

Package ‘Immprobe’

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Type Package

Title Sparse high-dimensional linear mixed modeling with a partitioned empirical Bayes ECM algorithm (LMM-PROBE).

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Author Anja Zgodic, Alex McLain

Maintainer Anja Zgodic <azgodic@email.sc.edu>

Description Linear Mixed Modeling using the PROBE algorithm. This package is in development.

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Encoding UTF-8

RoxygenNote 7.2.0

Depends R (>= 3.5.0), Rcpp (>= 1.0.8.3), snow (>= 0.4.4), snowfall (>= 1.84.6.1), tidyr (>= 1.2.0), lme4 (>= 1.1.29)

LinkingTo Rcpp, RcppArmadillo

NeedsCompilation yes

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Description

Linear Mixed Modeling using the PROBE algorithm. This package is in development.

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Maintainer

Anja Zgodic <azgodic@email.sc.edu>

Author(s)

Anja Zgodic, Alex McLain

Immprobe	<i>Sparse high-dimensional linear mixed modeling with PaRtitiOned empirical Bayes ECM (LMM-PROBE) algorithm.</i>
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Description

Sparse high-dimensional linear mixed modeling with PaRtitiOned empirical Bayes ECM (LMM-PROBE) algorithm. Currently, the package offers functionality for two scenarios. Scenario 1: only a random intercept; Scenario 2: a random intercept and a random slope. We are actively expanding the package for more flexibility and scenarios.

Arguments

Y	A matrix containing the outcome Y.
Z	A matrix containing the sparse fixed-effect predictors on which to apply the Immprobe algorithm.
V	A matrix containing non-sparse predictors for the random effects. This matrix is currently only programmed for two scenarios. Scenario 1: only a random intercept, where V is a matrix with one column containing ID's. Scenario 2: a random intercept and a random slope, where V is a matrix with two columns. The first column is ID and the second column is a continuous variable (e.g. time) for which a random slope is to be estimated.
alpha	Type I error; significance level.
ep	Value against which to compare convergence criterion, we recommend 0.05.
B	The number of groups to categorize estimated coefficients in to calculate correlation ρ . We recommend five.
adj	A factor multiplying Silverman's 'rule of thumb' in determining the bandwidth for density estimation, same as the 'adjust' argument of R's density function. Default is three.

<code>maxit</code>	Maximum number of iterations the algorithm will run for. Default is 10000.
<code>cpus</code>	The number of CPUS user would like to use for parallel computations. Default is four.
<code>LR</code>	A learning rate parameter r . Using zero corresponds to the implementation described in Zgodic et al.
<code>C</code>	A learning rate parameter c . Using one corresponds to the implementation described in Zgodic et al.

Value

A list of the output of the `lmmprobe` function, including

- `beta_hat`, `beta_hat_var` MAP estimates of the posterior expectation (`beta_hat`) and variance (`beta_hat_var`) of the prior mean (β) of the regression coefficients assuming $\gamma = 1$,
- `gamma` the posterior expectation of the latent γ variables,
- `preds` predictions of Y ,
- `PI_lower`, `PI_upper` lower and upper prediction intervals for the predictions,
- `sigma2_est` MAP estimate of the residual variance,
- `random_var` MAP estimate of the random effect(s) variance,
- `random_intercept` estimated random intercept terms,
- `random_slope` estimated random slope terms, if applicable.

References

Zgodic, A. and McLain, A. C. (2023). Sparse high-dimensional linear mixed modeling with a partitioned empirical Bayes ECM algorithm. arXiv preprint arXiv:XXXX.XXXXX.

Examples

```
library(lmmprobe)
data(SLE)
ep <- 0.05
alpha <- 0.05
Y = SLE$Y
Z = SLE$Z
V = SLE$V
full_res <- lmmprobe(Y = Y, Z = Z, V = V, ep = ep, alpha = alpha)
```

SLE

High-dimensional dataset for sparse linear mixed modeling.

Description

This is the Systemic Lupus Erythematosus (SLE) data used in the data analysis section of the LMM-PROBE reference. The dataset has 309 observations, 103 subjects, and 15387 predictors.

Usage

```
data(SLE)
```

Format

A data frame with 309 observations and the following list elements:

- Y First element of list, corresponding to the outcome to use in the `lmmprobe` function.
- Z Second element of list, corresponding to the high-dimesional matrix of sparse predictors for fixed effects.
- V Third element of list, corresponding to the low-dimesional matrix of non-sparse predictors for random effects. This matrix has either only one ID column, or one ID column with an additional column for a continuous variable for which a random slope is to be estimated.

References

Banchereau, R., Hong, S., Cantarel, B., Baldwin, N., Baisch, J., Edens, M., Cepika, A.-M., Acs, P., Turner, J., Anguiano, E., Vinod, P., Khan, S., Obermoser, G., Blankenship, D., Wakeland, E., Nassi, L., Gotte, A., Punaro, M., Liu, Y.-J., Banchereau, J., Rossello-Urgell, J., Wright, T., and Pascual, V. (2016), “Personalized Immunomonitoring Uncovers Molecular Networks that Stratify Lupus Patients,” *Cell*, 165, 551–565.

Zgodic, A. and McLain, A. C. (2023). Sparse high-dimensional linear mixed modeling with a partitioned empirical Bayes ECM algorithm. arXiv preprint [arXiv:XXXX.XXXXX](https://arxiv.org/abs/XXXX.XXXXX).

Examples

```
data(SLE)
Y = SLE$Y
Z = SLE$Z
V = SLE$V
```

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