

Package ‘pbdMPI’

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Description A simplified, efficient, interface to MPI for HPC clusters. It is a derivation and rethinking of the Rmpi package. pbdMPI embraces the prevalent parallel programming style on HPC clusters. Beyond the interface, a collection of functions for global work with distributed data and resource-independent RNG reproducibility is included. It is based on S4 classes and methods.

SystemRequirements OpenMPI (>= 1.5.4) on Linux, Mac, and FreeBSD.
MS-MPI (Microsoft MPI v7.1 (SDK) and Microsoft HPC Pack 2012 R2 MS-MPI Redistributable Package) on Windows.

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URL <https://pbdr.org/>

BugReports <https://github.com/snoweye/pbdMPI/issues>

NeedsCompilation yes

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pb(MPI)-package	<i>R Interface to MPI (Programming with Big Data in R Project)</i>
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Description

A simplified, efficient, interface to MPI for HPC clusters. It is a derivation and rethinking of the Rmpi package that embraces the prevalent parallel programming style on HPC clusters. Beyond the interface, a collection of functions for global work with distributed data is included. It is based on S4 classes and methods.

Details

This package requires an MPI library (OpenMPI, MPICH2, or LAM/MPI). Standard installation in an R session with
`> install.packages("pb(MPI)")`
should work in most cases.

On HPC clusters, **it is strongly recommended that you check with your HPC cluster documentation for specific requirements, such as module software environments.** Some module examples relevant to R and MPI are

```
$ module load openmpi
$ module load openblas
$ module load flexiblas
$ module load r
```

possibly giving specific versions and possibly with some upper case letters. Although module software environments are widely used, the specific module names and their dependence structure are not standard across cluster installations. The command

```
$ module avail
```

usually lists the available software modules on your cluster.

To install on the Unix command line after downloading the source file, use `R CMD INSTALL`.

If the MPI library is not found, after checking that you are loading the correct module environments, the following arguments can be used to specify its non-standard location on your system

Argument	Default
<code>-with-mpi-type</code>	OPENMPI
<code>-with-mpi-include</code>	<code>\${MPI_ROOT}/include</code>
<code>-with-mpi-libpath</code>	<code>\${MPI_ROOT}/lib</code>

```
-with-mpi          ${MPI_ROOT}
```

where `${MPI_ROOT}` is the path to the MPI root. See the package source file `pbdMPI/configure` for details.

Loading library(`pbdMPI`) sets a few global variables, including the environment `.pbd_env`, where many defaults are set, and initializes MPI. In most cases, the defaults should not be modified. Rather, the parameters of the functions that use them should be changed. **All codes must end with `finalize()` to cleanly exit MPI.**

Most functions are assumed to run as Single Program, Multiple Data (SPMD), i.e. in batch mode. SPMD is based on cooperation between parallel copies of a single program, which is more scalable than a manager-workers approach that is natural in interactive programming. Interactivity with an HPC cluster is more efficiently handled by a client-server approach, such as that enabled by the `remoter` package.

On most clusters, codes run with `mpirun` or `mpiexec` and `Rscript`, such as

```
> mpiexec -np 2 Rscript some_code.r
```

where `some_code.r` contains the entire SPMD program. The MPI Standard 4.0 recommends `mpiexec` over `mpirun`. Some MPI implementations may have minor differences between the two but under OpenMPI 5.0 they are synonyms that produce the same behavior.

The package source files provide several examples based on **pbdMPI**, such as

Directory	Examples
<code>pbdMPI/inst/examples/test_spmd/</code>	main SPMD functions
<code>pbdMPI/inst/examples/test_rmpi/</code>	analogues to Rmpi
<code>pbdMPI/inst/examples/test_parallel/</code>	analogues to parallel
<code>pbdMPI/inst/examples/test_performance/</code>	performance tests
<code>pbdMPI/inst/examples/test_s4/</code>	S4 extension
<code>pbdMPI/inst/examples/test_cs/</code>	client/server examples
<code>pbdMPI/inst/examples/test_long_vector/</code>	long vector examples

where `test_long_vector` needs a recompile with setting

```
#define MPI_LONG_DEBUG 1
```

in `pbdMPI/src/pkg_constant.h`.

The current version is mainly written and tested under OpenMPI environments on Linux systems (CentOS 7, RHEL 8, Xubuntu). Also, it is tested on macOS with Homebrew-installed OpenMPI and under MPICH2 environments on Windows systems, although the primary target systems are HPC clusters running Linux OS.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`allgather()`, `allreduce()`, `bcast()`, `gather()`, `reduce()`, `scatter()`.

Examples

```
## Not run:
### On command line, run each demo with 2 processors by
### (Use Rscript.exe on Windows systems)
# mpiexec -np 2 Rscript -e "demo(allgather,'pbdMPI',ask=F,echo=F)"
# mpiexec -np 2 Rscript -e "demo(allreduce,'pbdMPI',ask=F,echo=F)"
# mpiexec -np 2 Rscript -e "demo(bcast,'pbdMPI',ask=F,echo=F)"
# mpiexec -np 2 Rscript -e "demo(gather,'pbdMPI',ask=F,echo=F)"
# mpiexec -np 2 Rscript -e "demo(reduce,'pbdMPI',ask=F,echo=F)"
# mpiexec -np 2 Rscript -e "demo(scatter,'pbdMPI',ask=F,echo=F)"
### Or
# execmpi("demo(allgather,'pbdMPI',ask=F,echo=F)", nrank = 2L)
# execmpi("demo(allreduce,'pbdMPI',ask=F,echo=F)", nrank = 2L)
# execmpi("demo(bcast,'pbdMPI',ask=F,echo=F)", nrank = 2L)
# execmpi("demo(gather,'pbdMPI',ask=F,echo=F)", nrank = 2L)
# execmpi("demo(reduce,'pbdMPI',ask=F,echo=F)", nrank = 2L)
# execmpi("demo(scatter,'pbdMPI',ask=F,echo=F)", nrank = 2L)

## End(Not run)
```

allgather-methods

All Ranks Gather Objects from Every Rank

Description

This method lets all ranks gather objects from every rank in the same communicator. The default return is a list of length equal to `comm.size(comm)`.

Usage

```
allgather(x, x.buffer = NULL, x.count = NULL, displs = NULL,
          comm = .pbd_env$SPMD.CT$comm,
          unlist = .pbd_env$SPMD.CT$unlist)
```

Arguments

<code>x</code>	an object to be gathered from all ranks.
<code>x.buffer</code>	a buffer to hold the return object which probably has ‘size of <code>x</code> ’ times ‘ <code>comm.size(comm)</code> ’ with the same type as <code>x</code> .
<code>x.count</code>	a vector of length ‘ <code>comm.size(comm)</code> ’ containing all object lengths.
<code>displs</code>	<code>c(0L, cumsum(x.count))</code> by default.
<code>comm</code>	a communicator number.
<code>unlist</code>	apply <code>unlist</code> function to the gathered list before return.

Details

The arguments `x.buffer`, `x.count`, and `displs` can be left unspecified or `NULL` and are computed for you.

If `x.buffer` is specified, its type should be one of integer, double, or raw according to the type of `x`. Serialization and unserialization is avoided for atomic vectors if they are all the same size and `x.buffer` is specified, or if different sizes and both `x.buffer` and `x.count` are specified. A single vector instead of a list is returned in these cases.

Class array objects are gathered without serialization.

Complex objects can be gathered as serialization and unserialization is used on objects that are not of class "array" or atomic vectors.

The `allgather` is efficient due to the underlying MPI parallel communication and recursive doubling gathering algorithm that results in a sublinear ($\log_2(\text{comm.size}(\text{comm}))$) number of communication steps. Also, serialization is applied only locally and in parallel.

See `methods{"allgather"}` for S4 dispatch cases and the source code for further details.

Value

A list of length `comm.size(comm)`, containing the gathered objects from each rank, is returned to all ranks by default. An exception is for atomic vectors, when `x.buffer` is specified, where a list is never formed and a single vector is returned. In other cases, the `unlist = TRUE` parameter simply applies the `unlist()` function to this list before returning.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[gather\(\)](#), [allreduce\(\)](#), [reduce\(\)](#).

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples
N <- 5
```

```

x <- (1:N) + N * .comm.rank
y <- allgather(matrix(x, nrow = 1))
comm.print(y)

y <- allgather(x, double(N * .comm.size))
comm.print(y)

### Finish
finalize()
"
pbdMPI::execmpi(spmd.code, nranks = 2L)

```

allreduce-method

*All Ranks Receive a Reduction of Objects from Every Rank***Description**

This method lets all ranks receive a reduction of objects from every rank in the same communicator based on a given operation. The default return is an object like the input and the default operation is the sum.

Usage

```

allreduce(x, x.buffer = NULL, op = .pbd_env$SPMD.CT$op,
          comm = .pbd_env$SPMD.CT$comm)

```

Arguments

<code>x</code>	an object to be reduced from all ranks.
<code>x.buffer</code>	for atomic vectors, a buffer to hold the return object which has the same size and the same type as <code>x</code> .
<code>op</code>	the reduction operation to apply to <code>x</code> across all <code>comm</code> ranks. The default is normally sum.
<code>comm</code>	a communicator number.

Details

All ranks are presumed to have `x` of the same size and type.

Normally, `x.buffer` is `NULL` or unspecified, and is computed for you. If specified for atomic vectors, the type should be one of integer, double, or raw and be the same type as `x`.

The `allgather` is efficient due to the underlying MPI parallel communication and recursive doubling reduction algorithm that results in a sublinear ($\log_2(\text{comm.size}(\text{comm}))$) number of reduction and communication steps.

See `methods{"allreduce"}` for S4 dispatch cases and the source code for further details.

Value

The reduced object of the same type as `x` is returned to all ranks by default.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[allgather\(\)](#), [gather\(\)](#), [reduce\(\)](#).

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
y <- allreduce(matrix(x, nrow = 1), op = \"sum\")
comm.print(y)

y <- allreduce(x, double(N), op = \"prod\")
comm.print(y)

comm.set.seed(1234, diff = TRUE)
x <- as.logical(round(runif(N)))
y <- allreduce(x, logical(N), op = \"land\")
comm.print(y)

### Finish.
finalize()
"

pbdMPI::execmpi(spmd.code = spmd.code, nranks = 2L)
```

alltoall	<i>All to All</i>
----------	-------------------

Description

These functions make calls to `MPI_Alltoall()` and `MPI_Alltoallv()`.

Usage

```
spmd.alltoall.integer(x.send, x.recv, send.count, recv.count,
                      comm = .pbd_env$SPMD.CT$comm)
spmd.alltoall.double(x.send, x.recv, send.count, recv.count,
                     comm = .pbd_env$SPMD.CT$comm)
spmd.alltoall.raw(x.send, x.recv, send.count, recv.count,
                  comm = .pbd_env$SPMD.CT$comm)

spmd.alltoallv.integer(x.send, x.recv, send.count, recv.count,
                       sdispls, rdispls, comm = .pbd_env$SPMD.CT$comm)
spmd.alltoallv.double(x.send, x.recv, send.count, recv.count,
                      sdispls, rdispls, comm = .pbd_env$SPMD.CT$comm)
spmd.alltoallv.raw(x.send, x.recv, send.count, recv.count,
                   sdispls, rdispls, comm = .pbd_env$SPMD.CT$comm)
```

Arguments

<code>x.send</code>	an object to send.
<code>x.recv</code>	an object to receive
<code>send.count</code>	send counter
<code>recv.count</code>	recv counter
<code>sdispls</code>	send dis pls
<code>rdispls</code>	recv dis pls
<code>comm</code>	a communicator number.

Details

These are very low level functions. Use with cautions. Neigher S4 method nor long vector is supported.

Value

These are very low level functions. Use with cautions. Neigher S4 method nor long vector is supported.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`allgather()`, `allgatherv()`.

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript --vanilla [...].r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
n <- as.integer(2)
x <- 1:(.comm.size * n)
comm.cat("\nOriginal x:\n", quiet = TRUE)
comm.print(x, all.rank = TRUE)

x <- as.integer(x)
y <- spmd.alltoall.integer(x, integer(length(x)), n, n)
comm.cat("\n\nAlltoall y:\n", quiet = TRUE)
comm.print(y, all.rank = TRUE)

### Finish.
finalize()
"

# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

apply and lapply

Parallel Apply and Lapply Functions

Description

The functions are parallel versions of apply and lapply functions.

Usage

```
pbdApply(X, MARGIN, FUN, ..., pbd.mode = c("mw", "spmd", "dist"),
         rank.source = .pbd_env$SPMD.CT$rank.root,
         comm = .pbd_env$SPMD.CT$comm,
```

```

        barrier = TRUE)
pbdLapply(X, FUN, ..., pbd.mode = c("mw", "spmd", "dist"),
          rank.source = .pbd_env$SPMD.CT$rank.root,
          comm = .pbd_env$SPMD.CT$comm,
          bcast = FALSE, barrier = TRUE)
pbdSapply(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE,
          pbd.mode = c("mw", "spmd", "dist"),
          rank.source = .pbd_env$SPMD.CT$rank.root,
          comm = .pbd_env$SPMD.CT$comm,
          bcast = FALSE, barrier = TRUE)

```

Arguments

<code>X</code>	a matrix or array in <code>pbdApply()</code> or a list in <code>pbdLapply()</code> and <code>pbdSapply()</code> .
<code>MARGIN</code>	<code>MARGIN</code> as in the <code>apply()</code> .
<code>FUN</code>	as in the <code>apply()</code> .
<code>...</code>	optional arguments to <code>FUN</code> .
<code>simplify</code>	as in the <code>sapply()</code> .
<code>USE.NAMES</code>	as in the <code>sapply()</code> .
<code>pbd.mode</code>	mode of distributed data <code>X</code> .
<code>rank.source</code>	a rank of source where <code>X</code> broadcast from.
<code>comm</code>	a communicator number.
<code>bcast</code>	if bcast to all ranks.
<code>barrier</code>	if barrier for all ranks.

Details

All functions are majorly called in manager/workers mode (`pbd.model = "mw"`), and just work the same as their serial version.

If `pbd.mode = "mw"`, the `X` in `rank.source` (manager) will be distributed to the workers, then `FUN` will be applied to the new data, and results gathered to `rank.source`. "In SPMD, the manager is one of workers." ... is also `scatter()` from `rank.source`.

If `pbd.mode = "spmd"`, the same copy of `X` is expected on all ranks, and the original `apply()`, `lapply()`, or `sapply()` will operate on part of `X`. An explicit `allgather()` or `gather()` will be needed to aggregate the results.

If `pbd.mode = "dist"`, different `X` are expected on all ranks, i.e. 'distinct or distributed' `X`, and original `apply()`, `lapply()`, or `sapply()` will operate on the distinct `X`. An explicit `allgather()` or `gather()` will be needed to aggregate the results.

In SPMD, it is better to split data into pieces, so that `X` is a local piece of a global matrix. If the "apply" dimension is local, the base `apply()` function can be used.

Value

A list or a matrix will be returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r
```

```
spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
```

```
.comm.size <- comm.size()
.comm.rank <- comm.rank()
```

```
### Example for pbdApply.
N <- 100
x <- matrix((1:N) + N * .comm.rank, ncol = 10)
y <- pbdApply(x, 1, sum, pbd.mode = \"mw\")
comm.print(y)
```

```
y <- pbdApply(x, 1, sum, pbd.mode = \"spmd\")
comm.print(y)
```

```
y <- pbdApply(x, 1, sum, pbd.mode = \"dist\")
comm.print(y)
```

```
### Example for pbdApply for 3D array.
N <- 60
x <- array((1:N) + N * .comm.rank, c(3, 4, 5))
dimnames(x) <- list(lat = paste(\"lat\", 1:3, sep = \"\"),
                     lon = paste(\"lon\", 1:4, sep = \"\"),
                     time = paste(\"time\", 1:5, sep = \"\"))
comm.print(x[, , 1:2])
```

```
y <- pbdApply(x, c(1, 2), sum, pbd.mode = \"mw\")
comm.print(y)
```

```
y <- pbdApply(x, c(1, 2), sum, pbd.mode = \"spmd\")
comm.print(y)
```

```
y <- pbdApply(x, c(1, 2), sum, pbd.mode = \"dist\")
comm.print(y)
```

```
### Example for pbdLapply.
```

```

N <- 100
x <- split((1:N) + N * .comm.rank, rep(1:10, each = 10))
y <- pbdLapply(x, sum, pbd.mode = \"mw\")
comm.print(unlist(y))

y <- pbdLapply(x, sum, pbd.mode = \"spmd\")
comm.print(unlist(y))

y <- pbdLapply(x, sum, pbd.mode = \"dist\")
comm.print(unlist(y))

### Finish.
finalize()
"
pbdMPI::execmpi(spmd.code, nranks = 2L)

```

bcast-method

*A Rank Broadcast an Object to Every Rank***Description**

This method lets a rank broadcast an object to every rank in the same communicator. The default return is the object.

Usage

```

bcast(x, rank.source = .pbd_env$SPMD.CT$rank.source,
      comm = .pbd_env$SPMD.CT$comm)

```

Arguments

<code>x</code>	an object to be broadcast from all ranks.
<code>rank.source</code>	a rank of source where <code>x</code> broadcast from.
<code>comm</code>	a communicator number.

Details

The same copy of `x` is sent to all ranks.

See `methods{"bcast"}` for S4 dispatch cases and the source code for further details.

Value

Every rank has `x` returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`scatter()`.

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Examples.
x <- matrix(1:5, nrow = 1)
y <- bcast(x)
comm.print(y)

### Finish.
finalize()
"

pbdMPI::execmpi(spmd.code, nranks = 2L)
```

comm.chunk

comm.chunk

Description

Given a total number of items, N , `comm.chunk` splits the number into chunks. Tailored especially for situations in SPMD style programming, potentially returning different results to each rank. Optionally, results for all ranks can be returned to all.

Usage

```
comm.chunk(
  N,
  form = "number",
  type = "balance",
  lo.side = "right",
  rng = FALSE,
  all.rank = FALSE,
  p = NULL,
  rank = NULL,
  comm = .pbd_env$SPMD.CT$comm,
  ...
)
```

Arguments

N	The number of items to split into chunks.
form	Output a chunk as a single "number", as a "vector" of items from 1:N, or as a "seq" three parameters 'c(from, to, by)' of the base 'seq()' function (replaced deprecated "iopair" for offset and length in a file). Forms "ldim" and "bldim" are available only with type "equal" and are intended for setting "ddmatrix" (see package pbdDMAT) slots.
type	Is the primary load and location balance specification. The choices are: "balance" the chunks so they differ by no more than 1 item (used most frequently and default); "cycle" is the same as "balance" in terms of load but differs on location in that chunks are not contiguous, rather are assigned in a cycled way to ranks (note that "balance" and "cycle" are the same if 'form' is "number"); "equal" maximizes the number of same size chunks resulting in one or more smaller or even zero size chunks carrying the leftover (required by pbdDMAT block-cyclic layouts).
lo.side	If exact balance is not possible, put the smaller chunks on the "left" (low ranks) or on the "right" (high ranks).
rng	If TRUE, set up different L'Ecuyer random number generator streams. Switch to stream i with <code>comm.set.stream(i)</code> , where i is a global index. If form = "vector" random streams are set up for each index in the vector and only those needed by each rank are kept. If form = "number", each rank will use a different stream, set by default (so <code>comm.set.stream</code> does not need to be used). Additional ... parameter seed, passed to <code>comm.set.seed</code> , can be set for reproducibility.
all.rank	FALSE returns only the chunk for rank r. TRUE returns a vector of length p (when form="number"), and a list of length p (when form="vector") each containing the output for the corresponding rank.
p	The number of chunks (processors). Normally, it is NOT specified and defaults to NULL, which assigns <code>comm.size(comm)</code> .
rank	The rank of returned chunk. Normally, it is NOT specified and defaults to NULL, which assigns <code>comm.rank(comm)</code> . Note that ranks are numbered from 0 to p-1, whereas the list elements for <code>all.rank=TRUE</code> are numbered 1 to p.
comm	The communicator that determines MPI rank numbers.
...	If rng = TRUE, then a seed parameter should be provided for <code>comm.set.seed</code> .

Details

Various chunking options are possible when the number does not split evenly into equal chunks. The output form can be a number, a vector of items, or a few other special forms intended for pbdR components.

Value

A numeric value from 0:N or a vector giving a subset of 1:N (depending on form) for the rank. If `all.rank` is TRUE, a vector or a list of vectors, respectively.

Examples

```
## Not run:
## Note that the p and rank parameters are provided by comm.size() and
## comm.rank(), respectively, when running SPMD in parallel. Normally, they
## are not specified unless testing in serial mode (as in this example).
library(pbdIO)

comm.chunk(16, all.rank = TRUE, p = 5)
comm.chunk(16, type = "equal", all.rank = TRUE, p = 5)
comm.chunk(16, type = "equal", lo.side = "left", all.rank = TRUE, p = 5)
comm.chunk(16, p = 5, rank = 0)
comm.chunk(16, p = 5, lo.side = "left", rank = 0)

## End(Not run)
```

communicator

Communicator Functions

Description

The functions provide controls to communicators.

Usage

```
barrier(comm = .pbd_env$SPMD.CT$comm)
comm.is.null(comm = .pbd_env$SPMD.CT$comm)
comm.rank(comm = .pbd_env$SPMD.CT$comm)
comm.localrank(comm = .pbd_env$SPMD.CT$comm)
comm.size(comm = .pbd_env$SPMD.CT$comm)
comm.dup(comm, newcomm)
comm.free(comm = .pbd_env$SPMD.CT$comm)
init(set.seed = TRUE)
finalize(mpi.finalize = .pbd_env$SPMD.CT$mpi.finalize)
is.finalized()

comm.abort(errorcode = 1, comm = .pbd_env$SPMD.CT$comm)
comm.split(comm = .pbd_env$SPMD.CT$comm, color = 0L, key = 0L,
           newcomm = .pbd_env$SPMD.CT$newcomm)
comm.disconnect(comm = .pbd_env$SPMD.CT$comm)
comm.connect(port.name, info = .pbd_env$SPMD.CT$info,
             rank.root = .pbd_env$SPMD.CT$rank.root,
             comm = .pbd_env$SPMD.CT$comm,
             newcomm = .pbd_env$SPMD.CT$newcomm)
comm.accept(port.name, info = .pbd_env$SPMD.CT$info,
            rank.root = .pbd_env$SPMD.CT$rank.root,
            comm = .pbd_env$SPMD.CT$comm,
            newcomm = .pbd_env$SPMD.CT$newcomm)
```

```

port.open(info = .pbd_env$SPMD.CT$info)
port.close(port.name)
serv.publish(port.name, serv.name = .pbd_env$SPMD.CT$serv.name,
             info = .pbd_env$SPMD.CT$info)
serv.unpublish(port.name, serv.name = .pbd_env$SPMD.CT$serv.name,
               info = .pbd_env$SPMD.CT$info)
serv.lookup(serv.name = .pbd_env$SPMD.CT$serv.name,
            info = .pbd_env$SPMD.CT$info)

intercomm.merge(intercomm = .pbd_env$SPMD.CT$intercomm,
                 high = 0L, comm = .pbd_env$SPMD.CT$comm)
intercomm.create(local.comm = .pbd_env$SPMD.CT$comm,
                 local.leader = .pbd_env$SPMD.CT$rank.source,
                 peer.comm = .pbd_env$SPMD.CT$intercomm,
                 remote.leader = .pbd_env$SPMD.CT$rank.dest,
                 tag = .pbd_env$SPMD.CT$tag,
                 newintercomm = .pbd_env$SPMD.CT$newcomm)

comm.c2f(comm = .pbd_env$SPMD.CT$comm)

```

Arguments

<code>comm</code>	a communicator number.
<code>mpi.finalize</code>	if MPI should be shutdown.
<code>set.seed</code>	if a random seed preset.
<code>port.name</code>	a port name with default maximum length 1024 characters for OpenMPI.
<code>info</code>	a info number.
<code>rank.root</code>	a root rank.
<code>newcomm</code>	a new communicator number.
<code>color</code>	control of subset assignment.
<code>key</code>	control of rank assignment.
<code>serv.name</code>	a service name.
<code>errorcode</code>	an error code to abort MPI.
<code>intercomm</code>	a intercommunicator number.
<code>high</code>	used to order the groups within comm.
<code>local.comm</code>	a local communicator number.
<code>local.leader</code>	the leader number of local communicator.
<code>peer.comm</code>	a peer communicator number.
<code>remote.leader</code>	the remote leader number of peer communicator.
<code>newintercomm</code>	a new intercommunicator number.
<code>tag</code>	a tag number.

Details

Another functions are direct calls to MPI library.

`barrier()` blocks all processors until everyone call this.

`comm.is.null()` returns -1 if the array of communicators is not allocated, i.e. `init()` is not called yet. It returns 1 if the communicator is not initialized, i.e. NULL. It returns 0 if the communicator is initialized.

`comm.rank()` returns the processor's rank for the given `comm`.

`comm.size()` returns the total processes for the given `comm`.

`comm.dup()` duplicate a newcomm from `comm`.

`comm.free()` free a `comm`.

`init()` initializes a MPI world, and set two global variables `.comm.size` and `.comm.rank` in `.GlobalEnv`. A random seed will be preset by default (`Sys.getpid() + Sys.time()`) to the package **rlcuyer**.

`finalize()` frees memory and finishes a MPI world if `mpi.finalize = TRUE`. `is.finalized()` checks if MPI is already finalized.

`comm.abort()` aborts MPI.

`comm.split()` create a newcomm by color and key.

`comm.disconnect()` frees a `comm`.

`comm.connect()` connects a newcomm.

`comm.accept()` accepts a newcomm.

`port.open()` opens a port and returns the port name.

`port.close()` closes a port by name.

`serv.publish()` publishes a service via `port.name`.

`serv.unpublish()` unpublishes a service via `port.name`.

`serv.lookup()` lookup the `serv.name` and returns the port name.

`intercomm.merge()` merges the `intercomm` to intracommunicator.

`intercomm.create()` creates a new `intercomm` from two peer intracommunicators.

`comm.c2f()` returns an integer for Fortran MPI support.

Value

Most function return an invisible state of MPI call.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples .
comm.print(.comm.size)
comm.print(.comm.rank, all.rank = TRUE)
comm.print(comm.rank(), rank.print = 1)
comm.print(comm.c2f())

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

gather-methods

A Rank Gathers Objects from Every Rank

Description

This method lets one rank gather objects from every rank in the same communicator. The default return is a list of length equal to comm size.

Usage

```
gather(x, x.buffer = NULL, x.count = NULL, displs = NULL,
       rank.dest = .pbd_env$SPMD.CT$rank.root,
       comm = .pbd_env$SPMD.CT$comm,
       unlist = .pbd_env$SPMD.CT$unlist)
```

Arguments

<code>x</code>	an object to be gathered from all ranks.
<code>x.buffer</code>	a buffer to hold the return object which probably has 'size of x' times 'comm.size(comm)' with the same type of x.
<code>x.count</code>	a vector of length 'comm.size(comm)' containing all object lengths.
<code>displs</code>	c(0L, cumsum(x.count)) by default.
<code>rank.dest</code>	a rank of destination where all x gather to.
<code>comm</code>	a communicator number.
<code>unlist</code>	apply unlist function to the gathered list before return.

Details

The arguments `x.buffer`, `x.count`, and `displs` can be left unspecified or `NULL` and are computed for you.

If `x.buffer` is specified, its type should be one of integer, double, or raw according to the type of `x`. Serialization and unserialization is avoided for atomic vectors if they are all the same size and `x.buffer` is specified, or if different sizes and both `x.buffer` and `x.count` are specified. A single vector instead of a list is returned in these cases.

Class array objects are gathered without serialization.

Complex objects can be gathered as serialization and unserialization is used on objects that are not of class "array" or atomic vectors.

The gather is efficient due to the underlying MPI parallel communication and recursive doubling gathering algorithm that results in a sublinear ($\log_2(\text{comm.size}(\text{comm}))$) number of communication steps. Also, serialization is applied only locally and in parallel.

See `methods{"gather"}` for S4 dispatch cases and the source code for further details.

Value

Only `rank.dest` (by default rank 0) receives the gathered object. All other ranks receive `NULL`. See `allgather()` for a description of the gathered object.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`allgather()`, `allreduce()`, `reduce()`.

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
y <- gather(matrix(x, nrow = 1))
comm.print(y)
```

```

y <- gather(x, double(N * .comm.size))
comm.print(y)

### Finish.
finalize()
"
pbdMPI::execmpi(spmc.code, nranks = 2L)

```

Get Configures Used at Compiling Time

Functions to Get MPI and/or pbdMPI Configures Used at Compiling Time

Description

These functions are designed to get MPI and/or pbdMPI configures that were usually needed at the time of pbdMPI installation. In particular, to configure, link, and compile with ‘libmpi*.so’ or so.

Usage

```

get.conf(arg, arch = '', package = "pbdMPI", return = FALSE)
get.lib(arg, arch, package = "pbdPROF")
get.sysenv(flag)

```

Arguments

arg	an argument to be searched in the configuration file
arch	system architecture
package	package name
return	to return (or print if FALSE) the search results or not
flag	a system flag that is typically used in windows environment set.

Details

get.conf() and get.lib() are typically used by ‘pbd*/configure.ac’, ‘pbd*/src/Makevars.in’, and/or ‘pbd*/src/Makevar.win’ to find the default configurations from ‘pbd*/etc\${R_ARCH}/Makconf’.

get.sysenv() is only called by ‘pbdMPI/src/Makevars.win’ to obtain possible MPI dynamic/static library from the environment variable ‘MPI_ROOT’ preset by users.

Value

Typically, there are no return values, but the values are cat() to screen or stdin.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
library(pbdMPI)
if(Sys.info()["sysname"] != "Windows"){
  get.conf("MPI_INCLUDE_PATH"); cat("\n")
  get.conf("MPI_LIBPATH"); cat("\n")
  get.conf("MPI_LIBNAME"); cat("\n")
  get.conf("MPI_LIBS"); cat("\n")
} else{
  get.conf("MPI_INCLUDE", "/i386"); cat("\n")
  get.conf("MPI_LIB", "/i386"); cat("\n")

  get.conf("MPI_INCLUDE", "/x64"); cat("\n")
  get.conf("MPI_LIB", "/x64"); cat("\n")
}

## End(Not run)
```

get job id

Divide Job ID by Ranks

Description

This function obtains job id which can be used to divide jobs.

Usage

```
get.jid(n, method = .pbd_env$SPMD.CT$divide.method[1], all = FALSE,
        comm = .pbd_env$SPMD.CT$comm, reduced = FALSE)
```

Arguments

n	total number of jobs.
method	a way to divide jobs.
all	indicate if return all id for each processor.
comm	a communicator number.
reduced	indicate if return should be a reduced representation.

Details

`n` is total number of jobs needed to be divided into all processors (`comm.size(comm)`), i.e. `1:n` will be split according to the rank of processor (`comm.rank(comm)`) and method. Job id will be returned. Currently, three possible methods are provided.

"block" will use return id's which are nearly equal size blocks. For example, 7 jobs in 4 processors will have `jid=1` for rank 0, `jid=2,3` for rank 1, `jid=4,5` for rank 2, and `jid=6,7` for rank 3.

"block0" will use return id's which are nearly equal size blocks, in the opposite direction of "block". For example, 7 jobs in 4 processors will have `jid=1,2` for rank 0, `jid=3,4` for rank 1, `jid=5,6` for rank 2, and `jid=7` for rank 3.

"cycle" will use return id's which are nearly equal size in cycle. For example, 7 jobs in 4 processors will have `jid=1,5` for rank 0, `jid=2,6` for rank 1, `jid=3,7` for rank 2, and `jid=4` for rank 3.

Value

`get.jid()` returns a vector containing job id for each individual processor if `all = FALSE`. While it returns a list containing all job id for all processor if `all = TRUE`. The list has length equal to `comm.size`.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`task.pull()` and `comm.chunk()`.

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r
```

```
spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
```

```
### Examples.
comm.cat("\>>> block\n", quiet = TRUE)
jid <- get.jid(7, method = "block")
comm.print(jid, all.rank = TRUE)
```

```
comm.cat("\>>> cycle\n", quiet = TRUE)
jid <- get.jid(7, method = "cycle")
comm.print(jid, all.rank = TRUE)
```

```

comm.cat("\">>>> block (all)\n\", quiet = TRUE)
alljid <- get.jid(7, method = \"block\", all = TRUE)
comm.print(alljid)

comm.cat("\">>>> cycle (all)\n\", quiet = TRUE)
alljid <- get.jid(7, method = \"cycle\", all = TRUE)
comm.print(alljid)

### Finish.
finalize()
"

pbdMPI::execmpi(spmc.code, nranks = 2L)

```

global all pairs	<i>Global All Pairs</i>
------------------	-------------------------

Description

This function provide global all pairs.

Usage

```

comm.allpairs(N, diag = FALSE, symmetric = TRUE,
              comm = .pbd_env$SPMD.CT$comm)

```

Arguments

N	number of elements for matching, (i, j) for all $1 \leq i, j \leq N$.
diag	if matching the same elements, (i, i) for all i.
symmetric	if matching upper triangular elements. TRUE for $i \geq j$ only, otherwise for all (i, j).
comm	a communicator number.

Details

The function generates all combinations of N elements.

Value

The function returns a gbd matrix in row blocks with 2 columns named i and j. The number of rows is dependent on the options diag and symmetric. If diag = TRUE and symmetric = FALSE, then this case has the maximum number of rows, N^2 .

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`comm.dist()`.

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Examples.
id.matrix <- comm.allpairs(comm.size() + 1)
comm.print(id.matrix, all.rank = TRUE)

### Finish.
finalize()
"

# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

global any and all *Global Any and All Functions*

Description

These functions are global any and all applying on distributed data for all ranks.

Usage

```
comm.any(x, na.rm = FALSE, comm = .pbd_env$SPMD.CT$comm)
comm.all(x, na.rm = FALSE, comm = .pbd_env$SPMD.CT$comm)

comm.allcommon(x, comm = .pbd_env$SPMD.CT$comm,
               lazy.check = .pbd_env$SPMD.CT$lazy.check)
```

Arguments

<code>x</code>	a vector.
<code>na.rm</code>	if NA removed or not.
<code>comm</code>	a communicator number.
<code>lazy.check</code>	if TRUE, then <code>allreduce</code> is used to check all ranks, otherwise, <code>allgather</code> is used.

Details

These functions will apply `any()` and `all()` locally, and apply `allgather()` to get all local results from other ranks, then apply `any()` and `all()` on all local results.

`comm.allcommon()` is to check if `x` is exactly the same across all ranks. This is a vectorized operation on `x` where the input and output have the same length of vector, while `comm.any()` and `comm.all()` return a scalar.

Note that `lazy.check = TRUE` is faster as number of cores is large, but it may cause some inconsistency in some cases. `lazy.check = FALSE` is much slower, but it provides more accurate checking.

Value

The global check values (TRUE, FALSE, NA) are returned to all ranks.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Examples.
if(comm.rank() == 0){
  a <- c(T, F, NA)
} else{
  a <- T
}

comm.any(a)
comm.all(a)
comm.any(a, na.rm = TRUE)
comm.all(a, na.rm = TRUE)

comm.allcommon(1:3)
if(comm.rank() == 0){
  a <- 1:3
} else{
  a <- 3:1
}
```

```

comm.allcommon.integer(a)

### Finish.
finalize()
"
# execmpi(spmc.code, nranks = 2L)

## End(Not run)

```

global as.gbd

Global As GBD Function

Description

This function redistributes a regular matrix existed in rank.source and turns it in a gbd matrix in row blocks.

Usage

```

comm.as.gbd(X, balance.method = .pbd_env$SPMD.IO$balance.method,
            rank.source = .pbd_env$SPMD.CT$rank.source,
            comm = .pbd_env$SPMD.CT$comm)

```

Arguments

X a regular matrix in rank.source and to be redistributed as a gbd.
balance.method a balance method.
rank.source a rank of source where elements of x scatter from.
comm a communicator number.

Details

X matrix in rank.source will be redistributed as a gbd matrix in row blocks.

This function will first set NULL to X if it is not located in rank.source, then called `comm.load.balance()` to redistributed the one located in rank.source to all other ranks.

Value

A X.gbd will be returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`comm.load.balance()`, `comm.read.table()` and `comm.write.table()`.

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Examples.
X <- matrix(1:15, ncol = 3)
X.gbd <- comm.as.gbd(X)
comm.print(X.gbd, all.rank = TRUE)

### Finish.
finalize()
"

pbdMPI::execmpi(spmd.code, nranks = 2L)
```

global balanc

Global Balance Functions

Description

These functions are global balance methods for gbd data.frame (or matrix) distributed in row blocks.

Usage

```
comm.balance.info(X.gbd, balance.method = .pbd_env$SPMD.IO$balance.method[1],
                  comm = .pbd_env$SPMD.CT$comm)
comm.load.balance(X.gbd, bal.info = NULL,
                  balance.method = .pbd_env$SPMD.IO$balance.method[1],
                  comm = .pbd_env$SPMD.CT$comm)
comm.unload.balance(new.X.gbd, bal.info, comm = .pbd_env$SPMD.CT$comm)
```

Arguments

<code>X.gbd</code>	a gbd data.frame (or matrix).
<code>balance.method</code>	a balance method.
<code>bal.info</code>	a balance information returned from <code>comm.balance.info()</code> . If NULL, then this will be generated inside <code>comm.load.balance()</code> .
<code>new.X.gbd</code>	a new gbd of <code>X.gbd</code> (may be generated from <code>comm.load.balance()</code>).
<code>comm</code>	a communicator number.

Details

A typical use is to balance an input dataset `X.gbd` from `comm.read.table()`. Since by default, a two dimension `data.frame` is distributed in row blocks, but each processor (rank) may not (or closely) have the same number of rows. These functions redistribute the `data.frame` (and maybe matrix) according to the specified way in `bal.info`.

Currently, there are three balance methods are supported, `block` (uniform distributed but favor higher ranks), `block0` (as `block` but favor lower ranks), and `block.cyclic` (as `block` cyclic with one big block in one cycle).

Value

`comm.balance.info()` returns a list containing balance information based on the input `X.gbd` and `balance.method`.

`comm.load.balance()` returns a new `gbd data.frame` (or matrix).

`comm.unload.balance()` also returns the new `gbd data.frame` back to the original `X.gbd`.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`comm.read.table()`, `comm.write.table()`, and `comm.as.gbd()`.

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Get two gbd row-block data.frame.
da.block <- iris[get.jid(nrow(iris), method = \"block\"),]
da.block0 <- iris[get.jid(nrow(iris), method = \"block0\"),]

### Load balance one and unload it.
bal.info <- comm.balance.info(da.block0)
da.new <- comm.load.balance(da.block0)
da.org <- comm.unload.balance(da.new, bal.info)

### Check if all are equal.
comm.print(c(sum(da.new != da.block), sum(da.org != da.block0)),
```

```

        all.rank = TRUE)

### Finish.
finalize()
"
# execmpi(spmc.code, nranks = 2L)

## End(Not run)

```

global base

Global Base Functions

Description

These functions are global base functions applying on distributed data for all ranks.

Usage

```

comm.length(x, comm = .pbd_env$SPMD.CT$comm)
comm.sum(..., na.rm = TRUE, comm = .pbd_env$SPMD.CT$comm)
comm.mean(x, na.rm = TRUE, comm = .pbd_env$SPMD.CT$comm)
comm.var(x, na.rm = TRUE, comm = .pbd_env$SPMD.CT$comm)
comm.sd(x, na.rm = TRUE, comm = .pbd_env$SPMD.CT$comm)

```

Arguments

x	a vector.
...	as in <code>sum()</code> .
na.rm	logical, if remove NA and NaN.
comm	a communicator number.

Details

These functions will apply globally `length()`, `sum()`, `mean()`, `var()`, and `sd()`.

Value

The global values are returned to all ranks.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

if(comm.size() != 2){
  comm.cat("\n2 processors are required.\n", quiet = TRUE)
  finalize()
}

### Examples.
a <- 1:(comm.rank() + 1)

b <- comm.length(a)
comm.print(b)
b <- comm.sum(a)
comm.print(b)
b <- comm.mean(a)
comm.print(b)
b <- comm.var(a)
comm.print(b)
b <- comm.sd(a)
comm.print(b)

### Finish.
finalize()
"

# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

global distance function

Global Distance for Distributed Matrices

Description

These functions globally compute distance for all ranks.

Usage

```
comm.dist(X.gbd, method = "euclidean", diag = FALSE, upper = FALSE,
          p = 2, comm = .pbd_env$SPMD.CT$comm,
          return.type = c("common", "gbd"))
```

Arguments

<code>X.gbd</code>	a gbd matrix.
<code>method</code>	as in <code>dist()</code> .
<code>diag</code>	as in <code>dist()</code> .
<code>upper</code>	as in <code>dist()</code> .
<code>p</code>	as in <code>dist()</code> .
<code>comm</code>	a communicator number.
<code>return.type</code>	returning type for the distance.

Details

The distance function is implemented for a distributed matrix.

The return type `common` is only useful when the number of rows of the matrix is small since the returning matrix is $N * N$ for every rank where N is the total number of rows of `X.gbd` of all ranks.

The return type `gbd` returns a gbd matrix (distributed across all ranks, and the gbd matrix has 3 columns, named "i", "j", and "value", where (i, j) is the global indices of the i -th and j -th rows of `X.gbd`, and value is the corresponding distance. The (i, j) is ordered as a distance matrix.

Value

A full distance matrix is returned from the `common` return type. Suppose $N.gbd$ is total rows of `X.gbd`, then the distance will have $N.gbd * (N.gbd - 1) / 2$ elements and the distance matrix will have $N.gbd^2$ elements.

A gbd distance matrix with 3 columns is returned from the `gbd` return type.

Warning

The distance or distance matrix could be huge.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[comm.allpairs\(\)](#) and [comm.pairwise\(\)](#).

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Examples.
comm.set.seed(123456, diff = TRUE)

X.gbd <- matrix(runif(6), ncol = 3)
dist.X.common <- comm.dist(X.gbd)
dist.X.gbd <- comm.dist(X.gbd, return.type = \"gbd\")

### Verify.
dist.X <- dist(do.call(\"rbind\", allgather(X.gbd)))
comm.print(all(dist.X == dist.X.common))

### Verify 2.
dist.X.df <- do.call(\"rbind\", allgather(dist.X.gbd))
comm.print(all(dist.X == dist.X.df[, 3]))
comm.print(dist.X)
comm.print(dist.X.df)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

global match.arg

Global Argument Matching

Description

A binding for `match.arg()` that uses `comm.stop()` rather so that the error message (if there is one) is managed according to the rules of `.pbd_env$SPMD.CT`.

Usage

```
comm.match.arg(arg, choices, several.ok=FALSE, ...,
               all.rank = .pbd_env$SPMD.CT$print.all.rank,
               rank.print = .pbd_env$SPMD.CT$rank.source,
               comm = .pbd_env$SPMD.CT$comm,
               mpi.finalize = .pbd_env$SPMD.CT$mpi.finalize,
               quit = .pbd_env$SPMD.CT$quit)
```

Arguments

<code>arg, choices, several.ok</code>	see <code>match.arg()</code>
<code>...</code>	ignored.
<code>all.rank</code>	if all ranks print (default = FALSE).
<code>rank.print</code>	rank for printing if not all ranks print (default = 0).
<code>comm</code>	communicator for printing (default = 1).
<code>mpi.finalize</code>	if MPI should be shutdown.
<code>quit</code>	if quit R when errors happen.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

global pairwise	<i>Global Pairwise Evaluations</i>
-----------------	------------------------------------

Description

This function provides global pairwise evaluations.

Usage

```
comm.pairwise(X, pairid.gbd = NULL,
  FUN = function(x, y, ...){ return(as.vector(dist(rbind(x, y), ...))) },
  ..., diag = FALSE, symmetric = TRUE, comm = .pbd_env$SPMD.CT$comm)
```

Arguments

<code>X</code>	a common matrix across ranks, or a gbd matrix. (See details.)
<code>pairid.gbd</code>	a pair-wise id in a gbd format. (See details.)
<code>FUN</code>	a function to be evaluated for given pairs.
<code>...</code>	extra variables for FUN.
<code>diag</code>	if matching the same elements, (i, i) for all i.
<code>symmetric</code>	if matching upper triangular elements. TRUE for i >= j only, otherwise for all (i, j).
<code>comm</code>	a communicator number.

Details

This function evaluates the objective function $\text{FUN}(X[i,], X[j,])$ (usually distance of two elements) on any given pair (i, j) of a matrix X .

The input X should be in common across all ranks if `pairid.gbd` is provided, e.g. from `comm.pairwise()`. i.e. X is exactly the same in every ranks, but `pairid.gbd` is different and in gbd format indicating the row pair (i, j) should be evaluated. The returning gbd matrix is ordered and indexed by `pairid.gbd`.

Note that checking consistence of X across all ranks is not implemented within this function since that drops performance and may be not accurate.

The input X should be a gbd format in row major blocks (i.e. $X.\text{gbd}$) if `pairid.gbd` is `NULL`. A internal pair indices will be built implicitly for evaluation. The returning gbd matrix is ordered and indexed by $X.\text{gbd}$.

Value

This function returns a common matrix with 3 columns named `i`, `j`, and `value`. Each value is the returned value and computed by $\text{FUN}(X[i,], X[j,])$ where (i, j) is the global index as ordered in a distance matrix for i -th row and j -th columns.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[comm.pairwise\(\)](#), and [comm.dist\(\)](#).

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Examples.
comm.set.seed(123456, diff = FALSE)
X <- matrix(rnorm(10), ncol = 2)
id.matrix <- comm.allpairs(nrow(X))

### Method original.
dist.org <- dist(X)
```

```

### Method 1.
dist.common <- comm.pairwise(X, pairid.gbd = id.matrix)

### Method 2.
# if(comm.rank() != 0){
#   X <- matrix(0, nrow = 0, ncol = 4)
# }
X.gbd <- comm.as.gbd(X)    ### The other way.
dist.gbd <- comm.pairwise(X.gbd)

### Verify.
d.org <- as.vector(dist.org)
d.1 <- do.call("\nc", allgather(dist.common[, 3]))
d.2 <- do.call("\nc", allgather(dist.gbd[, 3]))
comm.print(all(d.org == d.1))
comm.print(all(d.org == d.2))

### Finish.
finalize()
"

# execmpi(spmc.code, nranks = 2L)

## End(Not run)

```

global print and cat *Global Print and Cat Functions*

Description

The functions globally print or cat a variable from specified processors, by default messages is shown on screen.

Usage

```

comm.print(x, all.rank = .pbd_env$SPMD.CT$print.all.rank,
           rank.print = .pbd_env$SPMD.CT$rank.source,
           comm = .pbd_env$SPMD.CT$comm,
           quiet = .pbd_env$SPMD.CT$print.quiet,
           flush = .pbd_env$SPMD.CT$msg.flush,
           barrier = .pbd_env$SPMD.CT$msg.barrier,
           con = stdout(), ...)

comm.cat(..., all.rank = .pbd_env$SPMD.CT$print.all.rank,
         rank.print = .pbd_env$SPMD.CT$rank.source,
         comm = .pbd_env$SPMD.CT$comm,
         quiet = .pbd_env$SPMD.CT$print.quiet, sep = " ", fill = FALSE,
         labels = NULL, append = FALSE, flush = .pbd_env$SPMD.CT$msg.flush,
         barrier = .pbd_env$SPMD.CT$msg.barrier, con = stdout())

```

Arguments

x	a variable to be printed.
...	variables to be cat.
all.rank	if all ranks print (default = FALSE).
rank.print	rank for printing if not all ranks print (default = 0).
comm	communicator for printing (default = 1).
quiet	FALSE for printing rank number.
sep	sep argument as in the cat() function.
fill	fill argument as in the cat() function.
labels	labels argument as in the cat() function.
append	labels argument as in the cat() function.
flush	if flush con.
barrier	if barrier con.
con	stdout() is the default to print message.

Details

Warning: These two functions use barrier() to make sure the well printing process on screen, so should be called by all processors to avoid a deadlock. A typical misuse is called inside a condition check, such as if(.comm.rank == 0) comm.cat(...).

rank.print can be a integer vector containing the ranks of processors which print messages.

Value

A print() or cat() is called for the specified processors and the messages of the input variables is shown on screen by default.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
```

```

### Example.
comm.print(comm.rank(), rank.print = 1)

### Finish.
finalize()
"
# execmpi(spmc.code, nranks = 2L)

## End(Not run)

```

global range, max, and min

Global Range, Max, and Min Functions

Description

These functions are global range, max and min applying on distributed data for all ranks.

Usage

```

comm.range(..., na.rm = FALSE, comm = .pbd_env$SPMD.CT$comm)
comm.max(..., na.rm = FALSE, comm = .pbd_env$SPMD.CT$comm)
comm.min(..., na.rm = FALSE, comm = .pbd_env$SPMD.CT$comm)

```

Arguments

...	an 'numeric' objects.
na.rm	if NA removed or not.
comm	a communicator number.

Details

These functions will apply `range()`, `max()` and `min()` locally, and apply `allgather` to get all local results from other ranks, then apply `range()`, `max()` and `min()` on all local results.

Value

The global values (range, max, or min) are returned to all ranks.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

if(comm.size() != 2){
  comm.cat("\n2 processors are required.\n", quiet = TRUE)
  finalize()
}

### Examples.
a <- 1:(comm.rank() + 1)

b <- comm.range(a)
comm.print(b)
b <- comm.max(a)
comm.print(b)
b <- comm.min(a)
comm.print(b)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

global reading

Global Reading Functions

Description

These functions are global reading from specified file.

Usage

```
comm.read.table(file, header = FALSE, sep = "", quote = "\"'",
  dec = ".",
  na.strings = "NA", colClasses = NA, nrow = -1, skip = 0,
  check.names = TRUE, fill = !blank.lines.skip,
  strip.white = FALSE,
  blank.lines.skip = TRUE, comment.char = "#",
  allowEscapes = FALSE,
  flush = FALSE,
  fileEncoding = "", encoding = "unknown",
```

```

read.method = .pbd_env$SPMD.IO$read.method[1],
balance.method = .pbd_env$SPMD.IO$balance.method[1],
comm = .pbd_env$SPMD.CT$comm)

comm.read.csv(file, header = TRUE, sep = ",", quote = "\"",
dec = ".", fill = TRUE, comment.char = "", ...,
read.method = .pbd_env$SPMD.IO$read.method[1],
balance.method = .pbd_env$SPMD.IO$balance.method[1],
comm = .pbd_env$SPMD.CT$comm)

comm.read.csv2(file, header = TRUE, sep = ";", quote = "\"",
dec = ",", fill = TRUE, comment.char = "", ...,
read.method = .pbd_env$SPMD.IO$read.method[1],
balance.method = .pbd_env$SPMD.IO$balance.method[1],
comm = .pbd_env$SPMD.CT$comm)

```

Arguments

file	as in read.table().
header	as in read.table().
sep	as in read.table().
quote	as in read.table().
dec	as in read.table().
na.strings	as in read.table().
colClasses	as in read.table().
nrows	as in read.table().
skip	as in read.table().
check.names	as in read.table().
fill	as in read.table().
strip.white	as in read.table().
blank.lines.skip	as in read.table().
comment.char	as in read.table().
allowEscapes	as in read.table().
flush	as in read.table().
fileEncoding	as in read.table().
encoding	as in read.table().
...	as in read.csv*().
read.method	either "gbd" or "common".
balance.method	balance method for read.method = "gbd" as nrows = -1 and skip = 0 are set.
comm	a communicator number.

Details

These functions will apply `read.table()` locally and sequentially from rank 0, 1, 2, ...

By default, rank 0 reads the file only, then scatter to other ranks for small datasets (`.pbd_env$SPMD.IO$max.read.size`) in `read.method = "gbd"`. (bcast to others in `read.method = "common"`.)

As dataset size increases, the reading is performed from each ranks and read portion of rows in "gbd" format as described in **pbdDEMO** vignettes and used in **pmclust**.

`comm.load.balance()` is called for "gbd" method as `nrows = -1` and `skip = 0` are set. Note that the default method "block" is the better way for performance in general that distributes equally and leaves residuals on higher ranks evenly. "block0" is the other way around. "block.cyclic" is only useful for converting to `ddmatrix` as in **pbdDMAT**.

Value

A distributed `data.frame` is returned.

All factors are disable and read as characters or as what data should be.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`comm.load.balance()` and `comm.write.table()`

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

smpd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Check.
if(comm.size() != 2){
  comm.stop("\"2 processors are required.\")
}

### Manually distributed iris.
da <- iris[get.jid(nrow(iris)),]

### Dump data.
comm.write.table(da, file = \"iris.txt\", quote = FALSE, sep = \"\\t\",
```

```

        row.names = FALSE)

### Read back in.
da.gbd <- comm.read.table("iris.txt", header = TRUE, sep = "\\t\\t",
                          quote = "\\")
comm.print(c(nrow(da), nrow(da.gbd)), all.rank = TRUE)

### Read in common.
da.common <- comm.read.table("iris.txt", header = TRUE, sep = "\\t\\t",
                             quote = "\\", read.method = "common")
comm.print(c(nrow(da.common), sum(da.common != iris)))

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)

```

global Rprof

A Rprof Function for SPMD Routines

Description

A Rprof function for use with parallel codes executed in the batch SPMD style.

Usage

```

comm.Rprof(filename = "Rprof.out", append = FALSE, interval = 0.02,
            memory.profiling = FALSE, gc.profiling = FALSE,
            line.profiling = FALSE, numfiles = 100L, bufsize = 10000L,
            all.rank = .pbd_env$SPMD.CT$Rprof.all.rank,
            rank.Rprof = .pbd_env$SPMD.CT$rank.source,
            comm = .pbd_env$SPMD.CT$comm)

```

Arguments

filename	as in Rprof() .
append	as in Rprof() .
interval	as in Rprof() .
memory.profiling	as in Rprof() .
gc.profiling	as in Rprof() .
line.profiling	as in Rprof() .
numfiles	as in Rprof() .
bufsize	as in Rprof() .

<code>all.rank</code>	if calling Rprof on all ranks (default = FALSE).
<code>rank.Rprof</code>	rank for calling Rprof if <code>all.rank</code> = FALSE (default = 0).
<code>comm</code>	a communicator number.

Details

as in `Rprof()`.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

global sort	<i>Global Quick Sort for Distributed Vectors or Matrices</i>
-------------	--

Description

This function globally sorts distributed data for all ranks.

Usage

```
comm.sort(x, decreasing = FALSE, na.last = NA,
          comm = .pbd_env$SPMD.CT$comm,
          status = .pbd_env$SPMD.CT$status)
```

Arguments

<code>x</code>	a vector.
<code>decreasing</code>	logical. Should the sort order be increasing or decreasing?
<code>na.last</code>	for controlling the treatment of NAs. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed.
<code>comm</code>	a communicator number.
<code>status</code>	a status number.

Details

The distributed quick sort is implemented for this functions.

Value

The returns are the same size of `x` but in global sorting order.

Warning

All ranks may not have a NULL x.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
comm.set.seed(123456, diff = TRUE)
x <- c(rnorm(5 + .comm.rank * 2), NA)
# x <- sample(1:5, 5 + .comm.rank * 2, replace = TRUE)
comm.end.seed()

if(.comm.rank == 1){
  x <- NULL    ### Test for NULL or 0 vector
}

y <- allgather(x)
comm.print(y)

y <- comm.sort(x)
y <- allgather(y)
comm.print(y)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

global stop and warning

Global Stop and Warning Functions

Description

These functions are global stop and warning applying on distributed data for all ranks, and are called by experts only. These functions may lead to potential performance degradation and system termination.

Usage

```
comm.stop(..., call. = TRUE, domain = NULL,
          all.rank = .pbd_env$SPMD.CT$print.all.rank,
          rank.print = .pbd_env$SPMD.CT$rank.source,
          comm = .pbd_env$SPMD.CT$comm,
          mpi.finalize = .pbd_env$SPMD.CT$mpi.finalize,
          quit = .pbd_env$SPMD.CT$quit)

comm.warning(..., call. = TRUE, immediate. = FALSE, domain = NULL,
            all.rank = .pbd_env$SPMD.CT$print.all.rank,
            rank.print = .pbd_env$SPMD.CT$rank.source,
            comm = .pbd_env$SPMD.CT$comm)

comm.warnings(...,
              all.rank = .pbd_env$SPMD.CT$print.all.rank,
              rank.print = .pbd_env$SPMD.CT$rank.source,
              comm = .pbd_env$SPMD.CT$comm)

comm.stopifnot(..., call. = TRUE, domain = NULL,
               all.rank = .pbd_env$SPMD.CT$print.all.rank,
               rank.print = .pbd_env$SPMD.CT$rank.source,
               comm = .pbd_env$SPMD.CT$comm,
               mpi.finalize = .pbd_env$SPMD.CT$mpi.finalize,
               quit = .pbd_env$SPMD.CT$quit)
```

Arguments

...	variables to be cat.
call.	see stop() and warnings().
immediate.	see stop() and warnings().
domain	see stop() and warnings().
all.rank	if all ranks print (default = FALSE).
rank.print	rank for printing if not all ranks print (default = 0).
comm	communicator for printing (default = 1).

```

mpi.finalize    if MPI should be shutdown.
quit           if quit R when errors happen.

```

Details

These functions will respectively apply `stop()`, `warning()`, `warnings()`, and `stopifnot()` locally.

Value

`comm.stop()` and `comm.stopifnot()` terminate all ranks, `comm.warning()` returns messages, and `comm.warnings()` print the message.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```

## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

if(comm.size() != 2){
  comm.cat("\n2 processors are required.\n", quiet = TRUE)
  finalize()
}

### Examples.
comm.warning("\ntest warning.\n")
comm.warnings()
comm.stop("\ntest stop.\n")
comm.stopifnot(1 == 2)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)

```

global timer*A Timing Function for SPMD Routines*

Description

A timing function for use with parallel codes executed in the batch SPMD style.

Usage

```
comm.timer(timed, comm = .pbd_env$SPMD.CT$comm)
```

Arguments

timed	expression to be timed.
comm	a communicator number.

Details

Finds the min, mean, and max execution time across all independent processes executing the operation timed.

Author(s)

Drew Schmidt.

References

Programming with Big Data in R Website: <https://pbdr.org/>

global which, which.max, and which.min*Global Which Functions*

Description

These functions are global which, which.max and which.min applying on distributed data for all ranks.

Usage

```
comm.which(x, arr.ind = FALSE, useNames = TRUE,  
           comm = .pbd_env$SPMD.CT$comm)  
comm.which.max(x, comm = .pbd_env$SPMD.CT$comm)  
comm.which.min(x, comm = .pbd_env$SPMD.CT$comm)
```

Arguments

<code>x</code>	a 'logical' vector or array as in <code>which()</code> , or an 'numeric' objects in <code>which.max()</code> and <code>which.min()</code> .
<code>arr.ind</code>	logical, as in <code>which()</code> .
<code>useNames</code>	logical, as in <code>which()</code> .
<code>comm</code>	a communicator number.

Details

These functions will apply `which()`, `which.max()` and `which.min()` locally, and apply `allgather()` to get all local results from other ranks.

Value

The global values (`which()`, `which.max()`, or `which.min()`) are returned to all ranks.

`comm.which()` returns with two columns, 'rank id' and 'index of TRUE'.

`comm.which.max()` and `comm.which.min()` return with three values, 'the _smallest_ rank id', 'index of the _first_ maximum or minimum', and 'max/min value of x'.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[comm.read.table\(\)](#)

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

if(comm.size() != 2){
  comm.cat("\n2 processors are required.\n", quiet = TRUE)
  finalize()
}

### Examples.
a <- 1:(comm.rank() + 1)
```

```

b <- comm.which(a == 2)
comm.print(b)
b <- comm.which.max(a)
comm.print(b)
b <- comm.which.min(a)
comm.print(b)

### Finish.
finalize()
"
# execmpi(spmc.code, nranks = 2L)

## End(Not run)

```

global writing

Global Writing Functions

Description

These functions are global writing applying on distributed data for all ranks.

Usage

```

comm.write(x, file = "data", ncolumns = if(is.character(x)) 1 else 5,
           append = FALSE, sep = " ", comm = .pbd_env$SPMD.CT$comm)
comm.write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ",
                 eol = "\n", na = "NA", dec = ".", row.names = TRUE,
                 col.names = TRUE, qmethod = c("escape", "double"),
                 fileEncoding = "", comm = .pbd_env$SPMD.CT$comm)

comm.write.csv(..., comm = .pbd_env$SPMD.CT$comm)
comm.write.csv2(..., comm = .pbd_env$SPMD.CT$comm)

```

Arguments

x	as in write() or write.table().
file	as in write() or write.table().
ncolumns	as in write*().
append	as in write*().
sep	as in write*().
quote	as in write*().
eol	as in write*().
na	as in write*().
dec	as in write*().

row.names	as in write*().
col.names	as in write*().
qmethod	as in write*().
fileEncoding	as in write*().
...	as in write*().
comm	a communicator number.

Details

These functions will apply write*() locally and sequentially from rank 0, 1, 2, ...

By default, rank 0 makes the file, and rest of ranks append the data.

Value

A file will be returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[comm.load.balance\(\)](#) and [comm.read.table\(\)](#)

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

smpd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
if(comm.size() != 2){
  comm.cat("\n2 processors are required.\n", quiet = TRUE)
  finalize()
}

### Examples.
comm.write((1:5) + comm.rank(), file = "test.txt")

### Finish.
finalize()
"
```

```
# execmpi(spmc.code, nranks = 2L)

## End(Not run)
```

info

Info Functions

Description

The functions call MPI info functions.

Usage

```
info.create(info = .pbd_env$SPMD.CT$info)
info.set(info = .pbd_env$SPMD.CT$info, key, value)
info.free(info = .pbd_env$SPMD.CT$info)
info.c2f(info = .pbd_env$SPMD.CT$info)
```

Arguments

info	a info number.
key	a character string to be set.
value	a character string to be set associate with key.

Details

These functions are for internal functions. Potentially, they set information for initialization of manager and workers.

Value

An invisible state of MPI call is returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
info.create(0L)
info.set(0L, \"file\", \"appschema\")
info.free(0L)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

irecv-method

A Rank Receives (Nonblocking) an Object from the Other Rank

Description

This method lets a rank receive (nonblocking) an object from the other rank in the same communicator. The default return is the object sent from the other rank.

Usage

```
irecv(x.buffer = NULL, rank.source = .pbd_env$SPMD.CT$rank.source,
      tag = .pbd_env$SPMD.CT$tag, comm = .pbd_env$SPMD.CT$comm,
      request = .pbd_env$SPMD.CT$request,
      status = .pbd_env$SPMD.CT$status)
```

Arguments

<code>x.buffer</code>	a buffer to store x sent from the other rank.
<code>rank.source</code>	a source rank where x sent from
<code>tag</code>	a tag number.
<code>comm</code>	a communicator number.
<code>request</code>	a request number.
<code>status</code>	a status number.

Details

A corresponding `send()/isend()` should be evoked at the corresponding rank `rank.source`.

Warning: `irecv()` is not safe for **R** since **R** is not a thread safe package that a dynamic returning object requires certain blocking or barrier at some where. Current, the default method is equivalent to the default method of `recv()`.

Value

An object is returned by default.

Methods

For calling `spmd.irecv.*()`:

`signature(x = "ANY")`

`signature(x = "integer")`

`signature(x = "numeric")`

`signature(x = "raw")`

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[recv\(\)](#), [send\(\)](#), [isend\(\)](#).

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
if(.comm.rank == 0){
  y <- send(matrix(x, nrow = 1))
} else if(.comm.rank == 1){
```

```

    y <- irecv()
  }
  comm.print(y, rank.print = 1)

  ### Finish.
  finalize()
  "
  # execmpi(spmc.code, nranks = 2L)

  ## End(Not run)

```

is.comm.null	<i>Check if a MPI_COMM_NULL</i>
--------------	---------------------------------

Description

The functions check MPI_COMM_NULL.

Usage

```
is.comm.null(comm = .pbd_env$SPMD.CT$comm)
```

Arguments

comm a comm number.

Details

These functions are for internal uses.

Value

TRUE if input comm is MPI_COMM_NULL, otherwise FALSE.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
is.comm.null(0L)
is.comm.null(1L)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

isend-method

A Rank Send (Nonblocking) an Object to the Other Rank

Description

This method lets a rank send (nonblocking) a object to the other rank in the same communicator. The default return is NULL.

Usage

```
isend(x, rank.dest = .pbd_env$SPMD.CT$rank.dest,
      tag = .pbd_env$SPMD.CT$tag,
      comm = .pbd_env$SPMD.CT$comm,
      request = .pbd_env$SPMD.CT$request,
      check.type = .pbd_env$SPMD.CT$check.type)
```

Arguments

<code>x</code>	an object to be sent from a rank.
<code>rank.dest</code>	a rank of destination where x send to.
<code>tag</code>	a tag number.
<code>comm</code>	a communicator number.
<code>request</code>	a request number.
<code>check.type</code>	if checking data type first for handshaking.

Details

A corresponding `recv()` or `irecv()` should be evoked at the corresponding rank `rank.dest`.
See details of `send()` for the arguments `check.type`.

Value

A NULL is returned by default.

Methods

For calling `spmd.isend.*()`:

```
signature(x = "ANY")
signature(x = "integer")
signature(x = "numeric")
signature(x = "raw")
```

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel,
and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[send\(\)](#), [recv\(\)](#), [irecv\(\)](#).

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
if(.comm.rank == 0){
  y <- isend(matrix(x, nrow = 1))
} else if(.comm.rank == 1){
  y <- recv()
}
```

```
comm.print(y, rank.print = 1)

### Finish.
finalize()
"
# execmpi(spmc.code, nranks = 2L)

## End(Not run)
```

MPI array pointers	<i>Set or Get MPI Array Pointers in R</i>
--------------------	---

Description

The function set/get a point address in R where the point point to a structure containing MPI arrays.

Usage

```
arrange.mpi.pts()
```

Details

Since Rmpi/pbdMPI pre-allocate memory to store comm, status, datatype, info, request, this function provides a variable in R to let different APIs share the same memory address.

If the package loads first, then this sets ‘`.__MPI_APTS__`’ in the `.GlobalEnv` of R. If the package does not load before other MPI APIs, then this gives a structure pointer to external memory according to ‘`.__MPI_APTS__`’, i.e. allocated by other MPI APIs.

pbdMPI/R/arrange.mpi.pts provides the R code, and pbdMPI/src/pkg_*.c provides the details of this call.

Value

‘`.__MPI_APTS__`’ is set in `.GlobalEnv` of R.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### See source code for the details.

## End(Not run)
```

Description

These functions are designed to get or print MPI_COMM pointer and its address when the SPMD code in R be a foreign application of other applications.

Usage

```
get.mpi.comm.ptr(comm = .pbd_env$SPMD.CT$comm, show.msg = FALSE)
addr.mpi.comm.ptr(comm.ptr)
```

Arguments

comm	a communicator number.
comm.ptr	a communicator pointer.
show.msg	if showing message for debug only.

Details

get.mpi.comm.ptr() returns an R external pointer that points to the address of the comm.
 addr.mpi.comm.ptr() takes the R external points, and prints the address of the comm. This function is mainly for debugging.

Value

get.mpi.comm.ptr() returns an R external pointer.
 addr.mpi.comm.ptr() prints the comm pointer address and the address of MPI_COMM_WORLD.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
### Save code in a file "demo.r" and run with 22processors by
### SHELL> mpiexec -np 2 Rscript demo.r

smd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
```

```
ptr1 <- get.mpi.comm.ptr(1, show.msg = TRUE)
addr.mpi.comm.ptr(ptr1)

comm.split(color = as.integer(comm.rank()/2), key = comm.rank())

ptr1.new <- get.mpi.comm.ptr(1, show.msg = TRUE)
addr.mpi.comm.ptr(ptr1.new)

### Finish.
finalize()
"

pbdMPI::execmpi(spmc.code = spmd.code, nranks = 2L)
```

probe

Probe Functions

Description

The functions call MPI probe functions.

Usage

```
probe(rank.source = .pbd_env$SPMD.CT$rank.source,
      tag = .pbd_env$SPMD.CT$tag, comm = .pbd_env$SPMD.CT$comm,
      status = .pbd_env$SPMD.CT$status)
iprobe(rank.source = .pbd_env$SPMD.CT$rank.source,
       tag = .pbd_env$SPMD.CT$tag, comm = .pbd_env$SPMD.CT$comm,
       status = .pbd_env$SPMD.CT$status)
```

Arguments

rank.source	a source rank where an object sent from.
tag	a tag number.
comm	a communicator number.
status	a status number.

Details

These functions are for internal functions. Potentially, they set/get probe for receiving data.

Value

An invisible state of MPI call is returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### See source code of spmd.recv.default() for an example.

## End(Not run)
```

recv-method

A Rank Receives (Blocking) an Object from the Other Rank

Description

This method lets a rank receive (blocking) an object from the other rank in the same communicator. The default return is the object sent from the other rank.

Usage

```
recv(x.buffer = NULL, rank.source = .pbd_env$SPMD.CT$rank.source,
     tag = .pbd_env$SPMD.CT$tag, comm = .pbd_env$SPMD.CT$comm,
     status = .pbd_env$SPMD.CT$status,
     check.type = .pbd_env$SPMD.CT$check.type)
```

Arguments

<code>x.buffer</code>	a buffer to store <code>x</code> sent from the other rank.
<code>rank.source</code>	a source rank where <code>x</code> sent from
<code>tag</code>	a tag number.
<code>comm</code>	a communicator number.
<code>status</code>	a status number.
<code>check.type</code>	if checking data type first for handshaking.

Details

A corresponding `send()` should be evoked at the corresponding rank `rank.source`.

These are high level S4 methods. By default, `check.type` is TRUE and an additional `send()/recv()` will make a handshaking call first, then deliver the data next. i.e. an integer vector of length two (type and length) will be deliver first between `send()` and `recv()` to ensure a buffer (of right type and right size/length) is properly allocated at the `rank.dest` side.

Currently, four data types are considered: integer, double, raw/byte, and default/raw.object. The default method will make a `serialize()` call first to convert the general R object into a raw vector before sending it away. After the raw vector is received at the `rank.dest` side, the vector will be `unserialize()` back to the R object format.

check.type set as FALSE will stop the additional handhsaking call, but the buffer should be prepared carefully by the user self. This is typically for the advanced users and more specifically calls are needed. i.e. calling those spmd.send.integer with spmd.recv.integer correspondingly.

check.type also needs to be set as FALSE for more efficient calls such as isend()/recv() or send()/irecv(). Currently, no check types are implemented in those mixed calls.

Value

An object is returned by default and the buffer will be overwritten implicitly.

Methods

For calling spmd.recv.*():

```
signature(x = "ANY")
```

```
signature(x = "integer")
```

```
signature(x = "numeric")
```

```
signature(x = "raw")
```

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[irecv\(\)](#), [send\(\)](#), [isend\(\)](#).

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r
```

```
spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()
```

```
### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
if(.comm.rank == 0){
  y <- send(matrix(x, nrow = 1))
} else if(.comm.rank == 1){
  y <- recv()
```

```

}
comm.print(y, rank.print = 1)

### Finish.
finalize()
"

pbdMPI::execmpi(spmc.code, nranks = 2L)

```

reduce-method

A Rank Receive a Reduction of Objects from Every Rank

Description

This method lets a rank receive a reduction of objects from every rank in the same communicator based on a given operation. The default return is an object as the input.

Usage

```

reduce(x, x.buffer = NULL, op = .pbd_env$SPMD.CT$op,
       rank.dest = .pbd_env$SPMD.CT$rank.source,
       comm = .pbd_env$SPMD.CT$comm)

```

Arguments

<code>x</code>	an object to be gathered from all ranks.
<code>x.buffer</code>	a buffer to hold the return object which probably has <code>x</code> with the same type of <code>x</code> .
<code>op</code>	a reduction operation applied on combine all <code>x</code> .
<code>rank.dest</code>	a rank of destination where all <code>x</code> reduce to.
<code>comm</code>	a communicator number.

Details

By default, the object is reduced to `.pbd_env$SPMD.CT$rank.source`, i.e. *rank 0L*.

All `x` on all ranks are likely presumed to have the same size and type.

`x.buffer` can be `NULL` or unspecified. If specified, the type should be either integer or double specified correctly according to the type of `x`.

See `methods{"reduce"}` for S4 dispatch cases and the source code for further details.

Value

The reduced object of the same type as `x` is returned by default.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[allgather\(\)](#), [gather\(\)](#), [reduce\(\)](#).

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initial.
suppressMessages(library(pbdMPI, quietly = TRUE))
init()
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
y <- reduce(matrix(x, nrow = 1), op = \"sum\")
comm.print(y)

y <- reduce(x, double(N), op = \"prod\")
comm.print(y)

x <- as.logical(round(runif(N)))
y <- reduce(x, logical(N), op = \"land\")
comm.print(y)

### Finish.
finalize()
"

pbdMPI::execmpi(spmd.code = spmd.code, nranks = 2L)
```

scatter-method

A Rank Scatter Objects to Every Rank

Description

This method lets a rank scatter objects to every rank in the same communicator. The default input is a list of length equal to ‘comm size’ and the default return is an element of the list.

Usage

```
scatter(x, x.buffer = NULL, x.count = NULL, displs = NULL,
       rank.source = .pbd_env$SPMD.CT$rank.source,
       comm = .pbd_env$SPMD.CT$comm)
```

Arguments

<code>x</code>	an object of length ‘comm size’ to be scattered to all ranks.
<code>x.buffer</code>	a buffer to hold the return object which probably has ‘size of element of <code>x</code> ’ with the same type of the element of <code>x</code> .
<code>x.count</code>	a vector of length ‘comm size’ containing all object lengths.
<code>displs</code>	<code>c(0L, cumsum(x.count))</code> by default.
<code>rank.source</code>	a rank of source where elements of <code>x</code> scatter from.
<code>comm</code>	a communicator number.

Details

All elements of `x` are likely presumed to have the same size and type.

`x.buffer`, `x.count`, and `displs` can be `NULL` or unspecified. If specified, the type should be one of integer, double, or raw specified correctly according to the type of `x`.

If `x.count` is specified, then the `spmd.scatterv.*()` is called.

Value

An element of `x` is returned according to the rank id.

Methods

For calling `spmd.scatter.*()`:

```
signature(x = "ANY", x.buffer = "missing", x.count = "missing")
signature(x = "integer", x.buffer = "integer", x.count = "missing")
signature(x = "numeric", x.buffer = "numeric", x.count = "missing")
signature(x = "raw", x.buffer = "raw", x.count = "missing")
```

For calling `spmd.scatterv.*()`:

```
signature(x = "ANY", x.buffer = "missing", x.count = "integer")
signature(x = "ANY", x.buffer = "ANY", x.count = "integer")
signature(x = "integer", x.buffer = "integer", x.count = "integer")
signature(x = "numeric", x.buffer = "numeric", x.count = "integer")
signature(x = "raw", x.buffer = "raw", x.count = "integer")
```

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also[bcast\(\)](#).**Examples**

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r
```

```
spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- split(1:(N * .comm.size), rep(1:.comm.size, N))
y <- scatter(lapply(x, matrix, nrow = 1))
comm.print(y)
y <- scatter(x, double(N))
comm.print(y)

### Finish.
finalize()
"

pbdMPI::execmpi(spmd.code, nranks = 2L)
```

seed for RNG

*Parallel random number generation with reproducible results***Description**

These functions control the parallel-capable L'Ecuyer-CMRG pseudo-random number generator (RNG) on clusters and in multicore parallel applications for reproducible results. Reproducibility is possible across different node and core configurations by associating the RNG streams with an application vector.

Usage

```
comm.set.seed(
  seed = NULL,
  diff = TRUE,
  state = NULL,
  streams = NULL,
  comm = .pbd_env$SPMD.CT$comm
)
comm.set.stream(
  name = NULL,
```

```

    reset = FALSE,
    state = NULL,
    comm = .pbd_env$SPMD.CT$comm
  )
  comm.get.streams(
    comm = .pbd_env$SPMD.CT$comm,
    seed = FALSE
  )

```

Arguments

seed	In <code>comm.set.seed</code> , a single value interpreted as an integer. In <code>comm.get.streams</code> , a logical if TRUE, return includes the current local <code>.Random.seed</code> .
diff	Logical indicating if the parallel instances should have different random streams.
state	In function <code>comm.set.seed</code> : This parameter is deprecated. In function <code>comm.set.stream</code> : If non-NULL it restarts a stream from a previously saved state <code><- comm.set.stream()</code> . A stream state is a list with one named element, which is the 6-element L'Ecuyer-CMRG <code>.Random.seed</code> , probably captured earlier with <code>state <- comm.set.stream()</code> . The stream name, if different from a provided parameter name, has precedence, but a warning is produced. Further, the requesting rank must own the stream.
streams	An vector of sequential integers specifying the streams to be prepared on the current rank. Typically, this is used by <code>'comm.chunk()'</code> to prepare correct streams for each rank, which are aligned with the vector being chunk-ed.
name	Stream number that is coercible to character, indicating to start or continue generating from that stream.
reset	If true, reset the requested stream back to its beginning.
comm	The communicator that determines MPI rank numbers.

Details

This implementation uses the function `nextRNGStream` in package `parallel` to set up streams appropriate for working on a cluster system with MPI. The main difference from `parallel` is that it adds a reproducibility capability with vector-based streams that works across different numbers of nodes or cores by associating streams with an application vector.

Vector-based streams are best set up with the higher level function `comm.chunk` instead of using `comm.set.stream` directly. `comm.chunk` will set up only the streams that each rank needs and provides the stream numbers necessary to switch between them with `comm.set.stream`.

The function uses `parallel`'s `nextRNGStream()` and sets up the parallel stream seeds in the `.pbd_env$RNG` environment, which are then managed with `comm.set.stream`. There is only one communication broadcast in this implementation that ensures all ranks have the same seed as rank 0. Subsequently, each rank maintains only its own streams.

When rank-based streams are set up, `comm.chunk` with `form = "number"` and `rng = TRUE` parameters, streams are different for each rank and switching is not needed. Vector-based streams are obtained with `form = "vector"` and `rng = TRUE` parameters. In this latter case, the vector returned to each rank contains the stream numbers (and vector components) that the rank owns. Switch with

`comm.set.stream(v)`, where `v` is one of the stream numbers. Switching back and forth is allowed, with each stream continuing where it left off.

RNG Notes R sessions connected by MPI begin like other R sessions as discussed in [Random](#). On first use of random number generation, each rank computes its own seed from a combination of clock time and process id (unless it reads a previously saved workspace, which is not recommended). Because of asynchronous execution, imperfectly synchronized node clocks, and likely different process ids, this almost guarantees unique seeds and most likely results in independent streams. However, this is not reproducible and not guaranteed. Both reproducibility and guarantee are brought by the use of the L'Ecuyer-CMRG generator implementation in [nextRNGStream](#) and the use of `comm.set.seed` and [comm.set.stream](#) adaptation for parallel computing on cluster systems.

At a high level, the L'Ecuyer-CMRG pseudo-random number generator can take jumps (advance the seed) in its stream (about 2^{191} long) so that distant substreams can be assigned. The [nextRNGStream](#) implementation takes jumps of 2^{127} (about $1.7e38$) to provide up to 2^{64} (about $1.8e19$) independent streams. See <https://stat.ethz.ch/R-manual/R-devel/library/parallel/doc/parallel.pdf> for more details.

In situations that require the same stream on all ranks, a simple [set.seed](#) from base R and the default RNG will suffice. `comm.set.seed` will also accomplish this with the `diff = FALSE` parameter if switching between same and different streams is needed.

Value

`comm.set.seed` engages the L'Ecuyer-CMRG RNG and invisibly returns the previous RNG in use (Output of `RNGkind()[1]`). Capturing it, enables the restoration of the previous RNG with [RNGkind](#). See examples of use in `demo/seed_rank.r` and `demo/seed_vec.r`.

`comm.set.stream` invisibly returns the current stream number as character.

`comm.get.streams` returns the current stream name and other stream names available to the rank as a character string. Optionally, the local `.Random.seed` is included. This function is a debugging aid for distributed random streams.

All three functions manage and use the environment `.pbd_env$RNG`.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Pierre L'Ecuyer, Simard, R., Chen, E.J., and Kelton, W.D. (2002) An Object-Oriented Random-Number Package with Many Long Streams and Substreams. *Operations Research*, 50(6), 1073-1075.

<https://www.iro.umontreal.ca/~lecuyer/myftp/papers/streams00.pdf>

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`comm.chunk()`

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
suppressMessages(library(pbdMPI, quietly = TRUE))

comm.print(RNGkind())
comm.print(runif(5), all.rank = TRUE)

set.seed(1357)
comm.print(runif(5), all.rank = TRUE)

old.kind = comm.set.seed(1357)
comm.print(RNGkind())
comm.print(runif(5), all.rank = TRUE)

comm.set.stream(reset = TRUE)
comm.print(runif(5), all.rank = TRUE)

comm.set.seed(1357, diff = TRUE)
comm.print(runif(5), all.rank = TRUE)

state <- comm.set.stream() ### save each rank's stream state
comm.print(runif(5), all.rank = TRUE)

comm.set.stream(state = state) ### set current RNG to state
comm.print(runif(5), all.rank = TRUE)

RNGkind(old.kind)
set.seed(1357)
comm.print(RNGkind())
comm.print(runif(5), all.rank = TRUE)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

send-method

A Rank Send (blocking) an Object to the Other Rank

Description

This method lets a rank send (blocking) an object to the other rank in the same communicator. The default return is NULL.

Usage

```
send(x, rank.dest = .pbd_env$SPMD.CT$rank.dest,
     tag = .pbd_env$SPMD.CT$tag,
     comm = .pbd_env$SPMD.CT$comm,
     check.type = .pbd_env$SPMD.CT$check.type)
```

Arguments

<code>x</code>	an object to be sent from a rank.
<code>rank.dest</code>	a rank of destination where <code>x</code> send to.
<code>tag</code>	a tag number.
<code>comm</code>	a communicator number.
<code>check.type</code>	if checking data type first for handshaking.

Details

A corresponding `recv()` should be evoked at the corresponding rank `rank.dest`.

These are high level S4 methods. By default, `check.type` is TRUE and an additional `send()/recv()` will make a handshaking call first, then deliver the data next. i.e. an integer vector of length two (type and length) will be deliver first between `send()` and `recv()` to ensure a buffer (of right type and right size/length) is properly allocated at the `rank.dest` side.

Currently, four data types are considered: integer, double, raw/byte, and default/raw.object. The default method will make a `serialize()` call first to convert the general R object into a raw vector before sending it away. After the raw vector is received at the `rank.dest` side, the vector will be `unserialize()` back to the R object format.

`check.type` set as FALSE will stop the additional handhsaking call, but the buffer should be prepared carefully by the user self. This is typically for the advanced users and more specifically calls are needed. i.e. calling those `spmd.send.integer` with `spmd.recv.integer` correspondingly.

`check.type` also needs to be set as FALSE for more efficient calls such as `isend()/recv()` or `send()/irecv()`. Currently, no check types are implemented in those mixed calls.

Value

A NULL is returned by default.

Methods

For calling `spmd.send.*()`:

```
signature(x = "ANY")
signature(x = "integer")
signature(x = "numeric")
signature(x = "raw")
```

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[isend\(\)](#), [recv\(\)](#), [irecv\(\)](#).

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
if(.comm.rank == 0){
  y <- send(matrix(x, nrow = 1))
} else if(.comm.rank == 1){
  y <- recv()
}
comm.print(y, rank.print = 1)

### Finish.
finalize()
"

pbdMPI::execmpi(spmd.code, nranks = 2L)
```

sendrecv-method

Send and Receive an Object to and from Other Ranks

Description

This method lets a rank send an object to the other rank and receive an object from another rank in the same communicator. The default return is x.

Usage

```

sendrecv(x, x.buffer = NULL,
  rank.dest = (comm.rank(.pbd_env$SPMD.CT$comm) + 1) %%
    comm.size(.pbd_env$SPMD.CT$comm),
  send.tag = .pbd_env$SPMD.CT$tag,
  rank.source = (comm.rank(.pbd_env$SPMD.CT$comm) - 1) %%
    comm.size(.pbd_env$SPMD.CT$comm),
  recv.tag = .pbd_env$SPMD.CT$tag,
  comm = .pbd_env$SPMD.CT$comm, status = .pbd_env$SPMD.CT$status)

```

Arguments

<code>x</code>	an object to be sent from a rank.
<code>x.buffer</code>	a buffer to store <code>x</code> sent from the other rank.
<code>rank.dest</code>	a rank of destination where <code>x</code> send to.
<code>send.tag</code>	a send tag number.
<code>rank.source</code>	a source rank where <code>x</code> sent from.
<code>recv.tag</code>	a receive tag number.
<code>comm</code>	a communicator number.
<code>status</code>	a status number.

Details

A corresponding `sendrecv()` should be evoked at the corresponding ranks `rank.dest` and `rank.source`. `rank.dest` and `rank.source` can be as `integer(NULL)` to create a silent `sendrecv` operation which is more efficient than setting `rank.dest` and `rank.source` to be equal.

Value

A `x` is returned by default.

Methods

For calling `spmd.sendrecv.*()`:

```

signature(x = "ANY", x.buffer = "ANY")
signature(x = "integer", x.buffer = "integer")
signature(x = "numeric", x.buffer = "numeric")
signature(x = "raw", x.buffer = "raw")

```

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[sendrecv.replace\(\)](#).

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.size
y <- sendrecv(matrix(x, nrow = 1))
comm.print(y, rank.print = 1)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

sendrecv.replace-method

Send and Receive an Object to and from Other Ranks

Description

This method lets a rank send an object to the other rank and receive an object from another rank in the same communicator. The default return is x.

Usage

```
sendrecv.replace(x,
  rank.dest = (comm.rank(.pbd_env$SPMD.CT$comm) + 1) %%
    comm.size(.pbd_env$SPMD.CT$comm),
  send.tag = .pbd_env$SPMD.CT$tag,
  rank.source = (comm.rank(.pbd_env$SPMD.CT$comm) - 1) %%
    comm.size(.pbd_env$SPMD.CT$comm),
```

```
recv.tag = .pbd_env$SPMD.CT$tag,  
comm = .pbd_env$SPMD.CT$comm, status = .pbd_env$SPMD.CT$status)
```

Arguments

x	an object to be sent from a rank.
rank.dest	a rank of destination where x send to.
send.tag	a send tag number.
rank.source	a source rank where x sent from.
recv.tag	a receive tag number.
comm	a communicator number.
status	a status number.

Details

A corresponding `sendrecv.replace()` should be evoked at the corresponding ranks `rank.dest` and `rank.source`.

`rank.dest` and `rank.source` can be `as.integer(NULL)` to create a silent `sendrecv` operation which is more efficient than setting `rank.dest` and `rank.source` to be equal.

Warning: `sendrecv.replace()` is not safe for R since R is not a thread safe package that a dynamic returning object requires certain blocking or barrier at some where. The replaced object or memory address ‘MUST’ return correctly. This is almost equivalent to `sendrecv()`.

Value

A x is returned by default.

Methods

For calling `spmd.sendrecv.replace.*()`:

```
signature(x = "ANY")  
signature(x = "integer")  
signature(x = "numeric")  
signature(x = "raw")
```

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[sendrecv\(\)](#).

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.size
x <- sendrecv.replace(matrix(x, nrow = 1))
comm.print(x, rank.print = 1)

### Finish.
finalize()
"
# execmpi(spmd.code, nrank = 2L)

## End(Not run)
```

Set global pbd options

Set Global pbdR Options

Description

This is an advanced function to set pbdR options.

Usage

```
pbd_opt(..., bytext = "", envir = .GlobalEnv)
```

Arguments

...	in argument format option = value to set .pbd_env\$option <- value inside the envir.
bytext	in text format "option = value" to set .pbd_env\$option <- value inside the envir.
envir	by default the global environment is used.

Details

... allows multiple options in `envir$.pbd_env`, but only in a simple way.

`bytext` allows to assign options by text in `envir$.pbd_env`, but can assign advanced objects. For example, `"option$suboption <- value"` will set `envir$.pbd_env$option$suboption <- value`.

Value

No value is returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Drew Schmidt.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[.pbd_env](#), [SPMD.CT\(\)](#), [SPMD.OP\(\)](#), [SPMD.IO\(\)](#), [SPMD.TP\(\)](#), and [.mpiopt_init\(\)](#).

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 4 processors by
### SHELL> mpiexec -np 4 Rscript demo.r

### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))

### Examples.
ls(.pbd_env)
pbd_opt(ICTXT = c(2, 2))
pbd_opt(bytext = "grid.new <- list(); grid.new$ICTXT <- c(4, 4)")
pbd_opt(BLDIM = c(16, 16), bytext = "grid.new$BLDIM = c(8, 8)")
ls(.pbd_env)
.pbd_env$ICTXT
.pbd_env$BLDIM
.pbd_env$grid.new

### Finish.
finalize()

## End(Not run)
```

sourcetag

Functions to Obtain source and tag

Description

The functions extract MPI_ANY_SOURCE, MPI_ANY_TAG, MPI_status.source and MPI_status.tag.

Usage

```
anysource()  
anytag()  
get.sourcetag(status = .pbd_env$SPMD.CT$status)
```

Arguments

status a status number.

Details

These functions are for internal uses.

Value

Corresponding status will be returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:  
### Save code in a file "demo.r" and run with 2 processors by  
### SHELL> mpiexec -np 2 Rscript demo.r  
  
spmd.code <- "  
### Initialize  
suppressMessages(library(pbdMPI, quietly = TRUE))  
.comm.size <- comm.size()  
.comm.rank <- comm.rank()  
if(.comm.size < 2)  
  comm.stop("\nAt least two processors are required.\n")  
  
### Examples.
```

```

if(.comm.rank != 0){
  send(as.integer(.comm.rank * 10), rank.dest = 0L,
       tag = as.integer(.comm.rank + 10))
}
if(.comm.rank == 0){
  for(i in 1:(.comm.size - 1)){
    ret <- recv(x.buffer = integer(1),
               rank.source = anysource(), tag = anytag())
    sourcetag <- get.sourcetag()
    print(c(sourcetag, ret))
  }
}

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)

```

SPMD Control

Default control in pbdMPI.

Description

These variables provide default values for most functions in the package.

Format

The environment `.pbd_env` contains several objects with parameters for communicators and methods.

Details

The elements of `.pbd_env$SPMD.CT` are default values for various controls

Elements	Default	Meaning
<code>comm</code>	0L	communicator index
<code>intercomm</code>	2L	inter communicator index
<code>info</code>	0L	info index
<code>newcomm</code>	1L	new communicator index
<code>op</code>	"sum"	the operation
<code>port.name</code>	"spmdport"	the operation
<code>print.all.rank</code>	FALSE	whether all ranks print message
<code>print.quiet</code>	FALSE	whether rank is added to print/cat
<code>rank.root</code>	0L	the rank of root
<code>rank.source</code>	0L	the rank of source
<code>rank.dest</code>	1L	the rank of destination

request	0L	the request index
serv.name	"spmdserv"	the service name
status	0L	the status index
tag	0L	the tag number
unlist	FALSE	whether to unlist a return
divide.method	"block"	default method for jid
mpi.finalize	TRUE	shutdown MPI on finalize()
quit	TRUE	quit when errors occur
msg.flush	TRUE	flush each comm.cat/comm.print
msg.barrier	TRUE	include barrier in comm.cat/comm.print
Rprof.all.rank	FALSE	call Rprof on all ranks
lazy.check	TRUE	use lazy check on all ranks

The elements of `.pbd_env$SPMD.OP` list the implemented operations for `reduce()` and `allreduce()`. Currently, implemented operations are "sum", "prod", "max", "min", "land", "band", "lor", "bor", "lxor", "bxor".

The elements of `.SPMD.IO` are default values for functions in `comm_read.r` and `comm_balance.r`.

Elements	Default	Meaning
max.read.size	5.2e6	max of reading size (5 MB)
max.test.lines	500	max of testing lines
read.method	"gbd"	default reading method
balance.method	"block"	default load balance method

where `balance.method` is only used for "gbd" reading method when `nrows = -1` and `skip = 0` are set.

The elements of `.pbd_env$SPMD.TP` are default values for task pull settings

Elements	Default	Meaning
bcast	FALSE	whether to <code>bcast()</code> objects to all ranks
barrier	TRUE	if call <code>barrier()</code> for all ranks
try	TRUE	if use <code>try()</code> in works
try.silent	FALSE	if silent the <code>try()</code> message

See [task.pull\(\)](#) for details.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

SPMD Control Functions

Sets of controls in pbdMPI.

Description

These sets of controls are used to provide default values in this package. The values are not supposed to be changed in general.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[.pbd_env.](#)

Task Pull

Functions for Task Pull Parallelism

Description

These functions are designed for SPMD but assume that rank 0 is a manager and the rest are workers.

Usage

```
task.pull(jids, FUN, ..., rank.manager = .pbd_env$SPMD.CT$rank.root,
          comm = .pbd_env$SPMD.CT$comm, bcast = .pbd_env$SPMD.TP$bcast,
          barrier = .pbd_env$SPMD.TP$barrier,
          try = .pbd_env$SPMD.TP$try,
          try.silent = .pbd_env$SPMD.TP$try.silent)

task.pull.workers(FUN = function(jid, ...){ return(jid) }, ...,
                  rank.manager = .pbd_env$SPMD.CT$rank.root,
                  comm = .pbd_env$SPMD.CT$comm,
                  try = .pbd_env$SPMD.TP$try,
                  try.silent = .pbd_env$SPMD.TP$try.silent)
task.pull.manager(jids, rank.manager = .pbd_env$SPMD.CT$rank.root,
                  comm = .pbd_env$SPMD.CT$comm)
```

Arguments

<code>jids</code>	all job ids (a vector of positive integers).
<code>FUN</code>	a function to be evaluated by workers.
<code>...</code>	extra parameters for <code>FUN</code> .
<code>rank.manager</code>	rank of the manager from where <code>jid</code> is sent.
<code>comm</code>	a communicator number.
<code>bcast</code>	if bcast to all ranks.
<code>barrier</code>	if barrier for all ranks.
<code>try</code>	whether to use <code>try()</code> to avoid crashes. CAUTION: <code>try = FALSE</code> is not safe and can crash all MPI/R jobs.
<code>try.silent</code>	turn off error messages from <code>try()</code> .

Details

All of these functions are designed to emulate a manager/workers paradigm in an SPMD environment. If your chunk workloads are known and similar, consider a direct SPMD solution.

`FUN` is a user defined function which has `jid` as its first argument and other variables are given in `...`

The manager will be queried by workers whenever a worker finishes a job to see if more jobs are available.

Value

A list with length `comm.size() - 1` will be returned to the manager and `NULL` to the workers. Each element of the list contains the returns `ret` of their `FUN` results.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

[get.jid\(\)](#).

Examples

```
## Not run:
### Under command mode, run the demo with 2 processors by
### (Use Rscript.exe for windows system)
# mpiexec -np 2 Rscript -e "demo(task_pull,'pbdMPI',ask=F,echo=F)"
### Or
# execmpi("demo(task_pull,'pbdMPI',ask=F,echo=F)", nranks = 2L)
```

```
## End(Not run)
```

Utility *execmpi*

Execute MPI code in system

Description

This function basically saves code in a `spmd.file` and executes MPI via R's system call e.g. `system("mpiexec -np 1 Rscript spmd.file")`.

Usage

```
execmpi(spmd.code = NULL, spmd.file = NULL,
        mpicmd = NULL, nranks = 1L, rscmd = NULL, verbose = TRUE,
        disable.current.mpi = TRUE, mpiopt = NULL, rsopt = NULL)
runmpi(spmd.code = NULL, spmd.file = NULL,
        mpicmd = NULL, nranks = 1L, rscmd = NULL, verbose = TRUE,
        disable.current.mpi = TRUE, mpiopt = NULL, rsopt = NULL)
```

Arguments

<code>spmd.code</code>	SPMD code to be run via <code>mpicmd</code> and <code>Rscript</code> .
<code>spmd.file</code>	a file contains SPMD code to be run via <code>mpicmd</code> and <code>Rscript</code> .
<code>mpicmd</code>	MPI executable command. If <code>NULL</code> , system default will be searched.
<code>nranks</code>	number of processes to run the SPMD code invoked by <code>mpicmd</code> .
<code>rscmd</code>	<code>Rscript</code> executable command. If <code>NULL</code> , system default will be searched.
<code>verbose</code>	print SPMD code outputs and MPI messages.
<code>disable.current.mpi</code>	force to finalize the current MPI comm if any, for unix-alike system only.
<code>mpiopt</code>	MPI options appended after <code>-np nranks --oversubscribe</code> .
<code>rsopt</code>	<code>Rscript</code> options appended after <code>Rscript</code> .

Details

When the `spmd.code` is `NULL`: The code should be already saved in the file named `spmd.file` for using.

When the `spmd.code` is not `NULL`: The `spmd.code` will be dumped to a temp file (`spmd.file`) via the call `writeLines(spmd.code, conn)` where `conn <- file(spmd.file, open = "wt")`. The file will be closed after the dumping.

When `spmd.file` is ready (either dumped from `spmd.code` or provided by the user), the steps below will be followed: If `spmd.file = NULL`, then a temporary file will be generated and used to dump `spmd.code`.

For Unix-alike systems, the command `cmd <- paste(mpicmd, "-np", nrank, mpiopt, rscmd, rscmd spmd.file, ">", log.file, " 2>&1 & echo \"PID=$!\" &")` is executed via `system(cmd, intern = TRUE, wait = FALSE, ignore.stdout = TRUE, ignore.stderr = TRUE)`. The `log.file` is a temporary file to save the outputs from the `spmd.code`. The results saved to the `log.file` will be read back in and `cat` and return to R.

For OPENMPI, the `"--oversubscribe"` is added before `mpiopt` as `mpiopt <- paste("--oversubscribe", mpiopt, sep = " ")` and is passed to `cmd` thereon.

For Windows, the `cmd` will be `paste(mpicmd, "-np", nrank, mpiopt, rscmd, rsopt spmd.file)` and is executed via `system(cmd, intern = TRUE, wait = FALSE, ignore.stdout = TRUE, ignore.stderr = TRUE)`.

Value

Basically, only the PID of the MPI job (in background) will be returned in Linux-alike systems. For Windows, the MPI job is always wait until it is complete.

Note

For Unix-alike systems, in new R and MPI, the `pbdrMPI::execmpi(...)` may carry the current MPI comm into `system(cmd, ...)` calls. Because the comm has been established/loaded by the `init()` call because of `::`, the `mpiexec` inside the `system(cmd, ...)` calls will be confused with the exist comm.

Consider that `pbdrMPI::execmpi(...)` is typically called in interactive mode (or actually only done for CRAN check in most case), an argument `disable.current.mpi = TRUE` is added/needed to finalize the existing comm first before `system(cmd, ...)` be executed.

This function is NOT recommended for running SPMD programs. The recommended way is to run under shell command.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Drew Schmidt.

References

Programming with Big Data in R Website: <https://pbdr.org/>

See Also

`pbdrCS::pbdrScript()`.

Examples

```
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.file <- tempfile()
cat("
suppressMessages(library(pbdMPI, quietly = TRUE))
allreduce(2)
```

```
finalize()
", file = spmd.file)
pbdMPI::execmpi(spmd.file = spmd.file, nranks = 2L)
```

wait

Wait Functions

Description

The functions call MPI wait functions.

Usage

```
wait(request = .pbd_env$SPMD.CT$request,
      status = .pbd_env$SPMD.CT$status)
waitany(count, status = .pbd_env$SPMD.CT$status)
waitsome(count)
waitall(count)
```

Arguments

request	a request number.
status	a status number.
count	a count number.

Details

These functions are for internal uses. Potentially, they wait after some nonblocking MPI calls.

Value

An invisible state of MPI call is returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com>, George Ostrouchov, Drew Schmidt, Pragneshkumar Patel, and Hao Yu.

References

Programming with Big Data in R Website: <https://pbdr.org/>

Examples

```
## Not run:
### Save code in a file "demo.r" and run with 2 processors by
### SHELL> mpiexec -np 2 Rscript demo.r

spmd.code <- "
### Initialize
suppressMessages(library(pbdMPI, quietly = TRUE))
.comm.size <- comm.size()
.comm.rank <- comm.rank()

### Examples.
N <- 5
x <- (1:N) + N * .comm.rank
if(.comm.rank == 0){
  isend(list(x))
}
if(.comm.rank == 1){
  y <- irecv(list(x))
}
wait()
comm.print(y, rank.print = 1L)

### Finish.
finalize()
"
# execmpi(spmd.code, nranks = 2L)

## End(Not run)
```

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