

Package ‘parglms’

September 23, 2026

Title support for parallelized estimation of GLMs/GEEs

Version 1.44.0

Author VJ Carey <stvjc@channing.harvard.edu>

Description This package provides support for parallelized estimation of GLMs/GEEs, catering for dispersed data.

Suggests RUnit, sandwich, MASS, knitr, GenomeInfoDb, GenomicRanges, gwascat, BiocStyle, rmarkdown

VignetteBuilder knitr

Depends methods

Imports BiocGenerics, BatchJobs, foreach, doParallel

Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

LazyLoad yes

BiocViews statistics, genetics

ByteCompile TRUE

git_url <https://git.bioconductor.org/packages/parglms>

git_branch RELEASE_3_23

git_last_commit f59813e

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-09-22

Contents

parglms-package	2
parGLM-methods	2
Index	4

parGLMs-package

support for parallelized estimation of GLMs/GEEs

Description

This package provides support for parallelized estimation of GLMs/GEEs, catering for dispersed data.

Details

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

In version 0.0.0 we established an approach to fitting GLM from data that have been persistently dispersed and managed by a [Registry](#).

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Maintainer: VJ Carey <stvjc@channing.harvard.edu>

References

This package shares an objective with the bigglm methods of biglm. In bigglm, a small-RAM-footprint algorithm is employed, with sequential chunking to update statistics in each iteration. In parGLM the footprint is likewise controllable, but statistics in each iteration are evaluated in parallel over chunks.

Examples

```
showMethods("parGLM")
```

parGLM-methods

fit GLM-like models with parallelized contributions to sufficient statistics

Description

This package addresses the problem of fitting GLM-like models in a scalable way, recognizing that data may be dispersed, with chunks processed in parallel, to create low-dimensional summaries from which model fits may be constructed.

Methods

`signature(formula = "formula", store = "Registry")` The model data are assumed to lie in the `file.dir/jobs/*` folders, with `file.dir` defined in the store, which is an instance of [Registry](#).

Additional arguments must be supplied:

family a function that serves as a family for `stats::glm`

binit a vector of initial values for regression parameter estimation, must conform to expectations of formula

maxit an integer giving the maximum number of iterations allowed

tol a numeric giving the tolerance criterion

Failure to specify these triggers a fatal error.

The Registry instance can be modified to include a list element 'extractor'. This must be a function with arguments `store`, and `codei`. The standard extraction function is

```
function(store, i) loadResult(store, i)
```

It must return a data frame, conformant with the expectations of formula. Limited checking is performed.

The predict method computes the linear predictor on data identified by `jobid` in a BatchJobs registry. Results are returned as output of `foreach` over the jobids specified in the predict call.

Note that setting option `parGLM.showiter` to TRUE will provide a message tracing progress of the optimization.

Examples

```
if (require(MASS) & require(BatchJobs)) {
  # here is the 'sharding' of a small dataset
  data(anorexia) # N = 72
  # in .BatchJobs.R:
  # best setting for sharding a small dataset on a small machine:
  # cluster.functions = BatchJobs::makeClusterFunctionsInteractive()
  myr = makeRegistry("abc", file.dir=tempfile())
  chs = chunk(1:nrow(anorexia), n.chunks=18) # 4 recs/chunk
  f = function(x) {library(MASS); data(anorexia); anorexia[x,]}
  batchMap(myr, f, chs)
  submitJobs(myr) # now getResult(myr,1) gives back a data.frame
  waitForJobs(myr) # simple dispersal
  # now myr is populated
  oldopt = options()$parGLM.showiter
  options(parGLM.showiter=TRUE)
  pp = parGLM( Postwt ~ Treat + Prewt, myr,
    family=gaussian, binit = c(0,0,0,0), maxit=10, tol=.001 )
  print(summary(theLM <- lm(Postwt~Treat+Prewt, data=anorexia)))
  print(pp$coefficients - coef(theLM))
  if (require(sandwich)) {
    hc0 <- vcovHC(theLM, type="HC0")
    print(pp$robust.variance - hc0)
  }
}
predict(pp, store=myr, jobids=2:3)
options(parGLM.showiter=oldopt)
```

Index

- * **methods**

- parGLM-methods, [2](#)

- * **modeling**

- parGLM-methods, [2](#)

- * **package**

- parGLMs-package, [2](#)

parGLM (parGLM-methods), [2](#)

parGLM, formula, Registry-method
(parGLM-methods), [2](#)

parGLM-methods, [2](#)

parGLMs (parGLMs-package), [2](#)

parGLMs-package, [2](#)

predict (parGLM-methods), [2](#)

print (parGLM-methods), [2](#)

Registry, [2](#), [3](#)

summary (parGLM-methods), [2](#)