>xgb_dump_file</code>	Name of file saved using 'xgb.dump' function.
<code>parent_invalid_value_treatment</code>	Invalid value treatment at the top MiningField level.
<code>child_invalid_value_treatment</code>	Invalid value treatment at the model segment MiningField level.
<code>...</code>	Further arguments passed to or from other methods.

## Details

The `xgboost` function takes as its input either an `xgb.DMatrix` object or a numeric matrix. The input field information is not stored in the R model object, hence the field information must be passed on as inputs. This enables the PMML to specify field names in its model representation. The R model object does not store information about the fitted tree structure either. However, this information can be extracted from the `xgb.model.dt.tree` function and the file saved using the `xgb.dump` function. The `xgboost` library is therefore needed in the environment and this saved file is needed as an input as well.

The following objectives are currently supported: `multi:softprob`, `multi:softmax`, `binary:logistic`.

The pmml exporter will throw an error if the `xgboost` model only has one tree.

The exporter only works with numeric matrices. Sparse matrices must be converted to `matrix` objects before training an `xgboost` model for the export to work correctly.

## Value

PMML representation of the `xgb.Booster` object.

## Author(s)

Tridivesh Jena

## References

[xgboost: Extreme Gradient Boosting](#)

## See Also

[pmml](#), [PMML schema](#)

**Examples**

```

## Not run:
# Example using the xgboost package example model.

library(xgboost)
data(agaricus.train, package = "xgboost")
data(agaricus.test, package = "xgboost")

train <- agaricus.train
test <- agaricus.test

model1 <- xgboost(
  data = train$data, label = train$label,
  max_depth = 2, eta = 1, nthread = 2,
  nrounds = 2, objective = "binary:logistic"
)

# Save the tree information in an external file:
xgb.dump(model1, "model1.dumped.trees")

# Convert to PMML:
pmml(model1,
  input_feature_names = colnames(train$data),
  output_label_name = "prediction1",
  output_categories = c("0", "1"),
  xgb_dump_file = "model1.dumped.trees"
)

# Multinomial model using iris data:
model2 <- xgboost(
  data = as.matrix(iris[, 1:4]),
  label = as.numeric(iris[, 5]) - 1,
  max_depth = 2, eta = 1, nthread = 2, nrounds = 2,
  objective = "multi:softprob", num_class = 3
)

# Save the tree information in an external file:
xgb.dump(model2, "model2.dumped.trees")

# Convert to PMML:
pmml(model2,
  input_feature_names = colnames(as.matrix(iris[, 1:4])),
  output_label_name = "Species",
  output_categories = c(1, 2, 3), xgb_dump_file = "model2.dumped.trees"
)

## End(Not run)

```

**Description**

Rename a variable in the `xform_wrap` transform object.

**Usage**

```
rename_wrap_var(wrap_data, xform_info = NA, ...)
```

**Arguments**

<code>wrap_data</code>	Wrapper object obtained by using the <code>xform_wrap</code> function on the raw data.
<code>xform_info</code>	Specification of details of the renaming.
<code>...</code>	Further arguments passed to or from other methods.

**Details**

Once input data is wrapped by the `xform_wrap` function, it is somewhat involved to rename a variable inside. This function makes it easier to do so. Given an variable named **InputVar** and the name one wishes to rename it to, **OutputVar**, the rename command options are:

```
xform_info="InputVar -> OutputVar"
```

There are two methods in which the variables can be referred to. The first method is to use its column number; given the **data** attribute of the **boxData** object, this would be the order at which the variable appears. This can be indicated in the format "column#". The second method is to refer to the variable by its name. This method will work even if the renamed value already exists; in which case there will be two variables with the same name.

If no input variable name is provided, the original object is returned with no renamings performed.

**Value**

R object containing the raw data, the transformed data and data statistics.

**Author(s)**

Tridivesh Jena

**See Also**

[xform\\_wrap](#)

**Examples**

```
# Load the standard iris dataset, already built into R
data(iris)

# First wrap the data
iris_box <- xform_wrap(iris)

# We wish to refer to the variables "Sepal.Length" and
# "Sepal.Width" as "SL" and "SW"
iris_box <- rename_wrap_var(iris_box, "column1->SL")
```

```
iris_box <- rename_wrap_var(iris_box, "Sepal.Width->SW")
```

---

save_pmml	<i>Save a pmml object as an external PMML file.</i>
-----------	---

---

## Description

Save a pmml object to an external PMML file more efficient further processing.

## Usage

```
save_pmml(doc, name, version = 4.3)
```

## Arguments

doc	The pmml model.
name	The name of the external file where the PMML is to be saved.
version	The PMML version with which the PMML model is compliant.

## Author(s)

Tridivesh Jena

## Examples

```
## Not run:  
# Make a gbm model:  
library(gbm)  
data(audit)  
  
mod <- gbm(Adjusted ~ .,  
  data = audit[, -c(1, 4, 6, 9, 10, 11, 12)],  
  n.trees = 3,  
  interaction.depth = 4  
)  
  
# Export to PMML:  
pmod <- pmml(mod)  
  
# Save to an external file:  
save_pmml(pmod, "GBMModel.pmml")  
  
## End(Not run)
```

---

xform_discretize	<i>Discretize a continuous variable as indicated by interval mappings in accordance with the PMML element <b>Discretize</b>.</i>
------------------	--

---

### Description

Discretize a continuous variable as indicated by interval mappings in accordance with the PMML element **Discretize**.

### Usage

```
xform_discretize(wrap_object, xform_info, table, default_value = NA,
  map_missing_to = NA, ...)
```

### Arguments

wrap_object	Output of xform_wrap or another transformation function.
xform_info	Specification of details of the transformation. This may be a name of an external file or a list of data frames. Even if only 1 variable is to be transformed, the information for that transform should be given as a list with 1 element.
table	Name of external CSV file containing the map from input to output values.
default_value	Value to be given to the transformed variable if the value of the input variable does not lie in any of the defined intervals. If 'xform_info' is a list, this is a vector with each element corresponding to the corresponding list element.
map_missing_to	Value to be given to the transformed variable if the value of the input variable is missing. If 'xform_info' is a list, this is a vector with each element corresponding to the corresponding list element.
...	Further arguments passed to or from other methods.

### Details

Create a discrete variable from a continuous one as indicated by interval mappings. The discrete variable value depends on interval in which the continuous variable value lies. The mapping from intervals to discrete values can be given in an external table file referred to in the transform command or as a list of data frames.

Given a list of intervals and the discrete value each interval is linked to, a discrete variable is defined with the value indicated by the interval where it lies in. If a continuous variable **InVar** of data type **InType** is to be converted to a variable **OutVar** of data type **OutType**, the transformation command is in the format:

```
xform_info = "[InVar->OutVar][InType->OutType]", table="TableFileName",
  default_value="defVal", map_missing_to="missingVal"
```

where **TableFileName** is the name of the CSV file containing the interval to discrete value map. The data types of the variables can be any of the ones defined in the PMML format including integer, double or string. **defVal** is the default value of the transformed variable and if any of the input values are missing, **missingVal** is the value of the transformed variable.

The arguments `InType`, `OutType`, `default_value` and `map_missing_to` are optional. The CSV file containing the table should not have any row and column identifiers, and the values given must be in the same order as in the `map` command. If the data types of the variables are not given, the data types of the input variables are attempted to be determined from the **boxData** argument. If that is not possible, the data types are assumed to be string.

Intervals are either given by the left or right limits, in which case the other limit is considered as infinite. It may also be given by both the left and right limits separated by the character ":". An example of how intervals should be defined in the external file are:

```
rightVal1),outVal1
rightVal2],outVal2
[leftVal1:rightVal3),outVal3
(leftVal2:rightVal4],outVal4
(leftVal,outVal5
```

which, given an input value **inVal** and the output value to be calculated **out**, means that:

```
if(inVal < rightVal1) out=outVal1
f(inVal <= rightVal2) out=outVal2
if( (inVal >= leftVal1) and (inVal < rightVal3) ) out=outVal3
if( (inVal > leftVal2) and (inVal <= rightVal4) ) out=outVal4
if(inVal > leftVal) out=outVal5
```

It is also possible to give the information about the transforms without an external file, using a list of data frames. Each data frame defines a discretization operation for 1 input variable. The first row of the data frame gives the original field name, the derived field name, the left interval, the left value, the right interval and the right value. The second row gives the data type of the values as listed in the first row. The second row with the data types of the fields is not required. If not given, all fields are assumed to be strings. In this input format, the `'default_value'` and `'map_missing_to'` parameters should be vectors. The first element of each vector will correspond to the derived field defined in the 1st element of the `'xform_info'` list etc. Although somewhat more complicated, this method is designed to not require any external features. Further, once the initial list is constructed, modifying it is a simple operation; making this a better method to use if the parameters of the transformation are to be modified frequently and/or automatically. This is made more clear in the example below.

### Value

R object containing the raw data, the transformed data and data statistics.

### Author(s)

Tridivesh Jena

### See Also

[xform\\_wrap](#)

**Examples**

```

# First wrap the data
iris_box <- xform_wrap(iris)
## Not run:
# Convert the continuous variable "Sepal.Length" to a discrete
# variable "dsl". The intervals to be used for this transformation is
# given in a file, "intervals.csv", whose content is, for example,:
#
# 5],val1
# (5:6],22
# (6,val2
#
# This will be used to create a discrete variable named "dsl" of dataType
# "string" such that:
#   if(Sepal.length <= 5) then dsl = "val1"
#   if((Sepal.Length > 5) and (Sepal.Length <= 6)) then dsl = "22"
#   if(Sepal.Length > 6) then dsl = "val2"
#
# Give "dsl" the value 0 if the input variable value is missing.
iris_box <- xform_discretize(iris_box,
  xform_info = "[Sepal.Length -> dsl][double -> string]",
  table = "intervals.csv", map_missing_to = "0"
)

## End(Not run)

# A different transformation using a list of data frames, of size 1:
t <- list()
m <- data.frame(rbind(
  c(
    "Petal.Length", "dis_pl", "leftInterval", "leftValue",
    "rightInterval", "rightValue"
  ),
  c(
    "double", "integer", "string", "double", "string",
    "double"
  ),
  c("0", 0, "open", NA, "Open", 0),
  c(NA, 1, "closed", 0, "Open", 1),
  c(NA, 2, "closed", 1, "Open", 2),
  c(NA, 3, "closed", 2, "Open", 3),
  c(NA, 4, "closed", 3, "Open", 4),
  c("[4", 5, "closed", 4, "Open", NA)
))

# Give column names to make it look nice; not necessary!
colnames(m) <- c(
  "Petal.Length", "dis_pl", "leftInterval", "leftValue",
  "rightInterval", "rightValue"
)

# A textual representation of the data frame is:

```



```

# Petal.Length dis_pl leftInterval leftValue rightInterval rightValue
# 1 Petal.Length dis_pl leftInterval leftValue rightInterval rightValue
# 2      double integer      string      double      string      double
# 3      0)      0      open      <NA>      Open      0
# 4      <NA>      1      closed      0      Open      1
# 5      <NA>      2      closed      1      Open      2
# 6      <NA>      3      closed      2      Open      3
# 7      <NA>      4      closed      3      Open      4
# 8      (4      5      closed      4      Open      <NA>
#
# This is a transformation that defines a derived field 'dis_pl'
# which has the integer value '0' if the original field
# 'Petal.Length' has a value less than 0. The derived field has a
# value '1' if the input is greater than or equal to 0 and less
# than 1. Note that the values of the 1st column after row 2 have
# been deliberately given NA values in the middle. This is to
# show that that column is meant for a textual representation of
# the transformation as defined for the method involving external
# files; however in this method their values are not used.

# Add the data frame to a list. The default values and the missing
# values should be given as a vector, each element of the vector
# corresponding to the element at the same index in the list. If
# these values are not given as a vector, they will be used for the
# first list element only.
t[[1]] <- m
def <- c(11)
mis <- c(22)
iris_box <- xform_discretize(iris_box,
  xform_info = t, default_value = def,
  map_missing_to = mis
)

# Make a simple model to see the effect.
fit <- lm(Petal.Width ~ ., iris_box$data[, -5])
pmml(fit, transforms = iris_box)

```

---

xform\_function

*Add a function transformation to a xform\_wrap object.*


---

## Description

Add a function transformation to a xform\_wrap object.

## Usage

```
xform_function(wrap_object, orig_field_name, new_field_name = "newField",
  new_field_data_type = "numeric", expression, map_missing_to = NA)
```

**Arguments**

wrap_object	Output of xform_wrap or another transformation function
orig_field_name	String specifying name(s) of the original data field(s) being used in the transformation
new_field_name	Name of the new field created by the transformation
new_field_data_type	Data type of the new field created by the transformation
expression	String expression specifying the transformation
map_missing_to	Value to be given to the transformed variable if the value of any input variable is missing

**Details**

Calculate the expression provided in expression for every row in the wrap\_object\$data data frame. The expression argument must represent a valid R expression, and any functions used in expression must be defined in the current environment.

The name of the new field is optional (a default name is provided), but an error will be thrown if attempting to create a field with a name that already exists in the xform\_wrap object.

**Value**

R object containing the raw data, the transformed data and data statistics. The data data frame will contain a new new\_field\_name column, and field\_data will contain a new new\_field\_name row.

**See Also**

[xform\\_wrap](#)

**Examples**

```
# Load the standard iris dataset:
data(iris)

# Wrap the data:
iris_box <- xform_wrap(iris)

# Perform a transform on the Sepal.Length field:
# the value is squared and then divided by 100
iris_box <- xform_function(iris_box,
  orig_field_name = "Sepal.Length",
  new_field_name = "Sepal.Length.Transformed",
  expression = "(Sepal.Length^2)/100"
)

# Combine two fields to create another new feature:
iris_box <- xform_function(iris_box,
  orig_field_name = "Sepal.Width, Petal.Width",
```

```

    new_field_name = "Width.Sum",
    expression = "Sepal.Width + Sepal.Length"
  )

# Create linear model using the derived features:
fit <- lm(Petal.Length ~
Sepal.Length.Transformed + Width.Sum, data = iris_box$data)

# Create pmml from the fit:
fit_pmml <- pmml(fit, transform = iris_box)

```

---

xform_map	<i>Implement a map between discrete values in accordance with the PMML element <b>MapValues</b>.</i>
-----------	--

---

### Description

Implement a map between discrete values in accordance with the PMML element **MapValues**.

### Usage

```
xform_map(wrap_object, xform_info, table = NA, default_value = NA,
map_missing_to = NA, ...)
```

### Arguments

wrap_object	Output of xform_wrap or another transformation function.
xform_info	Specification of details of the transformation. It can be a text giving the external file name or a list of data frames. Even if only 1 variable is to be transformed, the information for that map should be given as a list with 1 element.
table	Name of external CSV file containing the map from input to output values.
default_value	The default value to be given to the transformed variable. If 'xform_info' is a list, this is a vector with each element corresponding to the corresponding list element.
map_missing_to	Value to be given to the transformed variable if the value of the input variable is missing. If 'xform_info' is a list, this is a vector with each element corresponding to the corresponding list element.
...	Further arguments passed to or from other methods.

### Details

Map discrete values of an input variable to a discrete value of the transformed variable. The map can be given in an external table file referred to in the transform command or as a list of data frames, each data frame defining a map transform for one variable.

Given a map from the combination of variables **InVar1**, **InVar2**, ... to the transformed variable **OutVar**, where the variables have the data types **InType1**, **InType2**, ... and **OutType**, the map command is in the format:

```
xform_info = "[InVar1,InVar2,... -> OutVar][InType1,InType2,... -> OutType]"
table = "TableFileName", default_value = "defVal", map_missing_to = "missingVal"
```

where **TableFileName** is the name of the CSV file containing the map. The map can be a N to 1 map where N is greater or equal to 1. The data types of the variables can be any of the ones defined in the PMML format including integer, double or string. **defVal** is the default value of the transformed variable and if any of the map input values are missing, **missingVal** is the value of the transformed variable.

The arguments InType, OutType, default\_value and map\_missing\_to are optional. The CSV file containing the table should not have any row and column identifiers, and the values given must be in the same order as in the map command. If the data types of the variables are not given, the data types of the input variables are attempted to be determined from the **boxData** argument. If that is not possible, the data type is assumed to be string.

It is also possible to give the maps to be implemented without an external file using a list of data frames. Each data frame defines a map for 1 input variable. Given a data frame with N+1 columns, it is assumed that the map is a N to 1 map where the last column of the data frame corresponds to the derived field. The 1st row is assumed to be the names of the fields and the second row the data types of the fields. The rest of the rows define the map; each combination of the input values in a row is mapped to the value in the last column of that row. The second row with the data types of the fields is not required. If not given, all fields are assumed to be strings. In this input format, the 'default\_value' and 'map\_missing\_to' parameters should be vectors. The first element of each vector will correspond to the derived field defined in the 1st element of the 'xform\_info' list etc. These are made clearer in the example below.

## Value

R object containing the raw data, the transformed data and data statistics.

## Author(s)

Tridivesh Jena

## See Also

[xform\\_wrap](#), [pmml](#)

## Examples

```
# Load the standard audit dataset, part of the pmml package:
data(audit)

# First wrap the data:
audit_box <- xform_wrap(audit)
## Not run:
# One of the variables, "Sex", has 2 possible values: "Male"
# and "Female". If these string values have to be mapped to a
# numeric value, a file has to be created, say "MapGender.csv"
# whose content is, for example:
#
# Male,1
```

```

# Female,2
#
# Transform the variable "Gender" to a variable "d_gender"
# such that:
#   if Sex = "Male" then d_sex = "1"
#   if Sex = "Female" then d_sex = "0"
#
# Give "d_sex" the value 0 if the input variable value is
# missing.
audit_box <- xform_map(audit_box,
  xform_info = "[Sex -> d_sex][string->integer]",
  table = "MapGender.csv", map_missing_to = "0"
)

## End(Not run)
# Same as above, with an extra variable, but using data frames.
# The top 2 rows gives the variable names and their data types.
# The rest represent the map. So for example, the third row
# indicates that when the input variable "Sex" has the value
# "Male" and the input variable "Employment" has
# the value "PSLocal", the output variable "d_sex" should have
# the value 1.
t <- list()
m <- data.frame(
  c("Sex", "string", "Male", "Female"),
  c("Employment", "string", "PSLocal", "PSState"),
  c("d_sex", "integer", 1, 0)
)
t[[1]] <- m

# Give default value as a vector and missing value as a string,
# this is only possible as there is only one map defined. If
# default values is not given, it will simply not be given in
# the PMML file as well. In general, the default values and the
# missing values should be given as a vector, each element of
# the vector corresponding to the element at the same index in
# the list. If these values are not given as a vector, they will
# be used for the first list element only.
audit_box <- xform_map(audit_box,
  xform_info = t, default_value = c(3),
  map_missing_to = "2"
)

# check what the pmml looks like
fit <- lm(Adjusted ~ ., data = audit_box$data)
pmml(fit, transforms = audit_box)

```

**Description**

Normalize continuous values in accordance with the PMML element **NormContinuous**.

**Usage**

```
xform_min_max(wrap_object, xform_info = NA, map_missing_to = NA, ...)
```

**Arguments**

wrap_object	Output of xform_wrap or another transformation function.
xform_info	Specification of details of the transformation.
map_missing_to	Value to be given to the transformed variable if the value of the input variable is missing.
...	Further arguments passed to or from other methods.

**Details**

Given input data in a xform\_wrap format, normalize the given data values to lie between provided limits.

Given an input variable named **InputVar**, the name of the transformed variable **OutputVar**, the desired minimum value the transformed variable may have **low\_limit**, the desired maximum value the transformed variable may have **high\_limit**, and the desired value of the transformed variable if the input variable value is missing **missingVal**, the **xform\_min\_max** command including all the optional parameters is in the format:

```
formInfo = "InputVar -> OutputVar[low_limit,high_limit]"
map_missing_to = "missingVal"
```

There are two methods in which the variables can be referred to. The first method is to use its column number; given the **data** attribute of the **boxData** object, this would be the order at which the variable appears. This can be indicated in the format "column#". The second method is to refer to the variable by its name.

The name of the transformed variable is optional; if the name is not provided, the transformed variable is given the name: "derived\_" + *original\_variable\_name*

Similarly, the low and high limit values are optional; they have the default values of 0 and 1 respectively. **missingValue** is an optional parameter as well. It is the value of the derived variable if the input value is missing.

If no input variable names are provided, by default all numeric variables are transformed. Note that in this case a replacement value for missing input values cannot be specified; the same applies to the **low\_limit** and **high\_limit** parameters.

**Value**

R object containing the raw data, the transformed data and data statistics.

**Author(s)**

Tridivesh Jena

**See Also**[xform\\_wrap](#)**Examples**

```
# Load the standard iris dataset:
data(iris)

# First wrap the data:
iris_box <- xform_wrap(iris)

# Normalize all numeric variables of the loaded iris dataset to lie
# between 0 and 1. These would normalize "Sepal.Length", "Sepal.Width",
# "Petal.Length", "Petal.Width" to the 4 new derived variables named
# derived_Sepal.Length, derived_Sepal.Width, derived_Petal.Length,
# derived_Petal.Width.
xform_min_max(iris_box)

# Normalize the 1st column values of the dataset (Sepal.Length) to lie
# between 0 and 1 and give the derived variable the name "dsl"
xform_min_max(iris_box, xform_info = "column1 -> dsl")

# Repeat the above operation; adding the new transformed variable to
# the iris_box object
iris_box <- xform_min_max(iris_box, xform_info = "column1 -> dsl")

# Transform Sepal.Width(the 2nd column)
# The new transformed variable will be given the default name
# "derived_Sepal.Width"
xform_min_max(iris_box, xform_info = "column2")

# Repeat the same operation as above, this time using the variable name
xform_min_max(iris_box, xform_info = "Sepal.Width")

# Repeat the same operation as above, assign the transformed variable,
# "derived_Sepal.Width". the value of 0.5 if the input value of the
# "Sepal.Width" variable is missing
xform_min_max(iris_box, xform_info = "Sepal.Width", "map_missing_to=0.5")

# Transform Sepal.Width(the 2nd column) to lie between 2 and 3.
# The new transformed variable will be given the default name
# "derived_Sepal.Width"
xform_min_max(iris_box, xform_info = "column2->[2,3]")

# Repeat the above transformation, this time the transformed variable
# lies between 0 and 10
iris_box <- xform_min_max(iris_box, xform_info = "column2->[,10]")
```

---

xform_norm_discrete	<i>Normalize discrete values in accordance with the PMML element <b>NormDiscrete</b>.</i>
---------------------	---

---

### Description

Normalize discrete values in accordance with the PMML element **NormDiscrete**.

### Usage

```
xform_norm_discrete(wrap_object, xform_info = NA, inputVar = NA,
  map_missing_to = NA, ...)
```

### Arguments

wrap_object	Output of xform_wrap or another transformation function.
xform_info	Specification of details of the transformation: the name of the input variable to be transformed.
inputVar	The input variable name in the data on which the transformation is to be applied
map_missing_to	Value to be given to the transformed variable if the value of the input variable is missing.
...	Further arguments passed to or from other methods.

### Details

Define a new derived variable for each possible value of a categorical variable. Given a categorical variable **catVar** with possible discrete values **A** and **B**, this will create 2 derived variables **catVar\_A** and **catVar\_B**. If, for example, the input value of **catVar** is **A** then **catVar\_A** equals 1 and **catVar\_B** equals 0.

Given an input variable, **InputVar** and **missingVal**, the desired value of the transformed variable if the input variable value is missing, the xform\_norm\_discrete command including all optional parameters is in the format:

```
xform_info="inputVar=input_variable, map_missing_to=missingVal"
```

There are two methods in which the input variable can be referred to. The first method is to use its column number; given the **data** attribute of the **boxData** object, this would be the order at which the variable appears. This can be indicated in the format "column#". The second method is to refer to the variable by its name.

The **xform\_info** and **inputVar** parameters provide the same information. While either one may be used when using this function, at least one of them is required. If both parameters are given, the **inputVar** parameter is used as the default.

The output of this transformation is a set of transformed variables, one for each possible value of the input variable. For example, given possible values of the input variable **val1**, **val2**, ... these transformed variables are by default named **InputVar\_val1**, **InputVar\_val2**, ...



**Value**

R object containing the raw data, the transformed data and data statistics.

**Author(s)**

Tridivesh Jena

**See Also**

[xform\\_wrap](#)

**Examples**

```
# Load the standard iris dataset, already available in R
data(iris)

# First wrap the data
iris_box <- xform_wrap(iris)

# Discretize the "Species" variable. This will find all possible
# values of the "Species" variable and define new variables. The
# parameter name used here should be replaced by the new preferred
# parameter name as shown in the next example below.
#
# "Species_setosa" such that it is 1 if
#   "Species" equals "setosa", else 0;
# "Species_versicolor" such that it is 1 if
#   "Species" equals "versicolor", else 0;
# "Species_virginica" such that it is 1 if
#   "Species" equals "virginica", else 0

iris_box <- xform_norm_discrete(iris_box, inputVar = "Species")

# Exact same operation performed with a different parameter name.
# Use of this new parameter is the preferred method as the previous
# parameter will be deprecated soon.

iris_box <- xform_wrap(iris)
iris_box <- xform_norm_discrete(iris_box, xform_info = "Species")
```

---

xform\_wrap

*Wrap data in a data transformations object.*

---

**Description**

Wrap data in a data transformations object.

**Usage**

```
xform_wrap(data, use_matrix = FALSE)
```

## Arguments

<code>data</code>	The raw data set.
<code>use_matrix</code>	Boolean value indicating whether data should be stored in matrix format as well.

## Details

Wrap raw data read in an R object. This object can then be passed to various transform functions, and the data in it transformed.

The object consists of the data itself and various properties for each data variable. Since the data is not always required to be in matrix format as well as a data frame, the 'use\_matrix' value lets the user decide if the data should be stored in both formats, giving the user a choice in reducing the speed of the transformation operations and the memory required. If there is not enough information about the data, they are given default values; the data is assumed to be the original data of data type string. The variable names are assumed to be **X1**, **X2**, ... This information is then used by the transformation functions to calculate the derived variable values.

## Value

An R object containing information on the data to be transformed.

## Author(s)

Tridivesh Jena

## See Also

[pmml](#)

## Examples

```
# Load the standard iris dataset
data(iris)

# Make a object for the iris dataset to use with
# transformation functions
iris_box <- xform_wrap(iris)

# Output only the transformations in PMML format.
# This example will output just an empty "LocalTransformations"
# element as no transformations were performed.
pmml(NULL, transforms = iris_box)

# The following will also work
pmml(, transforms = iris_box)
```

---

xform_z_score	<i>Perform a z-score normalization on continuous values in accordance with the PMML element <b>NormContinuous</b>.</i>
---------------	--

---

### Description

Perform a z-score normalization on continuous values in accordance with the PMML element **NormContinuous**.

### Usage

```
xform_z_score(wrap_object, xform_info = NA, map_missing_to = NA, ...)
```

### Arguments

wrap_object	Output of xform_wrap or another transformation function.
xform_info	Specification of details of the transformation.
map_missing_to	Value to be given to the transformed variable if the value of the input variable is missing.
...	Further arguments passed to or from other methods.

### Details

Perform a z-score normalization on data given in xform\_wrap format.

Given an input variable named **InputVar**, the name of the transformed variable **OutputVar**, and the desired value of the transformed variable if the input variable value is missing **missingVal**, the xform\_z\_score command including all the optional parameters is:

```
xform_info="InputVar -> OutputVar", map_missing_to="missingVal"
```

Two methods can be used to refer to the variables. The first method is to use its column number; given the **data** attribute of the **boxData** object, this would be the order at which the variable appears. This can be indicated in the format "column#". The second method is to refer to the variable by its name.

The name of the transformed variable is optional; if the name is not provided, the transformed variable is given the name: "derived\_" + *original\_variable\_name*

**missingValue**, an optional parameter, is the value to be given to the output variable if the input variable value is missing. If no input variable names are provided, by default all numeric variables are transformed. Note that in this case a replacement value for missing input values cannot be specified.

### Value

R object containing the raw data, the transformed data and data statistics.

### Author(s)

Tridivesh Jena

**See Also**[xform\\_wrap](#)**Examples**

```
# Load the standard iris dataset, already built into R
data(iris)

# First wrap the data
iris_box <- xform_wrap(iris)

# Perform a z-transform on all numeric variables of the loaded
# iris dataset. These would be Sepal.Length, Sepal.Width,
# Petal.Length, and Petal.Width. The 4 new derived variables
# will be named derived_Sepal.Length, derived_Sepal.Width,
# derived_Petal.Length, and derived_Petal.Width
xform_z_score(iris_box)

# Perform a z-transform on the 1st column of the dataset (Sepal.Length)
# and give the derived variable the name "dsl"
xform_z_score(iris_box, xform_info = "column1 -> dsl")

# Repeat the above operation; adding the new transformed variable
# to the iris_box object
iris_box <- xform_z_score(iris_box, xform_info = "column1 -> dsl")

# Transform Sepal.Width(the 2nd column)
# The new transformed variable will be given the default name
# "derived_Sepal.Width"
xform_z_score(iris_box, xform_info = "column2")

# Repeat the same operation as above, this time using the variable
# name
xform_z_score(iris_box, xform_info = "Sepal.Width")

# Repeat the same operation as above, assign the transformed variable
# "derived_Sepal.Width". The value of 1.0 if the input value of the
# "Sepal.Width" variable is missing. Add the new information to the
# iris_box object.
iris_box <- xform_z_score(iris_box,
  xform_info = "Sepal.Width",
  "map_missing_to=1.0"
)
```

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