Package 'parallelly'

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Title Enhancing the 'parallel' Package

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VignetteBuilder parallelly

Description Utility functions that enhance the 'parallel' package and support the built-in parallel backends of the 'future' package. For example, availableCores() gives the number of CPU cores available to your R process as given by the operating system, 'cgroups' and Linux containers, R options, and environment variables, including those set by job schedulers on high-performance compute clusters. If none is set, it will fall back to parallel::detectCores(). Another example is 'parallel::makeCluster(type = ``RPSOCK")', which is backward compatible with 'parallel::makeCluster()' while doing a better job in setting up remote cluster workers without the need for configuring the firewall to do port-forwarding to your local computer.

License LGPL (>= 2.1)

LazyLoad TRUE

ByteCompile TRUE

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`as.cluster` *Coerce an Object to a Cluster Object*

Description

Coerce an Object to a Cluster Object

Usage

```
as.cluster(x, ...)

## S3 method for class 'cluster'
as.cluster(x, ...)

## S3 method for class 'list'
as.cluster(x, ...)

## S3 method for class 'SOCKnode'
as.cluster(x, ...)

## S3 method for class 'SOCK0node'
as.cluster(x, ...)

## S3 method for class 'RichSOCKnode'
```

```
as.cluster(x, ...)

## S3 method for class 'cluster'
c(..., recursive = FALSE)
```

Arguments

x	An object to be coerced.
recursive	Not used.
...	Additional arguments passed to the underlying coercion method. For `c(...)`, the clusters and cluster nodes to be combined.

Value

An object of class `cluster`.

`c(...)` combine multiple clusters and / or cluster nodes into one cluster returned as an of class `cluster`. A warning will be produced if there are duplicated nodes in the resulting cluster.

Examples

```
cl1 <- makeClusterPSOCK(2, dryrun = TRUE)
cl2 <- makeClusterPSOCK(c("n1", "server.remote.org"), dryrun = TRUE)
cl <- c(cl1, cl2)
print(cl)
```

---

autoStopCluster *Automatically Stop a Cluster when Garbage Collected*

Description

Registers a finalizer to a cluster such that the cluster will be stopped when garbage collected

Usage

```
autoStopCluster(cl, debug = FALSE)
```

Arguments

cl	A cluster object created by for instance `makeClusterPSOCK()` or `parallel::makeCluster()`.
debug	If TRUE, then debug messages are produced when the cluster is garbage collected.

Details

The cluster is stopped using `stopCluster(cl)`. An alternative to explicitly call this function on an existing `cluster` object, is to create the `cluster` object using `makeClusterPSOCK()` with argument `autoStop = TRUE`.

Value

The cluster object with attribute gcMe set.

Examples

```
cl <- makeClusterPSOCK(2, dryrun = TRUE)
cl <- autoStopCluster(cl)
print(cl)
rm(list = "cl")
gc()
```

---

availableConnections *Number of Available and Free Connections*

Description

The number of connections that can be open at the same time in R is *typically* 128, where the first three are occupied by the always open stdin(), stdout(), and stderr() connections, which leaves 125 slots available for other types of connections. Connections are used in many places, e.g. reading and writing to file, downloading URLs, communicating with parallel R processes over a socket connections (e.g. parallel::makeCluster() and makeClusterPSOCK()), and capturing standard output via text connections (e.g. utils::capture.output()).

Usage

```
availableConnections()

freeConnections()
```

Value

A non-negative integer, or +Inf if the available number of connections is greater than 16384, which is a limit be set via option parallelly.availableConnections.tries.

How to increase the limit

In R (>= 4.4.0), it is possible to *increase* the limit of 128 connections to a greater number via command-line option --max-connections=N, e.g.

```
$ Rscript -e "parallelly::availableConnections()"
[1] 128

$ Rscript --max-connections=512 -e "parallelly::availableConnections()"
[1] 512
```

For R (< 4.4.0), the limit can only be changed by rebuilding R from source, because the limited is hardcoded as a

```
#define NCONNECTIONS 128
```

in 'src/main/connections.c'.

How the limit is identified

Since the limit *might* changed, for instance in custom R builds or in future releases of R, we do not want to assume that the limit is 128 for all R installation. Unfortunately, it is not possible to query R for what the limit is. Instead, `availableConnections()` infers it from trial-and-error. Specifically, it attempts to open as many concurrent connections as possible until it fails. For efficiency, the result is memoized throughout the current R session.

References

1. 'WISH: Increase limit of maximum number of open connections (currently 125+3)', 2016-07-09, https://github.com/HenrikBengtsson/Wishlist-for-R/issues/28

See Also

`base::showConnections()`.

Examples

```
total <- availableConnections()
message("You can have ", total, " connections open in this R installation")
free <- freeConnections()
message("There are ", free, " connections remaining")
```

---

availableCores *Get Number of Available Cores on The Current Machine*

Description

The current/main R session counts as one, meaning the minimum number of cores available is always at least one.

Usage

```
availableCores(
  constraints = NULL,
  methods = getOption2("parallelly.availableCores.methods", c("system",
   "/proc/self/status", "cgroups.cpuset", "cgroups.cpuquota", "cgroups2.cpuset.cpus",
    "cgroups2.cpuset.cpus.effective", "cgroups2.cpu.max", "nproc", "mc.cores",
   "BiocParallel", "_R_CHECK_LIMIT_CORES_", "Bioconductor", "LSF", "PJM", "PBS", "SGE",
    "Slurm", "HTCondor", "fallback", "custom")),
  na.rm = TRUE,
  logical = getOption2("parallelly.availableCores.logical", TRUE),
```

```
  default = c(current = 1L),
 threadsPerWorker = getOption2("parallelly.availableCores.threadsPerWorker", 1L),
  which = c("min", "max", "all"),
  fraction = getOption2("parallelly.availableCores.fraction", 1),
  omit = getOption2("parallelly.availableCores.omit", 0L),
  max = getOption2("parallelly.availableCores.max", Inf)
)
```

Arguments

constraints	An optional character specifying under what constraints ("purposes") we are requesting the values. For instance, on systems where multicore processing is not supported (i.e. Windows), using `constraints = "multicore"` will force a single core to be reported. Using `constraints = "connections"`, will append `"connections"` to the `methods` argument. It is possible to specify multiple constraints, e.g. `constraints = c("connections", "multicore")`.
methods	A character vector specifying how to infer the number of available cores.
na.rm	If TRUE, only non-missing settings are considered/returned.
logical	Passed to `detectCores(logical = logical)`, which, *if supported*, returns the number of logical CPUs (TRUE) or physical CPUs/cores (FALSE). At least as of R 4.2.2, `detectCores()` ignores this argument on Linux. This argument is only used if argument `methods` includes `"system"`.
default	The default number of cores to return if no non-missing settings are available.
threadsPerWorker	(positive integer) Number of CPU cores, or threads, to reserve for each parallel worker. The number of cores is divided by this number, rounding down, with a minimum of one. Applied before `fraction` and `omit`. The default is one, which means one worker per CPU core.
which	A character specifying which settings to return. If `"min"` (default), the minimum value is returned. If `"max"`, the maximum value is returned (be careful!) If `"all"`, all values are returned.
fraction	(numeric; in (0,1]) Fraction of cores to keep. Applied before `omit`. `availableCores(fraction = 0.5)` is equivalent to `max(1, floor(0.5 * availableCores()))` and `availableCores(fraction = 0.7, omit = 1)` is equivalent to `max(1, floor(0.7 * availableCores()) - 1)`.
omit	(integer; non-negative) Number of cores to not include.
max	(integer; positive) Maximum number of cores returned. `availableCores(..., max = n)` is short for `min(n, availableCores(...), na.rm = TRUE)`.

Details

The following settings ("methods") for inferring the number of cores are supported:

- `"system"` - Query `detectCores(logical = logical)`. If it returns a missing value, which happens on platforms where the number of cores cannot be detected, such as webR, then 1 is used.

- "/proc/self/status" - Query Cpus_allowed_list of /proc/self/status. Since this list may include CPUs that are not online, only CPUs that are also online according to /sys/devices/system/cpu/online are counted.
- "cgroups.cpuset" - On Unix, query control group (cgroup v1) *affinity* value cpuset.cpus.
- "cgroups.cpuquota" - On Unix, query control group (cgroup v1) *quota* value cpu.cfs_quota_us / cpu.cfs_period_us.
- "cgroups2.cpuset.cpus" - On Unix, query control group (cgroup v2) *affinity* value cpuset.cpus.
- "cgroups2.cpuset.cpus.effective" - On Unix, query control group (cgroup v2) *effective affinity* value cpuset.cpus.effective.
- "cgroups2.cpu.max" - On Unix, query control group (cgroup v2) *quota* value cpu.max.
- "nproc" - On Unix, query system command nproc.
- "mc.cores" - If available, returns the value of option mc.cores. Note that mc.cores is defined as the number of *additional* R processes that can be used in addition to the main R process. This means that with mc.cores = 0 all calculations should be done in the main R process, i.e. we have exactly one core available for our calculations. The mc.cores option defaults to environment variable MC_CORES (and is set accordingly when the **parallel** package is loaded). The mc.cores option is used by for instance mclapply() of the **parallel** package.
- "connections" or "connections-N" - Query the current number of available R connections per freeConnections(). This is the maximum number of socket-based **parallel** cluster nodes that are possible to launch, because each one needs its own R connection. The "connections-N" form (e.g. connections-16) works like "connections" but uses freeConnections() - N as the upper limit, leaving N connections free for other purposes. The exception is when the result is zero or less, then 1L is still returned, because availableCores() should always return a positive integer.
- "BiocParallel" - Query environment variable BIOCPARALLEL_WORKER_NUMBER (integer), which is defined and used by **BiocParallel** (>= 1.27.2). If the former is set, this is the number of cores considered.
- "_R_CHECK_LIMIT_CORES_" - Query environment variable _R_CHECK_LIMIT_CORES_ (logical or "warn") used by R CMD check and set to true by R CMD check --as-cran. In addition, package **parallelly** sets _R_CHECK_LIMIT_CORES_=true when *loaded* if it detects that R CMD is running and *builds* package vignettes via R CMD build and R CMD check, which is something R CMD check does not do itself. If _R_CHECK_LIMIT_CORES_ is set to a non-false value, then a maximum of 2 cores is considered.
- "Bioconductor" - Query environment variable IS_BIOC_BUILD_MACHINE (logical) used by the Bioconductor (>= 3.16) build and check system. If set to true, then a maximum of 4 cores is considered.
- "LSF" - Query Platform Load Sharing Facility (LSF)/OpenLava environment variable LSB_DJOB_NUMPROC. Jobs with multiple (CPU) slots can be submitted on LSF using bsub -n 2 -R "span[hosts=1]" < hello.sh.
- "PJM" - Query Fujitsu Technical Computing Suite (that we choose to shorten as "PJM") environment variables PJM_VNODE_CORE and PJM_PROC_BY_NODE. The first is set when submitted with pjsub -L vnode-core=8 hello.sh.
- "PBS" - Query TORQUE/PBS environment variables PBS_NUM_PPN and NCPUS. Depending on PBS system configuration, these *resource* parameters may or may not default to one. An example of a job submission that results in this is qsub -l nodes=1:ppn=2, which requests one node with two cores.

- "SGE" - Query the "Grid Engine" scheduler environment variable NSLOTS. An example of a job submission that results in this is qsub -pe smp 2 (or qsub -pe by_node 2), which requests two cores on a single machine. If the job spans multiple machines, e.g. qsub -pe mpi 16, NSLOTS is the total number of slots on all machines. Because of this, the number of slots allotted to the current machine according to the file that PE_HOSTFILE specifies is used instead, if available. In processes launched by qrsh -inherit, PE_HOSTFILE is not set. On the machine running the job script, the file is searched for in the job's spool folder via SGE_JOB_SPOOL_DIR. Known Grid Engine schedulers are Oracle Grid Engine (OGE; acquired Sun Microsystems in 2010), Univa Grid Engine (UGE; fork of open-source SGE 6.2u5), Altair Grid Engine (AGE; acquired Univa Corporation in 2020), Son of Grid Engine (SGE aka SoGE; open-source fork of SGE 6.2u5), and
- "Slurm" - Query Simple Linux Utility for Resource Management (Slurm) environment variable SLURM_CPUS_ON_NODE, which is the number of CPUs that Slurm has allotted to the job on the current machine. For example, sbatch --ntasks=4 --cpus-per-task=2 hello.sh gives eight CPUs, when all tasks are assigned to the same machine. This is the number of cores available to the 'hello.sh' job script, and similarly to the interactive shell of salloc. In a task launched by srun (as indicated by SLURM_STEP_ID being set), the CPUs on the machine are shared with the other tasks on that machine. In this case, SLURM_CPUS_PER_TASK is used, if set, e.g. --cpus-per-task=2, otherwise the CPUs are split equally among the tasks of the job step on the current machine according to SLURM_STEP_TASKS_PER_NODE.
- "HTCondor" - Query HTCondor environment variables _CONDOR_MACHINE_AD and _CONDOR_JOB_AD. The slot's machine ClassAd file is queried for Cpus. If not available, the job ClassAd file is queried for CpusProvisioned (or Cpus).
- "custom" - If option parallelly.availableCores.custom is set and a function, then this function will be called (without arguments) and it's value will be coerced to an integer, which will be interpreted as a number of available cores. If the value is NA, then it will be ignored. It is safe for this custom function to call availableCores(); if done, the custom function will *not* be recursively called.

For any other value of a methods element, the R option with the same name is queried. If that is not set, the system environment variable is queried. If neither is set, a missing value is returned.

Value

Return a positive (>= 1) integer. If which = "all", then more than one value may be returned. Together with na.rm = FALSE missing values may also be returned.

Avoid ending up with zero cores

Note that some machines might have a limited number of cores, or the R process runs in a container or a cgroup that only provides a small number of cores. A real-world example is when you run R in webR – webR is single-core by design. Another example are free Posit Cloud accounts, which are limited to a single core. In such cases

```
ncores <- availableCores() - 1
```

may return zero, which is often not intended and is likely to give an error downstream. Instead, use:

```
ncores <- availableCores(omit = 1)
```

to put aside one of the cores from being used. Regardless how many cores you put aside, this function is guaranteed to return at least one core.

Advanced usage for package developers

It is possible to emulate a larger number of CPU cores than what the machine has. This can be useful to reproduce errors reported by users on large system. For instance, even if your machine only has 16 cores, you can trick `availableCores()` to believe there are 192 cores, by:

```
availableCores()
#> system
#>     16
options(parallelly.availableCores.methods = "system")
options(parallelly.availableCores.system = 192)
availableCores()
#> system
#>    192
freeConnections()
#> [1] 125
availableCores(constraints = "connections-16")
#> connections-16
#>            109
```

To achieve the same from outside of R, for instance when running `R CMD check`, set the corresponding environment variables, e.g.

```
$ export R_PARALLELLY_AVAILABLECORES_SYSTEM=192
$ export R_PARALLELLY_AVAILABLECORES_METHODS=system
$ Rscript -e parallelly::availableCores
system
   192
$ Rscript -e parallelly::availableCores --constraints="connections-16"
connections-16
          109
```

See Also

To get the set of available workers regardless of machine, see `availableWorkers()`.

Examples

```
message(paste("Number of cores available:", availableCores()))

## Not run:
options(mc.cores = 2L)
message(paste("Number of cores available:", availableCores()))

## End(Not run)

## Not run:
```

```
## IMPORTANT: availableCores() may return 1L
options(mc.cores = 1L)
ncores <- availableCores() - 1      ## ncores = 0
ncores <- availableCores(omit = 1)  ## ncores = 1
message(paste("Number of cores to use:", ncores))

## End(Not run)

## Not run:
## Use 50% of the available cores
ncores <- availableCores(fraction = 0.5)
message(paste("Number of cores to use:", ncores))

## Use 70% of the available cores, but leave one aside
ncores <- availableCores(fraction = 0.7, omit = 1)
message(paste("Number of cores to use:", ncores))

## End(Not run)

## Not run:
## Use 75% of the cores on the system but never more than four
options(parallelly.availableCores.custom = function() {
  ncores <- max(parallel::detectCores(), 1L, na.rm = TRUE)
  ncores <- min(as.integer(0.75 * ncores), 4L)
  max(1L, ncores)
})
message(paste("Number of cores available:", availableCores()))

## Use 50% of the cores according to availableCores(), e.g.
## allocated by a job scheduler or cgroups.
## Note that it is safe to call availableCores() here.
options(parallelly.availableCores.custom = function() {
  0.50 * parallelly::availableCores()
})
message(paste("Number of cores available:", availableCores()))

## End(Not run)

## Not run:
## Slurm job submitted with 'sbatch --ntasks=4 --cpus-per-task=2'
## Use one worker per task, each running two threads, instead of
## one worker per CPU core
nthreads <- as.integer(Sys.getenv("SLURM_CPUS_PER_TASK", "1"))
nworkers <- availableCores(threadsPerWorker = nthreads)
message(paste("Number of workers to use:", nworkers))

## End(Not run)
```

`availableWorkers` *Get Set of Available Workers*

Description

Get Set of Available Workers

Usage

```
availableWorkers(
  constraints = NULL,
  methods = getOption2("parallelly.availableWorkers.methods", c("mc.cores",
   "BiocParallel", "_R_CHECK_LIMIT_CORES_", "Bioconductor", "LSF", "PJM", "PBS", "SGE",
    "Slurm", "HTCondor", "custom", "cgroups.cpuset", "cgroups.cpuquota",
   "cgroups2.cpuset.cpus", "cgroups2.cpuset.cpus.effective", "cgroups2.cpu.max",
    "nproc", "/proc/self/status", "system", "fallback")),
  na.rm = TRUE,
  logical = getOption2("parallelly.availableCores.logical", TRUE),
  default = getOption2("parallelly.localhost.hostname", "localhost"),
 threadsPerWorker = getOption2("parallelly.availableCores.threadsPerWorker", 1L),
  which = c("auto", "min", "max", "all"),
  ...
)
```

Arguments

constraints	An optional character specifying under what constraints ("purposes") we are requesting the values. Using constraints = "connections", will append "connections" to the methods argument.
methods	A character vector specifying how to infer the number of available cores.
na.rm	If TRUE, only non-missing settings are considered/returned.
logical	Passed as-is to availableCores().
default	The default set of workers.
threadsPerWorker	(positive integer) Number of CPU cores, or threads, for each parallel worker. Each host is listed n %/% threadsPerWorker times, where n is the number of CPUs allotted on that host. Passed as-is to availableCores().
which	A character specifying which set / sets to return. If "auto" (default), the first non-empty set found. If "min", the minimum value is returned. If "max", the maximum value is returned (be careful!) If "all", all values are returned.
...	Additional named arguments pass to availableCores().

Details

The default set of workers for each method is rep("localhost", times = availableCores(methods = method, logical = logical)), which means that each will at least use as many parallel workers on the current machine that availableCores() allows for that method.

In addition, the following settings ("methods") are also acknowledged:

- "LSF" - Query Platform Load Sharing Facility (LSF)/OpenLava environment variable LSB_HOSTS.

- "PJM" - Query Fujitsu Technical Computing Suite (that we choose to shorten as "PJM") the hostname file given by environment variable PJM_O_NODEINF. The PJM_O_NODEINF file lists the hostnames of the nodes allotted. This function returns those hostnames each repeated availableCores() times, where availableCores() reflects PJM_VNODE_CORE. For example, for pjsub -L vnode=2 -L vnode-core=8 hello.sh, the PJM_O_NODEINF file gives two hostnames, and PJM_VNODE_CORE gives eight cores per host, resulting in a character vector of 16 hostnames (for two unique hostnames).
- "PBS" - Query TORQUE/PBS environment variable PBS_NODEFILE. If this is set and specifies an existing file, then the set of workers is read from that file, where one worker (node) is given per line. An example of a job submission that results in this is qsub -l nodes=4:ppn=2, which requests four nodes each with two cores.
- "SGE" - Query the "Grid Engine" scheduler environment variable PE_HOSTFILE. An example of a job submission that results in this is qsub -pe mpi 8 (or qsub -pe ompi 8), which requests eight cores on any number of machines. The workers are listed in the same order as the machines in PE_HOSTFILE, where the machine running the job script comes first. Known Grid Engine schedulers are Oracle Grid Engine (OGE; acquired Sun Microsystems in 2010), Univa Grid Engine (UGE; fork of open-source SGE 6.2u5), Altair Grid Engine (AGE; acquired Univa Corporation in 2020), Son of Grid Engine (SGE aka SoGE; open-source fork of SGE 6.2u5), and
- "Slurm" - Query Slurm environment variable SLURM_JOB_NODELIST (fallback to legacy SLURM_NODELIST) and parse set of nodes. Then query Slurm environment variable SLURM_JOB_CPUS_PER_NODE (fallback SLURM_TASKS_PER_NODE) to infer how many CPU cores Slurm has allotted to each of the nodes. For example, if SLURM_NODELIST="n1,n[03-05]" (expands to c("n1", "n03", "n04", "n05")) and SLURM_JOB_CPUS_PER_NODE="2(x2),3,2" (expands to c(2, 2, 3, 2)), then c("n1", "n1", "n03", "n03", "n04", "n04", "n04", "n05", "n05") is returned. Note that SLURM_CPUS_PER_TASK is not used to limit the number of workers per node. This means that the number of workers on the current machine equals availableCores() in the Slurm job script.
- "HTCondor" - Query HTCondor environment variables _CONDOR_MACHINE_AD and _CONDOR_JOB_AD. Currently, single-node jobs are assumed. If called on a multi-node job, it will only return the workers for the current node. Returns availableCores(methods = "HTCondor") localhost workers.
- "custom" - If option parallelly.availableWorkers.custom is set and a function, then this function will be called (without arguments) and it's value will be coerced to a character vector, which will be interpreted as hostnames of available workers. It is safe for this custom function to call availableWorkers(); if done, the custom function will *not* be recursively called.

Value

Return a character vector of workers, which typically consists of names of machines / compute nodes, but may also be IP numbers.

Known limitations

availableWorkers(methods = "HTCondor") currently assumes single-node jobs. If called on a multi-node job, it will only return the workers for the current node.

availableWorkers(methods = "Slurm") will expand SLURM_JOB_NODELIST using scontrol show hostnames "$SLURM_JOB_NODELIST", if available. If not available, then it attempts to parse the

compressed nodelist based on a best-guess understanding on what the possible syntax may be. One known limitation is that "multi-dimensional" ranges are not supported, e.g. `"a[1-2]b[3-4]"` is expanded by `scontrol` to `c("a1b3", "a1b4", "a2b3", "a2b4")`. If `scontrol` is not available, then any components that failed to be parsed are dropped with an informative warning message. If no components could be parsed, then the result of `methods = "Slurm"` will be empty.

See Also

To get the number of available workers on the current machine, see `availableCores()`.

Examples

```
message(paste("Available workers:",
        paste(sQuote(availableWorkers()), collapse = ", ")))

## Not run:
options(mc.cores = 2L)
message(paste("Available workers:",
        paste(sQuote(availableWorkers()), collapse = ", ")))

## End(Not run)

## Not run:
## Always use two workers on host 'n1' and one on host 'n2'
options(parallelly.availableWorkers.custom = function() {
  c("n1", "n1", "n2")
})
message(paste("Available workers:",
        paste(sQuote(availableWorkers()), collapse = ", ")))

## End(Not run)

## Not run:
## A 50% random subset of the available workers.
## Note that it is safe to call availableWorkers() here.
options(parallelly.availableWorkers.custom = function() {
  workers <- parallelly::availableWorkers()
  sample(workers, size = 0.50 * length(workers))
})
message(paste("Available workers:",
        paste(sQuote(availableWorkers()), collapse = ", ")))

## End(Not run)

## Not run:
## Slurm job submitted with 'sbatch --ntasks=4 --cpus-per-task=2'
## Use one worker per task, each running two threads, instead of
## one worker per CPU core
nthreads <- as.integer(Sys.getenv("SLURM_CPUS_PER_TASK", "1"))
workers <- availableWorkers(threadsPerWorker = nthreads)
message(paste("Workers to use:", paste(sQuote(workers), collapse = ", ")))
```

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

---

cloneNode *Clone one or more nodes*

Description

Clone one or more nodes

Usage

```
cloneNode(x, ...)
```

Arguments

x	A cluster node or a cluster.
...	Optional arguments overriding the recorded ones.

Value

An object of class `class(x)`.

Examples

```
cl <- makeClusterPSOCK(2)
print(cl)

## Terminate the second cluster node
parallel::stopCluster(cl[2])

## Show that cluster node #2 is no longer alive (wait a bit first)
Sys.sleep(1.0)
print(isNodeAlive(cl))
print(cl)

## "Restart" it
cl[2] <- cloneNode(cl[2])
print(cl)

## Check all nodes
print(isNodeAlive(cl))
```

freePort *Find a TCP port that can be opened*

Description

Find a TCP port that can be opened

Usage

```
freePort(ports = 1024:65535, default = "random", randomize = TRUE)
```

Arguments

ports	(integer vector, or character string) Zero or more TCP ports in [0, 65535] to scan. If "random", then a random set of ports is considered. If "auto", then the port given by environment variable R_PARALLEL_PORT is used, which may also specify "random". If R_PARALLEL_PORT is not set, the default is "random". The "auto" alternative is used for full backward compatibility with the **parallelly** package.
default	(integer) NA_integer_ or a port to returned if an available port could not be found. If "first", then ports[1]. If "random", then a random port among ports is used. If length(ports) == 0, then NA_integer_.
randomize	(logical) If TRUE, ports is randomly shuffled before searched. This shuffle does *not* forward the RNG seed.

Value

Returns an integer representing the first port among ports *that can be opened*. If none can be opened, then default is returned.

Validation of TCP port returned

This function attempts to validate that the TCP port returned is available and can be opened. Thus, it is likely that this port is available momentarily after freePort() returns. However, due to race conditions, there is always a risk that the port is taken by another process on the same system after freePort() returns but before, say, makeClusterPSOCK(), opens it.

Controlling the random set of TCP ports

For backward compatibility with the **parallel** package, the default set of ports freePort("random"), or freePort("auto") with environment variable R_PARALLEL_PORT=random samples from is 11000:11999. The set can be overridden by setting environment variable R_PARALLELLY_RANDOM_PORTS, e.g. R_PARALLELLY_RANDOM_PORTS="10001:10010,11000:54000".

Examples

```
# Make sure to undo any changes at the end
oenv <- Sys.getenv("R_PARALLELLY_RANDOM_PORTS")

# Get a random, free TCP port in 1024:65535
port <- freePort()
message("A free TCP port: ", port)

# Get a random, free TCP port in 11000:11999, which is what
# parallelly::makeClusterPSOCK() and parallel::makePSOCKcluster()
# default to (but the latter does not make sure it is available)
Sys.unsetenv("R_PARALLELLY_RANDOM_PORTS")
port <- freePort("random")
message("A free TCP port: ", port)

# Customize the range of ports to sample from to 30000:50000
Sys.setenv(R_PARALLELLY_RANDOM_PORTS = "30000:50000")
port <- freePort("random")
message("A free TCP port: ", port)

# Test if a specific port is free
isPortFree <- function(port) !is.na(freePort(port, default = NA_integer_))
message("TCP port 1024 is free: ", isPortFree(1024))

# Undo changes
Sys.setenv(R_PARALLELLY_RANDOM_PORTS = oenv)
```

---

isConnectionValid *Checks if a Connection is Valid*

Description

Get a unique identifier for an R connection and check whether or not the connection is still valid.

Usage

```
isConnectionValid(con)

connectionId(con)
```

Arguments

con	A connection.

Value

`isConnectionValid()` returns TRUE if the connection is still valid, otherwise FALSE. If FALSE, then character attribute `reason` provides an explanation why the connection is not valid.

connectionId() returns an non-negative integer, -1, or NA_integer_. For connections stdin, stdout, and stderr, 0, 1, and 2, are returned, respectively. For all other connections, an integer greater or equal to 3 based on the connection's internal pointer is returned. A connection that has been serialized, which is no longer valid, has identifier -1. Attribute raw_id returns the pointer string from which the above is inferred.

Connection Index versus Connection Identifier

R represents connections as indices using plain integers, e.g. idx <- as.integer(con). The three connections standard input ("stdin"), standard output ("stdout"), and standard error ("stderr") always exists and have indices 0, 1, and 2. Any connection opened beyond these will get index three or greater, depending on availability as given by base::showConnections(). To get the connection with a given index, use base::getConnection(). **Unfortunately, this index representation of connections is non-robust**, e.g. there are cases where two or more 'connection' objects can end up with the same index and if used, the written output may end up at the wrong destination and files and database might get corrupted. This can for instance happen if base::closeAllConnections() is used (*). **In contrast,** id <- connectionId(con) **gives an identifier that is unique to that 'connection' object.** This identifier is based on the internal pointer address of the object. The risk for two connections in the same R session to end up with the same pointer address is very small. Thus, in case we ended up in a situation where two connections con1 and con2 share the same index—as.integer(con1) == as.integer(con2)—they will never share the same identifier— connectionId(con1) != connectionId(con2). Here, isConnectionValid() can be used to check which one of these connections, if any, are valid.

(*) Note that there is no good reason for calling closeAllConnections() If called, there is a great risk that the files get corrupted etc. See (1) for examples and details on this problem. If you think there is a need to use it, it is much safer to restart R because that is guaranteed to give you a working R session with non-clashing connections. It might also be that closeAllConnections() is used because base::sys.save.image() is called, which might happen if R is being forced to terminate.

Connections Cannot be Serialized Or Saved

A 'connection' cannot be serialized, e.g. it cannot be saved to file to be read and used in another R session. If attempted, the connection will not be valid. This is a problem that may occur in parallel processing when passing an R object to parallel worker for further processing, e.g. the exported object may hold an internal database connection which will no longer be valid on the worker. When a connection is serialized, its internal pointer address will be invalidated (set to nil). In such cases, connectionId(con) returns -1 and isConnectionValid(con) returns FALSE.

References

1. 'BUG: A connection object may become corrupt and re-referenced to another connection (PATCH)', 2018-10-30.
2. R-devel thread PATCH: Asserting that 'connection' used has not changed + R_GetConnection2(), 2018-10-31.

See Also

See base::showConnections() for currently open connections and their indices. To get a connection by its index, use base::getConnection().

Examples

```
## R represents connections as plain indices
as.integer(stdin())          ## int 0
as.integer(stdout())         ## int 1
as.integer(stderr())         ## int 2

## The first three connections always exist and are always valid
isConnectionValid(stdin())   ## TRUE
connectionId(stdin())        ## 0L
isConnectionValid(stdout())  ## TRUE
connectionId(stdout())       ## 1L
isConnectionValid(stderr())  ## TRUE
connectionId(stderr())       ## 2L

## Connections cannot be serialized
con <- file(tempfile(), open = "w")
x <- list(value = 42, stderr = stderr(), con = con)
y <- unserialize(serialize(x, connection = NULL))
isConnectionValid(y$stderr)  ## TRUE
connectionId(y$stderr)       ##  2L
isConnectionValid(y$con)     ## FALSE with attribute 'reason'
connectionId(y$con)          ## -1L
close(con)
```

`isForkedChild` *Checks whether or not we are running in a forked child process*

Description

Checks whether or not we are running in a forked child process

Usage

```
isForkedChild()
```

Details

Examples of setups and functions that rely on *forked* parallelization are `parallel::makeCluster(n, type = "FORK")`, `parallel::mclapply()`, and `future::plan("multicore")`.

Value

(logical) Returns TRUE if the running in a forked child process, otherwise FALSE.

isForkedNode *Checks whether or not a Cluster Node Runs in a Forked Process*

Description

Checks whether or not a Cluster Node Runs in a Forked Process

Usage

```
isForkedNode(node, ...)
```

Arguments

node	A cluster node of class SOCKnode or SOCK0node.
...	Not used.

Value

(logical) Returns TRUE if the cluster node is running in a forked child process and FALSE if it does not. If it cannot be inferred, NA is returned.

isLocalhostNode *Checks whether or not a Cluster Node Runs on Localhost*

Description

Checks whether or not a Cluster Node Runs on Localhost

Usage

```
isLocalhostNode(node, ...)
```

Arguments

node	A cluster node of class SOCKnode or SOCK0node.
...	Not used.

Value

(logical) Returns TRUE if the cluster node is running on the current machine and FALSE if it runs on another machine. If it cannot be inferred, NA is returned.

isNodeAlive *Check whether or not the cluster nodes are alive*

Description

Check whether or not the cluster nodes are alive

Usage

```
isNodeAlive(x, ...)
```

Arguments

x	A cluster or a cluster node ("worker").
...	Not used.

Details

This function works by checking whether the cluster node process is running or not. This is done by querying the system for its process ID (PID), which is registered by `makeClusterPSOCK()` when the node starts. If the PID is not known, the NA is returned. On Unix and macOS, the PID is queried using `tools::pskill()` with fallback to `system("ps")`. On MS Windows, `system2("tasklist")` is used, which may take a long time if there are a lot of processes running. For details, see the *internal* `pid_exists()` function.

Value

A logical vector of length `length(x)` with values FALSE, TRUE, and NA. If it can be established that the process for a cluster node is running, then TRUE is returned. If it does not run, then FALSE is returned. If neither can be inferred, or it times out, then NA is returned.

See Also

Use `parallel::stopCluster()` to shut down cluster nodes. If that's not sufficient, `killNode()` may be attempted.

Examples

```
cl <- makeClusterPSOCK(2)

## Check if cluster node #2 is alive
print(isNodeAlive(cl[[2]]))

## Check all nodes
print(isNodeAlive(cl))
```

killNode *Terminate one or more cluster nodes using process signaling*

Description

Terminate one or more cluster nodes using process signaling

Usage

```
killNode(x, signal = tools::SIGTERM, ...)
```

Arguments

x	cluster or cluster node to terminate.
signal	An integer that specifies the signal level to be sent to the parallel R process. It's only tools::SIGINT (2) and tools::SIGTERM (15) that are supported on all operating systems (i.e. Unix, macOS, and MS Windows). All other signals are platform specific, cf. tools::pskill(). With the exception of MS Windows, as explained below, using SIGINT will trigger an R interrupt condition that can be caught with tryCatch() and withCallingHandlers() using an interrupt calling handler. When using SIGTERM, there will be no interrupt condition signaled, meaning your parallel R code does *not* have a chance to exit gracefully. Instead, the R process terminates rather abruptly, leaving behind its temporary folder. Importantly, contrary to Linux and macOS, it is not possible to get a cluster node running on MS Windows to exit gracefully. For example, despite using SIGINT, there is no interrupt condition signaled. As a matter of fact, on MS Windows, SIGINT works identically to SIGTERM, where they both terminate the cluster node abruptly without giving the R process a chance to exit gracefully. This means that R will *not* clean up after itself, e.g. its temporary directory will remain even after R terminates.
...	Not used.

Details

Note that the preferred way to terminate a cluster is via parallel::stopCluster(), because it terminates the cluster nodes by kindly asking each of them to nicely shut themselves down. Using killNode() is a much more severe approach. It abruptly terminates the underlying R process, possibly without giving the parallel worker a chance to terminate gracefully. For example, it might get terminated in the middle of writing to file. tools::pskill() is used to send the signal to the R process hosting the parallel worker.

If signal = tools::SIGTERM is used and success, this function will also close any existing socket connection to the node, if they exist. Moreover, if the node is running on the local host, this function will also attempt to remove the node's temporary directory, which is done because the node's R process might not have been exited gracefully.

Value

TRUE if the signal was successfully applied, FALSE if not, and NA if signaling is not supported on the specific cluster or node. *Warning*: With R (< 3.5.0), NA is always returned. This is due to a bug in R (< 3.5.0), where the signaling result cannot be trusted.

Known limitations

This function works only with cluster nodes of class `RichSOCKnode`, which were created by `makeClusterPSOCK()`. It does not work when using `parallel::makeCluster()` and friends.

See Also

Use `isNodeAlive()` to check whether one or more cluster nodes are alive.

Examples

```
cl <- makeClusterPSOCK(2)
print(isNodeAlive(cl))  ## [1] TRUE TRUE

res <- killNode(cl)
print(res)

## It might take a moment before the background
## workers are shutdown after having been signaled
Sys.sleep(1.0)

print(isNodeAlive(cl))  ## [1] FALSE FALSE
```

`makeClusterMPI` *Create a Rich Message Passing Interface (MPI) Cluster of R Workers for Parallel Processing*

Description

The `makeClusterMPI()` function creates an MPI cluster of R workers for parallel processing. This function utilizes `makeCluster(..., type = "MPI")` of the **parallel** package and tweaks the cluster in an attempt to avoid `stopCluster()` from hanging (1). *WARNING: This function is very much in a beta version and should only be used if* `parallel::makeCluster(..., type = "MPI")` *fails.*

Usage

```
makeClusterMPI(
  workers,
  ...,
  autoStop = FALSE,
  verbose = isTRUE(getOption("parallelly.debug"))
)
```

Arguments

workers	The number workers (as a positive integer).
autoStop	If TRUE, the cluster will be automatically stopped using stopCluster() when it is garbage collected, unless already stopped. See also autoStopCluster().
verbose	If TRUE, informative messages are outputted.
...	Optional arguments passed to makeCluster(workers, type = "MPI", ...).

Details

Creating MPI clusters requires that the **Rmpi** *and* **snow** *packages are installed.*

Value

An object of class c("RichMPIcluster", "MPIcluster", "cluster") consisting of a list of "MPInode" workers.

Alternative usage

In R (>= 4.5.0), an alternative to using cl <- parallelly::makeClusterMPI(workers) is:

```
cl <- parallel::makeCluster(workers, type = parallelly::RMPI)
```

References

1. R-sig-hpc thread Rmpi: mpi.close.Rslaves() 'hangs' on 2017-09-28.

See Also

makeClusterPSOCK() and parallel::makeCluster().

Examples

```
## Not run:
if (requireNamespace("Rmpi") && requireNamespace("snow")) {
  cl <- makeClusterMPI(2, autoStop = TRUE)
  print(cl)
  y <- parLapply(cl, X = 1:3, fun = sqrt)
  print(y)
  rm(list = "cl")
}

## End(Not run)
```

makeClusterPSOCK *Create a Rich PSOCK Cluster of R Workers for Parallel Processing*

Description

The makeClusterPSOCK() function creates a cluster of R workers for parallel processing. These R workers may be background R sessions on the current machine, R sessions on external machines (local or remote), or a mix of such. For external workers, the default is to use SSH to connect to those external machines. This function works similarly to makePSOCKcluster() of the **parallel** package, but provides additional and more flexible options for controlling the setup of the system calls that launch the background R workers, and how to connect to external machines.

Usage

```
makeClusterPSOCK(
  workers,
  makeNode = makeNodePSOCK,
  port = c("auto", "random"),
  user = NULL,
  ...,
  autoStop = FALSE,
  tries = getOption2("parallelly.makeNodePSOCK.tries", 3L),
  delay = getOption2("parallelly.makeNodePSOCK.tries.delay", 15),
  validate = getOption2("parallelly.makeNodePSOCK.validate", TRUE),
  verbose = isTRUE(getOption("parallelly.debug"))
)

makeNodePSOCK(
  worker = getOption2("parallelly.localhost.hostname", "localhost"),
  master = NULL,
  port,
  connectTimeout = getOption2("parallelly.makeNodePSOCK.connectTimeout", 2 * 60),
  timeout = getOption2("parallelly.makeNodePSOCK.timeout", 30 * 24 * 60 * 60),
  rscript = NULL,
  homogeneous = NULL,
  rscript_args = NULL,
  rscript_envs = NULL,
  rscript_libs = NULL,
  rscript_startup = NULL,
  rscript_call = getOption2("parallelly.makeNodePSOCK.rscript_call", NULL),
  rscript_sh = c("auto", "cmd", "sh", "none"),
  default_packages = c("datasets", "utils", "grDevices", "graphics", "stats", if
    (methods) "methods"),
  methods = TRUE,
  socketOptions = getOption2("parallelly.makeNodePSOCK.socketOptions", "no-delay"),
  useXDR = getOption2("parallelly.makeNodePSOCK.useXDR", FALSE),
  outfile = "/dev/null",
```

```
  renice = NA_integer_,
  rshcmd = getOption2("parallelly.makeNodePSOCK.rshcmd", NULL),
  user = NULL,
  revtunnel = NA,
  rshlogfile = NULL,
  rshopts = getOption2("parallelly.makeNodePSOCK.rshopts", NULL),
  rank = 1L,
  manual = FALSE,
  dryrun = FALSE,
  quiet = FALSE,
 setup_strategy = getOption2("parallelly.makeNodePSOCK.setup_strategy", "parallel"),
  calls = getOption2("parallelly.makeNodePSOCK.calls", FALSE),
  action = c("launch", "options"),
  verbose = FALSE
)
```

Arguments

workers	The hostnames of workers (as a character vector) or the number of localhost workers (as a positive integer).
makeNode	A function that creates a "SOCKnode" or "SOCK0node" object, which represents a connection to a worker.
port	The port number of the master used for communicating with all the workers (via socket connections). If an integer vector of ports, then a random one among those is chosen. If "random", then a random, *available* port is chosen in the range 11000:11999 or as specified by environment variable R_PARALLELLY_RANDOM_PORTS. If "auto" (default), then the default (single) port is taken from environment variable R_PARALLEL_PORT, otherwise "random" is used. *Note, do not use this argument to specify the port number used by* rshcmd*, which typically is an SSH client. Instead, if the SSH daemon runs on a different port than the default 22, specify the SSH port by appending it to the hostname, e.g.* "remote.server.org:2200" *or via SSH options '*-p*', e.g.* rshopts = c("-p", "2200").
user	(optional) The user name to be used when communicating with another host.
autoStop	If TRUE, the cluster will be automatically stopped using stopCluster() when it is garbage collected, unless already stopped. See also autoStopCluster().
tries, delay	Maximum number of attempts done to launch each node with makeNode() and the delay (in seconds) in-between attempts. If argument port specifies more than one port, e.g. port = "random" then a random port will be drawn and validated at most tries times. Arguments tries and delay are used only when setup_strategy == "sequential".
validate	If TRUE (default), after the nodes have been created, they are all validated that they work by inquiring about their session information, which is saved in attribute session_info of each node.
verbose	If TRUE, informative messages are outputted.
worker	The hostname or IP number of the machine where the worker should run. Attribute localhost can be set to TRUE or FALSE to manually indicate whether worker is the same as the local host.

`master` The hostname or IP number of the master / calling machine, as known to the workers. If NULL (default), then the default is `Sys.info()[["nodename"]]` unless `worker` is *localhost* or `revtunnel = TRUE` in case it is `"localhost"`.

`connectTimeout` The maximum time (in seconds) allowed for each socket connection between the master and a worker to be established (defaults to 2 minutes). *See note below on current lack of support on Linux and macOS systems.*

`timeout` The maximum time (in seconds) allowed to pass without the master and a worker communicate with each other (defaults to 30 days).

`rscript`, `homogeneous`
The system command for launching `Rscript` on the worker and whether it is installed in the same path as the calling machine or not. For more details, see below.

`rscript_args` Additional arguments to `Rscript` (as a character vector). This argument can be used to customize the R environment of the workers before they launches. For instance, use `rscript_args = c("-e", shQuote('setwd("/path/to")'))` to set the working directory to '`/path/to`' on *all* workers.

`rscript_envs` A named character vector environment variables to set or unset on worker at startup, e.g. `rscript_envs = c(FOO = "3.14", "HOME", "UNKNOWN", UNSETME = NA_character_)`. If an element is not named, then the value of that variable will be used as the name and the value will be the value of `Sys.getenv()` for that variable. Non-existing environment variables will be dropped. These variables are set using `Sys.setenv()`. A named element with value `NA_character_` will cause that variable to be unset, which is done via `Sys.unsetenv()`.

`rscript_libs` A character vector of R library paths that will be used for the library search path of the R workers. An asterisk (`"*"`) will be resolved to the default `.libPaths()` *on the worker*. That is, to prepend a folder, instead of replacing the existing ones, use `rscript_libs = c("new_folder", "*")`. To pass down a non-default library path currently set *on the main* R *session* to the workers, use `rscript_libs = .libPaths()`.

`rscript_startup`
An R expression or a character vector of R code, or a list with a mix of these, that will be evaluated on the R worker prior to launching the worker's event loop. For instance, use `rscript_startup = 'setwd("/path/to")'` to set the working directory to '`/path/to`' on *all* workers.

`rscript_call` An R expression or a character string of R code that is used to launch the worker event loop (default: `getOption("parallelly.makeNodePSOCK.rscript_call", NULL)`). If `NULL`, it defaults to `"workRSOCK<-tryCatch( parallel:::.workRSOCK, error=function(e) parallel:::.slaveRSOCK );workRSOCK()"`.

`rscript_sh` The type of shell used where `rscript` is launched, which should be `"sh"` is launched via a POSIX shell and `"cmd"` if launched via an MS Windows shell. This controls how shell command-line options are quoted, but also how R string expression are quoted when passed to `Rscript`. If `"none"`, then no quoting is done. If `"auto"` (default), and the cluster node is launched locally, then it is set to `"sh"` or `"cmd"` according to the current platform. *If launched remotely*, then it is set to `"sh"` based on the assumption remote machines typically launch commands via SSH in a POSIX shell. If the remote machines run MS Windows, use

rscript_sh = "cmd". If length(rscript_sh) is two, then rscript_sh[1] is for the inner and rscript_sh[2] is for the outer shell quoting of the Rscript call. More precisely, rscript_sh[1] is for Rscript arguments that need shell quoting (e.g. Rscript -e "<expr>"), and rscript_sh[2] is for the whole Rscript ... call. If length(rscript_sh) is one, then it is used for both the inner and the outer shell quoting.

default_packages
: A character vector or NULL that controls which R packages are attached on each cluster node during startup. An asterisk ("*") resolves to getOption("defaultPackages") *on the current machine*. If NULL, then the default set of packages R are attached.

methods
: If TRUE (default), then the **methods** package is also loaded. This is argument exists for legacy reasons due to how Rscript worked in R (< 3.5.0).

socketOptions
: A character string that sets R option socketOptions on the worker.

useXDR
: If FALSE (default), the communication between master and workers, which is binary, will use small-endian (faster), otherwise big-endian ("XDR"; slower).

outfile
: Where to direct the stdout and stderr connection output from the workers. If NULL, then no redirection of output is done, which means that the output is relayed in the terminal on the local computer. On Windows, the output is only relayed when running R from a terminal but not from a GUI.

renice
: A numerical 'niceness' (priority) to set for the worker processes.

rshcmd, rshopts
: The command (character vector) to be run on the master to launch a process on another host and any additional arguments (character vector). These arguments are only applied if machine is not *localhost*. For more details, see below.

revtunnel
: If TRUE, a reverse SSH tunnel is set up for each worker such that the worker R process sets up a socket connection to its local port (port + rank - 1) which then reaches the master on port port. If FALSE, then the worker will try to connect directly to port port on master. If NA, then TRUE or FALSE is inferred from inspection of rshcmd[1]. For more details, see below.

rshlogfile
: (optional) If a filename, the output produced by the rshcmd call is logged to this file, of if TRUE, then it is logged to a temporary file. The log file name is available as an attribute as part of the return node object. *Warning: This only works with SSH clients that support command-line option '-E out.log'*. For example, PuTTY's plink does *not* support this option, and any attempts to specify rshlogfile will cause the SSH connection to fail.

rank
: A unique one-based index for each worker (automatically set).

manual
: If TRUE the workers will need to be run manually. The command to run will be displayed.

dryrun
: If TRUE, nothing is set up, but a message suggesting how to launch the worker from the terminal is outputted. This is useful for troubleshooting.

quiet
: If TRUE, then no output will be produced other than that from using verbose = TRUE.

setup_strategy
: If "parallel" (default), the workers are set up concurrently, one after the other. If "sequential", they are set up sequentially.

calls	If TRUE, the call stack is recorded and revealed in the system call launching the cluster node. This can be useful when trying to identify which package and function created a particular cluster node.
action	This is an internal argument.
...	Optional arguments passed to `makeNode(workers[i], ..., rank = i)` where `i = seq_along(workers)`.

Value

An object of class `c("RichSOCKcluster", "SOCKcluster", "cluster")` consisting of a list of `"SOCKnode"` or `"SOCK0node"` workers (that also inherit from `RichSOCKnode`).

`makeNodePSOCK()` returns a `"SOCKnode"` or `"SOCK0node"` object representing an established connection to a worker.

Alternative usage

In R (>= 4.5.0), an alternative to using `cl <- parallelly::makeClusterPSOCK(workers)` is:

```
cl <- parallel::makeCluster(workers, type = parallelly::RPSOCK)
```

and in R (>= 4.6.0), it can also be created as:

```
cl <- parallel::makeCluster(workers, type = "RPSOCK")
```

where the 'R' in RPSOCK stands for "Rich", which reflects that the cluster returned is of class `RichSOCKcluster`, whereas the default is of class `SOCKcluster`.

Protection against CPU overuse

Using too many parallel workers on the same machine may result in overusing the CPU. For example, if an R script hard codes the number of parallel workers to 32, as in

```
cl <- makeClusterPSOCK(32)
```

it will use more than 100% of the CPU cores when running on machine with fewer than 32 CPU cores. For example, on a eight-core machine, this may run the CPU at 400% of its capacity, which has a significant negative effect on the current R process, but also on all other processes running on the same machine. This is also a problem on systems where R gets allotted a specific number of CPU cores, which is the case on high-performance compute (HPC) clusters, but also on other shared systems that limit user processes via Linux Control Groups (cgroups). For example, a free account on Posit Cloud is limited to a single CPU core. Parallelizing with 32 workers when only having access to a single core, will result in 3200% overuse and 32 concurrent R processes competing for this single CPU core.

To protect against CPU overuse by mistake, `makeClusterPSOCK()` will warn when parallelizing above 100%;

```
cl <- parallelly::makeClusterPSOCK(12, dryrun = TRUE)
Warning message:
In checkNumberOfLocalWorkers(workers) :
  Careful, you are setting up 12 localhost parallel workers with only
8 CPU cores available for this R process (per 'system'), which could
result in a 150% load. The soft limit is set to 100%. Overusing the
CPUs has negative impact on the current R process, but also on all
other processes of yours and others running on the same machine. See
help("parallelly.maxWorkers.localhost", package = "parallelly") for
further explanations and how to override the soft limit that triggered
```

Any attempts resulting in more than 300% overuse will be refused;

```
> cl <- parallelly::makeClusterPSOCK(25, dryrun = TRUE)
Error in checkNumberOfLocalWorkers(workers) :
  Attempting to set up 25 localhost parallel workers with only 8 CPU
cores available for this R process (per 'system'), which could result
in a 312% load. The hard limit is set to 300%. Overusing the CPUs has
negative impact on the current R process, but also on all other
processes of yours and others running on the same machine. See
help("parallelly.maxWorkers.localhost", package = "parallelly") for
further explanations and how to override the hard limit that triggered
this error
```

See parallelly.options for how to change the default thresholds. This built-in protection can be circumvented by specifying argument `workers` as an `AsIs` object, e.g. `workers = I(25)`. We recommend against using this, unless you know the CPU load for each parallel worker is very low. This might be safe to do so when the parallel tasks are mostly in a waiting state, e.g. polling a webserver.

Protection against CPU overuse via nested parallelism

Parallel workers on the current machine inherit the settings of the main R session. This means that `availableCores()` reports the same number of CPU cores in each worker as in the main R session. For example, on an eight-core machine, each of the eight workers in

```
cl <- makeClusterPSOCK(8)
```

reports eight CPU cores. If the code evaluated by the workers parallelizes further based on `availableCores()`, e.g.

```
y <- parallel::parLapply(cl, X, function(x) {
  parallel::mclapply(x, FUN = slow_fcn, mc.cores = parallelly::availableCores())
})
```

then there could be up to 64 R processes competing for eight CPU cores. To protect against this, set R option `mc.cores` to one in each worker using:

```
cl <- makeClusterPSOCK(8, rscript_startup = quote(options(mc.cores = 1L)))
```

This makes `availableCores()` report a single CPU core in each worker, and `parallel::mclapply()` run sequentially. This is not needed when using the cluster via the **future** framework, e.g. `plan(cluster, workers = cl)`, because futures are evaluated with `mc.cores` set to one on parallel workers.

Definition of *localhost*

A hostname is considered to be *localhost* if it equals:

- `"localhost"`,
- `"127.0.0.1"`, or
- `Sys.info()[["nodename"]]`.

It is also considered *localhost* if it appears on the same line as the value of `Sys.info()[["nodename"]]` in file '`/etc/hosts`'.

Default SSH client and options (arguments `rshcmd` and `rshopts`)

Arguments `rshcmd` and `rshopts` are only used when connecting to an external host.

The default method for connecting to an external host is via SSH and the system executable for this is given by argument `rshcmd`. The default is given by option `parallelly.makeNodePSOCK.rshcmd`. If that is not set, then the default is to use `ssh` on Unix-like systems, including macOS as well as Windows 10. On older MS Windows versions, which does not have a built-in `ssh` client, the default is to use (i) `plink` from the PuTTY project, and then (ii) the `ssh` client that is distributed with RStudio.

PuTTY puts itself on Windows' system `PATH` when installed, meaning this function will find PuTTY automatically if installed. If not, to manually set specify PuTTY as the SSH client, specify the absolute pathname of '`plink.exe`' in the first element and option `-ssh` in the second as in `rshcmd = c("C:/Path/PuTTY/plink.exe", "-ssh")`. This is because all elements of `rshcmd` are individually "shell" quoted and element `rshcmd[1]` must be on the system `PATH`.

Furthermore, when running R from RStudio on Windows, the `ssh` client that is distributed with RStudio will also be considered. This client, which is from MinGW MSYS, is searched for in the folder given by the `RSTUDIO_MSYS_SSH` environment variable—a variable that is (only) set when running RStudio. To use this SSH client outside of RStudio, set `RSTUDIO_MSYS_SSH` accordingly.

You can override the default set of SSH clients that are searched for by specifying them in argument `rshcmd` or via option `parallelly.makeNodePSOCK.rshcmd` using the format `<...>`, e.g. `rshcmd = c("<rstudio-ssh>", "<putty-plink>", "<ssh>")`. See below for examples.

If no SSH-client is found, an informative error message is produced.

Additional SSH command-line options may be specified via argument `rshopts`, which defaults to option `parallelly.makeNodePSOCK.rshopts`. For instance, a private SSH key can be provided as `rshopts = c("-i", "~/.ssh/my_private_key")`. PuTTY users should specify a PuTTY PPK file, e.g. `rshopts = c("-i", "C:/Users/joe/.ssh/my_keys.ppk")`. Contrary to `rshcmd`, elements of `rshopts` are not quoted.

Launching workers via an HPC job scheduler

On high-performance compute (HPC) clusters, SSH access to compute nodes is often disabled. Instead, parallel workers on other compute nodes that are part of the same job can be launched via the job scheduler. The following `rshcmd` types are supported for this:

- `"<srun>"` - Slurm's `srun`, which launches each worker as a single-CPU job step via `srun --exact --overlap --overc`. Since `srun` does not launch the worker via a shell, `rscript_sh[2]` defaults to `"none"` for this type.
- `"<qrsh>"` - Grid Engine's (SGE) `qrsh` via `qrsh -inherit -nostdin -V <worker>`
- `"<pjrsh>"` - Fujitsu Technical Computing Suite's (PJM) `pjrsh` via `pjrsh <worker>`
- `"<hpc>"` - Infers which of the above to use from the environment variables of the job that the current R process runs in, i.e. `"<srun>"` if `SLURM_JOB_ID` is set, `"<qrsh>"` if `PE_HOSTFILE` is set, and `"<pjrsh>"` if `PJM_JOBID` is set. It is an error if none of them is set, unless a fallback is given, e.g. `rshcmd = c("<hpc>", "<ssh>")`.

As with any `rshcmd`, these are only used for workers on *other* machines. Workers on the current machine are launched directly, which means `makeClusterPSOCK(availableWorkers(), rshcmd = "<hpc>")` works also for single-node jobs.

Accessing external machines that prompts for a password

IMPORTANT: With one exception, it is not possible to for these functions to log in and launch R *workers on external machines that requires a password to be entered manually for authentication.* The only known exception is the PuTTY client on Windows for which one can pass the password via command-line option '`-pw`', e.g. `rshopts = c("-pw", "MySecretPassword")`.

Note, depending on whether you run R in a terminal or via a GUI, you might not even see the password prompt. It is also likely that you cannot enter a password, because the connection is set up via a background system call.

The poor man's workaround for setup that requires a password is to manually log into the each of the external machines and launch the R workers by hand. For this approach, use `manual = TRUE` and follow the instructions which include cut'n'pasteable commands on how to launch the worker from the external machine.

However, a much more convenient and less tedious method is to set up key-based SSH authentication between your local machine and the external machine(s), as explain below.

Accessing external machines via key-based SSH authentication

The best approach to automatically launch R workers on external machines over SSH is to set up key-based SSH authentication. This will allow you to log into the external machine without have to enter a password.

Key-based SSH authentication is taken care of by the SSH client and not R. To configure this, see the manuals of your SSH client or search the web for "ssh key authentication".

Reverse SSH tunneling

If SSH is used, which is inferred from `rshcmd[1]`, then the default is to use reverse SSH tunneling (`revtunnel = TRUE`), otherwise not (`revtunnel = FALSE`). Using reverse SSH tunneling, avoids

complications from otherwise having to configure port forwarding in firewalls, which often requires static IP address as well as privileges to edit the firewall on your outgoing router, something most users don't have. It also has the advantage of not having to know the internal and / or the public IP address / hostname of the master. Yet another advantage is that there will be no need for a DNS lookup by the worker machines to the master, which may not be configured or is disabled on some systems, e.g. compute clusters.

Argument `rscript`

If `homogeneous` is FALSE, the `rscript` defaults to `"Rscript"`, i.e. it is assumed that the `Rscript` executable is available on the `PATH` of the worker. If `homogeneous` is TRUE, the `rscript` defaults to `file.path(R.home("bin"), "Rscript")`, i.e. it is basically assumed that the worker and the caller share the same file system and R installation.

When specified, argument `rscript` should be a character vector with one or more elements. Any asterisk (`"*"`) will be resolved to the above default `homogeneous`-dependent `Rscript` path. All elements are automatically shell quoted using `base::shQuote()`, except those that are of format `<ENVVAR>=<VALUE>`, that is, the ones matching the regular expression '`^[[:alpha:]_][[:alnum:]_]*=.*`". Another exception is when `rscript` inherits from 'AsIs'.

Default value of argument `homogeneous`

The default value of `homogeneous` is TRUE if and only if either of the following is fulfilled:

- `worker` is *localhost*
- `revtunnel` is FALSE and `master` is *localhost*
- `worker` is neither an IP number nor a fully qualified domain name (FQDN). A hostname is considered to be a FQDN if it contains one or more periods

In all other cases, `homogeneous` defaults to FALSE.

Connection timeout

Argument `connectTimeout` does *not* work properly on Unix and macOS due to limitation in R itself. For more details on this, please see R-devel thread 'BUG?: On Linux setTimeLimit() fails to propagate timeout error when it occurs (works on Windows)' on 2016-10-26 (https://stat.ethz.ch/pipermail/r-devel/2016-October/073309.html). When used, the timeout will eventually trigger an error, but it won't happen until the socket connection timeout `timeout` itself happens.

Communication timeout

If there is no communication between the master and a worker within the `timeout` limit, then the corresponding socket connection will be closed automatically. This will eventually result in an error in code trying to access the connection. This timeout is also what terminates a stray-running parallel cluster-node process.

Failing to set up local workers

When setting up a cluster of localhost workers, that is, workers running on the same machine as the master R process, occasionally a connection to a worker ("cluster node") may fail to be set up. When this occurs, an informative error message with troubleshooting suggestions will be produced. The most common reason for such localhost failures is due to port clashes. Retrying will often resolve the problem.

If R stalls when setting up a cluster of local workers, then it might be that you have a virtual private network (VPN) enabled that is configured to prevent you from connecting to `localhost`. To verify that this is the case, call the following from the terminal:

```
{local}$ ssh localhost "date"
```

This also freezed if the VPN intercepts connections to `localhost`. If this happens, try also:

```
{local}$ ssh 127.0.0.1 "date"
```

In rare cases, `127.0.0.1` might work when `localhost` does not. If the latter works, setting R option:

```
options(parallelly.localhost.hostname = "127.0.0.1")
```

should solve it (the default is `"localhost"`). You can set this automatically when R starts by adding it to your `~/.Rprofile` startup file. Alternatively, set environment variable `R_PARALLELLY_LOCALHOST_HOSTNAME=127.0.0.` in your `~/.Renviron` file.

If using `127.0.0.1` did not work around the problem, check your VPN settings and make sure it allows connections to `localhost` or `127.0.0.1`.

Failing to set up remote workers

A cluster of remote workers runs R processes on external machines. These external R processes are launched over, typically, SSH to the remote machine. For this to work, each of the remote machines needs to have R installed, which preferably is of the same version as what is on the main machine. For this to work, it is required that one can SSH to the remote machines. Ideally, the SSH connections use authentication based on public-private SSH keys such that the set up of the remote workers can be fully automated (see above). If `makeClusterPSOCK()` fails to set up one or more remote R workers, then an informative error message is produced. There are a few reasons for failing to set up remote workers. If this happens, start by asserting that you can SSH to the remote machine and launch '`Rscript`' by calling something like:

```
{local}$ ssh -l alice remote.server.org
{remote}$ Rscript --version
R scripting front-end version 4.2.2 (2022-10-31)
{remote}$ logout
{local}$
```

When you have confirmed the above to work, then confirm that you can achieve the same in a single command-line call;

```
{local}$ ssh -l alice remote.server.org Rscript --version
R scripting front-end version 4.2.2 (2022-10-31)
{local}$
```

The latter will assert that you have proper startup configuration also for *non-interactive* shell sessions on the remote machine.

If the remote machines are running on MS Windows, make sure to add argument `rscript_sh = "cmd"` when calling `makeClusterPSOCK()`, because the default is `rscript_sh = "sh"`, which assumes that the remote machines are Unix-like machines.

Another reason for failing to setup remote workers could be that they are running an R version that is not compatible with the version that your main R session is running. For instance, if we run R (>= 3.6.0) locally and the workers run R (< 3.5.0), we will get: `Error in unserialize(node$con) : error reading from conn` This is because R (>= 3.6.0) uses serialization format version 3 by default whereas R (< 3.5.0) only supports version 2. We can see the version of the R workers by adding `rscript_args = c("-e", shQuote("getRversion()"))` when calling `makeClusterPSOCK()`.

For package developers

When creating a `cluster` object, for instance via `parallel::makeCluster()` or `parallelly::makeClusterPSOCK()`, in a package help example, in a package vignette, or in a package test, we must *remember to stop the cluster at the end of all examples(*), vignettes, and unit tests*. This is required in order to not leave behind stray parallel `cluster` workers after our main R session terminates. On Linux and macOS, the operating system often takes care of terminating the worker processes if we forget, but on MS Windows such processes will keep running in the background until they time out themselves, which takes 30 days (sic!).
`R CMD check --as-cran` will indirectly detect these stray worker processes on MS Windows when running R (>= 4.3.0). They are detected, because they result in placeholder `Rscript<hexcode>` files being left behind in the temporary directory. The check NOTE to look out for (only in R (>= 4.3.0)) is:

```
* checking for detritus in the temp directory ... NOTE
Found the following files/directories:
  'Rscript1058267d0c10' 'Rscriptbd4267d0c10'
```

Those `Rscript<hexcode>` files are from background R worker processes, which almost always are parallel `cluster`:s that we forgot to stop at the end. To stop all `cluster` workers, use `parallel::stopCluster()` at the end of your examples(*), vignettes, and package tests for every `cluster` object that is created.

(*) Currently, examples are excluded from the detritus checks. This was validated with R-devel revision 82991 (2022-10-02).

Examples

```
## NOTE: Drop 'dryrun = TRUE' below in order to actually connect.  Add
## 'verbose = TRUE' if you run into problems and need to troubleshoot.

## ------------------------------------------------------------------
## Section 1. Setting up parallel workers on the local machine
## ------------------------------------------------------------------
```

```
## EXAMPLE: Two workers on the local machine
workers <- c("localhost", "localhost")
cl <- makeClusterPSOCK(workers, dryrun = TRUE, quiet = TRUE)


## EXAMPLE: Launch 124 workers on MS Windows 10, where half are
## running on CPU Group #0 and half on CPU Group #1.
## (https://lovickconsulting.com/2021/11/18/
##  running-r-clusters-on-an-amd-threadripper-3990x-in-windows-10-2/)
## The parallel workers are launched as:
## "%COMSPEC%" /c start /B /NODE 1 /AFFINITY 0xFFFFFFFFFFFFFFFE ...
## ...
## "%COMSPEC%" /c start /B /NODE 1 /AFFINITY 0xFFFFFFFFFFFFFFFE ...

## Temporarily disable CPU load protection for this example
oopts <- options(parallelly.maxWorkers.localhost = Inf)

ncores <- 124
cpu_groups <- c(0, 1)
cl <- lapply(cpu_groups, FUN = function(cpu_group) {
    parallelly::makeClusterPSOCK(ncores %/% length(cpu_groups),
      rscript = I(c(
        Sys.getenv("COMSPEC"), "/c", "start", "/B",
        "/NODE", cpu_group, "/AFFINITY", "0xFFFFFFFFFFFFFFFE",
        "*"
      )),
      dryrun = TRUE, quiet = TRUE
    )
})
## merge the two 62-node clusters into one with 124 nodes
cl <- do.call(c, cl)

## Re-enable CPU load protection
options(oopts)


## ------------------------------------------------------------------
## Section 2. Setting up parallel workers on remote machines
## ------------------------------------------------------------------
## EXAMPLE: Three remote workers
## Setup of three R workers on two remote machines are set up
## The parallel workers are launched as:
## '/usr/bin/ssh' -R 11058:localhost:11058 n1.remote.org ...
## '/usr/bin/ssh' -R 11059:localhost:11058 n2.remote.org ...
## '/usr/bin/ssh' -R 11060:localhost:11058 n1.remote.org ...
workers <- c("n1.remote.org", "n2.remote.org", "n1.remote.org")
cl <- makeClusterPSOCK(workers, dryrun = TRUE, quiet = TRUE)


## EXAMPLE: Two remote workers running on MS Windows.  Because the
## remote workers are MS Windows machines, we need to use
## rscript_sh = "cmd".
## The parallel workers are launched as:
```

```
## '/usr/bin/ssh' -R 11912:localhost:11912 mswin1.remote.org ...
## '/usr/bin/ssh' -R 11913:localhost:11912 mswin2.remote.org ...
workers <- c("mswin1.remote.org", "mswin2.remote.org")
cl <- makeClusterPSOCK(workers, rscript_sh = "cmd", dryrun = TRUE, quiet = TRUE)


## EXAMPLE: Local and remote workers
## Same setup when the two machines are on the local network and
## have identical software setups
cl <- makeClusterPSOCK(
  workers,
  revtunnel = FALSE, homogeneous = TRUE,
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: Three remote workers 'n1', 'n2', and 'n3' that can only be
## accessed via jumphost 'login.remote.org'
## The parallel workers are launched as:
## '/usr/bin/ssh' -R 11226:localhost:11226 -J login.remote.org n1 ...
## '/usr/bin/ssh' -R 11227:localhost:11226 -J login.remote.org n2 ...
## '/usr/bin/ssh' -R 11228:localhost:11226 -J login.remote.org n1 ...
workers <- c("n1", "n2", "n1")
cl <- makeClusterPSOCK(
  workers,
  rshopts = c("-J", "login.remote.org"),
  homogeneous = FALSE,
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: Remote worker running on Linux from MS Windows machine
## Connect to remote Unix machine 'remote.server.org' on port 2200
## as user 'bob' from a MS Windows machine with PuTTY installed.
## Using the explicit special rshcmd = "<putty-plink>", will force
## makeClusterPSOCK() to search for and use the PuTTY plink software,
## preventing it from using other SSH clients on the system search PATH.
## The parallel worker is launched as:
## 'plink' -l bob -P 2200 -i C:/Users/bobby/.ssh/putty.ppk remote.server.org ...
cl <- makeClusterPSOCK(
  "remote.server.org", user = "bob",
  rshcmd = "<putty-plink>",
  rshopts = c("-P", 2200, "-i", "C:/Users/bobby/.ssh/putty.ppk"),
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: Remote workers with specific setup
## Setup of remote worker with more detailed control on
## authentication and reverse SSH tunneling
## The parallel worker is launched as:
## '/usr/bin/ssh' -l johnny -v -R 11000:gateway:11942 remote.server.org ...
## "R_DEFAULT_PACKAGES=... 'nice' '/path/to/Rscript' --no-init-file ...
```

```
cl <- makeClusterPSOCK(
  "remote.server.org", user = "johnny",
  ## Manual configuration of reverse SSH tunneling
  revtunnel = FALSE,
  rshopts = c("-v", "-R 11000:gateway:11942"),
  master = "gateway", port = 11942,
  ## Run Rscript nicely and skip any startup scripts
  rscript = c("nice", "/path/to/Rscript"),
  rscript_args = c("--no-init-file"),
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: Remote worker running on Linux from RStudio on MS Windows
## Connect to remote Unix machine 'remote.server.org' on port 2200
## as user 'bob' from a MS Windows machine via RStudio's SSH client.
## Using the explicit special rshcmd = "<rstudio-ssh>", will force
## makeClusterPSOCK() to use the SSH client that comes with RStudio,
## preventing it from using other SSH clients on the system search PATH.
## The parallel worker is launched as:
## 'ssh' -l bob remote.server.org:2200 ...
cl <- makeClusterPSOCK(
  "remote.server.org:2200", user = "bob", rshcmd = "<rstudio-ssh>",
  dryrun = TRUE, quiet = TRUE
)


## ------------------------------------------------------------------
## Section 3. Setting up parallel workers on HPC cluster
## ------------------------------------------------------------------
## EXAMPLE: 'Grid Engine' is a high-performance compute (HPC) job
## scheduler where one can request compute resources on multiple nodes,
## each running multiple cores. Examples of Grid Engine schedulers are
## Oracle Grid Engine (formerly Sun Grid Engine), Univa Grid Engine,
## and Son of Grid Engine - all commonly referred to as SGE schedulers.
## Each SGE cluster may have its own configuration with their own way
## of requesting parallel slots. Here are a few examples:
##
##   ## Request 18 slots on a single host
##   qsub -pe smp 18 script.sh
##
##   ## Request 18 slots on one or more hosts
##   qsub -pe mpi 18 script.sh
##
## This will launch the job script 'script.sh' on one host, while have
## reserved in total 18 slots (CPU cores) on this host and possible
## other hosts.
##
## This example shows how to use the SGE command 'qrsh' to launch
## 18 parallel workers from R, which is assumed to have been launched
## by 'script.sh'.
##
## The parallel workers are launched as:
```

```
## 'qrsh' -inherit -nostdin -V comphost01 ...
## 'qrsh' -inherit -nostdin -V comphost01 ...
## ...
## 'qrsh' -inherit -nostdin -V comphost06 ...
cl <- makeClusterPSOCK(
  availableWorkers(),
  rshcmd = "qrsh", rshopts = c("-inherit", "-nostdin", "-V"),
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: The 'Fujitsu Technical Computing Suite' is a high-performance
## compute (HPC) job scheduler where one can request compute resources on
## multiple nodes, each running multiple cores.  For example,
##
##   pjsub -L vnode=3 -L vnode-core=18 script.sh
##
## reserves 18 cores on three nodes. The job script runs on the first
## with enviroment variables set to infer the other nodes, resulting in
## availableWorkers() to return 3 * 18 workers. When the HPC environment
## does not support SSH between compute nodes, one can use the 'pjrsh'
## command to launch the parallel workers.
##
## The parallel workers are launched as:
## 'pjrsh' comphost01 ...
## 'pjrsh' comphost01 ...
## ...
## 'pjrsh' comphost06 ...
cl <- makeClusterPSOCK(
  availableWorkers(),
  rshcmd = "pjrsh",
  dryrun = TRUE, quiet = TRUE
)



## ------------------------------------------------------------------
## Section 4. Setting up remote parallel workers in the cloud
## ------------------------------------------------------------------
## EXAMPLE: Remote worker running on AWS
## Launching worker on Amazon AWS EC2 running one of the
## Amazon Machine Images (AMI) provided by RStudio
## (https://www.louisaslett.com/RStudio_AMI/)
##
## The parallel worker is launched as:
## '/usr/bin/ssh' -R 11153:localhost:11153 -l ubuntu ...
## -o StrictHostKeyChecking=no -o IdentitiesOnly=yes ...
## -i ~/.ssh/my-private-aws-key.pem 1.2.3.4 ...
public_ip <- "1.2.3.4"
ssh_private_key_file <- "~/.ssh/my-private-aws-key.pem"
cl <- makeClusterPSOCK(
  ## Public IP number of EC2 instance
  public_ip,
```

```
  ## User name (always 'ubuntu')
  user = "ubuntu",
  ## Use private SSH key registered with AWS
  rshopts = c(
    "-o", "StrictHostKeyChecking=no",
    "-o", "IdentitiesOnly=yes",
    "-i", ssh_private_key_file
  ),
  ## Set up .libPaths() for the 'ubuntu' user
  ## and then install the future package
  rscript_startup = quote(local({
    p <- Sys.getenv("R_LIBS_USER")
    dir.create(p, recursive = TRUE, showWarnings = FALSE)
    .libPaths(p)
    install.packages("future")
  })),
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: Remote worker running on GCE
## Launching worker on Google Cloud Engine (GCE) running a
## container based VM (with a #cloud-config specification)
public_ip <- "1.2.3.4"
user <- "johnny"
ssh_private_key_file <- "~/.ssh/google_compute_engine"
cl <- makeClusterPSOCK(
  ## Public IP number of GCE instance
  public_ip,
  ## User name (== SSH key label (sic!))
  user = user,
  ## Use private SSH key registered with GCE
  rshopts = c(
    "-o", "StrictHostKeyChecking=no",
    "-o", "IdentitiesOnly=yes",
    "-i", ssh_private_key_file
  ),
  ## Launch Rscript inside Docker container
  rscript = c(
    "docker", "run", "--net=host", "rocker/r-parallel",
    "Rscript"
  ),
  dryrun = TRUE, quiet = TRUE
)



## ------------------------------------------------------------------
## Section 5. Parallel workers running locally inside virtual
## machines, Linux containers, etc.
## ------------------------------------------------------------------
## EXAMPLE: Two workers limited to 100% CPU process and 50 MiB of
## memory using Linux CGroups management. The 100% CPU quota limit
```

```
## constrain each worker to use at most one CPU worth of
## processing preventing them from overusing the machine, e.g.
## through unintended nested parallelization. The 50 MiB memory
## limit is strict - if a worker use more than this, the operating
## system will terminate the worker instantly.
## See 'man systemd.resource-control' for more details.
cl <- makeClusterPSOCK(2L,
  rscript = c("systemd-run", "--user", "--scope",
    "-p", "CPUQuota=100%",
    "-p", "MemoryMax=50M", "-p", "MemorySwapMax=50M",
    "*"
  ),
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: Two workers running in Docker on the local machine
## Setup of 2 Docker workers running rocker/r-parallel
##
## The parallel workers are launched as:
## R_DEFAULT_PACKAGES=... '/usr/bin/docker' 'run' '--net=host' 'rocker/r-parallel' ...
## R_DEFAULT_PACKAGES=... '/usr/bin/docker' 'run' '--net=host' 'rocker/r-parallel' ...
cl <- makeClusterPSOCK(
  rep("localhost", times = 2L),
  ## Launch Rscript inside Docker container
  rscript = c(
    "docker", "run", "--net=host", "rocker/r-parallel",
    "Rscript"
  ),
  ## IMPORTANT: Because Docker runs inside a virtual machine (VM) on macOS
  ## and MS Windows (not Linux), when the R worker tries to connect back to
  ## the default 'localhost' it will fail, because the main R session is
  ## not running in the VM, but outside on the host.  To reach the host on
  ## macOS and MS Windows, make sure to use master = "host.docker.internal"
  master = if (.Platform$OS.type == "unix") NULL else "host.docker.internal",
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: Two workers running via Linux container 'rocker/r-parallel' from
## DockerHub on the local machine using Apptainer (formerly Singularity)
##
## The parallel workers are launched as:
## R_DEFAULT_PACKAGES=... '/usr/bin/apptainer' 'exec' 'docker://rocker/r-parallel' ...
## R_DEFAULT_PACKAGES=... '/usr/bin/apptainer' 'exec' 'docker://rocker/r-parallel' ...
cl <- makeClusterPSOCK(
  rep("localhost", times = 2L),
  ## Launch Rscript inside Linux container
  rscript = c(
    "apptainer", "exec", "docker://rocker/r-parallel",
    "Rscript"
  ),
  dryrun = TRUE, quiet = TRUE
```

```
)


## EXAMPLE: One worker running in udocker on the local machine
## Setup of a single udocker.py worker running rocker/r-parallel
##
## The parallel worker is launched as:
## R_DEFAULT_PACKAGES=... 'udocker.py' 'run' 'rocker/r-parallel' ...
cl <- makeClusterPSOCK(
  "localhost",
  ## Launch Rscript inside Docker container (using udocker)
  rscript = c(
    "udocker.py", "run", "rocker/r-parallel",
    "Rscript"
  ),
  ## Manually launch parallel workers
  ## (need double shQuote():s because udocker.py drops one level)
  rscript_args = c(
    "-e", shQuote(shQuote("parallel:::.workRSOCK()"))
  ),
  dryrun = TRUE, quiet = TRUE
)


## EXAMPLE: One worker running in Wine for Linux on the local machine
## To install R for MS Windows in Wine, do something like:
##   winecfg  # In GUI, set 'Windows version' to 'Windows 10'
##   wget https://cran.r-project.org/bin/windows/base/R-4.5.2-win.exe
##   wine R-4.5.2-win.exe /SILENT
## Prevent packages from being installed to R's system library:
##   chmod ugo-w "$HOME/.wine/drive_c/Program Files/R/R-4.5.2/library/"
## Verify it works:
##   wine "C:/Program Files/R/R-4.5.2/bin/x64/Rscript.exe" --version
##
## The parallel worker is launched as:
## R_DEFAULT_PACKAGES=... WINEDEBUG=fixme-all R_LIBS_SITE= R_LIBS_USER= 'wine' ...
cl <- makeClusterPSOCK(1L,
  rscript = c(
    ## Silence Wine warnings
    "WINEDEBUG=fixme-all",
    ## Don't pass LC_* and R_LIBS* environments from host to Wine
    sprintf("%s=", grep("^(LC_|R_LIBS)", names(Sys.getenv()), value = TRUE)),
    "wine",
    "C:/Program Files/R/R-4.5.2/bin/x64/Rscript.exe"
  ),
  dryrun = TRUE, quiet = TRUE
)
```

---

makeClusterSequential *Create a "parallel" cluster running sequentially in the current session*

Description

The created cluster has only one node.

Usage

```
makeClusterSequential()
```

Details

Expression and function calls are evaluated in a local environment, inheriting the global environment.

Value

Returns a `cluster` object of class `sequential_cluster` of length one. The element is a cluster node of class `sequential_node`.

Alternative usage

In R (>= 4.5.0), an alternative to using `cl <- parallelly::makeClusterSequential()` is:

```
cl <- parallel::makeCluster(1L, type = parallelly::SEQ)
```

Requirements

This function is only defined for R (>= 4.4.0).

Works in webR

Contrary to other cluster types, a `makeClusterSequential()` cluster works in webR, meaning you can use it for code that rely on the **parallel** package, e.g. `y <- parLapply(cl, ...)`.

Examples

```
library(parallel)

cl <- makeClusterSequential()
print(cl)

y <- parLapply(cl, X = 1:3, fun = sqrt)
str(y)

pid <- Sys.getpid()
print(pid)
y <- clusterEvalQ(cl, Sys.getpid())
str(y)

abc <- 3.14
y <- clusterEvalQ(cl, { abc <- 42; abc })
str(y)
stopifnot(abc == 3.14)
```

```
clusterExport(cl, "abc", envir = environment())
rm(abc)
y <- clusterEvalQ(cl, { abc })
str(y)
stopifnot(y[[1]] == 3.14)
```

`serializedSize` *Calculate the size of an R object when it is serialized*

Description

This function goes through all the motions of serializing an object, but does nothing with the bytes other than to tally the total length.

Usage

```
serializedSize(obj)
```

Arguments

`obj`	An R object.

Value

(double) Number of bytes needed to serialize this object.

Author(s)

Mike FC

Examples

```
object.size(mtcars)
serializedSize(mtcars)
```

`supportsMulticore` *Check If Forked Processing ("multicore") is Supported*

Description

Certain parallelization methods in R rely on *forked* processing, e.g. `parallel::mclapply()`, `parallel::makeCluster(n, type = "FORK")`, `doMC::registerDoMC()`, and `future::plan("multicore")`. Process forking is done by the operating system and support for it in R is restricted to Unix-like operating systems such as Linux, Solaris, and macOS. R running on Microsoft Windows does not support forked processing. In R, forked processing is often referred to as "multicore" processing, which stems from the 'mc' of the `mclapply()` family of functions, which originally was in a package named **multicore** which later was incorporated into the **parallel** package. This function checks whether or not forked (aka "multicore") processing is supported in the current R session.

Usage

```
supportsMulticore(...)
```

Arguments

`...`	Internal usage only.

Value

TRUE if forked processing is supported and not disabled, otherwise FALSE.

Support for process forking

While R supports forked processing on Unix-like operating system such as Linux and macOS, it does not on the Microsoft Windows operating system.

For some R environments it is considered unstable to perform parallel processing based on *forking*. This is for example the case when using RStudio, cf. RStudio Inc. recommends against using forked processing when running R from within the RStudio software. This function detects when running in such an environment and returns `FALSE`, despite the underlying operating system supports forked processing. A warning will also be produced informing the user about this the first time this function is called in an R session. This warning can be disabled by setting R option `parallelly.supportsMulticore.unstable`, or environment variable `R_PARALLELLY_SUPPORTSMULTICORE_UNSTABLE` to `"quiet"`.

Enable or disable forked processing

It is possible to disable forked processing for futures by setting R option `parallelly.fork.enable` to `FALSE`. Alternatively, one can set environment variable `R_PARALLELLY_FORK_ENABLE` to `false`. Analogously, it is possible to override disabled forking by setting one of these to `TRUE`.

Why not forked processing?

One reason for *not* using forked parallel processing in R is that is not guaranteed to be stable in all environments or in all contexts, which also depends on which functions are called in the forked processes. Here is what R Core developer of the `parallel::mclapply()` family of functions said on R-devel (2020-04-29):

"Do NOT use `mcparallel()` *in packages except as a non-default option that user can set ... Multicore is intended for HPC applications that need to use many cores for computing-heavy jobs, but it does not play well with RStudio and more importantly you [as the developer] don't know the resource available so only the user can tell you when it's safe to use."*

Examples

```
## Check whether or not forked processing is supported
supportsMulticore()
```

---

zzz-parallelly.options

Options Used by the 'parallelly' Package

Description

Below are the R options and environment variables that are used by the **parallelly** package and packages enhancing it.

WARNING: Note that the names and the default values of these options may change in future versions of the package. Please use with care until further notice.

Configuring number of parallel workers

The below R options and environment variables control the default results of `availableCores()` and `availableWorkers()`.

`parallelly.availableCores.logical`**:** (logical) The default value of argument `logical` as used by `availableCores()`, `availableWorkers()`, and `availableCores()` for querying `parallel::detectCores(logic = logical)`. The default is `TRUE` just like it is for `parallel::detectCores()`.

`parallelly.availableCores.methods`**:** (character vector) Default lookup methods for `availableCores()`. (Default: `c("system", "/proc/self/status", "cgroups.cpuset", "cgroups.cpuquota", "cgroups2.cpuset.cpus", "cgroups2.cpuset.cpus.effective", "cgroups2.cpu.max", "nproc", "mc.cores", "BiocParallel", "_R_CHECK_LIMIT_CORES_", "Bioconductor", "LSF", "PJM", "PBS", "SGE", "Slurm", "HTCondor", "fallback", "custom")`)

`parallelly.availableCores.methods.excludes`**:** (character vector) Default lookup methods for `availableCores()` to be excluded. (Default: `NULL`)

`parallelly.availableCores.custom`**:** (function) If set and a function, then this function will be called (without arguments) by `availableCores()` where its value, coerced to an integer, is interpreted as a number of cores.

`parallelly.availableCores.fallback`: (integer) The default number of cores to use when no core-specifying settings are detected other than `"system"` and `"nproc"`. This options makes it possible to set the default number of cores returned by `availableCores()` / `availableWorkers()` yet allow users and schedulers to override it. In multi-tenant environment, such as HPC clusters, it is useful to set environment variable `R_PARALLELLY_AVAILABLECORES_FALLBACK` to `1`, which will set this option when the package is loaded.

`parallelly.availableCores.system`: (integer) The default number of "system" cores used instead of what is reported by `availableCores(which = "system")`. This option allows you to effectively override what `parallel::detectCores()` reports the system has.

`parallelly.availableCores.min`: (integer) The default minimum number of cores `availableCores()` is allowed to return. This can be used to force multiple cores on a single-core environment. If this is limit is applied, the names of the returned value are appended with an asterisk (`*`). (Default: `1L`)

`parallelly.availableCores.threadsPerWorker`: (integer; positive) The default number of CPU cores (threads) to reserve for each parallel worker, used by `availableCores()` and `availableWorkers()`. (Default: `1L`)

`parallelly.availableCores.fraction`: (numeric; in `[0,1]`) The default fraction of cores to keep.

`parallelly.availableCores.omit`: (integer; non-negative) The default number of cores to set aside, i.e. not to include.

`parallelly.availableCores.max`: (integer; positive) The default maximum number of cores to return.

`parallelly.availableWorkers.methods`: (character vector) Default lookup methods for `availableWorkers()`. (Default: `c("mc.cores", "BiocParallel", "_R_CHECK_LIMIT_CORES_", "Bioconductor", "LSF", "PJM", "PBS", "SGE", "Slurm", "HTCondor", "custom", "cgroups.cpuset", "cgroups.cpuquota", "cgroups2.cpuset.cpus", "cgroups2.cpuset.cpus.effective", "cgroups2.cpu.max", "nproc", "/proc/self/status", "system", "fallback")`)

`parallelly.availableWorkers.methods.excludes`: (character vector) Default lookup methods for `availableWorkers()` to be excluded. (Default: `NULL`)

`parallelly.availableWorkers.custom`: (function) If set and a function, then this function will be called (without arguments) by `availableWorkers()` where its value, coerced to a character vector, is interpreted as hostnames of available workers.

Configuring forked parallel processing

The below R options and environment variables control the default result of `supportsMulticore()`.

`parallelly.fork.enable`: (logical) Enable or disable *forked* processing. If `FALSE`, multicore futures becomes sequential futures. If `NA`, or not set (the default), the a set of best-practices rules decide whether should be supported or not.

`parallelly.supportsMulticore.disableOn`: (character vector) because the environment in which R runs is considered unstable for forked processing. If this vector contains `"rstudio_console"`, it is disabled when running R in the RStudio Console. If this vector contains `"rstudio_terminal"`, it is disabled when running R in the RStudio Terminal. (Default: `c("rstudio_console")`)

`parallelly.supportsMulticore.unstable`: (character) Controls whether a warning should be produced or not whenever multicore processing is automatically disabled per settings in option `parallelly.supportsMulticore.disableOn`. If `"warn"` (default), then an informative warning is produces the first time 'multicore' futures are used. If `"quiet"`, no warning is produced.

Configuring setup of parallel PSOCK clusters

The below R options and environment variables control the default results of `makeClusterPSOCK()` and its helper function `makeNodePSOCK()` that creates the individual cluster nodes.

`parallelly.maxWorkers.localhost`: (two numerics) Maximum number of localhost workers, relative to `availableCores()`, accepted and allowed. The first element specifies the "soft" limit, which triggers a warning, if exceeded. The second element specifies the "hard" limit, which triggers an error if exceeded. These limits exist to protect against CPU overuse of the current machine, which sometimes happens by mistake without the user causing it being aware. These limits can be disabled by setting them to `+Inf` (not recommended). If only the first exist, no error is produced (defaults to `c(1.0, 3.0)` corresponding to a maximum 100% and 300% use).

`parallelly.makeNodePSOCK.setup_strategy`: (character) If `"parallel"` (default), the PSOCK cluster nodes are set up concurrently. If `"sequential"`, they are set up sequentially.

`parallelly.makeNodePSOCK.validate`: (logical) If TRUE (default), after the nodes have been created, they are all validated that they work by inquiring about their session information, which is saved in attribute `session_info` of each node.

`parallelly.makeNodePSOCK.connectTimeout`: (numeric) The maximum time (in seconds) allowed for each socket connection between the master and a worker to be established (defaults to 2*60 seconds = 2 minutes).

`parallelly.makeNodePSOCK.timeout`: (numeric) The maximum time (in seconds) allowed to pass without the master and a worker communicate with each other (defaults to 30*24*60*60 seconds = 30 days).

`parallelly.makeNodePSOCK.useXDR`: (logical) If FALSE (default), the communication between master and workers, which is binary, will use small-endian (faster), otherwise big-endian ("XDR"; slower).

`parallelly.makeNodePSOCK.socketOptions`: (character string) If set to another value than `"NULL"`, then option `socketOptions` is set to this value on the workers during startup. See `base::socketConnection()` for details. (defaults to `"no-delay"`)

`parallelly.makeNodePSOCK.rscript_call`: (character string or R expression) The R expression that is used to start the R worker event loop on the worker node. (defaults to `"workRSOCK<-tryCatch(parallel:::.wo`

`parallelly.makeNodePSOCK.rshcmd`: (character vector) The command to be run on the master to launch a process on another host.

`parallelly.makeNodePSOCK.rshopts`: (character vector) Addition command-line options appended to `rshcmd`. These arguments are only applied when connecting to non-localhost machines.

`parallelly.makeNodePSOCK.tries`: (integer) The maximum number of attempts done to launch each node. Only used when setting up cluster nodes using the sequential strategy.

`parallelly.makeNodePSOCK.tries.delay`: (numeric) The number of seconds to wait before trying to launch a cluster node that failed to launch previously. Only used when setting up cluster nodes using the sequential strategy.

Options for debugging

`parallelly.debug`**:** (logical) If `TRUE`, extensive debug messages are generated. (Default: `FALSE`)

`parallelly.makeNodePSOCK.calls`**:** (logical) If TRUE, then the call stack that launched the cluster node is revealed as a string part of the system call such that it can be viewed using tools such as `ps`. (Default: `FALSE`)

Environment variables that set R options

All of the above R `parallelly.*` options can be set by corresponding environment variables `R_PARALLELLY_*` *when the* **parallelly** *package is loaded*. For example, if `R_PARALLELLY_MAKENODEPSOCK_SETUP_STRATEGY=` then option `parallelly.makeNodePSOCK.setup_strategy` is set to `"sequential"` (character). Similarly, if `R_PARALLELLY_AVAILABLECORES_FALLBACK="1"`, then option `parallelly.availableCores.fallback` is set to 1 (integer).

Backward compatibility with the future package

The functions in the **parallelly** package originates from the **future** package. Because they are widely used within the future ecosystem, we need to keep them backward compatible for quite a long time, in order for all existing packages and R scripts to have time to adjust. This also goes for the R options and the environment variables used to configure these functions. All options and environment variables used here have prefixes `parallelly.` and `R_PARALLELLY_`, respectively. Because of the backward compatibility with the **future** package, the same settings can also be controlled by options and environment variables with prefixes `future.` and `R_FUTURE_` until further notice, e.g. setting option `future.availableCores.fallback=1` is the same as setting option `parallelly.availableCores.fallback=1`, and setting environment variable `R_FUTURE_AVAILABLECORES_FALLBACK=1` is the same as setting `R_PARALLELLY_AVAILABLECORES_FALLBACK=1`.

`parallelly.future.reexports`**:** (character string) Controls whether a deprecation warning should be produced when `future::availableCores()`, `future::availableWorkers()`, `future::makeClusterPSOCK()`, or `future::supportsMulticore()` are called. If `"deprecated"` (default), a warning is produced. If `"defunct"`, an error is produced. If `"ignore"`, no warning or error is produced.

See Also

To set R options when R starts (even before the **parallelly** package is loaded), see the Startup help page. The **startup** package provides a friendly mechanism for configuring R's startup process.

Examples

```
# Set an R option:
options(parallelly.availableCores.fallback = 1L)
```

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