

Package: Rpadrino (via r-universe)

August 28, 2024

Title Interact with the 'PADRINO' IPM Database

Version 0.0.5

Description 'PADRINO' houses textual representations of Integral Projection Models which can be converted from their table format into full kernels to reproduce or extend an already published analysis. 'Rpadrino' is an R interface to this database. For more information on Integral Projection Models, see Easterling et al. (2000) [doi:10.1890/0012-9658\(2000\)081\[0694:SSSAAN\]2.0.CO;2](https://doi.org/10.1890/0012-9658(2000)081[0694:SSSAAN]2.0.CO;2), Merow et al. (2013) [doi:10.1111/2041-210X.12146](https://doi.org/10.1111/2041-210X.12146), Rees et al. (2014) [doi:10.1111/1365-2656.12178](https://doi.org/10.1111/1365-2656.12178), and Metcalf et al. (2015) [doi:10.1111/2041-210X.12405](https://doi.org/10.1111/2041-210X.12405). See Levin et al. (2021) for more information on 'ipmr', the engine that powers model reconstruction [doi:10.1111/2041-210X.13683](https://doi.org/10.1111/2041-210X.13683).

Depends R (>= 3.4.0), ipmr (>= 0.0.5)

Imports curl, ggplot2, magrittr, mvtnorm, purrr, rlang (>= 0.3.0), rmarkdown, tools, truncdist, utils

SystemRequirements libcurl: libcurl-devel (rpm) or libcurl4-openssl-dev (deb).

License GPL-3

Encoding UTF-8

LazyData true

BugReports <https://github.com/padrinoDB/Rpadrino/issues>

URL <https://github.com/padrinoDB/Rpadrino>,
<https://padrinoDB.github.io/Rpadrino/>

RoxygenNote 7.2.2

Suggests covr, knitr, maps, roxygen2, testthat

VignetteBuilder knitr

Config/testthat/parallel true

Config/testthat/edition 3

Repository <https://padrinodb.r-universe.dev>

RemoteUrl <https://github.com/padrinodb/rpadrino>

RemoteRef HEAD

RemoteSha 2a9a784d89ba4046ce1eff873fcfcad5d6958a7e

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pdb	<i>Selected models from the Padrino Database</i>
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Description

Selected models from the Padrino Database

Usage

pdb

Format

A list of data frames, each corresponding to a different table in the Padrino Database.

pdb_citations	<i>Access pieces of metadata from a pdb object</i>
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Description

These functions access pieces of specific pieces metadata from the Metadata table of a pdb object. The exception is `pdb_report`, which automatically generates a report with summary statistics and citation information for the pdb object.

Usage

pdb_citations(pdb, ipm_id = NULL)
pdb_species_accepted(pdb, ipm_id = NULL)
pdb_species_author(pdb, ipm_id = NULL)
pdb_genus(pdb, ipm_id = NULL)
pdb_family(pdb, ipm_id = NULL)
pdb_order(pdb, ipm_id = NULL)
pdb_class(pdb, ipm_id = NULL)
pdb_phylum(pdb, ipm_id = NULL)
pdb_kingdom(pdb, ipm_id = NULL)
pdb_org_type(pdb, ipm_id = NULL)
pdb_dicot_monocot(pdb, ipm_id = NULL)
pdb_angio_gymon(pdb, ipm_id = NULL)
pdb_authors(pdb, ipm_id = NULL)
pdb_journal(pdb, ipm_id = NULL)
pdb_pub_year(pdb, ipm_id = NULL)
pdb_doi(pdb, ipm_id = NULL)
pdb_comments(pdb, ipm_id = NULL)
pdb_appendix_link(pdb, ipm_id = NULL)
pdb_duration(pdb, ipm_id = NULL)
pdb_start_year(pdb, ipm_id = NULL)
pdb_start_month(pdb, ipm_id = NULL)
pdb_end_year(pdb, ipm_id = NULL)
pdb_end_month(pdb, ipm_id = NULL)
pdb_periodicity(pdb, ipm_id = NULL)

```
pdb_population_name(pdb, ipm_id = NULL)
pdb_number_populations(pdb, ipm_id = NULL)
pdb_lat(pdb, ipm_id = NULL)
pdb_lon(pdb, ipm_id = NULL)
pdb_altitude(pdb, ipm_id = NULL)
pdb_country(pdb, ipm_id = NULL)
pdb_continent(pdb, ipm_id = NULL)
pdb_ecoregion(pdb, ipm_id = NULL)
pdb_studied_sex(pdb, ipm_id = NULL)
pdb_eviction_used(pdb, ipm_id = NULL)
pdb_evict_type(pdb, ipm_id = NULL)
pdb_treatment(pdb, ipm_id = NULL)
pdb_has_time_lag(pdb, ipm_id = NULL)
pdb_has_age(pdb, ipm_id = NULL)

pdb_report(
  pdb,
  title = "",
  keep_rmd = TRUE,
  rmd_dest = getwd(),
  output_format = "html",
  render_output = TRUE,
  map = TRUE,
  translate_eqs = FALSE,
  block_eqs = FALSE,
  long_eq_length = 65
)
```

Arguments

<code>pdb</code>	A Padrino Database object.
<code>ipm_id</code>	The ID of the model. The default (NULL) returns all values in the <code>pdb</code> object.
<code>title</code>	The title for the created report.
<code>keep_rmd</code>	Keep the un-rendered Rmd file? Useful for manual editing.

rmd_dest	The folder to save the Rmd file at if keep_rmd = TRUE. The default is getwd().
output_format	The output format to create. Options are "html", "pdf", "word", "odt", "rtf", or "md".
render_output	A logical - should the document be rendered for inspection?
map	Create a map of studies included in the pdb object?
translate_eqs	A logical - should the mathematical equations of the IPM(s) also be included in the report? These are translated from R to Latex by make_ipm_report_body . Currently, this is only available for IPMs that do not have parameter set indexed terms.
block_eqs	If report_eqs = TRUE, should equations be reported in block format or as inline equations? This main difference for "pdf" formats is that equation numbering is done with tag{ }. For non-"pdf" formats, the difference is that equations are centered. Numbering may yield strange results for non-"pdf" formats.
long_eq_length	For longer equations, make_ipm_report tries to wrap these into multiple lines using \\. This parameter controls the number of characters per line. Default is 65. Ignored when block_eqs = FALSE.

Value

A named vector of the metadata. The names correspond to ipm_idss. For pdb_report, the file path to the rendered output, or to the .rmd file when render_output = FALSE.

pdb_download *Download PADRINO pdb objects*

Description

Download PADRINO from Github.

Usage

```
pdb_download(save = TRUE, destination = NULL)
```

```
pdb_save(pdb, destination = NULL)
```

```
pdb_load(path)
```

Arguments

save	Write the PDB object to a folder of text files?
destination	Where to write the pdb object to.
pdb	A pdb object.
path	The directory where the PADRINO tables are stored

Details

This does not currently support versioning because there is only one version. destination should be a folder name. When save = TRUE, a set of 12 text files will be saved in the destination folder. The files are tab-delimited. If you are not connected to the internet, pdb_download will load the internal pdb data object and return that instead.

Value

pdb_download and pdb_load return pdb objects. pdb_save returns a pdb object invisibly.

pdb_make_ipm	<i>Generate IPMs from Padrino objects</i>
--------------	---

Description

This function generates complete IPMs from objects created with pdb_make_proto_ipm.

Usage

```
pdb_make_ipm(proto_ipm_list, addl_args = list())
```

Arguments

proto_ipm_list Output from pdb_make_proto_ipm.
 addl_args A named list of additional arguments to pass to [make_ipm](#).

Details

The format of addl_args should be a nested list. The names of the outermost level should correspond to the ipm_id that the arguments apply to. Each entry of the outermost level should itself then be a named list where the names correspond to arguments to [make_ipm](#), and the values are the values for each argument. See examples.

Value

A list of IPMs.

Examples

```
## Not run:

data("pdb_ex")

proto <- pdb_make_proto_ipm(pdb_ex, ipm_id = "aaa341", det_stoch = "det")

ipm   <- pdb_make_ipm(proto)

proto <- pdb_make_proto_ipm(pdb_ex,
```

```

        ipm_id      = "aaaa55",
        det_stoch   = "stoch",
        kern_param  = "kern")

args <-list(

# The names in the outermost list should be ipm_id's

aaaa55 = list(

# The names in the inner list should be arguments to make_ipm()

report_progress = TRUE,
iterate         = TRUE,
iterations      = 100,
kernel_seq      = sample(2004:2014, 100, replace = TRUE)
)
)

ipm <- pdb_make_ipm(proto, addl_args = args)

## End(Not run)

```

`pdb_make_proto_ipm` *Generate proto_ipms from Padrino objects*

Description

This function generates `proto_ipm` objects from Padrino Database tables.

Usage

```

pdb_make_proto_ipm(pdb, ipm_id = NULL, det_stoch = "det", kern_param = "kern")

```

Arguments

<code>pdb</code>	A <code>pdb</code> object.
<code>ipm_id</code>	Optionally, one or more <code>ipm_id</code> 's to build. If empty, all models contained in the <code>pdb</code> object will be processed into <code>proto_ipm</code> 's.
<code>det_stoch</code>	A vector containing either "det" or "stoch". This determines whether we want to construct a deterministic or stochastic model. Default is "det". See details
<code>kern_param</code>	If <code>det_stoch = "stoch"</code> , then whether or not to construct a kernel resampled model, or a parameter resampled model. See details.

Details

proto_ipm objects contain all of the information needed to implement an IPM, but stop short of actually generating kernels. These are intermediate building blocks that can be modified before creating a full IPM so that things like perturbation analysis are a bit more straightforward.

When requesting many models, the det_stoch and kern_param parameters can also be vectors. These are matched with ipm_id by position. If the lengths of det_stoch and kern_param do not match the length ipm_id, they will be recycled until they do.

For stochastic models, there is sometimes the option of building either a kernel-resampled or a parameter resampled model. A kernel resampled model uses some point estimate for time and/or space varying parameters to generate kernels for each year/site/grouping factor. Parameter resampled models sample parameters from distributions. Padrino stores this information for some models when it is available in the literature, and tries to fail informatively when these distributions aren't available in the database.

Value

A list containing one or more proto_ipms. Names of the list will correspond to ipm_ids.

See Also

For more info on kern_param definitions:

Metcalf *et al.* (2015). Statistical modeling of annual variation for inference on stochastic population dynamics using Integral Projection Models. *Methods in Ecology and Evolution*. DOI: 10.1111/2041-210X.12405

pdb_subset

Subset a Padrino database object

Description

Subset a Padrino database object

Usage

```
pdb_subset(pdb, ipm_ids)
```

Arguments

pdb	A Padrino database object.
ipm_ids	The ipm_id's to subset the database to.

Details

Currently, the only variable to subset with is the ipm_id. Eventually, subsetting based on other variables will be possible with syntax similar to subset. At the moment, users will need to create a vector of ipm_ids based on searching and then pass that to subset. See Examples

Value

A new Padrino database object containing only the models specified in ipm_ids.

Examples

```
## Not run:

data(pdb)

poa_ind <- pdb$Metadata$ipm_id[pdb$Metadata$tax_family == "Poaceae"]

poa_db <- pdb_subset(pdb, ipm_ids = poa_ind)

## End(Not run)
```

print.pdb

Print a pdb object.

Description

Print a pdb object.

Usage

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

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

Arguments

x	A pdb object.
...	Only used by pdb_new_fun_form, otherwise ignored. See details and examples for usage in pdb_new_fun_form.

Value

x invisibly.

```
vital_rate_exprs.pdb_proto_ipm_list
```

Padrino methods for 'ipmr' generic functions

Description

Provides wrappers around ipmr generic functions to extract some quantities of interest from pdb_proto_ipm_lists and pdb_ipms.

Usage

```
## S3 method for class 'pdb_proto_ipm_list'
vital_rate_exprs(object)

## S3 method for class 'pdb_ipm'
vital_rate_exprs(object)

## S3 method for class 'pdb_proto_ipm_list'
kernel_formulae(object)

## S3 method for class 'pdb_ipm'
kernel_formulae(object)

## S3 method for class 'pdb_proto_ipm_list'
domains(object)

## S3 method for class 'pdb_ipm'
domains(object)

## S3 method for class 'pdb_proto_ipm_list'
parameters(object)

## S3 method for class 'pdb_ipm'
parameters(object)

## S3 method for class 'pdb_proto_ipm_list'
pop_state(object)

## S3 method for class 'pdb_ipm'
pop_state(object)

## S3 method for class 'pdb_ipm'
vital_rate_funs(ipm)

## S3 method for class 'pdb_ipm'
int_mesh(ipm, full_mesh = TRUE)
```

```

## S3 method for class 'pdb_ipm'
lambda(ipm, ...)

## S3 method for class 'pdb_ipm'
right_ev(ipm, iterations = 100, tolerance = 1e-10, ...)

## S3 method for class 'pdb_ipm'
left_ev(ipm, iterations = 100, tolerance = 1e-10, ...)

## S3 method for class 'pdb_ipm'
is_conv_to_asymptotic(ipm, tolerance = 1e-10, burn_in = 0.1)

## S3 method for class 'pdb_ipm'
conv_plot(ipm, iterations = NULL, log = FALSE, show_stable = TRUE, ...)

## S3 method for class 'pdb_ipm'
make_iter_kernel(ipm, ..., name_ps = NULL, f_forms = NULL)

## S3 method for class 'pdb_ipm'
mean_kernel(ipm)

pdb_new_fun_form(...)

## S3 replacement method for class 'pdb_proto_ipm_list'
parameters(object, ...) <- value

## S3 replacement method for class 'pdb_proto_ipm_list'
vital_rate_exprs(object, kernel = NULL, vital_rate = NULL) <- value

## S3 replacement method for class 'pdb_proto_ipm_list'
kernel_formulae(object, kernel) <- value

## S3 method for class 'pdb_ipm'
x[i]

```

Arguments

object	An object produced by <code>pdb_make_proto_ipm</code> or <code>pdb_make_ipm</code> .
ipm	A <code>pdb_ipm</code> .
full_mesh	Logical. Return the complete set of meshpoints or only the unique ones.
...	Usage depends on the function - see Details and Examples.
iterations	The number of times to iterate the model to reach convergence. Default is 100.
tolerance	Tolerance to evaluate convergence to asymptotic dynamics.
burn_in	The proportion of iterations to discard as burn in when assessing convergence.
log	Log-transform lambdas for plotting?
show_stable	Show horizontal line denoting stable population growth?

<code>name_ps</code>	For <code>pdb_ipm</code> objects that contain <code>age_x_size</code> IPMs, a named list. The names of the list should be the <code>ipm_ids</code> that are <code>age_x_size</code> models, and the values in the list should be the the name of the survival/growth kernels.
<code>f_forms</code>	For <code>pdb_ipm</code> objects that contain <code>age_x_size</code> IPMs, a named list. The names of the list should be the <code>ipm_ids</code> that are <code>age_x_size</code> models, and the values in the list should be the the name of the fecundity kernels. If multiple sub-kernels contribute to fecundity, we can also supply a string specifying how they are combined (e.g. <code>f_forms = "F + C"</code>).
<code>value</code>	The value to insert. See details and Examples.
<code>kernel</code>	Ignored, present for compatibility with <code>ipmr</code> .
<code>vital_rate</code>	Ignored, present for compatibility with <code>ipmr</code> .
<code>x</code>	A <code>pdb_ipm</code> object.
<code>i</code>	The index to extract

Details

There are number of uses for `...` which depend on the function used for them. These are described below.

Value

Most of these return named lists where names correspond to `ipm_ids`. The exception is `pdb_new_fun_form`, which returns a list of expressions. It is only intended for setting new expressions with `vital_rate_exprs<-`.

`pdb_new_fun_form`

This must be used when setting new expressions for vital rates and kernel formulae. The `...` argument should be a named list of named lists. The top most layer should be `ipm_id`'s. The next layer should be a list where the names are vital rates you wish to modify, and the values are the expressions you want to insert. See examples.

`make_iter_kernel`

The `...` here should be expressions representing the block kernel of the IPMs in question. The names of each expression should be the `ipm_id`, and the expressions should take the form of `c(<upper_left>, <upper_right>, <lower_left>, <lower_right>)` (i.e. a vector of symbols would create a matrix in row-major order). See examples.

`conv_plot/lambda`

The `...` are used pass additional arguments to `lambda` and `conv_plot`.

Examples

```
data(pdb)
my_pdb <- pdb_make_proto_ipm(pdb, c("aaaa17", "aaa310"))

# These values will be appended to the parameter list for each IPM, as they
```

```

# aren't currently present in them.

parameters(my_pdb) <- list(
  aaa310 = list(
    g_slope_2 = 0.0001,
    establishment_prob = 0.02
  ),
  aaaa17 = list(
    g_var = 4.2,
    germ_prob = 0.3
  )
)

# We can overwrite a parameter value with a new one as well. Old values aren't
# saved anywhere except in the pdb object, so be careful!

parameters(my_pdb) <- list(
  aaa310 = list(
    s_s = 0.93, # old value is 0.92
    gvar_i = 0.13 # old value is 0.127
  )
)

vital_rate_exprs(my_pdb) <- pdb_new_fun_form(
  list(
    aaa310 = list(mu_g = g_int + g_slope * size_1 + g_slope_2 * size_1^2),
    aaaa17 = list(sigmax2 = sqrt(g_var * exp(cf_v1 + cf_v2 * size_1))
  )
)

kernel_formulae(my_pdb) <- pdb_new_fun_form(
  list(
    aaaa17 = list(Y = recr_size * yearling_s * germ_prob * d_size),
    aaa310 = list(F = f_n * f_d * establishment_prob)
  )
)

my_ipms <- pdb_make_ipm(my_pdb)
iter_kerns <- make_iter_kernel(my_ipms, aaaa17 = c(0, F_yr, Y, P_yr))

```

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