

Package ‘pm4py’

January 7, 2020

Type Package

Title Interface to the 'PM4py' Process Mining Library

Version 1.2.7

Description Interface to 'PM4py' <<http://pm4py.org>>, a process mining library in 'Python'. This package uses the 'reticulate' package to act as a bridge between 'PM4Py' and the 'R' package 'bupaR'. It provides several process discovery algorithms, evaluation measures, and alignments.

License GPL-3

Encoding UTF-8

LazyData true

SystemRequirements Python (>= 3.6)

Imports reticulate (>= 1.11), bupaR, petrinetR, purrr, stringr

RoxygenNote 7.0.2

Suggests testthat, eventdataR

URL <https://github.com/fmannhardt/pm4py>

BugReports <https://github.com/fmannhardt/pm4py/issues>

NeedsCompilation no

Author Felix Mannhardt [aut, cre]

Maintainer Felix Mannhardt <felix.mannhardt@sintef.no>

Repository CRAN

Date/Publication 2020-01-07 18:40:02 UTC

R topics documented:

as_pm4py_marking	2
conformance	3
discovery	4
evaluation	6
install_pm4py	7

parameters	8
petrinet_check_relaxed_soundness	9
petrinet_check_wfnet	10
petrinet_synchronous_product	10
pm4py	12
pm4py_available	12
pm4py_version	13
version	13
write_pnml	14

Index	15
--------------	-----------

as_pm4py_marking	<i>Convert to a PM4Py marking</i>
------------------	-----------------------------------

Description

Converts a character vector of place identifiers to a PM4Py marking object.

Usage

```
as_pm4py_marking(x, petrinet)
```

Arguments

x	A character vector with (possible duplicate) place identifiers.
petrinet	A PM4Py Petri net.

Examples

```
if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4PY is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  net <- discovery_inductive(patients_completes)
  as_pm4py_marking(c("sink"), r_to_py(net$petrinet))
}
```

Description

Conformance between an Event Log and a Petri net

Usage

```
conformance_alignment(
  eventlog,
  petrinet,
  initial_marking,
  final_marking,
  parameters = default_parameters(eventlog),
  variant = variant_state_equation_a_star(),
  convert = TRUE
)

variant_state_equation_a_star()

variant_dijkstra_no_heuristics()
```

Arguments

eventlog	A bupaR or PM4PY event log.
petrinet	A bupaR or PM4PY Petri net.
initial_marking	A R vector with the place identifiers of the initial marking or a PM4PY marking. By default the initial marking of the bupaR Petri net will be used if available.
final_marking	A R vector with the place identifiers of the final marking or a PM4PY marking.
parameters	PM4PY conformance parameter. By default the <code>activity_key</code> from the bupaR event log is specified using param_activity_key .
variant	The conformance variant to be used.
convert	TRUE to automatically convert Python objects to their R equivalent. If you pass FALSE you can do manual conversion using the r-py-conversion function.

Value

A data frame describing the conformance result. In case of `conformance_alignment` a data frame of log and model moves.

Examples

```

if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4Py is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  # Discover a Petri net
  net <- discovery_inductive(patients_completes)

  # Align event log and Petri net
  a <- conformance_alignment(patients_completes,
                             net$petrinet,
                             net$initial_marking,
                             net$final_marking)

  # Alignment is returned as data frame
  head(a)
}

```

discovery

Petri net discovery algorithms

Description

PM4PY discovery algorithms that discover a Petri net and its initial and final marking. Currently the Inductive Miner and the Alpha Miner are implemented.

Usage

```

discovery_inductive(
  eventlog,
  parameters = default_parameters(eventlog),
  variant = variant_inductive_imdfb(),
  convert = TRUE
)

variant_inductive_imdfb()

variant_inductive_only_dfg()

discovery_alpha(
  eventlog,
  parameters = default_parameters(eventlog),
  variant = variant_alpha_classic(),
  convert = TRUE
)

```

```
)
variant_alpha_classic()
variant_alpha_plus()
```

Arguments

eventlog	A bupaR event log or an R data frame.
parameters	A named list of PM4PY parameters (see parameters) as required by the discovery method. By default, if the eventlog is a bupaR event log, the activity_key, timestamp_key, and caseid_key are automatically determined.
variant	The variant of the discovery algorithm to be used. For Inductive Miner currently only variant_inductive_imdfb is supported.
convert	TRUE to automatically convert Python objects to their R equivalent. If you pass FALSE you can do manual conversion using the r-py-conversion function.

Value

A named list with elements petrinet, initial_marking, and final_marking or the original Python object.

Examples

```
if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4PY is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  net <- discovery_inductive(patients_completes)

  # Show details of the obtained bupaR Petri net
  print(net$petrinet)

  # initial marking is a character vector
  print(net$initial_marking)

  # final marking is a character vector
  print(net$final_marking)

  # Petri net can be used with other bupaR functions
  petrinetR::render_PN(net$petrinet)

  # Keep an unconverted PM4PY Petri net for use in other PM4PY functions
  py_net <- discovery_inductive(patients_completes, convert = FALSE)
}
```

evaluation

Calculates evaluation measures for a Petri nets and an Event Log

Description

Calculates evaluation measures for a Petri nets and an Event Log

Usage

```
evaluation_all(  
    eventlog,  
    petrinet,  
    initial_marking,  
    final_marking,  
    parameters = default_parameters(eventlog),  
    convert = TRUE  
)  
  
evaluation_precision(  
    eventlog,  
    petrinet,  
    initial_marking,  
    final_marking,  
    parameters = default_parameters(eventlog),  
    variant = variant_precision_etconformance(),  
    convert = TRUE  
)  
  
variant_precision_etconformance()  
  
evaluation_fitness(  
    eventlog,  
    petrinet,  
    initial_marking,  
    final_marking,  
    parameters = default_parameters(eventlog),  
    variant = variant_fitness_token_based(),  
    convert = TRUE  
)  
  
variant_fitness_token_based()  
  
variant_fitness_alignment_based()
```

Arguments

eventlog A bupaR or PM4PY event log.

petrinet	A bupaR or PM4PY Petri net.
initial_marking	A R vector with the place identifiers of the initial marking or a PM4PY marking. By default the initial marking of the bupaR Petri net will be used if available.
final_marking	A R vector with the place identifiers of the final marking or a PM4PY marking.
parameters	PM4PY alignment parameter. By default the activity_key from the bupaR event log is specified using param_activity_key .
convert	TRUE to automatically convert Python objects to their R equivalent. If you pass FALSE you can do manual conversion using the r-py-conversion function.
variant	The evaluation variant to be used.

Value

A list with all available evaluation measures.

Examples

```
if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4PY is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  # Discover a Petri net
  net <- discovery_inductive(patients_completes)

  # Calculate evaluation measures for event log and Petri net
  evaluation_all(patients_completes,
                 net$petrinet,
                 net$initial_marking,
                 net$final_marking)
}
```

install_pm4py

Install PM4PY library

Description

Installs the pm4py package and its dependencies using pip since no Conda package is available. Further information on the parameters can be found in the reticulate package documentation: <https://rstudio.github.io/reticulate/> In some cases (multiple Python versions installed) it might be useful to specify the exact path to the conda binary.

Usage

```
install_pm4py(method = "auto", conda = "auto", ...)
```

Arguments

method	Installation method. By default, "auto" automatically finds a method that will work in the local environment. Change the default to force a specific installation method. Note that the "virtualenv" method is not available on Windows.
conda	Path to conda executable (or "auto" to find conda using the PATH and other conventional install locations).
...	Additional arguments passed to py_install().

Details

Additional requirements (a C++ compiler and GraphViz) of PM4PY might need to be installed to leverage all functionality; <http://pm4py.pads.rwth-aachen.de/installation/>

Examples

```
pm4py::install_pm4py()

# Specify path to conda
pm4py::install_pm4py(method = "conda", conda = "/home/user/miniconda3/bin/conda")
```

parameters

PM4Py parameter keys

Description

Convenience methods to use as PM4Py parameter keys.

Usage

```
param_activity_key(value)

param_attribute_key(value)

param_timestamp_key(value)

param_caseid_key(value)

param_resource_key(value)

default_parameters(eventlog)
```

Arguments

value	The value to add to the list.
eventlog	A bupaR or PM4PY event log.

Value

a list with the parameter key/value pair

Examples

```
param_activity_key("activity")

library(eventdataR)
data(patients)
default_parameters(patients)
```

```
petrinet_check_relaxed_soundness
      Check Relaxed soundness property
```

Description

Checks if the Petri net is relaxed sound

Usage

```
petrinet_check_relaxed_soundness(pn, im = NULL, fm = NULL, convert = TRUE)
```

Arguments

pn	Petri net
im	Initial marking of the Petri net (optional for workflow nets)
fm	Final marking of the Petri net (optional for workflow nets)
convert	TRUE to automatically convert Python objects to their R equivalent. If you pass FALSE you can do manual conversion using the r-py-conversion function.

Value

A single logical

Examples

```
if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4PY is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  net <- discovery_inductive(patients_completes)
  petrinet_check_relaxed_soundness(net$petrinet)
}
```

petrinet_check_wfnet *Check Workflow net property*

Description

Checks if the Petri net is a Workflow net

Usage

```
petrinet_check_wfnet(pn, convert = TRUE)
```

Arguments

pn	Petri net
convert	TRUE to automatically convert Python objects to their R equivalent. If you pass FALSE you can do manual conversion using the r-py-conversion function.

Value

A single logical

Examples

```
if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4PY is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  net <- discovery_inductive(patients_completes)
  petrinet_check_wfnet(net$petrinet)
}
```

petrinet_synchronous_product
Synchronous product Petri net

Description

Constructs the synchronous product net of two given Petri nets.

Usage

```
petrinet_synchronous_product(
  pn1,
  im1,
  fm1,
  pn2,
  im2,
  fm2,
  skip = ">>",
  convert = TRUE
)
```

Arguments

pn1	First Petri net
im1	Initial marking of the first Petri net
fm1	Final marking of the first Petri net
pn2	Second Petri net
im2	Initial marking of the second Petri net
fm2	Final marking of the second Petri net
skip	Symbol to be used as skip
convert	TRUE to automatically convert Python objects to their R equivalent. If you pass FALSE you can do manual conversion using the r-py-conversion function.

Value

A Petri net.

Examples

```
if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4PY is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  net <- discovery_inductive(patients_completes)
  petrinet_synchronous_product(net$petrinet,
                              net$initial_marking,
                              net$final_marking,
                              net$petrinet,
                              net$initial_marking,
                              net$final_marking)
}
```

 pm4py

PM4PY for R

Description

This package provides access to the Python Process Mining library PM4PY in R and provides conversion between bupaR and PM4PY data structures.

Usage

```
pm4py
```

Format

An object of class `python.builtin.module` (inherits from `python.builtin.object`) of length 2.

Details

To use this package, you need to have a Python environment (Conda or virtualenv) installed and install the PM4PY package and its dependencies. You can use the convenience function [install_pm4py](#) to let `reticulate` take care of install the right version. See the documentation of this function for further information.

When loaded, the object `pm4py` provides the low-level interface to the main PM4PY module. Use `$` to access sub modules of PM4PY as described in the `reticulate` documentation:

```
vignette("calling_python", package = "reticulate")
```

For parts of PM4PY wrapper functions are provided to transparently convert parameters and results to and from the corresponding bupaR S3 classes.

Examples

```
# Print the PM4PY version loaded
if (pm4py_available()) {
  print(pm4py$`__version__`)
}
```

 pm4py_available

Is the PM4Py module available

Description

Is the PM4Py module available

Usage

```
pm4py_available()
```

Value

TRUE is PM4Py is installed

Examples

```
if (pm4py_available()) {
  print(pm4py_version())
}
```

pm4py_version	<i>Returns PM4Py version used</i>
---------------	-----------------------------------

Description

Returns PM4Py version used

Usage

```
pm4py_version()
```

Value

package_version S3 class

Examples

```
if (pm4py_available()) {
  print(pm4py_version())
}
```

version	<i>This function is deprecated, please use pm4py_version.</i>
---------	---

Description

This function is deprecated, please use [pm4py_version](#).

Usage

```
version()
```

Value

package_version S3 class

write_pnml	<i>Write Petri net as PNML</i>
------------	--------------------------------

Description

Write Petri net as PNML

Usage

```
write_pnml(petrinet, file, initial_marking = NULL, final_marking = NULL)
```

Arguments

petrinet	A bupaR or PM4PY Petri net.
file	File name of the PNML file
initial_marking	A R vector with the place identifiers of the initial marking or a PM4PY marking. By default the initial marking of the bupaR Petri net will be used if available.
final_marking	A R vector with the place identifiers of the final marking or a PM4PY marking.

Examples

```
# don't test automatically since this writes a file

if (pm4py_available()) {
  library(eventdataR)
  data(patients)

  # As Inductive Miner of PM4PY is not life-cycle aware, keep only `complete` events:
  patients_completes <- patients[patients$registration_type == "complete", ]

  net <- discovery_inductive(patients_completes)
  write_pnml(net$petrinet,
             "test.pnml",
             net$initial_marking,
             net$final_marking)
}
```

Index

*Topic **datasets**

- pm4py, [12](#)
- as_pm4py_marking, [2](#)
- conformance, [3](#)
- conformance_alignment (conformance), [3](#)
- default_parameters (parameters), [8](#)
- discovery, [4](#)
- discovery_alpha (discovery), [4](#)
- discovery_inductive (discovery), [4](#)
- evaluation, [6](#)
- evaluation_all (evaluation), [6](#)
- evaluation_fitness (evaluation), [6](#)
- evaluation_precision (evaluation), [6](#)
- install_pm4py, [7](#), [12](#)
- param_activity_key, [3](#), [7](#)
- param_activity_key (parameters), [8](#)
- param_attribute_key (parameters), [8](#)
- param_caseid_key (parameters), [8](#)
- param_resource_key (parameters), [8](#)
- param_timestamp_key (parameters), [8](#)
- parameters, [5](#), [8](#)
- petrinet_check_relaxed_soundness, [9](#)
- petrinet_check_wfnet, [10](#)
- petrinet_synchronous_product, [10](#)
- pm4py, [12](#)
- pm4py_available, [12](#)
- pm4py_version, [13](#), [13](#)
- r-py-conversion, [3](#), [5](#), [7](#), [9–11](#)
- variant_alpha_classic (discovery), [4](#)
- variant_alpha_plus (discovery), [4](#)
- variant_dijkstra_no_heuristics (conformance), [3](#)
- variant_fitness_alignment_based (evaluation), [6](#)
- variant_fitness_token_based (evaluation), [6](#)
- variant_inductive_imdfb (discovery), [4](#)
- variant_inductive_only_dfg (discovery), [4](#)
- variant_precision_etconformance (evaluation), [6](#)
- variant_state_equation_a_star (conformance), [3](#)
- version, [13](#)
- write_pnml, [14](#)