### **NAME**

sem - semaphore for executing shell command lines in parallel

### **SYNOPSIS**

sem [--fg] [--id <id>] [--semaphoretimeout <secs>] [-j <num>] [--wait] command

#### DESCRIPTION

GNU sem is an alias for GNU parallel --semaphore.

It works as a tool for executing shell commands in parallel. GNU **sem** acts as a counting semaphore. When GNU **sem** is called with command it will start the command in the background. When *num* number of commands are running in the background, GNU **sem** will wait for one of these to complete before starting another command.

Before looking at the options you may want to check out the examples after the list of options. That will give you an idea of what GNU **sem** is capable of.

### **OPTIONS**

command

Command to execute. The command may be followed by arguments for the command.

--bg

Run command in background thus GNU **parallel** will not wait for completion of the command before exiting. This is the default.

See also: --fg

-j N

Run up to N commands in parallel. Default is 1 thus acting like a mutex.

```
--jobs N
```

-j N

--max-procs N

**-P** N

Run up to N commands in parallel. Default is 1 thus acting like a mutex.

```
--jobs +N
```

-j +N

--max-procs +N

**-P** +N

Add N to the number of CPU cores. Run up to this many jobs in parallel. For compute intensive jobs **-j** +0 is useful as it will run number-of-cpu-cores jobs simultaneously.

```
--jobs -N
```

-j -N

--max-procs -N

**-P** -N

Subtract N from the number of CPU cores. Run up to this many jobs in parallel. If the evaluated number is less than 1 then 1 will be used. See also

--use-cpus-instead-of-cores.

--jobs N%

-j N%

#### --max-procs N%

-P N%

Multiply N% with the number of CPU cores. Run up to this many jobs in parallel. If the evaluated number is less than 1 then 1 will be used. See also --use-cpus-instead-of-cores.

- -- jobs procfile
- -j procfile
- --max-procs procfile
- -P procfile

Read parameter from file. Use the content of *procfile* as parameter for *-j.* E.g. *procfile* could contain the string 100% or +2 or 10.

### --semaphorename name

--id name

Use **name** as the name of the semaphore. Default is the name of the controlling tty (output from **tty**).

The default normally works as expected when used interactively, but when used in a script *name* should be set. \$\$ or *my\_task\_name* are often a good value.

The semaphore is stored in ~/.parallel/semaphores/

--fg

Do not put command in background.

- --semaphoretimeout secs (alpha testing)
- --st secs (alpha testing)

If secs > 0: If the semaphore is not released within secs seconds, take it anyway.

If secs < 0: If the semaphore is not released within secs seconds, exit.

--wait

-W

Wait for all commands to complete.

# **EXAMPLE:** Gzipping \*.log

Run one gzip process per CPU core. Block until a CPU core becomes available.

```
for i in *.log ; do
   echo $i
   sem -j+0 gzip $i ";" echo done
done
sem --wait
```

## **EXAMPLE: Protecting pod2html from itself**

pod2html creates two files: pod2htmd.tmp and pod2htmi.tmp which it does not clean up. It uses these two files for a short time. But if you run multiple pod2html in parallel (e.g. in a Makefile with make -j) you need to protect pod2html from running twice at the same time. **sem** running as a mutex will do just that:

```
sem --fg --id pod2html pod2html foo.pod > foo.html
sem --fg --id pod2html rm -f pod2htmd.tmp pod2htmi.tmp
```

### **BUGS**

None known.

### REPORTING BUGS

Report bugs to <bug-parallel@gnu.org>.

#### **AUTHOR**

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# **DEPENDENCIES**

GNU sem uses Perl, and the Perl modules Getopt::Long, Symbol, Fcntl.

# **SEE ALSO**

parallel(1)