

# Package ‘parglms’

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**Title** support for parallelized estimation of GLMs/GEEs

**Version** 1.39.0

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**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

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**License** Artistic-2.0

**LazyLoad** yes

**BiocViews** statistics, genetics

**ByteCompile** TRUE

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**Description**

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

**Details**

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

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**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")
```

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parGLM-methods	<i>fit GLM-like models with parallelized contributions to sufficient statistics</i>
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**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)
```

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