

Matt Secret <secrestm@gene.com>

CRAN Submission psborrow2 0.0.3.2**Matt Secret** <secrestm@gene.com>

Fri, Mar 22, 2024 at 5:01 PM

To: Uwe Ligges <ligges@statistik.tu-dortmund.de>

Cc: CRAN <cran-submissions@r-project.org>

Thanks, Uwe!

Can you advise on the cmdstanr bit? In DESCRIPTION we have the repo in Additional_repositories. We also have a message on .onAttach() and include instructions in many of the vignettes. Maybe more info in README.md and the first vignette?

Best,

Matt

--

Matt Secret, MS

Senior Data Scientist

Real-World Data Science, PDD

Genentech, a member of the Roche Group

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On Fri, Mar 22, 2024 at 3:54 PM Uwe Ligges <ligges@statistik.tu-dortmund.de> wrote:

And in addition:

Please declare where to get cmdstanr from.

Best,

Uwe Ligges

On 22.03.2024 23:53, Uwe Ligges wrote:

>

>

> On 22.03.2024 20:40, CRAN Package Submission Form wrote:

>>

>> [This was generated from [CRAN.R-project.org/submit.html](https://cran.r-project.org/submit.html)]

>>

>> The following package was uploaded to CRAN:

>> =====

>>

>> Package Information:

>> Package: psborrow2

>> Version: 0.0.3.2

>> Title: Bayesian Dynamic Borrowing Analysis and Simulation

>> Author(s): Matt Secret [aut, cre]

>> (<<https://orcid.org/0000-0002-0939-4902>>), Isaac Gravestock

>> [aut], Craig Gower-Page [ctb], Genentech, Inc. [cph, fnd]

>> Maintainer: Matt Secret <secrestm@gene.com>

>> Depends: R (>= 4.1.0)

>> Suggests: cmdstanr, survival, flexsurv, testthat (>= 3.0), usethis (>=

>> 2.1.5), vdiffr, tibble, xml2, knitr, rmarkdown, bayesplot,

>> matrixcalc, WeightIt, MatchIt, BayesPPD, ggsvrfit, gbm,

>> ggplot2, cobalt, table1, gt, gtsummary

>> Description: Bayesian dynamic borrowing is an approach to incorporating

>> external data to supplement a randomized, controlled trial

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>> analysis in which external data are incorporated in a dynamic
>> way (e.g., based on similarity of outcomes); see Viele 2013
>> \doi{10.1002/pst.1589} for an overview. This package
>
> Pls write the dois as follows:
> ... see Viele (2013) <doi:10.1002/pst.1589> for ...
>
>
> Please fix and resubmit.
>
> Best,
> Uwe Ligges
>
>> implements the hierarchical commensurate prior approach to
>> dynamic borrowing as described in Hobbes 2011
>> \doi{10.1111/j.1541-0420.2011.01564.x}. There are three main
>> functionalities. First, 'psborrow2' provides a user-friendly
>> interface for applying dynamic borrowing on the study results
>> handles the Markov Chain Monte Carlo sampling on behalf of
>> the user. Second, 'psborrow2' provides a simulation
>> framework to compare different borrowing parameters (e.g.
>> full borrowing, no borrowing, dynamic borrowing) and other
>> trial and borrowing characteristics (e.g. sample size,
>> covariates) in a unified way. Third, 'psborrow2' provides a
>> set of functions to generate data for simulation studies, and
>> also allows the user to specify their own data generation
>> process.
>> License: Apache License 2.0
>> Imports: checkmate, glue, methods, graphics, posterior, generics,
>> Matrix, mvtnorm, future, simsurv
>>
>>
>> The maintainer confirms that he or she
>> has read and agrees to the CRAN policies.
>>
>> Submitter's comment: Updated to fix some NOTES on first submission around
>> formatting.
>>
>> =====
>>
>> Original content of DESCRIPTION file:
>>
>> Type: Package
>> Package: psborrow2
>> Title: Bayesian Dynamic Borrowing Analysis and Simulation
>> Version: 0.0.3.2
>> Authors@R: c(
>>   person(
>>     given = "Matt",
>>     family = "Secret",
>>     role = c("aut", "cre"),
>>     comment = c(ORCID = "0000-0002-0939-4902"),
>>     email = "secrestm@gene.com"
>>   ),
>>   person(
>>     given = "Isaac",
>>     family = "Gravestock",
>>     role = c("aut"),
>>     email = "isaac.gravestock@roche.com"
>>   ),
>>   person(
>>     given = "Craig",
>>     family = "Gower-Page",
>>     role = c("ctb"),

```

```

>> email = "craig.gower-page@roche.com"
>> ),
>> person("Genentech, Inc.", role = c("cph", "fnd"))
>> )
>> Description: Bayesian dynamic borrowing is an approach to
>> incorporating external
>> data to supplement a randomized, controlled trial analysis in which
>> external data are incorporated in a dynamic way (e.g., based on
>> similarity
>> of outcomes); see Viele 2013 \doi{10.1002/pst.1589} for an overview.
>> This package implements the hierarchical commensurate prior
>> approach to dynamic borrowing
>> as described in Hobbes 2011 \doi{10.1111/j.1541-0420.2011.01564.x}.
>> There are three main functionalities. First, 'psborrow2' provides
>> a user-friendly
>> interface for applying dynamic borrowing on the study results
>> handles the Markov Chain
>> Monte Carlo sampling on behalf of the user. Second, 'psborrow2'
>> provides a
>> simulation framework to compare different borrowing parameters
>> (e.g. full borrowing, no
>> borrowing, dynamic borrowing) and other trial and borrowing
>> characteristics
>> (e.g. sample size, covariates) in a unified way. Third,
>> 'psborrow2' provides
>> a set of functions to generate data for simulation studies, and
>> also allows
>> the user to specify their own data generation process.
>> URL: https://github.com/Genentech/psborrow2,
>> https://genentech.github.io/psborrow2/index.html
>> BugReports: https://github.com/Genentech/psborrow2/issues
>> License: Apache License 2.0
>> Encoding: UTF-8
>> Depends: R (>= 4.1.0)
>> Roxygen: list(markdown = TRUE)
>> RoxygenNote: 7.3.1
>> Config/testthat/edition: 3
>> Imports: checkmate, glue, methods, graphics, posterior, generics,
>> Matrix, mvtnorm, future, simsurv
>> Suggests: cmdstanr, survival, flexsurv, testthat (>= 3.0), usethis (>=
>> 2.1.5), vdiffr, tibble, xml2, knitr, rmarkdown, bayesplot,
>> matrixcalc, WeightIt, MatchIt, BayesPPD, ggsvrfit, gbm,
>> ggplot2, cobalt, table1, gt, gtsummary
>> Additional_repositories: https://mc-stan.org/r-packages/
>> Language: en-US
>> SystemRequirements: cmdstan
>> Collate: 'generics.R' 'prior_class.R' 'covariate_class.R'
>> 'add_covariates.R' 'prior_normal.R' 'treatment_class.R'
>> 'borrowing_class.R' 'outcome_class.R' 'analysis_class.R'
>> 'borrowing_details.R' 'borrowing_full.R'
>> 'borrowing_hierarchical_commensurate.R' 'borrowing_none.R'
>> 'check_data_matrix_has_columns.R' 'cmdstan.R'
>> 'create_analysis_obj.R' 'create_data_matrix.R'
>> 'treatment_details.R' 'sim_treatment_list.R' 'helpers.R'
>> 'outcome_bin_logistic.R' 'prior_exponential.R'
>> 'outcome_surv_weibull_ph.R' 'outcome_surv_exponential.R'
>> 'sim_outcome_list.R' 'sim_borrowing_list.R'
>> 'sim_covariate_list.R' 'sim_data_list.R' 'simulation_class.R'
>> 'create_simulation_obj.R' 'data.R'
>> 'make_analysis_object_list.R' 'make_model_string_data.R'
>> 'make_model_string_functions.R' 'make_model_string_model.R'
>> 'make_model_string_parameters.R'
>> 'make_model_string_transf_params.R' 'mcmc_sample.R'
>> 'mcmc_simulation_result.R' 'prior_half_cauchy.R'
>> 'outcome_cont_normal.R' 'package.R'

```

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>> 'prepare_stan_data_inputs.R' 'prior_bernoulli.R' 'prior_beta.R'
>> 'prior_cauchy.R' 'prior_gamma.R' 'prior_half_normal.R'
>> 'prior_poisson.R' 'sim_covariates.R' 'sim_estimate_bias.R'
>> 'sim_estimate_effect_variance.R' 'sim_estimate_mse.R'
>> 'sim_is_null_effect_covered.R' 'sim_is_true_effect_covered.R'
>> 'sim_samplesize.R' 'simulate_data_baseline.R' 'simulate_data.R'
>> 'simvar_class.R' 'trim_data_matrix.R' 'uniform_prior.R' 'zzz.R'
>> LazyData: true
>> VignetteBuilder: knitr
>> NeedsCompilation: no
>> Packaged: 2024-03-22 19:11:48 UTC; secrestm
>> Author: Matt Secret [aut, cre]
>> (<https://orcid.org/0000-0002-0939-4902>),
>> Isaac Gravestock [aut],
>> Craig Gower-Page [ctb],
>> Genentech, Inc. [cph, fnd]
>> Maintainer: Matt Secret <secrestm@gene.com>
>>
```