



**Barcelona
Supercomputing
Center**

Centro Nacional de Supercomputación

Introduction to MareNostrum IV

LifeSciences startup guide

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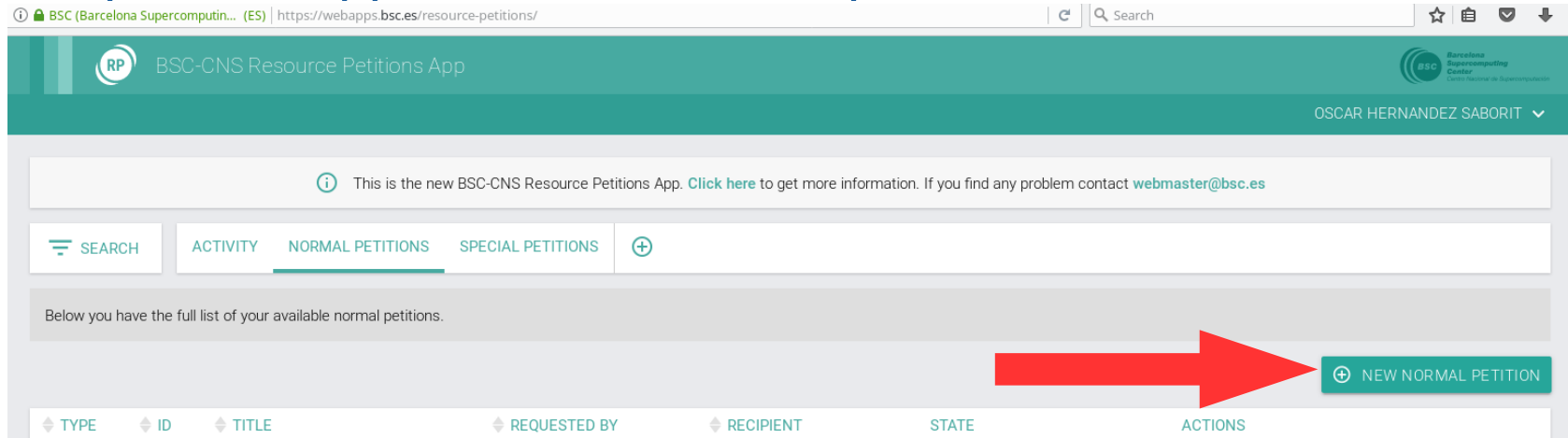
BSC Support Team

Barcelona, September 27th 2017

Requesting supercomputing resources

“ Through the “resource petitions” app available at:

<https://webapps.bsc.es/resource-petitions/>



“ Team leaders can issue “special petitions”

Intended for non-BSC personeel

BSC HPC access

« Access through SSH

- OpenSSH for Linux / OSX
- PuTTY for Windows

« On the facilities granted you can authenticate by:

- password
- SSH public keys



Shared Credentials

Shared users among:

- Data Transfer (dt01.bsc.es) >> Data management
- MareNostrum IV (mn1.bsc.es) >> 48 core nodes | 166000cpus
- Ultraviolet (bscsmp02.bsc.es) >> 96 cpus | 1.5 TB RAM
- CTE-POWER (plogin1.bsc.es) >> P8(160 cpus) | 2xTesla P100
- CTE-KNL (klogin1.bsc.es) >> 16*64 core xeon-phi
- Nord3 (nord3.bsc.es) >> 16 core nodes|
- Minotauro (mt01.bsc.es) >> 16/12 core nodes | 2* M2090/K80

Same \$HOME, \$USER and password

General Parallel Filesystem (GPFS)

« High performance parallel filesystem

« GPFS Filesystems on the cluster

- /gpfs/apps (Support vetted applications)
- /gpfs/home (User's home, backup)
- /gpfs/projects (Inputs, custom installations, backup)
- /gpfs/scratch (Temporary files, NO backup)
- /gpfs/archive (Long term storage, batch interaction)

Filesystem limits (Quota)

« Filesystem limit per user and/or group.

« Check with: `bsc_quota`

« Typical related problems:

- Job submission failure when `$HOME` is over quota
- Job execution failure when writing to over-quota filesystem

« Group-shared quota on `/gpfs/projects` and `/gpfs/scratch`

/gpfs/home Filesystem usage

☞ Few space (~40 GB per user)

☞ /gpfs/home Do:

- Store source code
- Store personal scripts



☞ /gpfs/home Don't:

- Use as production directory



/gpfs/archive Filesystem usage

“ You can check availability with `bsc_quota` and `dtquota`

“ /gpfs/archive Do:

- Store data you are not going to use soon
- Store processed final results



“ /gpfs/archive Don't:

- Execute commands interactively (`cp`, `mv`, ...)
- Try to put ACLs



Data Transfer Commands

« Set of commands to send data transfer jobs to queues

- Available in MareNostrum and dt01 & dt02

« Commands

- File movement: dtcp & dtmv
- Archiving & synchronizing: dttar & dtrsyc
- Job control: dtq & dtcancel

Node's local disk (/scratch)

☞ All nodes have disk for temporary files

- Accessible via \$TMPDIR
- Not shared between nodes (different to /gpfs/scratch)
- Content erased after execution

☞ Useful for temporary files

- Temporal data from MPI communication

☞ 200 GB disk

MareNostrum logins

3 external accessible logins:

- mn1.bsc.es
- mn2.bsc.es
- mn3.bsc.es

2 internal accessible logins:

- Login4
- Login5

No outgoing connections

- No downloads or uploads
- 5 minutes cpu time limit



Login usage



Manage & edit files

Small & medium compilations

Submit jobs to batch system

Check results and prepare scripts



Run production executions

Copy large amount of files

Long and heavy load graphical
interfaces

Compilers

⌞ Intel and GNU compiler suites available

⌞ Intel compilers available in:

- login1
- Interactive nodes (`$ salloc -p interactive`)

⌞ Several versions, managed by modules

- Fortran, C, C++
- Intel (licensed)
- GCC (Free Software)

⌞ MPI compilation also managed by modules through wrappers

- `mpicc`, `mpifort`...

Module Environment (I)

- « Open Source project
- « Environment variables and software dependencies management
- « Several versions of same program side-to-side (/gpfs/apps only)
- « Typical dependencies:
 - MPI libraries
 - Mathematical libraries

Module Environment (II)

Module commands:

Command	Option	Example	Info
avail	[program]	module avail	List modules available
list		module list	List loaded modules
purge		module purge	Unload all modules
load	<program[/version]>	module load gcc/5.1.0	Load a module
switch	<old> <new>	module switch intel gcc	Change a module by another

Batch System

« MareNostrum IV uses Platform SLURM as batch system

« Benefits of using jobscripts

- Defines resources needed
- Reusable
- Documents needs and requests
- Jobscripts are shellscripts with special markings



« Each submission is a job

SLURM commands

« Submit a job defined in job_script.cmd

- sbatch job_script.cmd

« Check status of jobs submitted:

- User's: squeue

« Cancel a job:

- scancel JobID

SLURM Common Parameters

Option	Comment	Example
-n -ntasks	Number of tasks	#SBATCH -n 32
-t --time	Wallclock limit	#SBATCH -t 01:00
-J --job-name	Job name	#SBATCH -J myjob
-o --output	Output file	#SBATCH -o %j.out
-e --error	Error file	#SBATCH -e %j.err
--qos	Queue	#SBATCH --qos debug
--exclusive	Exclusive mode	#SBATCH --exclusive
-D --workdir	Current working dir	#SBATCH -D= /my/path/
--reservation	Reservation	#SBATCH --reservation reserv_name

SLURM Extra Parameters: Process layout

« How to define specific load balance configurations:

Option	Comment	Example
--ntasks-per-core	Tasks per core	#SBATCH --ntasks-per-core 1
--ntasks-per-node	Tasks per node	#SBATCH --ntasks-per-node 48
-c --cpus-per-task	Cpus per task	#SBATCH -c 1

Generic MNIV example:

```
#SBATCH --ntasks-per-core 1
#SBATCH --ntasks-per-node 48
```

SLURM Extra Parameters: Memory layout

2 nodetypes:

« HIGH MEMORY NODES

- Total of 384GBytes per node (8G per core)
- Only 216 nodes available

#SBATCH --constraint=highmem

« LOW MEMORY NODES

- Total of 96GBytes per node (2G per core)
- Default nodes

Job queues

- « Jobs are assigned to queues (QoS)
- « Default queue automatically selected.
- « Specify when special need: debug, interactive, graphical...
- « Different queues have different limits and goals
- « Check your available queues and their limits:
 - `bsc_queues`
- « Example: `#SBATCH --qos debug`

Job Examples: Sequential

« Sequential

```
#!/bin/bash
```

```
#SBATCH -n 1
```

```
#SBATCH -o %J.out
```

```
#SBATCH -e %J.err
```

```
#SBATCH -t 01:00
```

```
hostname
```


Job Examples: Threaded

« Threaded (OpenMP, pthreads, ...)

```
#!/bin/bash
```

```
#SBATCH -n 1
```

```
#SBATCH --exclusive
```

```
#SBATCH -o %j.out
```

```
#SBATCH -e %j.err
```

```
#SBATCH -t 01:00
```

```
export OMP_NUM_THREADS=16
```

```
...
```

Job Examples: Typical MPI

❧ MPI (multiple nodes, OpenMPI)

```
#!/bin/bash
```

```
#SBATCH -n 96
```

```
#SBATCH -o %j.out
```

```
#SBATCH -e %j.err
```

```
#SBATCH -t 01:00
```

```
module purge
```

```
module load openmpi
```

```
mpirun ...
```

Job Examples: MPI + OpenMP

« MPI + Threads

```
#!/bin/bash  
  
#SBATCH -n 96  
  
#SBATCH -o %j.out  
  
#SBATCH -e %j.err  
  
#SBATCH --ntasks-per-node=4  
  
#SBATCH -t 01:00  
  
export OMP_NUM_THREADS=4  
  
module purge  
  
module load openmpi  
  
mpirun ...
```

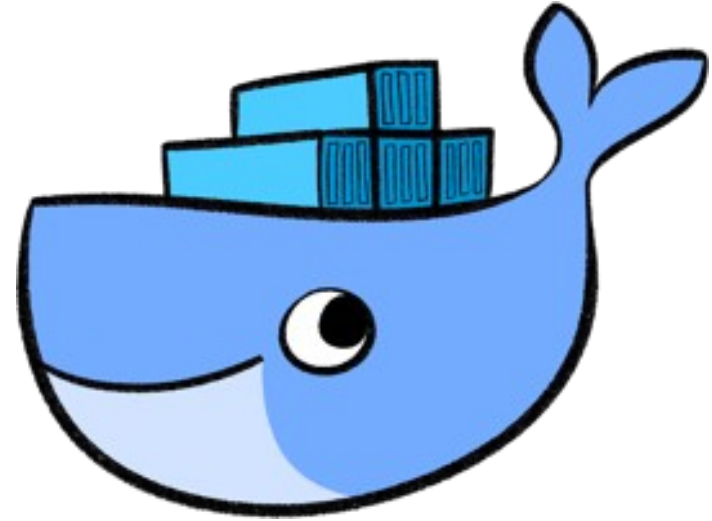
Container executions

“ We do know that it is a common practice

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Docker the most used platform



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Not available in our clusters



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« Why?

HPC Complex environment setup



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HPC Complex environment setup



- Root privileges
- High level abstraction features

Singularity

« Singularity is available in Nord3, Minotauro & Marenosturm4



Singularity

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« Why Singularity?

- Application level virtualization
- No root privileges



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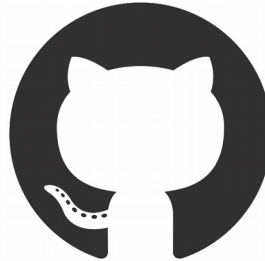


more info at <http://singularity.lbl.gov/faq>

We suggest

« Install singularity locally

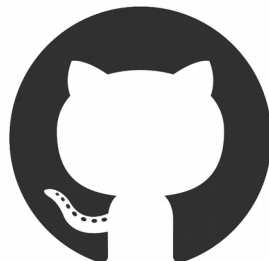
Available via git



We suggest

« Install singularity locally

Available via git



« Generate and edit your containers locally

```
$ sudo singularity shell --writable container.img
```

Always create folders in container for mountpoints:

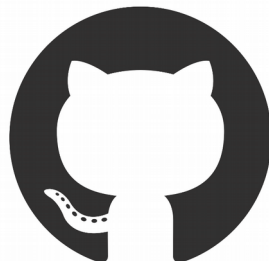
```
$mkdir /gpfs/home /gpfs/scratch /gpfs/projects /gpfs/apps
```



We suggest

« Install singularity locally

Available via git



« Generate and edit your containers locally

```
$ sudo singularity shell --writable container.img
```



« Upload them to GPFS for production runs

```
$ scp /local/path/container bscXX@dt01.bsc.es:/gpfs/path
```

- > Singularity run [container]
- > Singularity exec [container] [executable + args]

From Docker to Singularity

- « Singularity supports pulling containers from docker repos

- « Docker2singularity

Docker script that converts containers

Run the following script from your local machine

<https://github.com/singularityware/docker2singularity>

Support Contact practices

“ When contacting support remember to:



- Specify Job Ids, software version and environment (if applies), machine, username
- Not take for granted we know what you know, want or need

“ We don't know who you are but we care you do fine

“ We have no favorites

Thank you!

For further information please contact
support@bsc.es