

Package ‘gputools’

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Title A Few GPU Enabled Functions

Depends R (>= 3.1.2)

SystemRequirements Nvidia's CUDA toolkit (>= release 7.0)

Description Provides R interfaces to a handful of common functions implemented using the Nvidia CUDA toolkit. Some of the functions require at least GPU Compute Capability 1.3.
Thanks to Craig Stark at UC Irvine for donating time on his lab's Mac.

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URL <https://github.com/nullsatz/gputools/wiki>

BugReports <https://github.com/nullsatz/gputools/issues>

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chooseGpu	<i>Choose which GPU device to use</i>
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Description

Selects the GPU device to use for computation. This is only useful on a machine equipped with multiple GPU devices. The numbering starts at 0 and is assigned by the CUDA capable driver. Choosing a device can only be done before any other GPU operation and only once per thread.

Usage

chooseGpu(deviceId = 0)

Arguments

deviceId an integer >= 0 designating the GPU to use for computation.

Value

chooseGpu should print out an integer specifying the device id chosen or an error message.

cpuMatMult	<i>Perform Matrix Multiplication</i>
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Description

Performs matrix multiplication using R’s BLAS. This function is merely a wrapper for the BLAS dgemm function.

Usage

cpuMatMult(a, b)

Arguments

a	a numeric matrix.
b	a numeric matrix.

Value

A numeric matrix. The matrix is just the product of arguments 'a' and 'b'.

Examples

```
matA <- matrix(runif(2*3), 2, 3)
matB <- matrix(runif(3*4), 3, 4)
cpuMatMult(matA, matB)
```

*getGpuId**Discover the Id of the current GPU device*

Description

Queries the CUDA driver for the GPU device currently assigned to this thread. This is the id of the device that will be used for computation. If you wish to use a different device, use the `chooseGpu` function.

Usage

```
getGpuId()
```

Value

The function returns a single integer indicating the id of the GPU device currently selected to carry out computation according to the CUDA driver.

Examples

```
getGpuId()
```

Description

The correlation coefficient will be calculated for each pair x_i , y_j where x_i is a column of x and y_j is a column of y . Currently, Pearson's and Kendall's correlation coefficient are implemented. Pearson's may be calculated for data sets containing NAs in which case, the implementation behaves as R-native `cor` function with `use="pairwise.complete"`.

Usage

```
gpuCor(x, y = NULL, use = "everything", method = "pearson")
```

Arguments

<code>x</code>	a matrix of floating point values in which each column is a random variable.
<code>y</code>	a matrix of floating point values in which each column is a random variable.
<code>use</code>	a string. A character string giving a method for computing in the presence of missing values. Options are "everything" or "pairwise.complete.obs". This currently only affects the "pearson" method.
<code>method</code>	a string. Either "pearson" or "kendall".

Value

For method "pearson", a list with matrices 'pairs', 'coefficients', and 'ts'. The matrix entry i, j for pairs represents the number of pairs of entries x_i^k, y_j^k (the k -th entry from x_i and y_j respectively). These are the number of entries actually used to calculate the coefficients. Entry i, j of the coefficients matrix is the correlation coefficient for x_i, y_j . Entry i, j of the ts matrix is the t-score of the i, j entry of the coefficient matrix. If `use="pairwise.complete.obs"` then only the pairs where both entries are not NA are used in the computations.

For method "kendall", a list of matrices 'pairs' as above and 'coefficients' as follows. The matrix 'coefficients' is a matrix of floating point numbers where entry i, j is the correlation coefficient for x_i, y_j . Calculation of t-scores for the kendall coefficients is not yet implemented.

See Also

`cor`

Examples

```
numAvars <- 5
numBvars <- 10
numSamples <- 30
A <- matrix(runif(numAvars*numSamples), numSamples, numAvars)
B <- matrix(runif(numBvars*numSamples), numSamples, numBvars)
gpuCor(A, B, method="pearson")
```

```
gpuCor(A, B, method="kendall")
A[3,2] <- NA
gpuCor(A, B, use="pairwise.complete.obs", method="pearson")
```

gpuCrossprod
Perform Matrix Cross-product with a GPU

Description

Performs matrix cross-product using a GPU. This function is merely a couple of wrappers for the CUBLAS cublasSgemm function.

Usage

```
gpuCrossprod(a, b=NULL)
```

Arguments

a a matrix of floating point values.
b a matrix of floating point values. A null value defaults to 'a'.

Value

A matrix of single precision floating point values. The matrix is the cross-product of arguments 'a' and 'b', i.e., $t(a) * b$.

Examples

```
matA <- matrix(runif(3*2), 3, 2)
matB <- matrix(runif(3*4), 3, 4)
gpuCrossprod(matA, matB)
```

gpuDist
Compute Distances Between Vectors on a GPU

Description

This function computes the distance between each vector of the 'points' argument using the metric specified by 'method'.

Usage

```
gpuDist(points, method = "euclidean", p = 2.0)
```

Arguments

points	a matrix of floating point numbers in which each row is a vector in \mathbb{R}^n space where n is <code>ncol(points)</code> .
method	a string representing the name of the metric to use to calculate the distance between the vectors of 'points'. Currently supported values are: "binary", "canberra", "euclidean", "manhattan", "maximum", and "minkowski".
p	a floating point parameter for the Minkowski metric.

Value

a class of type "dist" containing floating point numbers representing the distances between vectors from the 'points' argument.

See Also

`dist`

Examples

```
numVectors <- 5
dimension <- 10
Vectors <- matrix(runif(numVectors*dimension), numVectors, dimension)
gpuDist(Vectors, "euclidean")
gpuDist(Vectors, "maximum")
gpuDist(Vectors, "manhattan")
gpuDist(Vectors, "minkowski", 4)
```

gpuDistClust

Compute Distances and Hierarchical Clustering for Vectors on a GPU

Description

This function takes a set of vectors and performs clustering on them. The function will first calculate the distance between all of the pairs of vectors and then use the distances to cluster the vectors. Both of these steps are done on the GPU.

Usage

```
gpuDistClust(points, distmethod = "euclidean", clustmethod = "complete")
```

Arguments

points	a matrix of floating point numbers in which each row is a vector in \mathbb{R}^n space where n is <code>ncol(points)</code> .
distmethod	a string representing the name of the metric to use to calculate the distance between the vectors of 'points'. Currently supported values are: "binary", "canberra", "euclidean", "manhattan", "maximum".

clustmethod a string representing the name of the clustering method to be applied to distances. Currently supported method names include "average", "centroid", "complete", "flexible", "flexible group", "mcquitty", "median", "single", "ward", and "wpgma".

Value

Copied from the native R function 'hclust' documentation. A class of type "hclust" with the following attributes.

merge an n-1 by 2 matrix. Row i of 'merge' describes the merging of clusters at step i of the clustering. If an element j in the row is negative, then observation -j was merged at this stage. If j is positive then the merge was with the cluster formed at the (earlier) stage j of the algorithm. Thus negative entries in 'merge' indicate agglomerations of singletons, and positive entries indicate agglomerations of non-singletons. Copied from the native R function 'hclust' documentation.

order a vector giving the permutation of the original observations suitable for plotting, in the sense that a cluster plot using this ordering and matrix 'merge' will not have crossings of the branches.

height a set of n-1 non-decreasing real values. The clustering height: that is, the value of the criterion associated with the clustering 'method' for the particular agglomeration.

See Also

[gpuDist](#), [gpuHclust](#).

Examples

```
numVectors <- 5
dimension <- 10
Vectors <- matrix(runif(numVectors*dimension), numVectors, dimension)
myClust <- gpuDistClust(Vectors, "maximum", "mcquitty")
plot(myClust)
```

gpuGlm

Fitting generalized linear models using GPU-enabled QR decomposition

Description

Most of this documentation is copied from R's documentation for glm. gpuGlm is used to fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution.

Note: The QR decomposition employed by gpuLm is optimized for speed and uses minimal pivoting.

Usage

```
gpuGlm(formula, family = gaussian, data, weights, subset,
na.action, start = NULL, etastart, mustart, offset, useSingle = TRUE,
control = gpuGlm.control(useSingle, ...), model = TRUE,
method = "gpuGlm.fit", x = FALSE, y = TRUE, contrasts = NULL, ...)

gpuGlm.fit(x, y, weights = rep(1, nobs), start = NULL, etastart = NULL,
mustart = NULL, offset = rep(0, nobs), family = gaussian(), useSingle,
control = gpuGlm.control(useSingle), intercept = TRUE)
```

Arguments

formula	an object of class " formula " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
family	a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. (See family for details of family functions.)
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>glm</code> is called.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of options , and is na.fail if that is unset. The 'factory-fresh' default is na.omit . Another possible value is NULL, no action. Value na.exclude can be useful.
start	starting values for the parameters in the linear predictor.
etastart	starting values for the linear predictor.
mustart	starting values for the vector of means.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset .
useSingle	whether to use single precision arithmetic on the gpu. Only the 'TRUE' option is implemented so far.
control	a list of parameters for controlling the fitting process. See the documentation for glm.control for details.
model	a logical value indicating whether <i>model frame</i> should be included as a component of the returned value.

method	the method to be used in fitting the model. The default method "gpuGlm.fit" uses iteratively reweighted least squares (IWLS). The only current alternative is "model.frame" which returns the model frame and does no fitting.
x, y	For gpuGlm: logical values indicating whether the response vector and model matrix used in the fitting process should be returned as components of the returned value. For gpuGlm.fit: x is a design matrix of dimension $n \times p$, and y is a vector of observations of length n.
contrasts	an optional list. See the contrasts.arg of model.matrix.default.
intercept	logical. Should an intercept be included in the <i>null</i> model?
...	For gpuGlm: arguments to be passed by default to glm.control : see argument control. For weights: further arguments passed to or from other methods.

Details

A typical predictor has the form `response ~ terms` where response is the (numeric) response vector and terms is a series of terms which specifies a linear predictor for response. For binomial and quasibinomial families the response can also be specified as a [factor](#) (when the first level denotes failure and all others success) or as a two-column matrix with the columns giving the numbers of successes and failures. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed.

A specification of the form `first:second` indicates the the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the *cross* of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in weights being inversely proportional to the dispersions); or equivalently, when the elements of weights are positive integers w_i , that each response y_i is the mean of w_i unit-weight observations. For a binomial GLM prior weights are used to give the number of trials when the response is the proportion of successes: they would rarely be used for a Poisson GLM.

`gpuGlm.fit` is the workhorse function: it is not normally called directly but can be more efficient where the response vector and design matrix have already been calculated.

If more than one of `etastart`, `start` and `mustart` is specified, the first in the list will be used. It is often advisable to supply starting values for a [quasi](#) family, and also for families with unusual links such as `gaussian("log")`.

All of weights, subset, offset, `etastart` and `mustart` are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula.

For the background to warning messages about 'fitted probabilities numerically 0 or 1 occurred' for binomial GLMs, see Venables & Ripley (2002, pp. 197–8).

Value

`gpuGlm` returns an object of class inheriting from "glm" which inherits from the class "lm". See later in this section.

The function `summary` (i.e., `summary.glm`) can be used to obtain or print a summary of the results and the function `anova` (i.e., `anova.glm`) to produce an analysis of variance table.

The generic accessor functions `coefficients`, `effects`, `fitted.values` and `residuals` can be used to extract various useful features of the value returned by `glm`.

`weights` extracts a vector of weights, one for each case in the fit (after subsetting and `na.action`).

An object of class "glm" is a list containing at least the following components:

<code>coefficients</code>	a named vector of coefficients
<code>residuals</code>	the <i>working</i> residuals, that is the residuals in the final iteration of the IWLS fit. Since cases with zero weights are omitted, their working residuals are NA.
<code>fitted.values</code>	the fitted mean values, obtained by transforming the linear predictors by the inverse of the link function.
<code>rank</code>	the numeric rank of the fitted linear model.
<code>family</code>	the <code>family</code> object used.
<code>linear.predictors</code>	the linear fit on link scale.
<code>deviance</code>	up to a constant, minus twice the maximized log-likelihood. Where sensible, the constant is chosen so that a saturated model has deviance zero.
<code>aic</code>	A version of Akaike's <i>An Information Criterion</i> , minus twice the maximized log-likelihood plus twice the number of parameters, computed by the <code>aic</code> component of the family. For binomial and Poisson families the dispersion is fixed at one and the number of parameters is the number of coefficients. For gaussian, Gamma and inverse gaussian families the dispersion is estimated from the residual deviance, and the number of parameters is the number of coefficients plus one. For a gaussian family the MLE of the dispersion is used so this is a valid value of AIC, but for Gamma and inverse gaussian families it is not. For families fitted by quasi-likelihood the value is NA.
<code>null.deviance</code>	The deviance for the null model, comparable with deviance. The null model will include the offset, and an intercept if there is one in the model. Note that this will be incorrect if the link function depends on the data other than through the fitted mean: specify a zero offset to force a correct calculation.
<code>iter</code>	the number of iterations of IWLS used.
<code>weights</code>	the <i>working</i> weights, that is the weights in the final iteration of the IWLS fit.
<code>prior.weights</code>	the weights initially supplied, a vector of 1s if none were.
<code>df.residual</code>	the residual degrees of freedom.
<code>df.null</code>	the residual degrees of freedom for the null model.
<code>y</code>	if requested (the default) the y vector used. (It is a vector even for a binomial model.)
<code>x</code>	if requested, the model matrix.
<code>model</code>	if requested (the default), the model frame.
<code>converged</code>	logical. Was the IWLS algorithm judged to have converged?
<code>boundary</code>	logical. Is the fitted value on the boundary of the attainable values?

call	the matched call.
formula	the formula supplied.
terms	the terms object used.
data	the data argument.
offset	the offset vector used.
control	the value of the control argument used.
method	the name of the fitter function used, currently always "gpuGlm.fit".
contrasts	(where relevant) the contrasts used.
xlevels	(where relevant) a record of the levels of the factors used in fitting.
na.action	(where relevant) information returned by model.frame on the special handling of NAs.

In addition, non-empty fits will have components `qr`, `R` and `effects` relating to the final weighted linear fit.

Objects of class "glm" are normally of class `c("glm", "lm")`, that is inherit from class "lm", and well-designed methods for class "lm" will be applied to the weighted linear model at the final iteration of IWLS. However, care is needed, as extractor functions for class "glm" such as [residuals](#) and `weights` do **not** just pick out the component of the fit with the same name.

If a [binomial](#) glm model was specified by giving a two-column response, the weights returned by `prior.weights` are the total numbers of cases (factored by the supplied case weights) and the component `y` of the result is the proportion of successes.

Author(s)

The original R implementation of glm was written by Simon Davies working for Ross Ihaka at the University of Auckland, but has since been extensively re-written by members of the R Core team.

The design was inspired by the S function of the same name described in Hastie & Pregibon (1992).

This function was adapted for Nvidia's CUDA-supporting GPGPUs by Mark Seligman at Rapid Biologics LLC. <http://www.rapidbiologics.com>

References

- Dobson, A. J. (1990) *An Introduction to Generalized Linear Models*. London: Chapman and Hall.
- Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.
- McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models*. London: Chapman and Hall.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. New York: Springer.

See Also

[anova.glm](#), [summary.glm](#), etc. for glm methods, and the generic functions [anova](#), [summary](#), [effects](#), [fitted.values](#), and [residuals](#).

[lm](#) for non-generalized *linear* models (which SAS calls GLMs, for 'general' linear models).

[loglin](#) for fitting log-linear models (which binomial and Poisson GLMs are) to contingency tables.

Examples

```
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
print(d.AD <- data.frame(treatment, outcome, counts))
glm.D93 <- gpuGlm(counts ~ outcome + treatment, family=poisson())
anova(glm.D93)
summary(glm.D93)

# A Gamma example, from McCullagh & Nelder (1989, pp. 300-2)
clotting <- data.frame(
  u = c(5,10,15,20,30,40,60,80,100),
  lot1 = c(118,58,42,35,27,25,21,19,18),
  lot2 = c(69,35,26,21,18,16,13,12,12))
summary(gpuGlm(lot1 ~ log(u), data=clotting, family=Gamma))
summary(gpuGlm(lot2 ~ log(u), data=clotting, family=Gamma))
```

gpuGranger

Perform Granger Causality Tests for Vectors on a GPU

Description

This function performs, with the aid of a GPU, Granger Causality Tests on permutations of pairs of columns of the input matrices 'x' and 'y'.

Usage

```
gpuGranger(x, y=NULL, lag)
```

Arguments

- | | |
|-----|--|
| x | a matrix of floating point values. Each column represents a sequence of observations for a single random variable. |
| y | an optional matrix of floating point values. Each column represents a sequence of observations for a single random variable. |
| lag | a positive integer by which to offset the sequence of observations to calculate the coefficient for Granger causality. |

Value

a list of two single precision floating point matrices both of the same dimension. The two matrices are fStatistics and pValues. The fStatistics matrix holds the F-statistics from the Granger causality tests. Each element of the pValues matrix is the p-value for the corresponding element of the fStatistics matrix.

If y is NULL, the test is run on permutations of pairs of columns of x. To find the Granger causality F-statistic estimating the answer to "Does variable x[,j] Granger-cause variable x[,i]?", look at fStatistics[i, j] and pValues[i, j].

If `y` is not `NULL`, the test is run on permutations of pairs (`x[,i]`, `y[,j]`). To find the Granger causality F-statistic estimating the answer to "Does variable `y[,j]` Granger-cause variable `x[,i]`?", look at `fStatistics[i,j]` and `pValues[i,j]`.

Examples

```
# permutations of pairs of cols of just x
numRandVars <- 5
numSamples <- 20
randVarSequences <- matrix(runif(numRandVars*numSamples), numSamples,
numRandVars)
gpuGranger(randVarSequences, lag = 5)

# pairs of cols, one from x and one from y
numXRandVars <- 5
numXSamples <- 20
x <- matrix(runif(numXRandVars*numXSamples), numXSamples, numXRandVars)

numYRandVars <- 3
numYSamples <- 20
y <- matrix(runif(numYRandVars*numYSamples), numYSamples, numYRandVars)

result <- gpuGranger(x, y, lag = 5)
print(result)
```

gpuHclust

Perform Hierarchical Clustering for Vectors with a GPU

Description

This function performs clustering on a set of points. The distance between each pair of points should be calculated first using a function like `'gpuDist'` or `'dist'`.

Usage

```
gpuHclust(distances, method = "complete")
```

Arguments

<code>distances</code>	a class of type "dist" containing floating point numbers representing distances between points. R's native <code>dist</code> function and the <code>gpuDist</code> function produce output of this type.
<code>method</code>	a string representing the name of the clustering method to be applied to distances. Currently supported method names include "average", "centroid", "complete", "flexible", "flexible group", "mcquitty", "median", "single", "ward", and "wpgma".

Value

Copied from the native R function 'hclust' documentation. A class of type "hclust" with the following attributes.

merge	an n-1 by 2 matrix. Row i of 'merge' describes the merging of clusters at step i of the clustering. If an element j in the row is negative, then observation -j was merged at this stage. If j is positive then the merge was with the cluster formed at the (earlier) stage j of the algorithm. Thus negative entries in 'merge' indicate agglomerations of singletons, and positive entries indicate agglomerations of non-singletons. Copied from the native R function 'hclust' documentation.
order	a vector giving the permutation of the original observations suitable for plotting, in the sense that a cluster plot using this ordering and matrix 'merge' will not have crossings of the branches.
height	a set of n-1 non-decreasing real values. The clustering height: that is, the value of the criterion associated with the clustering 'method' for the particular agglomeration.

See Also

hclust, [gpuDistClust](#)

Examples

```
numVectors <- 5
dimension <- 10
Vectors <- matrix(runif(numVectors*dimension), numVectors, dimension)
distMat <- gpuDist(Vectors, "euclidean")
myClust <- gpuHclust(distMat, "single")
plot(myClust)
```

gpuLm

Fitting Linear Models using a GPU-enabled QR

Description

Most of this documentation is copied from R's documentation for `lm`. `gpuLm` is used to fit linear models using a GPU enabled QR decomposition. It can be used to carry out regression, single stratum analysis of variance and analysis of covariance (although [aov](#) may provide a more convenient interface for these).

Note: The QR decomposition employed by `gpuLm` is optimized for speed and uses minimal pivoting. If rank-revealing pivot is desired, then the function `gpuQR`, should be used. The most reliable determination of rank, however, will be obtained with the `svd` command.

Usage

```
gpuLm(formula, data, subset, weights, na.action,
      method = "qr", model = TRUE, x = FALSE, y = FALSE, qr = TRUE,
      singular.ok = TRUE, contrasts = NULL, useSingle = TRUE, offset, ...)
```

Arguments

formula	an object of class " formula " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>lm</code> is called.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process. Should be <code>NULL</code> or a numeric vector. If non- <code>NULL</code> , weighted least squares is used with weights <code>weights</code> (that is, minimizing $\sum(w \cdot e^2)$); otherwise ordinary least squares is used. See also 'Details',
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of options , and is na.fail if that is unset. The 'factory-fresh' default is na.omit . Another possible value is <code>NULL</code> , no action. Value na.exclude can be useful.
method	the method to be used; for fitting, currently only <code>method = "qr"</code> is supported; <code>method = "model.frame"</code> returns the model frame (the same as with <code>model = TRUE</code> , see below).
model, x, y, qr	logicals. If <code>TRUE</code> the corresponding components of the fit (the model frame, the model matrix, the response, the qr decomposition) are returned.
singular.ok	logical. If <code>FALSE</code> (the default in S but not in R) a singular fit is an error.
contrasts	an optional list. See the <code>contrasts.arg</code> of model.matrix.default .
useSingle	an optional logical. In the future, setting this to <code>FALSE</code> will result in using double precision arithmetic on the gpu, but this is not yet implemented
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be <code>NULL</code> or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one are specified their sum is used. See model.offset .
...	additional arguments to be passed to the low level regression fitting functions (see below).

Details

Models for `lm` are specified symbolically. A typical model has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for response. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with duplicates removed. A specification of the form `first:second` indicates the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the *cross* of `first` and `second`. This is the same as `first + second + first:second`.

If the formula includes an `offset`, this is evaluated and subtracted from the response.

If response is a matrix a linear model is fitted separately by least-squares to each column of the matrix.

See `model.matrix` for some further details. The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula (see `aov` and `demo(glm.vr)` for an example).

A formula has an implied intercept term. To remove this use either $y \sim x - 1$ or $y \sim 0 + x$. See `formula` for more details of allowed formulae.

Non-NULL weights can be used to indicate that different observations have different variances (with the values in `weights` being inversely proportional to the variances); or equivalently, when the elements of `weights` are positive integers w_i , that each response y_i is the mean of w_i unit-weight observations (including the case that there are w_i observations equal to y_i and the data have been summarized).

`lm` calls the lower level functions `lm.fit`, etc, see below, for the actual numerical computations. For programming only, you may consider doing likewise.

All of `weights`, `subset` and `offset` are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula.

Value

`lm` returns an object of class `"lm"` or for multiple responses of class `c("mlm", "lm")`.

The functions `summary` and `anova` are used to obtain and print a summary and analysis of variance table of the results. The generic accessor functions `coefficients`, `effects`, `fitted.values` and `residuals` extract various useful features of the value returned by `lm`.

An object of class `"lm"` is a list containing at least the following components:

<code>coefficients</code>	a named vector of coefficients
<code>residuals</code>	the residuals, that is response minus fitted values.
<code>fitted.values</code>	the fitted mean values.
<code>rank</code>	the numeric rank of the fitted linear model.
<code>weights</code>	(only for weighted fits) the specified weights.
<code>df.residual</code>	the residual degrees of freedom.
<code>call</code>	the matched call.
<code>terms</code>	the <code>terms</code> object used.
<code>contrasts</code>	(only where relevant) the contrasts used.
<code>xlevels</code>	(only where relevant) a record of the levels of the factors used in fitting.
<code>offset</code>	the offset used (missing if none were used).
<code>y</code>	if requested, the response used.
<code>x</code>	if requested, the model matrix used.
<code>model</code>	if requested (the default), the model frame used.
<code>na.action</code>	(where relevant) information returned by <code>model.frame</code> on the special handling of NAs.

In addition, non-null fits will have components `assign`, `effects` and (unless not requested) `qr` relating to the linear fit, for use by extractor functions such as `summary` and `effects`.

Using time series

Considerable care is needed when using `lm` with time series.

Unless `na.action = NULL`, the time series attributes are stripped from the variables before the regression is done. (This is necessary as omitting NAs would invalidate the time series attributes, and if NAs are omitted in the middle of the series the result would no longer be a regular time series.)

Even if the time series attributes are retained, they are not used to line up series, so that the time shift of a lagged or differenced regressor would be ignored. It is good practice to prepare a data argument by `ts.intersect(..., dframe = TRUE)`, then apply a suitable `na.action` to that data frame and call `gpuLm` with `na.action = NULL` so that residuals and fitted values are time series.

Note

Offsets specified by `offset` will not be included in predictions by `predict.lm`, whereas those specified by an offset term in the formula will be.

Author(s)

The design was inspired by the `S` function of the same name described in Chambers (1992). The implementation of model formula by Ross Ihaka was based on Wilkinson & Rogers (1973).

This function was adapted for Nvidia's CUDA-supporting GPGPUs by Mark Seligman at Rapid Biologics LLC. <http://www.rapidbiologics.com>

References

Chambers, J. M. (1992) Linear models. Chapter 4 of Statistical Models in S eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Wilkinson, G. N. and Rogers, C. E. (1973) Symbolic descriptions of factorial models for analysis of variance. *Applied Statistics*, 22, 392–9.

See Also

`summary.lm` for summaries and `anova.lm` for the ANOVA table; `aov` for a different interface.

The generic functions `coef`, `effects`, `residuals`, `fitted`, `vcov`.

`predict.lm` (via `predict`) for prediction, including confidence and prediction intervals; `confint` for confidence intervals of *parameters*.

`lm.influence` for regression diagnostics, and `glm` for **generalized** linear models.

The underlying low level functions, `lm.fit` for plain, and `lm.wfit` for weighted regression fitting.

More `lm()` examples are available e.g., in `anscombe`, `attitude`, `freeny`, `LifeCycleSavings`, `longley`, `stackloss`, `swiss`.

`biglm` in package **biglm** for an alternative way to fit linear models to large datasets (especially those with many cases).

Examples

```
# require(graphics)

## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2,10,20, labels=c("Ctl","Trt"))
weight <- c(ctl, trt)
anova(lm.D9 <- gpuLm(weight ~ group))
summary(lm.D90 <- gpuLm(weight ~ group - 1))# omitting intercept
summary(resid(lm.D9) - resid(lm.D90)) #- residuals almost identical

opar <- par(mfrow = c(2,2), oma = c(0, 0, 1.1, 0))
plot(lm.D9, las = 1) # Residuals, Fitted, ...
par(opar)

## model frame :
stopifnot(identical(gpuLm(weight ~ group, method = "model.frame"),
model.frame(lm.D9)))

### less simple examples in "See Also" above
```

gpuLm.defaultTol

Function to switch tolerance depending on precision

Description

This function was written by Mark Seligman at Rapid Biologics, <http://rapidbiologics.com>

The function `gpuLm.fit` calls this function to determine a default tolerance. So `gpuLm.defaultTol` should *not* need to be used directly.

Usage

```
gpuLm.defaultTol(useSingle = TRUE)
```

Arguments

<code>useSingle</code>	logical. If TRUE, a tolerance will be returned appropriate for single precision arithmetic. If FALSE, a tolerance will be returned appropriate for double precision arithmetic.
------------------------	---

Value

a floating point number representing a tolerance to be used by `gpuLm.fit`

See Also

[gpuLm.fit](#) [gpuLm](#)

gpuLm.fit

*Fitter functions for gpu enabled linear models***Description**

The C code called by this function was written by Mark Seligman at Rapid Biologics, <http://rapidbiologics.com>

The function `gpuLm` calls this function to fit linear models. So `gpuLm.fit` should *not* need to be used directly.

Usage

```
gpuLm.fit(x, y, w = NULL, offset = NULL, method = "qr",
          useSingle, tol = gpuLm.defaultTol(useSingle), singular.ok = TRUE, ...)
```

Arguments

<code>x</code>	design matrix of dimension $n * p$.
<code>y</code>	vector of observations of length n , or a matrix with n rows.
<code>w</code>	vector of weights (length n) to be used in the fitting process for the <code>wfit</code> functions. Weighted least squares is used with weights w , i.e., $\sum(w * e^2)$ is minimized.
<code>offset</code>	numeric of length n). This can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting.
<code>method</code>	currently, only <code>method="qr"</code> is supported.
<code>useSingle</code>	logical. If TRUE, the gpu will use single precision arithmetic. In the future, if FALSE the gpu may use double precision arithmetic, but this is not implemented yet.
<code>tol</code>	tolerance for the <code>qr</code> decomposition. Default is $1e-7$.
<code>singular.ok</code>	logical. If FALSE, a singular model is an error.
<code>...</code>	currently disregarded.

Value

	a list with components
<code>coefficients</code>	p vector
<code>residuals</code>	n vector or matrix
<code>fitted.values</code>	n vector or matrix
<code>effects</code>	(not null fits) n vector of orthogonal single-df effects. The first rank of them correspond to non-aliased coefficients, and are named accordingly.
<code>weights</code>	n vector — <i>only</i> for the <code>*wfit*</code> functions.
<code>rank</code>	integer, giving the rank
<code>df.residual</code>	degrees of freedom of residuals
<code>qr</code>	(not null fits) the QR decomposition, see <code>qr</code> .

See Also

[gpuLm](#) which should usually be used for linear least squares regression

Examples

```
require(utils)
set.seed(129)
n <- 7 ; p <- 2
X <- matrix(rnorm(n * p), n,p) # no intercept!
y <- rnorm(n)
w <- rnorm(n)^2

str(lmw <- gpuLm.fit(x=X, y=y, w=w))
```

gpuLsfit

Least squares fit using GPU-enabled QR decomposition

Description

The least squares estimate of β in the model

$$Y = X\beta + \epsilon$$

is found.

Most of this documentation is copied from R's documentation for `lsfit`. The function `gpuLsfit` performs a least-squares fit using a GPU enabled QR decomposition.

Note: The QR decomposition employed by `gpuLm` is optimized for speed and uses minimal pivoting. If more precise pivoting is desired, then either the function `gpuQR` or, better still, `svd` should be used.

Usage

```
gpuLsfit(x, y,
  wt = NULL, intercept = TRUE, useSingle = TRUE,
  tolerance=gpuLm.defaultTol(useSingle),
  yname = NULL)
```

Arguments

<code>x</code>	a matrix whose rows correspond to cases and whose columns correspond to variables.
<code>y</code>	the responses, possibly a matrix if you want to fit multiple left hand sides.
<code>wt</code>	an optional vector of weights for performing weighted least squares.
<code>intercept</code>	whether or not an intercept term should be used.
<code>useSingle</code>	whether to use single precision arithmetic on the gpu. Only the 'TRUE' option is implemented so far.
<code>tolerance</code>	the tolerance to be used in the matrix decomposition. This defaults to 1e-04 for single-precision GPU computation.
<code>yname</code>	names to be used for the response variables.

Details

If weights are specified then a weighted least squares is performed with the weight given to the j th case specified by the j th entry in `wt`.

If any observation has a missing value in any field, that observation is removed before the analysis is carried out. This can be quite inefficient if there is a lot of missing data.

The implementation is via a modification of the LINPACK subroutines which allow for multiple left-hand sides.

Value

A list with the following named components:

<code>coef</code>	the least squares estimates of the coefficients in the model (β as stated above).
<code>residuals</code>	residuals from the fit.
<code>intercept</code>	indicates whether an intercept was fitted.
<code>qr</code>	the QR decomposition of the design matrix.

Author(s)

This function was adapted for Nvidia's CUDA-supporting GPGPUs by Mark Seligman at Rapid Biologics LLC. <http://www.rapidbiologics.com>

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

See Also

[lsfit](#), [lm](#), [ls.print](#), [ls.diag](#)

Examples

```
##-- Using the same data as the lm(.) example:  
lsD9 <- gpuLsfit(x = unclass(gl(2,10)), y = weight)  
ls.print(lsD9)
```

 gpuMatMult

Perform Matrix Multiplication with a GPU

Description

Performs matrix multiplication using a GPU. This function is merely a wrapper for the CUBLAS cublasDgemm function.

Usage

```
gpuMatMult(a, b)
```

Arguments

a	a numeric matrix.
b	a numeric matrix.

Value

A numeric matrix. The matrix is just the product of arguments 'a' and 'b'.

Examples

```
matA <- matrix(runif(2*3), 2, 3)
matB <- matrix(runif(3*4), 3, 4)
gpuMatMult(matA, matB)
```

 gpuMi

B spline based mutual information

Description

This function estimates the mutual information for permutations of pairs of columns of a matrix using a B spline approach on a GPU device. Please note, the data must be values from the interval [0.0, 1.0].

Usage

```
gpuMi(x, y = NULL, bins = 2, splineOrder = 1)
```

Arguments

x	a matrix of floating point numbers from the interval [0.0, 1.0]. Each column represents a list of samples of a random variable. The mutual information between each column of x and each column of y will be computed. If y is NULL then each pair of columns of x will be compared.
y	a matrix of floating point numbers from the interval [0.0, 1.0]. Each column represents a list of samples of a random variable. The mutual information between each column of x and each column of y will be computed. If y is NULL then each pair of columns of x will be compared.
bins	a single integer value representing the number of equal intervals that [0.0, 1.0] will be divided into in order to determine the bins in which to place each value of the columns of x and y. In the case of splineOrder = 1, this determines the histogram for traditional mutual information. For splineOrder > 1, a single value may be placed in multiple adjoining bins with varying weights on membership.
splineOrder	a single integer value giving the degree of the spline polynomials used to define both the number of bins a single value will be placed in and the weight of membership given to the value.

Value

a matrix of single precision floating point values of order ncol(y) by ncol(x). Entry (i, j) of this matrix represents the mutual information calculation for (y_i, x_j) .

References

Carten O. Daub, Ralf Steuer, Joachim Selbig, and Sebastian Kloska. 2004. Estimating mutual information using B-spline functions – an improved similarity measure for analysing gene expression data. *BMC Bioinformatics*. 5:118. Available from <http://www.biomedcentral.com/1471-2105/5/118>

Examples

```
# get 3 random variables each with 20 samples
x <- matrix(runif(60), 20, 3)
y <- matrix(runif(60), 20, 3)
# do something interesting
y[,2] <- 3.0 * (x[,1] + x[,3])
z <- gpuMi(x, y, bins = 10, splineOrder = 3)
print(z)
```

Description

gpuQR estimates the QR decomposition for a matrix using column pivoting and householder matrices. The work is done on a GPU.

Note: a rank-revealing pivoting scheme is employed, potentially resulting in pivot distinctly different from ordinary "qr".

Usage

```
gpuQr(x, tol = 1e-07)
```

Arguments

x	a matrix of floating point numbers. This is the matrix that will be decomposed into Q and R factors.
tol	a floating point value. It is used for estimating the rank of matrix x.

Value

an object of class 'qr'. This object has members qr, qraux, pivot, rank. It is meant to be identical to the output of R's base function 'qr'. From the documentation for R's 'qr' function: The attribute qr is a matrix with the same dimension as 'x'. The upper triangle contains the R of the QR decomposition. The lower triangle contains partial information to construct Q. The attribute qraux is a vector of length 'ncol(x)' contains more information to construct Q. The attribute rank is a single integer representing an estimation of the rank of input matrix x based on the results of the QR decomposition. In some cases, this rank can be wildly different from the actual rank of the matrix x and so is only an estimation. The attribute pivot contains the permutation applied to columns of x in the process of calculating the QR decomposition.

Author(s)

The low-level implementation of this function for Nvidia's CUDA-supporting GPGPUs was written by Mark Seligman at Rapid Biologics LLC. <http://www.rapidbiologics.com>

References

Bischof, C. B. and Van Loan, C. F. (1987) The WY Representation for Products of Householder Matrices SIAM J Sci. and Stat. Comp, 8, s2-s13.

Bjorck, Ake (1996) Numerical methods for least squares problems. SIAM.

Golub, Gene H. and Van Loan, C. F. (1996) Matrix Computations, Ed. 3, ch. 5.

Examples

```
# get some random data of any shape at all
x <- matrix(runif(25), 5, 5)
qr <- gpuQr(x)
print(qr)
```


gpuSolve

*Estimate the solution to a matrix vector equation***Description**

This function estimates the solution to an equation of the form $x * b = y$ where x is a matrix, b is an unknown vector, and y is a known vector. It does much calculation on a GPU. If the y argument is omitted, the function returns the inverse of x .

The function uses R's base 'qr' and then applies the gpu to the result to get the final solution.

Usage

```
gpuSolve(x, y=NULL)
```

Arguments

x a matrix of floating point numbers.
 y a vector of floating point numbers of length `nrow(x)`.

Value

a vector or matrix of floating point numbers. If y is not null, then the value is an estimate of the vector b of length `ncol(x)` where $x * b = y$. If y is null or omitted, the value is a matrix, an estimate of a matrix multiplicative pseudo inverse of x .

Examples

```
x <- matrix(runif(100), 10, 10)
y <- runif(10)
b <- gpuSolve(x, y)
cat("Solution:\n")
print(b)
x.inverse <- gpuSolve(x)
cat("an estimate of a pseudo inverse for x:\n")
print(x.inverse)
```

gpuTcrossprod

*Perform Matrix Transposed Cross-product with a GPU***Description**

Performs transposed matrix cross-product using a GPU. This function is merely a couple of wrappers for the CUBLAS `cublasSgemm` function.

Usage

```
gpuTcrossprod(a, b)
```

Arguments

a a matrix of floating point values.

b a matrix of floating point values. If null, defaultsto 'a'.

Value

A matrix of single precision floating point values. The matrix is the transposed cross-product of arguments 'a' and 'b', i.e., $a * t(b)$.

Examples

```
matA <- matrix(runif(2*3), 2, 3)
matB <- matrix(runif(4*3), 4, 3)
gpuTcrossprod(matA, matB)
```

 gpuTtest

T-Test Estimator with a GPU

Description

Given the number of samples and a Pearson correlation coefficient, this function estimates the t-score on a GPU. If an entry in goodPairs is zero or one then you may get a NaN as the t-test result.

Usage

```
gpuTtest(goodPairs, coeffs)
```

Arguments

goodPairs a vector of positive integer values. Value i represents the number of samples used to calculate the i-th value of the 'coeffs' argument.

coeffs a vector of floating point values representing Pearson correlation coefficients.

Value

a vector of single precision floating point values. The i-th entry is an estimate of the t-score of the i-th entry of the 'coeffs' argument.

See Also

[gpuCor](#).

Examples

```
goodPairs <- rpois(10, lambda=5)
coeffs <- runif(10)
gpuTtest(goodPairs, coeffs)
```

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