

# HPC Tutorial

Last updated: October 23 2020

For Linux Users

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Acknowledgement: VSCentrum.be



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## **Audience:**

This HPC Tutorial is designed for **researchers** at the **UGent** and affiliated institutes who are in need of computational power (computer resources) and wish to explore and use the High Performance Computing (HPC) core facilities of the Flemish Supercomputing Centre (VSC) to execute their computationally intensive tasks.

The audience may be completely unaware of the HPC concepts but must have some basic understanding of computers and computer programming.

## **Contents:**

This **Beginners Part** of this tutorial gives answers to the typical questions that a new HPC user has. The aim is to learn how to make use of the HPC.

Beginners Part		
Questions	chapter	title
What is a HPC exactly?	<b>1</b>	<a href="#">Introduction to HPC</a>
Can it solve my computational needs?		
How to get an account?	<b>2</b>	<a href="#">Getting an HPC Account</a>
How do I connect to the HPC and transfer my files and programs?	<b>3</b>	<a href="#">Connecting to the HPC infrastructure</a>
How to start background jobs?	<b>4</b>	<a href="#">Running batch jobs</a>
How to start jobs with user interaction?	<b>5</b>	<a href="#">Running interactive jobs</a>
Where do the input and output go?	<b>6</b>	<a href="#">Running jobs with input/output data</a>
Where to collect my results?		
Can I speed up my program by exploring parallel programming techniques?	<b>7</b>	<a href="#">Multi core jobs/Parallel Computing</a>
How do I use the HPC-UGent web portal?	<b>8</b>	<a href="#">Using the HPC-UGent web portal</a>
Troubleshooting	<b>9</b>	<a href="#">Troubleshooting</a>
What are the rules and priorities of jobs?	<b>10</b>	<a href="#">HPC Policies</a>
FAQ	<b>11</b>	<a href="#">Frequently Asked Questions</a>

The **Advanced Part** focuses on in-depth issues. The aim is to assist the end-users in running their own software on the HPC.

Advanced Part		
Questions	chapter	title
What are the optimal Job Specifications?	12	Fine-tuning Job Specifications
Can I start many jobs at once?	13	Multi-job submission
Can I compile my software on the HPC?	14	Compiling and testing your software on the HPC
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Do you have more program examples for me?	16	Program examples
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Need a remote display with more features?	20	Graphical applications with X2Go
Want to use the HPC-UGent GPU cluster?	21	HPC-UGent GPGPU cluster

The **Software-specific Best Practices Part** focuses on specific programs.

Software-specific Best Practices Part		
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The **Annexes** contains some useful reference guides.

Annex	
Title	chapter
HPC Quick Reference Guide	A
TORQUE options	B
Useful Linux Commands	C

### Notification:

In this tutorial specific commands are separated from the accompanying text:

```
$ commands
```

These should be entered by the reader at a command line in a terminal on the UGent-HPC. They appear in all exercises preceded by a \$ and printed in **bold**. You'll find those actions in a grey frame.

**Button** are menus, buttons or drop down boxes to be pressed or selected.

“Directory” is the notation for directories (called “folders” in Windows terminology) or specific files. (e.g., “/user/home/gent/vsc400/vsc40000”)

“Text” Is the notation for text to be entered.

**Tip:** A “Tip” paragraph is used for remarks or tips.

### **More support:**

Before starting the course, the example programs and configuration files used in this Tutorial must be copied to your home directory, so that you can work with your personal copy. If you have received a new VSC-account, all examples are present in an “/apps/gent/tutorials/Intro-HPC/examples” directory.

```
$ cp -r /apps/gent/tutorials/Intro-HPC/examples ~/  
$ cd  
$ ls
```

They can also be downloaded from the VSC website at <https://www.vscentrum.be>. Apart from this HPC Tutorial, the documentation on the VSC website will serve as a reference for all the operations.

**Tip:** The users are advised to get self-organised. There are only limited resources available at the HPC staff, which are best effort based. The HPC staff cannot give support for code fixing. The user applications and own developed software remain solely the responsibility of the end-user.

More documentation can be found at:

1. VSC documentation: <https://www.vscentrum.be/user-portal>
2. External documentation (TORQUE, Moab): <http://docs.adaptivecomputing.com>

This tutorial is intended for users who want to connect and work on the HPC of the **UGent**.

This tutorial is available in a Windows, Mac or Linux version.

This tutorial is available for UAntwerpen, UGent, KU Leuven, UHasselt and VUB users.

Request your appropriate version at hpc@ugent.be.

### **Contact Information:**

We welcome your feedback, comments and suggestions for improving the HPC Tutorial (contact: hpc@ugent.be).

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4. Follow us on Twitter: <http://twitter.com/HPCUGent>

Mailing-lists:

1. Announcements: hpc-announce@lists.ugent.be (for official announcements and communications)
2. Users: hpc-users@lists.ugent.be (for discussions between users)

# Glossary

**NFS** Network File System, a protocol for sharing file systems across a network, often used on Unix(-like) operating systems.

**NIC** Network Interface Controller, a (virtualized) hardware component that connects a computer to a network.

**REST** REpresentational State Transfer is a software architectural style that defines a set of constraints to be used for creating web services.

**YAML** A human-readable text-based data serialization format.

**cluster** A group of compute nodes.

**compute node** The computational units on which batch or interactive jobs are processed. A compute node is pretty much comparable to a single personal computer. It contains one or more sockets, each holding a single CPU. Some nodes also contain one or more GPGPUs. The compute node is equipped with memory (RAM) that is accessible by all its CPUs.

**core** An individual compute unit inside a CPU. A CPU typically contains one or more cores.

**CPU** A central processing unit. A CPU is a consumable resource. A compute node typically contains one or more CPUs.

**distributed memory system** Computing system consisting of many compute nodes connected by a network, each with their own memory. Accessing memory on a neighbouring node is possible but requires explicit communication.

**FLOPS** FLOPS is short for “Floating-point Operations Per second”, i.e., the number of (floating-point) computations that a processor can perform per second.

**FTP** File Transfer Protocol, used to copy files between distinct machines (over a network.) FTP is unencrypted, and as such blocked on certain systems. SFTP or SCP are secure alternatives to FTP.

**GPGPU** A general purpose graphical processing unit. A GPGPU is a consumable resource. A GPGPU is a GPU that is used for highly parallel general purpose calculations. A compute node may contain zero, one or more GPGPUs.

**grid** A group of clusters.

**Heat** Heat is the OpenStack orchestration service, which can manage multiple composite cloud applications using templates, through both an OpenStack-native REST API and a CloudFormation-compatible Query API.

**Heat Orchestration Template** A [Heat](#) Orchestration Template (HOT) is a text file which describes the infrastructure for a cloud application. Because HOT files are text files in a YAML-based format, they are readable and writable by humans, and can be managed using a version control system. HOT is one of the template formats supported by Heat, along with the older CloudFormation-compatible CFN format.

**Horizon** Horizon is the name of the [OpenStack Dashboard](#).

**HPC** High Performance Computing, high performance computing and multiple-task computing on a supercomputer. The UGent-HPC is the HPC infrastructure at the UGent.

**InfiniBand** A high speed switched fabric computer network communications link used in HPC.

**job constraints** A set of conditions that must be fulfilled for the job to start.

**L1d** Level 1 data cache, often called **primary cache**, is a static memory integrated with the CPU core that is used to store data recently accessed by a CPU and also data which may be required by the next operations.

**L2d** Level 2 data cache, also called **secondary cache**, is a memory that is used to store recently accessed data and also data, which may be required for the next operations. The goal of having the level 2 cache is to reduce data access time in cases when the same data was already accessed before..

**L3d** Level 3 data cache. Extra cache level built into motherboards between the microprocessor and the main memory.

**LAN** Local Area Network.

**Linux** An operating system, similar to UNIX.

**LLC** The Last Level Cache is the last level in the memory hierarchy before main memory. Any memory requests missing here must be serviced by local or remote DRAM, with significant increase in latency when compared with data serviced by the cache memory.

**login node** On HPC clusters, login nodes serve multiple functions. From a login node you can submit and monitor batch jobs, analyse computational results, run editors, plots, debuggers, compilers, do housekeeping chores as adjust shell settings, copy files and in general manage your account. You connect to these servers when want to start working on the UGent-HPC.

**memory** A quantity of physical memory (RAM). Memory is provided by compute nodes. It is required as a constraint or consumed as a consumable resource by jobs. Within Moab, memory is tracked and reported in megabytes (MB).

**metrics** A measure of some property, activity or performance of a computer sub-system. These metrics are visualised by graphs in, e.g., Ganglia.

**Moab** Moab is a job scheduler, which allocates resources for jobs that are requesting resources.

**modules** HPC uses an open source software package called “Environment Modules” (Modules for short) which allows you to add various path definitions to your shell environment.

**MPI** MPI stands for Message-Passing Interface. It supports a parallel programming method designed for distributed memory systems, but can also be used well on shared memory systems.

**node** See [compute node](#).

**node attribute** A node attribute is a non-quantitative aspect of a node. Attributes typically describe the node itself or possibly aspects of various node resources such as processors or memory. While it is probably not optimal to aggregate node and resource attributes together in this manner, it is common practice. Common node attributes include processor architecture, operating system, and processor speed. Jobs often specify that resources be allocated from nodes possessing certain node attributes.

**OpenStack** OpenStack (<https://www.openstack.org>) is a free and open-source software platform for cloud computing, mostly deployed as infrastructure-as-a-service (IaaS), whereby virtual servers and other resources are made available to customers.

**OpenStack Dashboard** OpenStack Dashboard (Horizon) provides administrators and users with a graphical interface to access, provision, and automate deployment of cloud-based resources. The design accommodates third party products and services, such as billing, monitoring, and additional management tools. The dashboard is also brandable for service providers and other commercial vendors who want to make use of it. The dashboard is one of several ways users can interact with OpenStack resources. Developers can automate access or build tools to manage resources using the native OpenStack API or the EC2 compatibility API..

**OpenStack Identity** OpenStack Identity (Keystone) provides a central directory of users mapped to the OpenStack services they can access. It acts as a common authentication system across the cloud operating system and can integrate with existing backend directory services. It supports multiple forms of authentication including standard username/password credentials and token-based systems. In the VSC cloud, it is integrated with the VSC account system..

**OpenStack Image** OpenStack Image (Glance) provides discovery, registration, and delivery services for disk and server images. Stored images can be used as a template. It can also be used to store and catalog an unlimited number of backups. The Image Service can store disk and server images in a variety of back-ends, including Swift..

**OpenStack Instance** OpenStack Instances are virtual machines, which are instances of a system image that is created upon request and which is configured when launched. With traditional virtualization technology, the state of the virtual machine is persistent, whereas OpenStack supports both persistent and ephemeral image creation.

**OpenStack Volume** OpenStack Volume is a detachable block storage device. Each volume can be attached to only one instance at a time.

**PBS, TORQUE or OpenPBS** are Open Source resource managers, which are responsible for collecting status and health information from compute nodes and keeping track of jobs

running in the system. It is also responsible for spawning the actual executable that is associated with a job, e.g., running the executable on the corresponding compute node. Client commands for submitting and managing jobs can be installed on any host, but in general are installed and used from the Login nodes.

**processor** A processing unit. A processor is a consumable resource. A processor can be a CPU or a (GP)GPU.

**queue** PBS/TORQUE queues, or “classes” as Moab refers to them, represent groups of computing resources with specific parameters. A queue with a 12 hour runtime or “walltime” would allow jobs requesting 12 hours or less to use this queue.

**scp** Secure Copy is a protocol to copy files between distinct machines. SCP or scp is used extensively on HPC clusters to stage in data from outside resources.

**scratch** Supercomputers generally have what is called scratch space: storage available for temporary use. Use the scratch filesystem when, for example you are downloading and uncompressing applications, reading and writing input/output data during a batch job, or when you work with large datasets. Scratch is generally a lot faster than the Data or Home filesystem.

**sftp** Secure File Transfer Protocol, used to copy files between distinct machines.

**share** A share is a remote, mountable file system. Users can mount and access a share on several hosts at a time.

**shared memory system** Computing system in which all of the CPUs share one global memory space. However, access times from a CPU to different regions of memory are not necessarily uniform. This is called NUMA: Non-uniform memory access. Memory that is closer to the CPU your process is running on will generally be faster to access than memory that is closer to a different CPU. You can pin processes to a certain CPU to ensure they always use the same memory.

**SSD** Solid-State Drive. This is a kind of storage device that is faster than a traditional hard disk drive.

**SSH** Secure Shell (SSH), sometimes known as Secure Socket Shell, is a Unix-based command interface and protocol for securely getting access to a remote computer. It is widely used by network administrators to control Web and other kinds of servers remotely. SSH is actually a suite of three utilities (slogin, ssh, and scp) that are secure versions of the earlier UNIX utilities, rlogin, rsh, and rcp. SSH commands are encrypted and secure in several ways. Both ends of the client/server connection are authenticated using a digital certificate, and passwords are protected by encryption. Popular implementations include OpenSSH on Linux/Mac and Putty on Windows.

**ssh-keys** OpenSSH is a network connectivity tool, which encrypts all traffic including passwords to effectively eliminate eavesdropping, connection hijacking, and other network-level attacks. SSH-keys are part of the OpenSSH bundle. On HPC clusters, ssh-keys allow password-less access between compute nodes while running batch or interactive parallel jobs.

**stack** In the context of [OpenStack](#), a stack is a collection of cloud resources which can be managed using the [Heat](#) orchestration engine.

**supercomputer** A computer with an extremely high processing capacity or processing power.

**swap space** A quantity of virtual memory available for use by batch jobs. Swap is a consumable resource provided by nodes and consumed by jobs.

**TLB** Translation Look-aside Buffer, a table in the CPU's memory that contains information about the virtual memory pages the CPU has accessed recently. The table cross-references a program's virtual addresses with the corresponding absolute addresses in physical memory that the program has most recently used. The TLB enables faster computing because it allows the address processing to take place independent of the normal address-translation pipeline.

**walltime** Walltime is the length of time specified in the job script for which the job will run on a batch system, you can visualise walltime as the time measured by a wall mounted clock (or your digital wrist watch). This is a computational resource.

**worker node** See [compute node](#).

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# Part I

## Beginner's Guide

# Chapter 1

## Introduction to HPC

### 1.1 What is HPC?

“**High Performance Computing**” (HPC) is computing on a “*Supercomputer*”, a computer with at the frontline of contemporary processing capacity – particularly speed of calculation and available memory.

While the supercomputers in the early days (around 1970) used only a few processors, in the 1990s machines with thousands of processors began to appear and, by the end of the 20th century, massively parallel supercomputers with tens of thousands of “off-the-shelf” processors were the norm. A large number of dedicated processors are placed in close proximity to each other in a computer cluster.

A **computer cluster** consists of a set of loosely or tightly connected computers that work together so that in many respects they can be viewed as a single system.

The components of a cluster are usually connected to each other through fast local area networks (“LAN”) with each *node* (computer used as a server) running its own instance of an operating system. Computer clusters emerged as a result of convergence of a number of computing trends including the availability of low cost microprocessors, high-speed networks, and software for high performance distributed computing.

Compute clusters are usually deployed to improve performance and availability over that of a single computer, while typically being more cost-effective than single computers of comparable speed or availability.

Supercomputers play an important role in the field of computational science, and are used for a wide range of computationally intensive tasks in various fields, including quantum mechanics, weather forecasting, climate research, oil and gas exploration, molecular modelling (computing the structures and properties of chemical compounds, biological macromolecules, polymers, and crystals), and physical simulations (such as simulations of the early moments of the universe, airplane and spacecraft aerodynamics, the detonation of nuclear weapons, and nuclear fusion).<sup>1</sup>

---

<sup>1</sup>Wikipedia: <http://en.wikipedia.org/wiki/Supercomputer>

## 1.2 What is the UGent-HPC?

The HPC is a collection of computers with Intel CPUs, running a Linux operating system, shaped like pizza boxes and stored above and next to each other in racks, interconnected with copper and fiber cables. Their number crunching power is (presently) measured in hundreds of billions of floating point operations (gigaflops) and even in teraflops.



The UGent-HPC relies on parallel-processing technology to offer UGent researchers an extremely fast solution for all their data processing needs.

The HPC currently consists of:

a set of different compute clusters. For an up to date list of all clusters and their hardware, see [https://vscdocumentation.readthedocs.io/en/latest/gent/tier2\\_hardware.html](https://vscdocumentation.readthedocs.io/en/latest/gent/tier2_hardware.html).

All the nodes in the HPC run “CentOS 7.7 (golett, phanpy, skitty, swalot, victimi)” with *cpuset* support and *BLCR* modules.

Two tools perform the **job management** and **job scheduling**:

1. TORQUE: a resource manager (based on PBS);
2. Moab: job scheduler and management tools.

## 1.3 What the HPC infrastructure is *not*

The HPC infrastructure is *not* a magic computer that automatically:

1. runs your PC-applications much faster for bigger problems;
2. develops your applications;
3. solves your bugs;
4. does your thinking;
5. ...
6. allows you to play games even faster.

The HPC does not replace your desktop computer.

## 1.4 Is the HPC a solution for my computational needs?

### 1.4.1 Batch or interactive mode?

Typically, the strength of a supercomputer comes from its ability to run a huge number of programs (i.e., executables) in parallel without any user interaction in real time. This is what is called “running in batch mode”.

It is also possible to run programs at the HPC, which require user interaction. (pushing buttons, entering input data, etc.). Although technically possible, the use of the HPC might not always be the best and smartest option to run those interactive programs. Each time some user interaction is needed, the computer will wait for user input. The available computer resources (CPU, storage, network, etc.) might not be optimally used in those cases. A more in-depth analysis with the HPC staff can unveil whether the HPC is the desired solution to run interactive programs. Interactive mode is typically only useful for creating quick visualisations of your data without having to copy your data to your desktop and back.

### 1.4.2 What are cores, processors and nodes?

In this manual, the terms core, processor and node will be frequently used, so it’s useful to understand what they are.

Modern servers, also referred to as *(worker)nodes* in the context of HPC, include one or more sockets, each housing a *multi-core processor* (next to memory, disk(s), network cards, …). A modern *processor* consists of multiple CPUs or *cores* that are used to execute *computations*.

### 1.4.3 Parallel or sequential programs?

#### Parallel programs

**Parallel computing** is a form of computation in which many calculations are carried out simultaneously. They are based on the principle that large problems can often be divided into smaller ones, which are then solved concurrently (“in parallel”).

Parallel computers can be roughly classified according to the level at which the hardware supports parallelism, with multicore computers having multiple processing elements within a single machine, while clusters use multiple computers to work on the same task. Parallel computing has become the dominant computer architecture, mainly in the form of multicore processors.

The two parallel programming paradigms most used in HPC are:

- OpenMP for shared memory systems (multithreading): on multiple cores of a single node
- MPI for distributed memory systems (multiprocessing): on multiple nodes

**Parallel programs** are more difficult to write than sequential ones, because concurrency introduces several new classes of potential software bugs, of which race conditions are the most common. Communication and synchronisation between the different subtasks are typically some of the greatest obstacles to getting good parallel program performance.

## Sequential programs

Sequential software does not do calculations in parallel, i.e., it only uses *one single core of a single workernode*. **It does not become faster by just throwing more cores at it:** it can only use one core.

It is perfectly possible to also run purely **sequential programs** on the HPC.

Running your sequential programs on the most modern and fastest computers in the HPC can save you a lot of time. But it also might be possible to run multiple instances of your program (e.g., with different input parameters) on the HPC, in order to solve one overall problem (e.g., to perform a parameter sweep). This is another form of running your sequential programs in parallel.

### 1.4.4 What programming languages can I use?

You can use *any* programming language, *any* software package and *any* library provided it has a version that runs on Linux, specifically, on the version of Linux that is installed on the compute nodes, CentOS 7.7 (golett, phanpy, skitty, swalot, victimi).

For the most common **programming languages**, a compiler is available on CentOS 7.7 (golett, phanpy, skitty, swalot, victimi). Supported and common programming languages on the HPC are C/C++, FORTRAN, Java, Perl, Python, MATLAB, R, etc.

Supported and commonly used compilers are GCC and Intel.

Additional software can be installed “*on demand*”. Please contact the HPC staff to see whether the HPC can handle your specific requirements.

### 1.4.5 What operating systems can I use?

All nodes in the HPC cluster run under CentOS 7.7 (golett, phanpy, skitty, swalot, victimi), which is a specific version of Red Hat Enterprise Linux. This means that all programs (executables) should be compiled for CentOS 7.7 (golett, phanpy, skitty, swalot, victimi).

Users can connect from any computer in the UGent network to the HPC, regardless of the Operating System that they are using on their personal computer. Users can use any of the common Operating Systems (such as Windows, macOS or any version of Linux/Unix/BSD) and run and control their programs on the HPC.

A user does not need to have prior knowledge about Linux; all of the required knowledge is explained in this tutorial.

### 1.4.6 What does a typical workflow look like?

A typical workflow looks like:

1. Connect to the login nodes with SSH (see [section 3.2](#))
2. Transfer your files to the cluster (see [section 3.3](#))

3. Optional: compile your code and test it (for compiling, see [chapter 14](#))
4. Create a job script and submit your job (see [chapter 4](#))
5. Get some coffee and be patient:
  - (a) Your job gets into the queue
  - (b) Your job gets executed
  - (c) Your job finishes
6. Study the results generated by your jobs, either on the cluster or after downloading them locally.

#### **1.4.7 What is the next step?**

When you think that the HPC is a useful tool to support your computational needs, we encourage you to acquire a VSC-account (as explained in [chapter 2](#)), read [chapter 3](#), “Setting up the environment”, and explore chapters [5](#) to [12](#) which will help you to transfer and run your programs on the HPC cluster.

Do not hesitate to contact the HPC staff for any help.

## Chapter 2

# Getting an HPC Account

### 2.1 Getting ready to request an account

All users of AUGent can request an account on the HPC, which is part of the Flemish Supercomputing Centre (VSC).

See [chapter 10](#) for more information on who is entitled to an account.

The VSC, abbreviation of Flemish Supercomputer Centre, is a virtual supercomputer centre. It is a partnership between the five Flemish associations: the Association KU Leuven, Ghent University Association, Brussels University Association, Antwerp University Association and the University Colleges-Limburg. The VSC is funded by the Flemish Government.

The UGent-HPC clusters use public/private key pairs for user authentication (rather than passwords). Technically, the private key is stored on your local computer and always stays there; the public key is stored on the HPC. Access to the HPC is granted to anyone who can prove to have access to the corresponding private key on his local computer.

#### 2.1.1 How do SSH keys work?

- an SSH public/private key pair can be seen as a lock and a key
- the SSH public key is equivalent with a *lock*: you give it to the VSC and they put it on the *door* that gives access to your account.
- the SSH private key is like a *physical key*: you don't hand it out to other people.
- anyone who has the key (and the optional password) can unlock the *door* and log in to the account.
- the *door* to your VSC account is special: it can have multiple *locks* (SSH public keys) attached to it, and you only need to open one *lock* with the corresponding *key* (SSH private key) to open the *door* (log in to the account).

Since all VSC clusters use Linux as their main operating system, you will need to get acquainted with using the command-line interface and using the terminal.

Launch a terminal from your desktop's application menu and you will see the bash shell. There are other shells, but most Linux distributions use bash by default.

Before requesting an account, you need to generate a pair of ssh keys. One popular way to do this on Linux is using the OpenSSH client included with Linux, which you can then also use to log on to the clusters.

### **2.1.2 Test OpenSSH**

Secure Shell (ssh) is a cryptographic network protocol for secure data communication, remote command-line login, remote command execution, and other secure network services between two networked computers. In short, ssh provides a secure connection between 2 computers via insecure channels (Network, Internet, telephone lines, ...).

“Secure” means that:

1. the User is authenticated to the System; and
2. the System is authenticated to the User; and
3. all data is encrypted during transfer.

OpenSSH is a FREE implementation of the SSH connectivity protocol. Linux comes with its own implementation of OpenSSH, so you don't need to install any third-party software to use it. Just open a terminal window and jump in!

On all popular Linux distributions, the OpenSSH software is readily available, and most often installed by default. You can check whether the OpenSSH software is installed by opening a terminal and typing:

```
$ ssh -V  
OpenSSH_7.4p1, OpenSSL 1.0.2k-fips 26 Jan 2017
```

To access the clusters and transfer your files, you will use the following commands:

1. ssh-keygen: to generate the ssh keys
2. ssh: to open a shell on a remote machine;
3. sftp: a secure equivalent of ftp;
4. scp: a secure equivalent of the remote copy command rcp.

### **2.1.3 Generate a public/private key pair with OpenSSH**

A key pair might already be present in the default location inside your home directory. Therefore, we first check if a key is available with the “list short” (“ls”) command:

```
$ ls ~/.ssh
```

If a key-pair is already available, you would normally get:

authorized_keys	id_rsa	id_rsa.pub	known_hosts
-----------------	--------	------------	-------------

Otherwise, the command will show:

ls: .ssh: No such file or directory
-------------------------------------

You can recognise a public/private key pair when a pair of files has the same name except for the extension “.pub” added to one of them. In this particular case, the private key is “id\_rsa” and public key is “id\_rsa.pub”. You may have multiple keys (not necessarily in the directory “~/.ssh”) if you or your operating system requires this.

You will need to generate a new key pair, when:

1. you don’t have a key pair yet
2. you forgot the passphrase protecting your private key
3. or your private key was compromised

For extra security, the private key itself can be encrypted using a “passphrase”, to prevent anyone from using your private key even when they manage to copy it. You have to “unlock” the private key by typing the passphrase. Be sure to never give away your private key, it is private and should stay private. You should not even copy it to one of your other machines, instead, you should create a new public/private key pair for each machine.

\$ ssh-keygen -t rsa -b 4096 Generating public/private rsa key pair. Enter file in which to save the key (/home/user/.ssh/id_rsa): Enter passphrase (empty for no passphrase): Enter same passphrase again: Your identification has been saved in /home/user/.ssh/id_rsa. Your public key has been saved in /home/user/.ssh/id_rsa.pub.
---

This will ask you for a file name to store the private and public key, and a passphrase to protect your private key. It needs to be emphasised that you really should choose the passphrase wisely! The system will ask you for it every time you want to use the private key that is every time you want to access the cluster or transfer your files.

**Without your key pair, you won’t be able to apply for a personal VSC account.**

#### 2.1.4 Using an SSH agent (optional)

Most recent Unix derivatives include by default an SSH agent (“gnome-keyring-daemon” in most cases) to keep and manage the user SSH keys. If you use one of these derivatives you **must** include the new keys into the SSH manager keyring to be able to connect to the HPC cluster. If not, SSH client will display an error message (see [chapter 3](#)) similar to this:

Agent admitted failure to sign using the key. Permission denied (publickey,gssapi-keyex,gssapi-with-mic).
--

This could be fixed using the ssh-add command. You can include the new private keys' identities in your keyring with:

```
$ ssh-add
```

**Tip:** Without extra options ssh-add adds any key located at \$HOME/.ssh directory, but you can specify the private key location path as argument, as example: ssh-add /path/to/my/id\_rsa.

```
$ ssh-add -l
```

After these changes the key agent will keep your SSH key to connect to the clusters as usual.

**Tip:** You should execute ssh-add command again if you generate a new SSH key.

Visit <https://wiki.gnome.org/Projects/GnomeKeyring/Ssh> for more information.

## 2.2 Applying for the account

Visit <https://account.vscentrum.be/>

You will be redirected to our WAYF (Where Are You From) service where you have to select your “Home Organisation”.

The screenshot shows a web browser window with the following details:

- Address Bar:** account.vscentrum.be
- Page Content:** WELCOME, VSC logo, Hogeschool-Universiteit Brussel dropdown, Save my preference checkboxes.
- Footer:** © FWO VScentrum.be

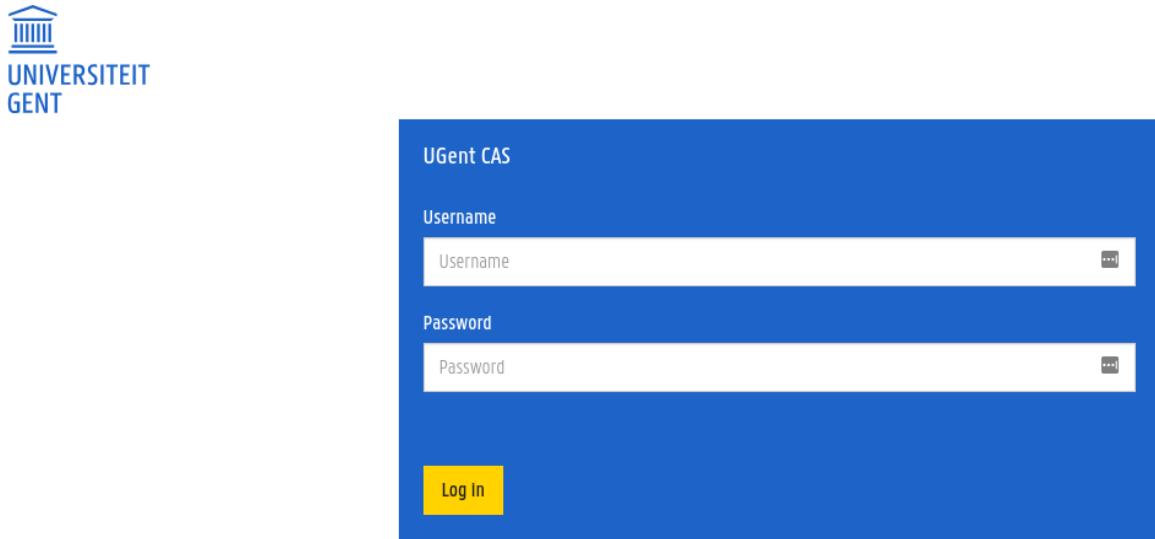
Select “UGent” in the dropdown box and optionally select “Save my preference” and “permanently”.

Click **Confirm**

You will now be taken to the authentication page of your institute.

You will now have to log in with CAS using your UGent account.

You either have a login name of maximum 8 characters, or a (non-UGent) email address if you are an external user. In case of problems with your UGent password, please visit: <https://password.ugent.be/>. After logging in, you may be requested to share your information. Click “Yes, continue”.



[CAS](#) is de Centrale Authenticatie Service van Universiteit Gent. Via CAS kan u zich op beveiligde UGent-webpagina's aanmelden.

[CAS](#) is the Central Authentication Service for UGent. CAS allows you to log on to secured UGent pages.

#### FAQ

- [Inloggen \(je aanmelden\) met je UGent account](#)
- [Wachtwoorden ingeven op een gedeelde of publieke computer](#)
- [Wachtwoord wijzigen?](#)
- [Wachtwoord vergeten?](#)
- [Hoe lang blijf ik ingelogd?](#)
- [Hoe log ik volledig uit?](#)
- [Problemen?](#)

#### FAQ

- [Log in with your UGent account](#)
- [Entering passwords on a shared or public computer](#)
- [Change password?](#)
- [Forgot password?](#)
- [How long do you remain logged in?](#)
- [How do I do a complete logout?](#)
- [Questions about your account or having problems logging in?](#)

After you log in using your UGent login and password, you will be asked to upload the file that contains your public key, i.e., the file “id\_rsa.pub” which you have generated earlier.

This file has been stored in the directory “`~/.ssh/`”.

After you have uploaded your public key you will receive an e-mail with a link to confirm your e-mail address. After confirming your e-mail address the VSC staff will review and if applicable approve your account.

### 2.2.1 Welcome e-mail

Within one day, you should receive a Welcome e-mail with your VSC account details.

```
Dear (Username),  
Your VSC-account has been approved by an administrator.  
Your vsc-username is vsc40000  
  
Your account should be fully active within one hour.  
  
To check or update your account information please visit  
https://account.vscentrum.be/  
  
For further info please visit https://www.vscentrum.be/user-portal  
  
Kind regards,  
-- The VSC administrators
```

Now, you can start using the HPC. You can always look up your VSC id later by visiting <https://account.vscentrum.be>.

### 2.2.2 Adding multiple SSH public keys (optional)

In case you are connecting from different computers to the login nodes, it is advised to use separate SSH public keys to do so. You should follow these steps.

1. Create a new public/private SSH key pair from the new computer. Repeat the process described in section [2.1.3](#).
2. Go to <https://account.vscentrum.be/django/account/edit>
3. Upload the new SSH public key using the **Add public key** section.
4. (optional) If you lost your key, you can delete the old key on the same page. You should keep at least one valid public SSH key in your account.
5. Take into account that it will take some time before the new SSH public key is active in your account on the system; waiting for 15-30 minutes should be sufficient.

## 2.3 Computation Workflow on the HPC

A typical Computation workflow will be:

1. Connect to the HPC
2. Transfer your files to the HPC
3. Compile your code and test it
4. Create a job script

5. Submit your job
6. Wait while
  - (a) your job gets into the queue
  - (b) your job gets executed
  - (c) your job finishes
7. Move your results

We'll take you through the different tasks one by one in the following chapters.

## Chapter 3

# Connecting to the HPC infrastructure

Before you can really start using the HPC clusters, there are several things you need to do or know:

1. You need to **log on to the cluster** using an SSH client to one of the login nodes. This will give you command-line access. The software you'll need to use on your client system depends on its operating system.
2. Before you can do some work, you'll have to **transfer the files** that you need from your desktop computer to the cluster. At the end of a job, you might want to transfer some files back.
3. Optionally, if you wish to use programs with a **graphical user interface**, you will need an X-server on your client system and log in to the login nodes with X-forwarding enabled.
4. Often several versions of **software packages and libraries** are installed, so you need to select the ones you need. To manage different versions efficiently, the VSC clusters use so-called **modules**, so you will need to select and load the modules that you need.

### 3.1 Connection restrictions

Since March 20th 2020, restrictions are in place that limit from where you can connect to the VSC HPC infrastructure, in response to security incidents involving several European HPC centres.

VSC login nodes are only directly accessible from within university networks, and from (most) Belgian commercial internet providers.

All other IP domains are blocked by default. If you are connecting from an IP address that is not allowed direct access, you have the following options to get access to VSC login nodes:

- Use an VPN connection to connect to the UGent network (recommended). See <https://helpdesk.ugent.be/vpn/en/> for more information.
- Register your IP address by accessing <https://firewall.hpc.kuleuven.be> (same URL regardless of the university your affiliated with) and log in with your UGent account.

- While this web connection is active new SSH sessions can be started.
  - Active SSH sessions will remain active even when this web page is closed.
- Contact your HPC support team (via hpc@ugent.be) and ask them to whitelist your IP range (e.g., for industry access, automated processes).

Trying to establish an SSH connection from an IP address that does not adhere to these restrictions will result in an immediate failure to connect, with an error message like:

```
ssh_exchange_identification: read: Connection reset by peer
```

## 3.2 First Time connection to the HPC infrastructure

If you have any issues connecting to the HPC after you've followed these steps, see [section 9.3](#) to troubleshoot.

### 3.2.1 Connect

Open up a terminal and enter the following command to connect to the HPC.

```
$ ssh vsc40000@login.hpc.ugent.be
```

Here, user vsc40000 wants to make a connection to the “hpcugent” cluster at UGent via the login node “login.hpc.ugent.be”, so replace vsc40000 with your own VSC id in the above command.

The first time you make a connection to the login node, you will be asked to verify the authenticity of the login node. Please check section [9.6](#) on how to do this.

A possible error message you can get if you previously saved your private key somewhere else than the default location (\$HOME/.ssh/id\_rsa):

```
$ Permission denied (publickey,gssapi-keyex,gssapi-with-mic).
```

In this case, use the -i option for the ssh command to specify the location of your private key. For example:

```
$ ssh -i /home/example/my_keys/id_rsa vsc40000@login.hpc.ugent.be
```

**Congratulations, you're on the HPC infrastructure now!** To find out where you have landed you can print the current working directory:

```
$ pwd  
/user/home/gent/vsc400/vsc40000
```

Your new private home directory is “/user/home/gent/vsc400/vsc40000”. Here you can create your own subdirectory structure, copy and prepare your applications, compile and test them and submit your jobs on the HPC.

```
$ cd /apps/gent/tutorials  
$ ls  
Intro-HPC/
```

This directory currently contains all training material for the ***Introduction to the HPC***. More relevant training material to work with the HPC can always be added later in this directory.

You can now explore the content of this directory with the “ls -l” (lists long) and the “cd” (change directory) commands:

As we are interested in the use of the **HPC**, move further to **Intro-HPC** and explore the contents up to 2 levels deep:

```
$ cd Intro-HPC
$ tree -L 2
.
`-- examples
    |-- Compiling-and-testing-your-software-on-the-HPC
    |-- Fine-tuning-Job-Specifications
    |-- Multi-core-jobs-Parallel-Computing
    |-- Multi-job-submission
    |-- Program-examples
    |-- Running-batch-jobs
    |-- Running-jobs-with-input
    |-- Running-jobs-with-input-output-data
    |-- example.pbs
    '-- example.sh
9 directories, 5 files
```

This directory contains:

1. This **HPC Tutorial** (in either a Mac, Linux or Windows version).
2. An **examples** subdirectory, containing all the examples that you need in this Tutorial, as well as examples that might be useful for your specific applications.

```
$ cd examples
```

**Tip:** Typing `cd ex` followed by  (the Tab-key) will generate the `cd examples` command. **Command-line completion** (also tab completion) is a common feature of the bash command line interpreter, in which the program automatically fills in partially typed commands.

**Tip:** For more exhaustive tutorials about Linux usage, see Appendix C

The first action is to copy the contents of the HPC examples directory to your home directory, so that you have your own personal copy and that you can start using the examples. The “-r” option of the copy command will also copy the contents of the sub-directories “recursively”.

```
$ cp -r /apps/gent/tutorials/Intro-HPC/examples ~/
```

Go to your home directory, check your own private examples directory, ... and start working.

```
$ cd
$ ls -l
```

Upon connecting you will see a login message containing your last login time stamp and a basic overview of the current cluster utilisation.

```
Last login: Mon Sep  3 14:00:00 2018 from helios.ugent.be
STEVIN HPC-UGent infrastructure status on Mon, 03 Sep 2018 14:30:00
```

cluster	-	full	-	free	-	part	-	total	-	running	-	queued
	nodes	nodes		free		nodes		jobs		jobs		jobs
golett	168	2		16		200		N/A		N/A		N/A
phanpy	15	0		1		16		N/A		N/A		N/A
swalot	0	0		0		128		N/A		N/A		N/A
skitty	69	2		0		73		N/A		N/A		N/A
victini	83	1		3		96		N/A		N/A		N/A

For a full view of the current loads and queues see:

<http://hpc.ugent.be/clusterstate/>

Updates on maintenance and unscheduled downtime can be found on

<https://www.ugent.be/hpc/en/infrastructure/status>

You can exit the connection at anytime by entering:

```
$ exit
logout
Connection to login.hpc.ugent.be closed.
```

### Tip: Setting your Language right:

You may encounter a warning message similar to the following one during connecting:

```
perl: warning: Setting locale failed.
perl: warning: Please check that your locale settings:
LANGUAGE = (unset),
LC_ALL = (unset),
LC_CTYPE = "UTF-8",
LANG = (unset)
    are supported and installed on your system.
perl: warning: Falling back to the standard locale ("C").
```

or any other error message complaining about the locale.

This means that the correct “locale” has not yet been properly specified on your local machine.  
Try:

```
$ locale
LANG=
LC_COLLATE="C"
LC_CTYPE="UTF-8"
LC_MESSAGES="C"
LC_MONETARY="C"
LC_NUMERIC="C"
LC_TIME="C"
LC_ALL=
```

A **locale** is a set of parameters that defines the user’s language, country and any special variant preferences that the user wants to see in their user interface. Usually a locale identifier consists of at least a language identifier and a region identifier.

**Note:** If you try to set a non-supported locale, then it will be automatically set to the default. Currently the default is en\_US.UTF-8 or en\_US, depending on whether your originally (non-supported) locale was UTF-8 or not.

Open the `.bashrc` on your local machine with your favourite editor and add the following lines:

```
$ nano ~/.bashrc
...
export LANGUAGE="en_US.UTF-8"
export LC_ALL="en_US.UTF-8"
export LC_CTYPE="en_US.UTF-8"
export LANG="en_US.UTF-8"
...
```

**Tip: vi:** To start entering text in vi: move to the place you want to start entering text with the arrow keys and type “`i`” to switch to insert mode. You can easily exit vi by entering: “`[ESC]:wq`” To exit vi without saving your changes, enter “`[ESC]:q!`”

or alternatively (if you are not comfortable with the Linux editors), again on your local machine:

```
$ echo "export LANGUAGE=\"en_US.UTF-8\" >> ~/.profile
$ echo "export LC_ALL=\"en_US.UTF-8\" >> ~/.profile
$ echo "export LC_CTYPE=\"en_US.UTF-8\" >> ~/.profile
$ echo "export LANG=\"en_US.UTF-8\" >> ~/.profile
```

You can now log out, open a new terminal/shell on your local machine and reconnect to the HPC, and you should not get these warnings anymore.

### 3.3 Transfer Files to/from the HPC

Before you can do some work, you’ll have to **transfer the files** you need from your desktop or department to the cluster. At the end of a job, you might want to transfer some files back.

The preferred way to transfer files is by using an `scp` or `sftp` via the secure OpenSSH protocol. Linux ships with an implementation of OpenSSH, so you don’t need to install any third-party software to use it. Just open a terminal window and jump in!

#### 3.3.1 Using `scp`

**Secure copy or SCP** is a tool (command) for securely transferring files between a local host (= your computer) and a remote host (the HPC). It is based on the Secure Shell (SSH) protocol. The `scp` command is the equivalent of the `cp` (i.e., `copy`) command, but can copy files to or from remote machines.

It’s easier to copy files directly to `$VSC_DATA` and `$VSC_SCRATCH` if you have symlinks to them in your home directory. See [the chapter titled “Uploading/downloading/editing files”, section “Symlinks for data/scratch” in the intro to Linux](#) for how to do this.

Open an additional terminal window and check that you’re working on your local machine.

```
$ hostname
<local-machine-name>
```

If you’re still using the terminal that is connected to the HPC, close the connection by typing “exit” in the terminal window.

For example, we will copy the (local) file “*localfile.txt*” to your home directory on the HPC cluster. We first generate a small dummy “*localfile.txt*”, which contains the word “Hello”. Use your own VSC account, which is something like “*vsc40000*”. Don’t forget the colon (:) at the end: if you forget it, it will just create a file named *vsc40000@login.hpc.ugent.be* on your local filesystem. You can even specify where to save the file on the remote filesystem by putting a path after the colon.

```
$ echo "Hello" > localfile.txt
$ ls -l
...
-rw-r--r-- 1 user  staff   6 Sep 18 09:37 localfile.txt
$ scp localfile.txt vsc40000@login.hpc.ugent.be:
localfile.txt      100%    6      0.0KB/s   00:00
```

Connect to the HPC via another terminal, print the working directory (to make sure you’re in the home directory) and check whether the file has arrived:

```
$ pwd
/user/home/gent/vsc400/vsc40000
$ ls -l
total 1536
drwxrwxr-x  2 vsc40000 131072 Sep 11 16:24 bin/
drwxrwxr-x  2 vsc40000 131072 Sep 17 11:47 docs/
drwxrwxr-x 10 vsc40000 131072 Sep 17 11:48 examples/
-rw-r--r--  1 vsc40000       6 Sep 18 09:44 localfile.txt
$ cat localfile.txt
Hello
```

The **scp** command can also be used to copy files from the cluster to your local machine. Let us copy the remote file “*intro-HPC-linux-gent.pdf*” from your “*docs*” subdirectory on the cluster to your local computer.

First, we will confirm that the file is indeed in the “*docs*” subdirectory. On the terminal on the HPC, enter:

```
$ cd ~/docs
$ ls -l
total 1536
-rw-r--r-- 1 vsc40000 Sep 11 09:53 intro-HPC-linux-gent.pdf
```

Now we will copy the file to the local machine. On the terminal on your own local computer, enter:

```
$ scp vsc40000@login.hpc.ugent.be:./docs/intro-HPC-linux-gent.pdf .
intro-HPC-linux-gent.pdf 100% 725KB 724.6KB/s   00:01
$ ls -l
total 899
-rw-r--r--  1 user  staff  741995 Sep 18 09:53 intro-HPC-linux-gent.pdf
-rw-r--r--  1 user  staff       6 Sep 18 09:37 localfile.txt
```

The file has been copied from the HPC to your local computer.

It’s also possible to copy entire directories (and their contents) with the **-r** flag. For example, if we want to copy the local directory *dataset* to **\$VSC\_SCRATCH**, we can use the following command (assuming you’ve created the *scratch* symlink):

```
$ scp -r dataset vsc40000@login.hpc.ugent.be:scratch
```

If you don't use the `-r` option to copy a directory, you will run into the following error:

```
$ scp dataset vsc40000@login.hpc.ugent.be:scratch
dataset: not a regular file
```

### 3.3.2 Using sftp

The **SSH File Transfer Protocol** (also **Secure File Transfer Protocol**, or **SFTP**) is a network protocol that provides file access, file transfer and file management functionalities over any reliable data stream. It was designed as an extension of the Secure Shell protocol (SSH) version 2.0. This protocol assumes that it is run over a secure channel, such as SSH, that the server has already authenticated the client, and that the identity of the client user is available to the protocol.

The sftp is an equivalent of the ftp command, with the difference that it uses the secure ssh protocol to connect to the clusters.

One easy way of starting a sftp session is

```
$ sftp vsc40000@login.hpc.ugent.be
```

Typical and popular commands inside an sftp session are:

<code>cd ~/examples/fibo</code>	Move to the examples/fibo subdirectory on the HPC (i.e., the remote machine)
<code>ls</code>	Get a list of the files in the current directory on the HPC.
<code>get fibo.py</code>	Copy the file "fibo.py" from the HPC
<code>get tutorial/HPC.pdf</code>	Copy the file "HPC.pdf" from the HPC, which is in the "tutorial" subdirectory.
<code>lcd test</code>	Move to the "test" subdirectory on your local machine.
<code>lcd ..</code>	Move up one level in the local directory.
<code>lls</code>	Get local directory listing
<code>put test.py</code>	Copy the local file test.py to the HPC.
<code>put test1.py test2.py</code>	Copy the local file test1.py to the HPC and rename it to test2.py.
<code>bye</code>	Quit the sftp session
<code>mget *.cc</code>	Copy all the remote files with extension ".cc" to the local directory.
<code>mput *.h</code>	Copy all the local files with extension ".h" to the HPC.

### 3.3.3 Using a GUI

If you prefer a GUI to transfer files back and forth to the HPC, you can use your file browser. Open your file browser and press

`Ctrl` + `I`

This should open up a address bar where you can enter a URL. Alternatively, look for the "connect to server" option in your file browsers menu.

Enter: `sftp://vsc40000@login.hpc.ugent.be/` and press enter.

You should now be able to browse files on the HPC in your file browser.

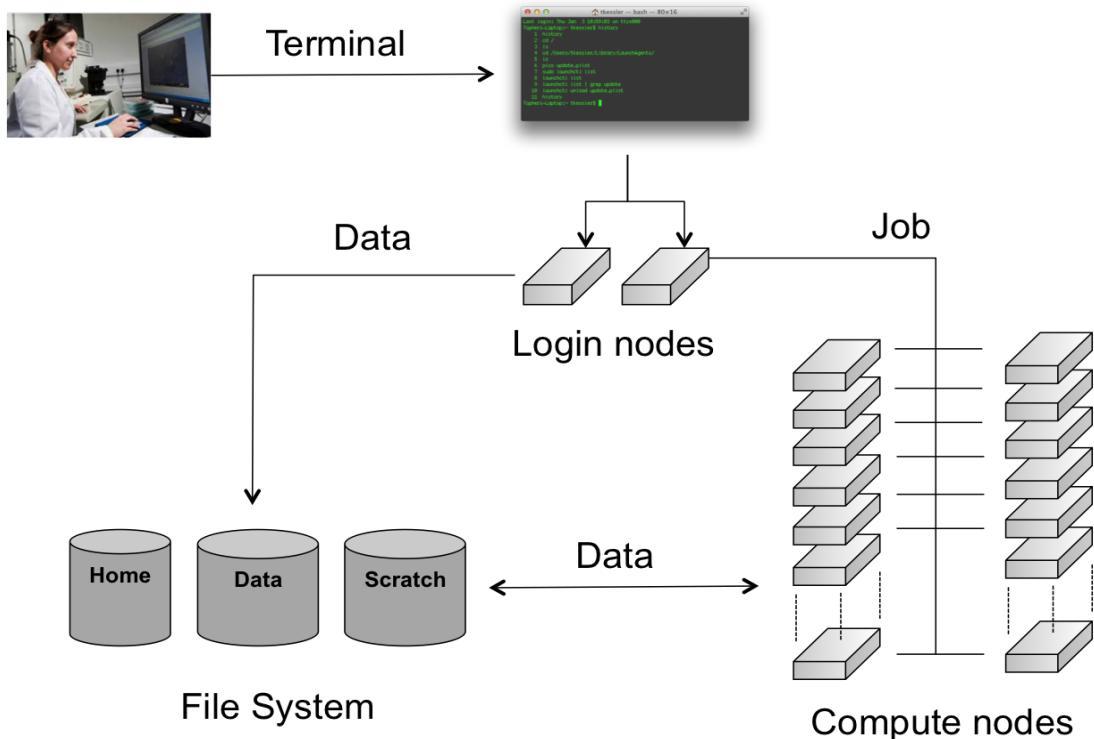
### 3.3.4 Fast file transfer for large datasets

See [the section on rsync in chapter 5 of the Linux intro manual](#).

## Chapter 4

# Running batch jobs

In order to have access to the compute nodes of a cluster, you have to use the job system. The system software that handles your batch jobs consists of two pieces: the queue- and resource manager **TORQUE** and the scheduler **Moab**. Together, TORQUE and Moab provide a suite of commands for submitting jobs, altering some of the properties of waiting jobs (such as reordering or deleting them), monitoring their progress and killing ones that are having problems or are no longer needed. Only the most commonly used commands are mentioned here.



When you connect to the HPC, you have access to (one of) the **login nodes** of the cluster. There you can prepare the work you want to get done on the cluster by, e.g., installing or compiling programs, setting up data sets, etc. The computations however, should not be performed on this login node. The actual work is done on the cluster's **compute nodes**. Each compute node

contains a number of CPU **cores**. The compute nodes are managed by the job scheduling software (Moab) and a Resource Manager (TORQUE), which decides when and on which compute nodes the jobs can run. It is usually not necessary to log on to the compute nodes directly and is only allowed on the nodes where you have a job running . Users can (and should) monitor their jobs periodically as they run, but do not have to remain connected to the HPC the entire time.

The documentation in this “Running batch jobs” section includes a description of the general features of job scripts, how to submit them for execution and how to monitor their progress.

## 4.1 Modules

Software installation and maintenance on a HPC cluster such as the VSC clusters poses a number of challenges not encountered on a workstation or a departmental cluster. We therefore need a system on the HPC, which is able to easily activate or deactivate the software packages that you require for your program execution.

### 4.1.1 Environment Variables

The program environment on the HPC is controlled by pre-defined settings, which are stored in environment (or shell) variables. For more information about environment variables, see [the chapter “Getting started”, section “Variables” in the intro to Linux](#).

All the software packages that are installed on the HPC cluster require different settings. These packages include compilers, interpreters, mathematical software such as MATLAB and SAS, as well as other applications and libraries.

### 4.1.2 The module command

In order to administer the active software and their environment variables, the module system has been developed, which:

1. Activates or deactivates *software packages* and their dependencies.
2. Allows setting and unsetting of *environment variables*, including adding and deleting entries from list-like environment variables.
3. Does this in a *shell-independent* fashion (necessary information is stored in the accompanying module file).
4. Takes care of *versioning aspects*: For many libraries, multiple versions are installed and maintained. The module system also takes care of the versioning of software packages. For instance, it does not allow multiple versions to be loaded at same time.
5. Takes care of *dependencies*: Another issue arises when one considers library versions and the dependencies they require. Some software requires an older version of a particular library to run correctly (or at all). Hence a variety of version numbers is available for important libraries. Modules typically load the required dependencies automatically.

This is all managed with the `module` command, which is explained in the next sections.

There is also a shorter `m1` command that does exactly the same as the `module` command and is easier to type. Whenever you see a `module` command, you can replace `module` with `m1`.

### 4.1.3 Available modules

A large number of software packages are installed on the HPC clusters. A list of all currently available software can be obtained by typing:

```
$ module available
```

It's also possible to execute `module av` or `module avail`, these are shorter to type and will do the same thing.

This will give some output such as:

```
$ module av 2>&1 | more
--- /apps/gent/SL6/sandybridge/modules/all ---
ABAQUS/6.12.1-linux-x86_64
AMOS/3.1.0-ictce-4.0.10
ant/1.9.0-Java-1.7.0_40
ASE/3.6.0.2515-ictce-4.1.13-Python-2.7.3
ASE/3.6.0.2515-ictce-5.5.0-Python-2.7.6
...
```

Or when you want to check whether some specific software, some compiler or some application (e.g., MATLAB) is installed on the HPC.

```
$ module av 2>&1 | grep -i -e "matlab"
MATLAB/2010b
MATLAB/2012b
MATLAB/2013b
```

As you are not aware of the capitals letters in the module name, we looked for a case-insensitive name with the “`-i`” option.

This gives a full list of software packages that can be loaded.

**The casing of module names is important:** lowercase and uppercase letters matter in module names.

### 4.1.4 Organisation of modules in toolchains

The amount of modules on the VSC systems can be overwhelming, and it is not always immediately clear which modules can be loaded safely together if you need to combine multiple programs in a single job to get your work done.

Therefore the VSC has defined so-called **toolchains**. A toolchain contains a C/C++ and Fortran compiler, a MPI library and some basic math libraries for (dense matrix) linear algebra and FFT. Two toolchains are defined on most VSC systems. One, the `intel` toolchain, consists of the Intel compilers, MPI library and math libraries. The other one, the `foss` toolchain, consists of Open Source components: the GNU compilers, OpenMPI, OpenBLAS and the standard LAPACK

and ScaLAPACK libraries for the linear algebra operations and the FFTW library for FFT. The toolchains are refreshed twice a year, which is reflected in their name.

E.g., `foss/2020a` is the first version of the `foss` toolchain in 2020.

The toolchains are then used to compile a lot of the software installed on the VSC clusters. You can recognise those packages easily as they all contain the name of the toolchain after the version number in their name (e.g., `Python/2.7.12-intel-2016b`). Only packages compiled with the same toolchain name and version can work together without conflicts.

#### 4.1.5 Loading and unloading modules

##### **module load**

To “activate” a software package, you load the corresponding module file using the `module load` command:

```
$ module load example
```

This will load the most recent version of *example*.

For some packages, multiple versions are installed; the load command will automatically choose the default version (if it was set by the system administrators) or the most recent version otherwise (i.e., the lexicographical last after the `/`).

**However, you should specify a particular version to avoid surprises when newer versions are installed:**

```
$ module load secondeexample/2.7-intel-2016b
```

The `ml` command is a shorthand for `module load`: `ml example/1.2.3` is equivalent to `module load example/1.2.3`.

Modules need not be loaded one by one; the two `module load` commands can be combined as follows:

```
$ module load example/1.2.3 secondeexample/2.7-intel-2016b
```

This will load the two modules as well as their dependencies (unless there are conflicts between both modules).

##### **module list**

Obviously, you need to be able to keep track of the modules that are currently loaded. Assuming you have run the `module load` commands stated above, you will get the following:

```
$ module list
Currently Loaded Modulefiles:
1) example/1.2.3
   -2016b
2) GCCcore/5.4.0
3) icc/2016.3.210-GCC-5.4.0-2.26
   -2016b
4) ifort/2016.3.210-GCC-5.4.0-2.26
   -2016b
5) impi/5.1.3.181-iccifort-2016.3.210-GCC-5.4.0-2.26
6) imkl/11.3.3.210-iimpi
7) intel/2016b
8) examplelib/1.2-intel
9) secondexample/2.7-intel
```

You can also just use the `ml` command without arguments to list loaded modules.

It is important to note at this point that other modules (e.g., `intel/2016b`) are also listed, although the user did not explicitly load them. This is because `secondexample/2.7-intel-2016b` depends on it (as indicated in its name), and the system administrator specified that the `intel/2016b` module should be loaded whenever *this* `secondexample` module is loaded. There are advantages and disadvantages to this, so be aware of automatically loaded modules whenever things go wrong: they may have something to do with it!

### module unload

To unload a module, one can use the `module unload` command. It works consistently with the `load` command, and reverses the latter's effect. However, the dependencies of the package are NOT automatically unloaded; you will have to unload the packages one by one. When the `secondexample` module is unloaded, only the following modules remain:

```
$ module unload secondexample
$ module list
Currently Loaded Modulefiles:
Currently Loaded Modulefiles:
1) example/1.2.3
   -2016.3.210-GCC-5.4.0-2.26
2) GCCcore/5.4.0
   -2016b
3) icc/2016.3.210-GCC-5.4.0-2.26
4) ifort/2016.3.210-GCC-5.4.0-2.26
   -2016b
5) impi/5.1.3.181-iccifort
6) imkl/11.3.3.210-iimpi
7) intel/2016b
8) examplelib/1.2-intel
```

To unload the `secondexample` module, you can also use `ml -secondexample`.

Notice that the version was not specified: there can only be one version of a module loaded at a time, so unloading modules by name is not ambiguous. However, checking the list of currently loaded modules is always a good idea, since unloading a module that is currently not loaded will *not* result in an error.

### 4.1.6 Purging all modules

In order to unload all modules at once, and hence be sure to start in a clean state, you can use:

```
$ module purge
```

This is always safe: the `cluster` module (the module that specifies which cluster jobs will get

submitted to) will not be unloaded (because it's a so-called “sticky” module).

#### 4.1.7 Using explicit version numbers

Once a module has been installed on the cluster, the executables or libraries it comprises are never modified. This policy ensures that the user's programs will run consistently, at least if the user specifies a specific version. **Failing to specify a version may result in unexpected behaviour.**

Consider the following example: the user decides to use the `example` module and at that point in time, just a single version 1.2.3 is installed on the cluster. The user loads the module using:

```
$ module load example
```

rather than

```
$ module load example/1.2.3
```

Everything works fine, up to the point where a new version of `example` is installed, 4.5.6. From then on, the user's `load` command will load the latter version, rather than the intended one, which may lead to unexpected problems. See for example [section 9.8](#).

Consider the following `example` modules:

```
$ module avail example/
example/1.2.3
example/4.5.6
```

Let's now generate a version conflict with the `example` module, and see what happens.

```
$ module av example/
example/1.2.3           example/4.5.6
$ module load example/1.2.3 example/4.5.6
Lmod has detected the following error: A different version of the 'example'
module is already loaded (see output of 'ml').
$ module swap example/4.5.6
```

Note: A `module swap` command combines the appropriate `module unload` and `module load` commands.

#### 4.1.8 Search for modules

With the `module spider` command, you can search for modules:

```
$ module spider example
-----
example:

Description:
This is just an example

Versions:
example/1.2.3
example/4.5.6
-----
For detailed information about a specific "example" module (including how to
load the modules) use the module's full name.
For example:

module spider example/1.2.3
```

It's also possible to get detailed information about a specific module:

```
$ module spider example/1.2.3
-----
example: example/1.2.3

Description:
This is just an example

You will need to load all module(s) on any one of the lines below before the "example/1.2.3" module is available to load.

cluster/golett
cluster/phumpy
cluster/swalot
cluster/skitty
cluster/victini

Help:

Description
=====
This is just an example

More information
=====
- Homepage: https://example.com
```

### 4.1.9 Get detailed info

To get a list of all possible commands, type:

```
$ module help
```

Or to get more information about one specific module package:

```
$ module help example/1.2.3
----- Module Specific Help for 'example/1.2.3' -----
This is just an example - Homepage: https://example.com/
```

#### 4.1.10 Save and load collections of modules

If you have a set of modules that you need to load often, you can save these in a *collection*. This will enable you to load all the modules you need with a single command.

In each `module` command shown below, you can replace `module` with `ml`.

First, load all modules you want to include in the collections:

```
$ module load example/1.2.3 secondeexample/2.7-intel-2016b
```

Now store it in a collection using `module save`. In this example, the collection is named `my-collection`.

```
$ module save my-collection
```

Later, for example in a jobscript or a new session, you can load all these modules with `module restore`:

```
$ module restore my-collection
```

You can get a list of all your saved collections with the `module savelist` command:

```
$ module savelist
Named collection list (For LMOD_SYSTEM_NAME = "C07-sandybridge"):
 1) my-collection
```

To get a list of all modules a collection will load, you can use the `module describe` command:

```
$ module describe my-collection
1) example/1.2.3                               6) imkl/11.3.3.210-iimpi
   -2016b
2) GCCcore/5.4.0                               7) intel/2016b
3) icc/2016.3.210-GCC-5.4.0-2.26            8) examplelib/1.2-intel
   -2016b
4) ifort/2016.3.210-GCC-5.4.0-2.26          9) secondeexample/2.7-intel
   -2016b
5) impi/5.1.3.181-iccifort-2016.3.210-GCC-5.4.0-2.26
```

To remove a collection, remove the corresponding file in `$HOME/.lmod.d`:

```
$ rm $HOME/.lmod.d/my-collection
```

#### 4.1.11 Getting module details

To see how a module would change the environment, you can use the `module show` command:

```
$ module show Python/2.7.12-intel-2016b
whatis("Description: Python is a programming language that lets you work more
quickly and integrate your systems more effectively. - Homepage: http://python.
org/")
conflict("Python")
load("intel/2016b")
load("bzip2/1.0.6-intel-2016b")
...
prepend_path(...)
setenv("EBEXTSLISTPYTHON", "setuptools-23.1.0,pip-8.1.2,nose-1.3.7,numpy-1.11.1,scipy
-0.17.1,ytz-2016.4", ...)
```

It's also possible to use the `ml show` command instead: they are equivalent.

Here you can see that the `Python/2.7.12-intel-2016b` comes with a whole bunch of extensions: `numpy`, `scipy`, ...

You can also see the modules the `Python/2.7.12-intel-2016b` module loads: `intel/2016b`, `bzip2/1.0.6-intel-2016b`, ...

If you're not sure what all of this means: don't worry, you don't have to know; just load the module and try to use the software.

## 4.2 Getting system information about the HPC infrastructure

### 4.2.1 Checking the general status of the HPC infrastructure

To check the general system state, check <https://www.ugent.be/hpc/en/infrastructure/status>. This has information about scheduled downtime, status of the system, ...

Note: the `qstat -q` command now only shows *your own jobs* on the UGent-HPC infrastructure (since May 2019), and can't be used any longer to access how "busy" each cluster is. For example:

```
$ qstat -q
Queue      Memory  CPU Time Walltime Node  Run Que Lm State
-----  -----
victini     --      --    72:00:00  --    3   9  --  E R
                                         --  --
                                         3   9

Please be aware that "qstat -q" only gives information about your own jobs.
```

### 4.2.2 Getting cluster state

You can check <http://hpc.ugent.be/clusterstate> to see information about the clusters: you can see the nodes that are down, free, partially filled with jobs, completely filled with jobs, ....

You can also get this information in text form (per cluster separately) with the `pbsmon` command:

```
$ module swap cluster/phumpy
$ pbsmon
2301 2302 2303 2304 2305 2306 2307
- . X J - - -
2308 2309 2310 2311 2312 2313 2314
j j J j - - j

2315 2316
- j

J full : 2 | X down : 1 |
j partial : 5 | x down_on_error : 0 |
- free : 7 | . offline : 1 |
| o other : 0 |

Node type:
ppn=24, physmem=503.6GB, swap=20.0GB, vmem=523.6GB, local disk=1117.0GB
```

pbsmon only outputs details of the cluster corresponding to the currently loaded `cluster` module (see [subsection 4.3.2](#)).

It also shows details about the nodes in a cluster. In the example, all nodes have 24 cores and 503.6 GB of memory.

### 4.3 Defining and submitting your job

Usually, you will want to have your program running in batch mode, as opposed to interactively as you may be accustomed to. The point is that the program must be able to start and run without user intervention, i.e., without you having to enter any information or to press any buttons during program execution. All the necessary input or required options have to be specified on the command line, or needs to be put in input or configuration files.

As an example, we will run a Perl script, which you will find in the examples subdirectory on the HPC. When you received an account to the HPC a subdirectory with examples was automatically generated for you.

Remember that you have copied the contents of the HPC examples directory to your home directory, so that you have your **own personal** copy (editable and over-writable) and that you can start using the examples. If you haven't done so already, run these commands now:

```
$ cd
$ cp -r /apps/gent/tutorials/Intro-HPC/examples ~/
```

First go to the directory with the first examples by entering the command:

```
$ cd ~/examples/Running-batch-jobs
```

Each time you want to execute a program on the HPC you'll need 2 things:

**The executable** The program to execute from the end-user, together with its peripheral input files, databases and/or command options.

**A batch job script**, which will define the computer resource requirements of the program,

the required additional software packages and which will start the actual executable. The HPC needs to know:

1. the type of compute nodes;
2. the number of CPUs;
3. the amount of memory;
4. the expected duration of the execution time (wall time: Time as measured by a clock on the wall);
5. the name of the files which will contain the output (i.e., stdout) and error (i.e., stderr) messages;
6. what executable to start, and its arguments.

Later on, the HPC user shall have to define (or to adapt) his/her own job scripts. For now, all required job scripts for the exercises are provided for you in the examples subdirectories.

List and check the contents with:

```
$ ls -l
total 512
-rw-r--r-- 1 vsc40000 193 Sep 11 10:34 fibo.pbs
-rw-r--r-- 1 vsc40000 609 Sep 11 10:25 fibo.pl
```

In this directory you find a Perl script (named “fibo.pl”) and a job script (named “fibo.pbs”).

1. The Perl script calculates the first 30 Fibonacci numbers.
2. The job script is actually a standard Unix/Linux shell script that contains a few extra comments at the beginning that specify directives to PBS. These comments all begin with **#PBS**.

We will first execute the program locally (i.e., on your current login-node), so that you can see what the program does.

On the command line, you would run this using:

```
$ ./fibonacci.pl
[0] -> 0
[1] -> 1
[2] -> 1
[3] -> 2
[4] -> 3
[5] -> 5
[6] -> 8
[7] -> 13
[8] -> 21
[9] -> 34
[10] -> 55
[11] -> 89
[12] -> 144
[13] -> 233
[14] -> 377
[15] -> 610
[16] -> 987
[17] -> 1597
[18] -> 2584
[19] -> 4181
[20] -> 6765
[21] -> 10946
[22] -> 17711
[23] -> 28657
[24] -> 46368
[25] -> 75025
[26] -> 121393
[27] -> 196418
[28] -> 317811
[29] -> 514229
```

Remark: Recall that you have now executed the Perl script locally on one of the login-nodes of the HPC cluster. Of course, this is not our final intention; we want to run the script on any of the compute nodes. Also, it is not considered as good practice, if you “abuse” the login-nodes for testing your scripts and executables. It will be explained later on how you can reserve your own compute-node (by opening an interactive session) to test your software. But for the sake of acquiring a good understanding of what is happening, you are pardoned for this example since these jobs require very little computing power.

The job script contains a description of the job by specifying the command that need to be executed on the compute node:

— fibo.pbs —

```
1 #!/bin/bash -l
2 cd $PBS_O_WORKDIR
3 ./fibonacci.pl
```

So, jobs are submitted as scripts (bash, Perl, Python, etc.), which specify the parameters related to the jobs such as expected runtime (walltime), e-mail notification, etc. These parameters can also be specified on the command line.

This job script that can now be submitted to the cluster’s job system for execution, using the qsub (Queue SUBmit) command:

```
$ qsub fibo.pbs
123456
```

The qsub command returns a job identifier on the HPC cluster. The important part is the number (e.g., “123456 ”); this is a unique identifier for the job and can be used to monitor and manage your job.

Remark: the modules that were loaded when you submitted the job will *not* be loaded when the job is started. You should always specify the module load statements that are required for your job in the job script itself.

To facilitate this, you can use a pre-defined module collection which you can restore using module restore, see section [4.1.10](#) for more information.

Your job is now waiting in the queue for a free workernode to start on.

Go and drink some coffee . . . but not too long. If you get impatient you can start reading the next section for more information on how to monitor jobs in the queue.

After your job was started, and ended, check the contents of the directory:

```
$ ls -l
total 768
-rw-r--r-- 1 vsc40000 vsc40000 44 Feb 28 13:33 fibo.pbs
-rw----- 1 vsc40000 vsc40000 0 Feb 28 13:33 fibo.pbs.e123456
-rw----- 1 vsc40000 vsc40000 1010 Feb 28 13:33 fibo.pbs.o123456
-rwxrwxr-x 1 vsc40000 vsc40000 302 Feb 28 13:32 fibo.pl
```

Explore the contents of the 2 new files:

```
$ more fibo.pbs.o123456
$ more fibo.pbs.e123456
```

These files are used to store the standard output and error that would otherwise be shown in the terminal window. By default, they have the same name as that of the PBS script, i.e., “fibo.pbs” as base name, followed by the extension “.o” (output) and “.e” (error), respectively, and the job number (‘123456 ’ for this example). The error file will be empty, at least if all went well. If not, it may contain valuable information to determine and remedy the problem that prevented a successful run. The standard output file will contain the results of your calculation (here, the output of the Perl script)

### 4.3.1 When will my job start?

In practice it’s impossible to predict when your job(s) will start, since most currently running jobs will finish before their requested walltime expires, and new jobs by may be submitted by other users that are assigned a higher priority than your job(s).

The UGent-HPC clusters use a fair-share scheduling policy (see [chapter 10](#)). There is no guarantee on when a job will start, since it depends on a number of factors. One of these factors is the priority of the job, which is determined by

- historical use: the aim is to balance usage over users, so infrequent (in terms of total compute time used) users get a higher priority

- requested resources (amount of cores, walltime, memory, . . .)
- time waiting in queue: queued jobs get a higher priority over time
- user limits: this avoids having a single user use the entire cluster. This means that each user can only use a part of the cluster.

Some other factors are how busy the cluster is, how many workernodes are active, the resources (e.g., number of cores, memory) provided by each workernode, . . .

It might be beneficial to request less resources (e.g., not requesting all cores in a workernode), since the scheduler often finds a “gap” to fit the job into more easily.

### 4.3.2 Specifying the cluster on which to run

To use other clusters, you can swap the `cluster` module. This is a special module that changes what modules are available for you, and what cluster your jobs will be queued in.

By default you are working on `victini`. To switch to, e.g., `skitty` you need to redefine the environment so you get access to all modules installed on the `skitty` cluster, and to be able to submit jobs to the `skitty` scheduler so your jobs will start on `skitty` instead of the default `victini` cluster.

```
$ module swap cluster/skitty
```

Note: the `skitty` modules may not work directly on the login nodes, because the login nodes do not have the same architecture as the `skitty` cluster, they have the same architecture as the `victini` cluster however, so this is why by default software works on the login nodes. See [section 9.9](#) for why this is and how to fix this.

```
$ module avail cluster/
-----
/etc/modulefiles/vsc
-----
cluster/golett (S)    cluster/phnpy (S)    cluster/skitty (S)    cluster/swalot
(S)      cluster/victini (S,L)

Where:
S:  Module is Sticky, requires --force to unload or purge
L:  Module is loaded

If you need software that is not listed, request it via https://www.ugent.be/hpc/en/
support/software-installation-request
```

As indicated in the output above, each `cluster` module is a so-called sticky module, i.e., it will not be unloaded when `module purge` (see [subsection 4.1.6](#)) is used.

The output of the various commands interacting with jobs (`qsub`, `stat`, . . .) all depend on which `cluster` module is loaded.

## 4.4 Monitoring and managing your job(s)

Using the job ID that qsub returned, there are various ways to monitor the status of your job. In the following commands, replace 12345 with the job ID qsub returned.

```
$ qstat 12345
```

To show on which compute nodes your job is running, at least, when it is running:

```
$ qstat -n 12345
```

To remove a job from the queue so that it will not run, or to stop a job that is already running.

```
$ qdel 12345
```

When you have submitted several jobs (or you just forgot about the job ID), you can retrieve the status of all your jobs that are submitted and are not yet finished using:

```
$ qstat
:
Job ID      Name      User      Time Use S Queue
-----
123456 .... mpi      vsc40000 0      Q short
```

Here:

**Job ID** the job's unique identifier

**Name** the name of the job

**User** the user that owns the job

**Time Use** the elapsed walltime for the job

**Queue** the queue the job is in

The state S can be any of the following:

State	Meaning
<b>Q</b>	The job is <b>queued</b> and is waiting to start.
<b>R</b>	The job is currently <b>running</b> .
<b>E</b>	The job is currently <b>exiting</b> after having run.
<b>C</b>	The job is <b>completed</b> after having run.
<b>H</b>	The job has a user or system <b>hold</b> on it and will not be eligible to run until the hold is removed.

User hold means that the user can remove the hold. System hold means that the system or an administrator has put the job on hold, very likely because something is wrong with it. Check with your helpdesk to see why this is the case.

## 4.5 Examining the queue

There is currently (since May 2019) no way to get an overall view of the state of the cluster queues for the UGent-HPC infrastructure, due to changes to the cluster resource management software (and also because a general overview is mostly meaningless since it doesn't give any indication of the resources requested by the queued jobs).

## 4.6 Specifying job requirements

Without giving more information about your job upon submitting it with **qsub**, default values will be assumed that are almost never appropriate for real jobs.

It is important to estimate the resources you need to successfully run your program, such as the amount of time the job will require, the amount of memory it needs, the number of CPUs it will run on, etc. This may take some work, but it is necessary to ensure your jobs will run properly.

### 4.6.1 Generic resource requirements

The **qsub** command takes several options to specify the requirements, of which we list the most commonly used ones below.

```
$ qsub -l walltime=2:30:00
```

For the simplest cases, only the amount of maximum estimated execution time (called "walltime") is really important. Here, the job requests 2 hours, 30 minutes. As soon as the job exceeds the requested walltime, it will be "killed" (terminated) by the job scheduler. There is no harm if you *slightly* overestimate the maximum execution time. If you omit this option, the queue manager will not complain but use a default value (one hour on most clusters).

If you want to run some final steps (for example to copy files back) before the walltime kills your main process, you have to kill the main command yourself before the walltime runs out and then copy the file back. See [section 17.3](#) for how to do this.

```
$ qsub -l mem=4gb
```

The job requests 4 GB of RAM memory. As soon as the job tries to use more memory, it will be "killed" (terminated) by the job scheduler. There is no harm if you *slightly* overestimate the requested memory.

```
$ qsub -l nodes=5:ppn=2
```

The job requests 5 compute nodes with two cores on each node (ppn stands for "processors per node", where "processors" here actually means "CPU cores").

```
$ qsub -l nodes=1:westmere
```

The job requests just one node, but it should have an Intel Westmere processor. A list with site-specific properties can be found in the next section or in the User Portal (“VSC hardware” section)<sup>1</sup> of the VSC website.

These options can either be specified on the command line, e.g.

```
$ qsub -l nodes=1:ppn=1,mem=2gb fibo.pbs
```

or in the job script itself using the #PBS-directive, so “fibo.pbs” could be modified to:

```
1 #!/bin/bash -l
2 #PBS -l nodes=1:ppn=1
3 #PBS -l mem=2gb
4 cd $PBS_O_WORKDIR
5 ./fibo.pl
```

Note that the resources requested on the command line will override those specified in the PBS file.

#### 4.6.2 Node-specific properties

The following table contains some node-specific properties that can be used to make sure the job will run on nodes with a specific CPU or interconnect. Note that these properties may vary over the different VSC sites.

To get a list of all properties defined for all nodes, enter

```
$ pbsnodes
```

This list will also contain properties referring to, e.g., network components, rack number, etc.

## 4.7 Job output and error files

At some point your job finishes, so you may no longer see the job ID in the list of jobs when you run *qstat* (since it will only be listed for a few minutes after completion with state “C”). After your job finishes, you should see the standard output and error of your job in two files, located by default in the directory where you issued the *qsub* command.

When you navigate to that directory and list its contents, you should see them:

```
$ ls -l
total 1024
-rw-r--r-- 1 vsc40000 609 Sep 11 10:54 fibo.pl
-rw-r--r-- 1 vsc40000 68 Sep 11 10:53 fibo.pbs
-rw----- 1 vsc40000 52 Sep 11 11:03 fibo.pbs.e123456
-rw----- 1 vsc40000 1307 Sep 11 11:03 fibo.pbs.o123456
```

In our case, our job has created both output (‘fibo.pbs.o123456’) and error files (‘fibo.pbs.e123456’) containing info written to *stdout* and *stderr* respectively.

Inspect the generated output and error files:

---

<sup>1</sup>URL: <https://vscdocumentation.readthedocs.io/en/latest/hardware.html>

```
$ cat fibo.pbs.o123456  
...  
$ cat fibo.pbs.e123456  
...
```

## 4.8 E-mail notifications

### 4.8.1 Generate your own e-mail notifications

You can instruct the HPC to send an e-mail to your e-mail address whenever a job begins, ends and/or aborts, by adding the following lines to the job script `fibo.pbs`:

```
1 #PBS -m b  
2 #PBS -m e  
3 #PBS -m a
```

or

```
1 #PBS -m abe
```

These options can also be specified on the command line. Try it and see what happens:

```
$ qsub -m abe fibo.pbs
```

The system will use the e-mail address that is connected to your VSC account. You can also specify an alternate e-mail address with the `-M` option:

```
$ qsub -m b -M john.smith@example.com fibo.pbs
```

will send an e-mail to `john.smith@example.com` when the job begins.

## 4.9 Running a job after another job

If you submit two jobs expecting that should be run one after another (for example because the first generates a file the second needs), there might be a problem as they might both be run at the same time.

So the following example might go wrong:

```
$ qsub job1.sh  
$ qsub job2.sh
```

You can make jobs that depend on other jobs. This can be useful for breaking up large jobs into smaller jobs that can be run in a pipeline. The following example will submit 2 jobs, but the second job (`job2.sh`) will be held (`H` status in `qstat`) until the first job successfully completes. If the first job fails, the second will be cancelled.

```
$ FIRST_ID=$(qsub job1.sh)  
$ qsub -W depend=afterok:$FIRST_ID job2.sh
```

`afterok` means “After OK”, or in other words, after the first job successfully completed.

It's also possible to use `afternotok` ("After not OK") to run the second job only if the first job exited with errors. A third option is to use `afterany` ("After any"), to run the second job after the first job (regardless of success or failure).

# Chapter 5

## Running interactive jobs

### 5.1 Introduction

Interactive jobs are jobs which give you an interactive session on one of the compute nodes. Importantly, accessing the compute nodes this way means that the job control system guarantees the resources that you have asked for.

Interactive PBS jobs are similar to non-interactive PBS jobs in that they are submitted to PBS via the command **qsub**. Where an interactive job differs is that it does not require a job script, the required PBS directives can be specified on the command line.

Interactive jobs can be useful to debug certain job scripts or programs, but should not be the main use of the UGent-HPC. Waiting for user input takes a very long time in the life of a CPU and does not make efficient usage of the computing resources.

The syntax for *qsub* for submitting an interactive PBS job is:

```
$ qsub -I <... pbs directives ...>
```

### 5.2 Interactive jobs, without X support

**Tip:** Find the code in “`~/examples/Running-interactive-jobs`”

First of all, in order to know on which computer you’re working, enter:

```
$ hostname -f  
gligar04.gastly.os
```

This means that you’re now working on the login node `gligar04.gastly.os` of the HPC cluster.

The most basic way to start an interactive job is the following:

```
$ qsub -I  
qsub: waiting for job 123456 to start  
qsub: job 123456 ready
```

There are two things of note here.

1. The “*qsub*” command (with the interactive -I flag) waits until a node is assigned to your interactive session, connects to the compute node and shows you the terminal prompt on that node.
2. You’ll see that your directory structure of your home directory has remained the same. Your home directory is actually located on a shared storage system. This means that the exact same directory is available on all login nodes and all compute nodes on all clusters.

In order to know on which compute-node you’re working, enter again:

```
$ hostname -f
node3200.victini.gent.vsc
```

Note that we are now working on the compute-node called “*node3200.victini.gent.vsc*”. This is the compute node, which was assigned to us by the scheduler after issuing the “*qsub -I*” command.

Now, go to the directory of our second interactive example and run the program “primes.py”. This program will ask you for an upper limit (> 1) and will print all the primes between 1 and your upper limit:

```
$ cd ~/examples/Running-interactive-jobs
$ ./primes.py
This program calculates all primes between 1 and your upper limit.
Enter your upper limit (>1): 50
Start Time: 2013-09-11 15:49:06
[Prime#1] = 1
[Prime#2] = 2
[Prime#3] = 3
[Prime#4] = 5
[Prime#5] = 7
[Prime#6] = 11
[Prime#7] = 13
[Prime#8] = 17
[Prime#9] = 19
[Prime#10] = 23
[Prime#11] = 29
[Prime#12] = 31
[Prime#13] = 37
[Prime#14] = 41
[Prime#15] = 43
[Prime#16] = 47
End Time: 2013-09-11 15:49:06
Duration: 0 seconds.
```

You can exit the interactive session with:

```
$ exit
```

Note that you can now use this allocated node for 1 hour. After this hour you will be automatically disconnected. You can change this “usage time” by explicitly specifying a “walltime”, i.e., the time that you want to work on this node. (Think of walltime as the time elapsed when watching the clock on the wall.)

You can work for 3 hours by:

```
$ qsub -I -l walltime=03:00:00
```

If the walltime of the job is exceeded, the (interactive) job will be killed and your connection to the compute node will be closed. So do make sure to provide adequate walltime and that you save your data before your (wall)time is up (exceeded)! When you do not specify a walltime, you get a default walltime of 1 hour.

## 5.3 Interactive jobs, with graphical support

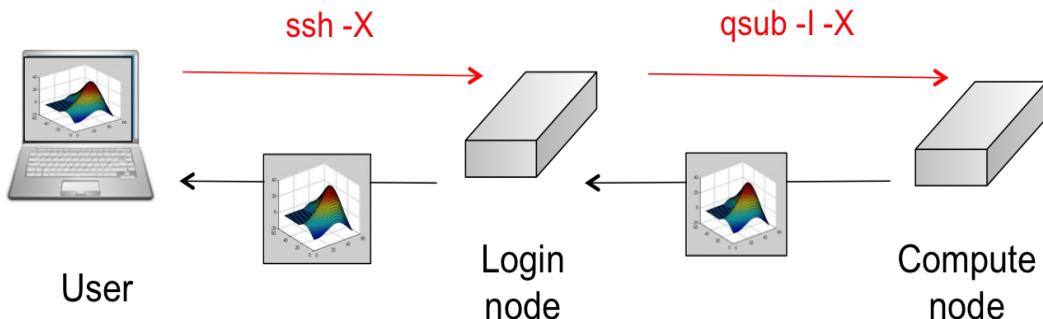
### 5.3.1 Software Installation

To display graphical applications from a Linux computer (such as the VSC clusters) on your machine, you need to install an X Window server on your local computer. An X Window server is packaged by default on most Linux distributions. If you have a graphical user interface this generally means that you are using an X Window server.

The X Window system (commonly known as **X11**, based on its current major version being 11, or shortened to simply **X**) is the system-level software infrastructure for the windowing GUI on Linux, BSD and other UNIX-like operating systems. It was designed to handle both local displays, as well as displays sent across a network. More formally, it is a computer software system and network protocol that provides a basis for graphical user interfaces (GUIs) and rich input device capability for networked computers.

### 5.3.2 Connect with X-forwarding

In order to get the graphical output of your application (which is running on a compute node on the HPC) transferred to your personal screen, you will need to reconnect to the HPC with X-forwarding enabled, which is done with the “-X” option.



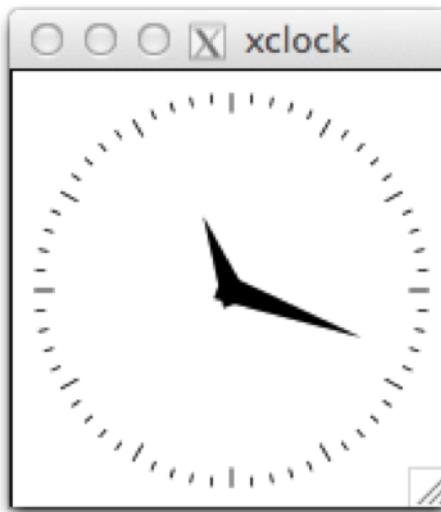
First exit and reconnect to the HPC with X-forwarding enabled:

```
$ exit  
$ ssh -X vsc40000@login.hpc.ugent.be  
$ hostname -f  
gligar04.gastly.os
```

We first check whether our GUIs on the login node are decently forwarded to your screen on your local machine. An easy way to test it is by running a small X-application on the login node. Type:

```
$ xclock
```

And you should see a clock appearing on your screen.



You can close your clock and connect further to a compute node with again your X-forwarding enabled:

```
$ qsub -I -X
qsub: waiting for job 123456 to start
qsub: job 123456 ready
$ hostname -f
node3200.victini.gent.vsc
$ xclock
```

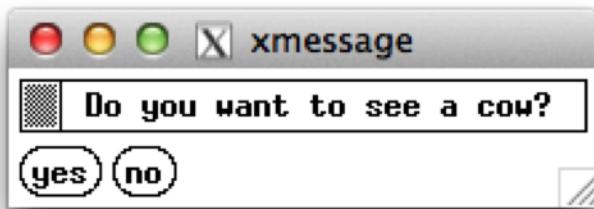
and you should see your clock again.

### 5.3.3 Run simple example

We have developed a little interactive program that shows the communication in 2 directions. It will send information to your local screen, but also asks you to click a button.

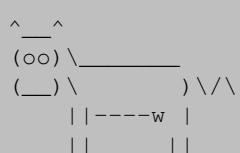
```
$ cd ~/examples/Running-interactive-jobs
$ ./message.py
```

You should see the following message appearing.



Click any button and see what happens.

```
-----  
< Enjoy the day! Mooh >  
-----
```



# Chapter 6

## Running jobs with input/output data

You have now learned how to start a batch job and how to start an interactive session. The next question is how to deal with input and output files, where your standard output and error messages will go to and where that you can collect your results.

### 6.1 The current directory and output and error files

#### 6.1.1 Default file names

First go to the directory:

```
$ cd ~/examples/Running-jobs-with-input-output-data
```

List and check the contents with:

```
$ ls -l
total 2304
-rwxrwxr-x 1 vsc40000 682 Sep 13 11:34 file1.py
-rw-rw-r-- 1 vsc40000 212 Sep 13 11:54 file1a.pbs
-rw-rw-r-- 1 vsc40000 994 Sep 13 11:53 file1b.pbs
-rw-rw-r-- 1 vsc40000 994 Sep 13 11:53 file1c.pbs
-rw-r--r-- 1 vsc40000 1393 Sep 13 10:41 file2.pbs
-rwxrwxr-x 1 vsc40000 2393 Sep 13 10:40 file2.py
-rw-r--r-- 1 vsc40000 1393 Sep 13 10:41 file3.pbs
-rwxrwxr-x 1 vsc40000 2393 Sep 13 10:40 file3.py
```

Now, let us inspect the contents of the first executable (which is just a Python script with execute permission).

— file1.py —

```
1 #!/usr/bin/env python
2 #
3 # VSC      : Flemish Supercomputing Centre
4 # Tutorial : Introduction to HPC
5 # Description: Writing to the current directory, stdout and stderr
6 #
7 import sys
8
9 # Step #1: write to a local file in your current directory
10 local_f = open("Hello.txt", 'w+')
11 local_f.write("Hello World!\n")
12 local_f.write("I am writing in the file:<Hello.txt>.\n")
13 local_f.write("in the current directory.\n")
14 local_f.write("Cheers!\n")
15 local_f.close()
16
17 # Step #2: Write to stdout
18 sys.stdout.write("Hello World!\n")
19 sys.stdout.write("I am writing to <stdout>.\n")
20 sys.stdout.write("Cheers!\n")
21
22 # Step #3: Write to stderr
23 sys.stderr.write("Hello World!\n")
24 sys.stderr.write("This is NO ERROR or WARNING.\n")
25 sys.stderr.write("I am just writing to <stderr>.\n")
26 sys.stderr.write("Cheers!\n")
```

The code of the Python script, is self explanatory:

1. In step 1, we write something to the file hello.txt in the current directory.
2. In step 2, we write some text to stdout.
3. In step 3, we write to stderr.

Check the contents of the first job script:

— file1a.pbs —

```
1 #!/bin/bash
2
3 #PBS -l walltime=00:05:00
4
5 # go to the (current) working directory (optional, if this is the
6 # directory where you submitted the job)
7 cd $PBS_O_WORKDIR
8
9 # the program itself
10 echo Start Job
11 date
12 ./file1.py
13 echo End Job
```

You'll see that there are NO specific PBS directives for the placement of the output files. All output files are just written to the standard paths.

Submit it:

```
$ qsub file1a.pbs
```

After the job has finished, inspect the local directory again, i.e., the directory where you executed the *qsub* command:

```
$ ls -l
total 3072
-rw-rw-r-- 1 vsc40000 90 Sep 13 13:13 Hello.txt
-rwxrwxr-x 1 vsc40000 693 Sep 13 13:03 file1.py*
-rw-rw-r-- 1 vsc40000 229 Sep 13 13:01 file1a.pbs
-rw----- 1 vsc40000 91 Sep 13 13:13 file1a.pbs.e123456
-rw----- 1 vsc40000 105 Sep 13 13:13 file1a.pbs.o123456
-rw-rw-r-- 1 vsc40000 143 Sep 13 13:07 file1b.pbs
-rw-rw-r-- 1 vsc40000 177 Sep 13 13:06 file1c.pbs
-rw-rw-r-- 1 vsc40000 1393 Sep 13 10:41 file2.pbs
-rwxrwxr-x 1 vsc40000 2393 Sep 13 10:40 file2.py*
-rw-rw-r-- 1 vsc40000 1393 Sep 13 10:41 file3.pbs
-rwxrwxr-x 1 vsc40000 2393 Sep 13 10:40 file3.py*
```

Some observations:

1. The file `Hello.txt` was created in the current directory.
2. The file `file1a.pbs.o123456` contains all the text that was written to the standard output stream (“`stdout`”).
3. The file `file1a.pbs.e123456` contains all the text that was written to the standard error stream (“`stderr`”).

Inspect their contents ... and remove the files

```
$ cat Hello.txt
$ cat file1a.pbs.o123456
$ cat file1a.pbs.e123456
$ rm Hello.txt file1a.pbs.o123456 file1a.pbs.e123456
```

**Tip:** Type `cat H` and press the Tab button (looks like ) , and it will **expand** into `cat Hello.txt`.

### 6.1.2 Filenames using the name of the job

Check the contents of the job script and execute it.

— file1b.pbs —

```

1 #!/bin/bash
2
3 #   Specify the "name" of the job
4 #PBS -N my_serial_job
5
6 cd $PBS_O_WORKDIR
7 echo Start Job
8 date
9 ./file1.py
10 echo End Job
$ qsub file1b.pbs

```

Inspect the contents again ... and remove the generated files:

```

$ ls
Hello.txt  file1a.pbs  file1c.pbs  file2.pbs  file3.pbs  my_serial_job.e123456
file1.py*  file1b.pbs  file2.py*   file3.py*  my_serial_job.o123456
$ rm Hello.txt my_serial_job.*

```

Here, the option “-N” was used to explicitly assign a name to the job. This overwrote the JOBNAME variable, and resulted in a different name for the *stdout* and *stderr* files. This name is also shown in the second column of the “qstat” command. If no name is provided, it defaults to the name of the job script.

### 6.1.3 User-defined file names

You can also specify the name of *stdout* and *stderr* files explicitly by adding two lines in the job script, as in our third example:

— file1c.pbs —

```

1 #!/bin/bash
2
3 # redirect standard output (-o) and error (-e)
4 #PBS -o stdout.$PBS_JOBID
5 #PBS -e stderr.$PBS_JOBID
6
7 cd $PBS_O_WORKDIR
8 echo Start Job
9 date
10 ./file1.py
11 echo End Job
$ qsub file1c.pbs
$ ls

```

## 6.2 Where to store your data on the HPC

The HPC cluster offers their users several locations to store their data. Most of the data will reside on the shared storage system, but all compute nodes also have their own (small) local disk.

### 6.2.1 Pre-defined user directories

Three different pre-defined user directories are available, where each directory has been created for different purposes. The best place to store your data depends on the purpose, but also the size and type of usage of the data.

The following locations are available:

Variable	Description
<i>Long-term storage</i> slow filesystem, intended for smaller files	
\$VSC_HOME	For your configuration files and other small files, see §6.2.2. The default directory is /user/gent/xxx/vsc40000. The same file system is accessible from all sites, i.e., you'll see the same contents in \$VSC_HOME on all sites.
\$VSC_DATA	A bigger “workspace”, for datasets, results, logfiles, etc. see §6.2.3. The default directory is /data/gent/xxx/vsc40000. The same file system is accessible from all sites.
<i>Fast temporary storage</i>	
\$VSC_SCRATCH_NODE	For <b>temporary</b> or transient data on the local compute node, where fast access is important; see §6.2.4. This space is available per node. The default directory is /tmp. On different nodes, you'll see different content.
\$VSC_SCRATCH	For <b>temporary</b> or transient data that has to be accessible from all nodes of a cluster (including the login nodes) The default directory is /scratch/gent/xxx/vsc40000. This directory is cluster- or site-specific: On different sites, and sometimes on different clusters on the same site, you'll get a different directory with different content.
\$VSC_SCRATCH_SITE	Currently the same as \$VSC_SCRATCH, but could be used for a scratch space shared across all clusters at a site in the future. See §6.2.4.
\$VSC_SCRATCH_GLOBAL	Currently the same as \$VSC_SCRATCH, but could be used for a scratch space shared across all clusters of the VSC in the future. See §6.2.4.
\$VSC_SCRATCH_CLUSTER	The scratch filesystem closest to this cluster.
\$VSC_SCRATCH_PHANPY	A separate (smaller) shared scratch filesystem, powered by SSDs. This scratch filesystem is intended for very I/O-intensive workloads.

Since these directories are not necessarily mounted on the same locations over all sites, you should always (try to) use the environment variables that have been created.

We elaborate more on the specific function of these locations in the following sections.

Note: `$VSC_SCRATCH_KYUKON` and `$VSC_SCRATCH` are the same directories (“kyukon” is the name of the storage cluster where the default shared scratch filesystem is hosted).

For documentation about VO directories, see [subsection 6.7.5](#).

### 6.2.2 Your home directory (`$VSC_HOME`)

Your home directory is where you arrive by default when you login to the cluster. Your shell refers to it as “~” (tilde), and its absolute path is also stored in the environment variable `$VSC_HOME`. Your home directory is shared across all clusters of the VSC.

The data stored here should be relatively small (e.g., no files or directories larger than a few megabytes), and preferably should only contain configuration files. Note that various kinds of configuration files are also stored here, e.g., by MATLAB, Eclipse, …

The operating system also creates a few files and folders here to manage your account. Examples are:

File or Directory	Description
<code>.ssh/</code>	This directory contains some files necessary for you to login to the cluster and to submit jobs on the cluster. Do not remove them, and do not alter anything if you don’t know what you are doing!
<code>.bash_profile</code>	When you login (type username and password) remotely via ssh, <code>.bash_profile</code> is executed to configure your shell before the initial command prompt.
<code>.bashrc</code>	This script is executed every time you start a session on the cluster: when you login to the cluster and when a job starts.
<code>.bash_history</code>	This file contains the commands you typed at your shell prompt, in case you need them again.

### 6.2.3 Your data directory (`$VSC_DATA`)

In this directory you can store all other data that you need for longer terms (such as the results of previous jobs, …). It is a good place for, e.g., storing big files like genome data.

The environment variable pointing to this directory is `$VSC_DATA`. This volume is shared across all clusters of the VSC. There are however no guarantees about the speed you will achieve on this volume. For guaranteed fast performance and very heavy I/O, you should use the scratch space instead. If you are running out of quota on your `$VSC_DATA` filesystem you can request a VO. See [section 6.7](#) on how to do this.

### 6.2.4 Your scratch space (`$VSC_SCRATCH`)

To enable quick writing from your job, a few extra file systems are available on the compute nodes. These extra file systems are called scratch folders, and can be used for storage of temporary and/or transient data (temporary results, anything you just need during your job, or your batch

of jobs).

You should remove any data from these systems after your processing them has finished. There are no guarantees about the time your data will be stored on this system, and we plan to clean these automatically on a regular base. The maximum allowed age of files on these scratch file systems depends on the type of scratch, and can be anywhere between a day and a few weeks. We don't guarantee that these policies remain forever, and may change them if this seems necessary for the healthy operation of the cluster.

Each type of scratch has its own use:

**Node scratch (\$VSC\_SCRATCH\_NODE).** Every node has its own scratch space, which is completely separated from the other nodes. On some clusters, it will be on a local disk in the node, while on other clusters it will be emulated through another file server. In many cases, it will be significantly slower than the cluster scratch as it typically consists of just a single disk. Some **drawbacks** are that the storage can only be accessed on that particular node and that the capacity is often very limited (e.g., 100 GB). The performance will depend a lot on the particular implementation in the cluster. In many cases, it will be significantly slower than the cluster scratch as it typically consists of just a single disk. However, if that disk is local to the node (as on most clusters), the performance will not depend on what others are doing on the cluster.

**Cluster scratch (\$VSC\_SCRATCH).** To allow a job running on multiple nodes (or multiple jobs running on separate nodes) to share data as files, every node of the cluster (including the login nodes) has access to this shared scratch directory. Just like the home and data directories, every user has its own scratch directory. Because this scratch is also available from the login nodes, you could manually copy results to your data directory after your job has ended. Also, this type of scratch is usually implemented by running tens or hundreds of disks in parallel on a powerful file server with fast connection to all the cluster nodes and therefore is often the fastest file system available on a cluster.

You may not get the same file system on different clusters, i.e., you may see different content on different clusters at the same institute.

**Site scratch (\$VSC\_SCRATCH\_SITE).** At the time of writing, the site scratch is just the same volume as the cluster scratch, and thus contains the same data. In the future it may point to a different scratch file system that is available across all clusters at a particular site, which is in fact the case for the cluster scratch on some sites.

**Global scratch (\$VSC\_SCRATCH\_GLOBAL).** At the time of writing, the global scratch is just the same volume as the cluster scratch, and thus contains the same data. In the future it may point to a scratch file system that is available across all clusters of the VSC, but at the moment of writing there are no plans to provide this.

### 6.2.5 Your UGent home drive and shares

In order to access data on your UGent share(s), you need to stage-in the data and stage-out afterwards. On the login nodes, it is possible to access your UGent home drive and shares. To allow this you need a ticket. This requires that you first authenticate yourself with your UGent username and password by running:

```
$ kinit yourugentusername@UGENT.BE  
Password for yourugentusername@UGENT.BE:
```

Now you should be able to access your files running

```
$ ls /UGent/yourugentusername  
home shares www
```

Please note the shares will only be mounted when you access this folder. You should specify your complete username - tab completion will not work.

If you want to use the UGent shares longer than 24 hours, you should ask a ticket for up to a week by running

```
$ kinit yourugentusername@UGENT.BE -r 7d
```

You can verify your authentication ticket and expiry dates yourself by running klist

```
$ klist  
...  
Valid starting     Expires            Service principal  
14/07/20 15:19:13  15/07/20 01:19:13  krbtgt/UGENT.BE@UGENT.BE  
                  renew until 21/07/20 15:19:13
```

Your ticket is valid for 10 hours, but you can renew it before it expires.

To renew your tickets, simply run

```
$ kinit -R
```

If you want your ticket to be renewed automatically up to the maximum expiry date, you can run

```
$ krenew -b -K 60
```

Each hour the process will check if your ticket should be renewed.

We strongly advise to disable access to your shares once it is no longer needed:

```
$ kdestroy
```

### 6.2.6 UGent shares with globus

In order to access your UGent home and shares inside the globus endpoint, you first have to generate authentication credentials on the endpoint. To do that, you have to ssh to the globus endpoint from a loginnode. You will be prompted for your UGent username and password to authenticate:

```
$ ssh globus01
UGent username:ugentusername
Password for ugentusername@UGENT.BE:
Shares are available in globus endpoint at /UGent/ugentusername/
Overview of valid tickets:
Ticket cache: KEYRING:persistent:xxxxxxxx:xxxxxxxx
Default principal: ugentusername@UGENT.BE

Valid starting     Expires            Service principal
29/07/20 15:56:43  30/07/20 01:56:43  krbtgt/UGENT.BE@UGENT.BE
                  renew until 05/08/20 15:56:40
Tickets will be automatically renewed for 1 week
Connection to globus01 closed.
```

Your shares will then be available at /UGent/ugentusername/ under the globus VSC tier2 endpoint. Tickets will be renewed automatically for 1 week, after which you'll need to run this again. We advise to disable access to your shares within globus once access is no longer needed:

```
$ ssh globus01 destroy
Successfully destroyed session
```

### 6.2.7 Pre-defined quotas

**Quota** is enabled on these directories, which means that the amount of data you can store there is limited. This holds for both the total size of all files as well as the total number of files that can be stored. The system works with a soft quota and a hard quota. You can temporarily exceed the soft quota, but you can never exceed the hard quota. The user will get warnings as soon as he exceeds the soft quota.

To see your a list of your current quota, visit the VSC accountpage: <https://account.vscentrum.be>. VO moderators can see a list of VO quota usage per member of their VO via <https://account.vscentrum.be/django/vo/>.

The rules are:

1. You will only receive a warning when you have reached the soft limit of either quota.
2. You *will* start losing data and get I/O errors when you reach the hard limit. In this case, data loss will occur since nothing can be written anymore (this holds both for new files as well as for existing files), until you free up some space by removing some files. Also note that you *will not* be warned when data loss occurs, so keep an eye open for the general quota warnings!
3. The same holds for running jobs that need to write files: when you reach your hard quota, jobs will crash.

We do realise that quota are often observed as a nuisance by users, especially if you're running low on it. However, it is an essential feature of a shared infrastructure. Quota ensure that a single user cannot accidentally take a cluster down (and break other user's jobs) by filling up the available disk space. And they help to guarantee a fair use of all available resources for all users. Quota also help to ensure that each folder is used for its intended purpose.

## 6.3 Writing Output files

**Tip:** Find the code of the exercises in “`~/examples/Running-jobs-with-input-output-data`”

In the next exercise, you will generate a file in the `$VSC_SCRATCH` directory. In order to generate some CPU- and disk-I/O load, we will

1. take a random integer between 1 and 2000 and calculate all primes up to that limit;
2. repeat this action 30.000 times;
3. write the output to the “`primes_1.txt`” output file in the `$VSC_SCRATCH`-directory.

Check the Python and the PBS file, and submit the job: Remember that this is already a more serious (disk-I/O and computational intensive) job, which takes approximately 3 minutes on the HPC.

```
$ cat file2.py
$ cat file2.pbs
$ qsub file2.pbs
$ qstat
$ ls -l
$ echo $VSC_SCRATCH
$ ls -l $VSC_SCRATCH
$ more $VSC_SCRATCH/primes_1.txt
```

## 6.4 Reading Input files

**Tip:** Find the code of the exercise “`file3.py`” in  
“`~/examples/Running-jobs-with-input-output-data`”.

In this exercise, you will

1. Generate the file “`primes_1.txt`” again as in the previous exercise;
2. open the this file;
3. read it line by line;
4. calculate the average of primes in the line;
5. count the number of primes found per line;
6. write it to the “`primes_2.txt`” output file in the `$VSC_SCRATCH`-directory.

Check the Python and the PBS file, and submit the job:

```
$ cat file3.py
$ cat file3.pbs
$ qsub file3.pbs
$ qstat
$ ls -l
$ more $VSC_SCRATCH/primes_2.txt
...
```

## 6.5 How much disk space do I get?

### 6.5.1 Quota

The available disk space on the HPC is limited. The actual disk capacity, shared by all users, can be found on the “Available hardware” page on the website. (<https://vscdocumentation.readthedocs.io/en/latest/hardware.html>) As explained in subsection 6.2.7, this implies that there are also limits to:

- the amount of disk space; and
- the number of files

that can be made available to each individual HPC user.

The quota of disk space and number of files for each HPC user is:

Volume	Max. disk space	Max. # Files
HOME	3 GB	20000
DATA	25 GB	100000
SCRATCH	25 GB	100000

**Tip:** The first action to take when you have exceeded your quota is to clean up your directories. You could start by removing intermediate, temporary or log files. Keeping your environment clean will never do any harm.

**Tip:** If you obtained your VSC account via UGent, you can get (significantly) more storage quota in the DATA and SCRATCH volumes by joining a Virtual Organisation (VO), see section 6.7 for more information. In case of questions, contact hpc@ugent.be.

### 6.5.2 Check your quota

You can consult your current storage quota usage on the UGent-HPC shared filesystems via the VSC accountpage, see the "Usage" section at <https://account.vscentrum.be>.

VO moderators can inspect storage quota for all VO members via <https://account.vscentrum.be/django/vo/>.

To check your storage usage on the local scratch filesystems on VSC sites other than UGent, you can use the “show\_quota” command (when logged into the login nodes of that VSC site).

Once your quota is (nearly) exhausted, you will want to know which directories are responsible for the consumption of your disk space. You can check the size of all subdirectories in the current

directory with the “du” (**Disk Usage**) command:

```
$ du  
256 ./ex01-matlab/log  
1536 ./ex01-matlab  
768 ./ex04-python  
512 ./ex02-python  
768 ./ex03-python  
5632 .
```

This shows you first the aggregated size of all subdirectories, and finally the total size of the current directory “.” (this includes files stored in the current directory).

If you also want this size to be “human readable” (and not always the total number of kilobytes), you add the parameter “-h”:

```
$ du -h  
256K ./ex01-matlab/log  
1.5M ./ex01-matlab  
768K ./ex04-python  
512K ./ex02-python  
768K ./ex03-python  
5.5M .
```

If the number of lower level subdirectories starts to grow too big, you may not want to see the information at that depth; you could just ask for a summary of the current directory:

```
$ du -s  
5632 .  
$ du -s -h  
5.5M .
```

If you want to see the size of any file or top-level subdirectory in the current directory, you could use the following command:

```
$ du -s -h *  
1.5M ex01-matlab  
512K ex02-python  
768K ex03-python  
768K ex04-python  
256K example.sh  
1.5M intro-HPC.pdf
```

Finally, if you don’t want to know the size of the data in your current directory, but in some other directory (e.g., your data directory), you just pass this directory as a parameter. The command below will show the disk use in your home directory, even if you are currently in a different directory:

```
$ du -h $VSC_HOME/*  
22M /user/home/gent/vsc400/vsc40000/dataset01  
36M /user/home/gent/vsc400/vsc40000/dataset02  
22M /user/home/gent/vsc400/vsc40000/dataset03  
3.5M /user/home/gent/vsc400/vsc40000/primes.txt
```

## 6.6 Groups

Groups are a way to manage who can access what data. A user can belong to multiple groups at a time. **Groups can be created and managed without any interaction from the system administrators.**

Please note that changes are not instantaneous: it may take about an hour for the changes to propagate throughout the entire HPC infrastructure.

To change the group of a directory and its underlying directories and files, you can use:

```
$ chgrp -R groupname directory
```

### 6.6.1 Joining an existing group

1. Get the group name you want to belong to.
2. Go to <https://account.vscentrum.be/django/group/new> and fill in the section named “Join group”. You will be asked to fill in the group name and a message for the moderator of the group, where you identify yourself. This should look something like Figure 6.6.1.
3. After clicking the submit button, a message will be sent to the moderator of the group, who will either approve or deny the request. You will be a member of the group shortly after the group moderator approves your request.

### 6.6.2 Creating a new group

1. Go to <https://account.vscentrum.be/django/group/new> and scroll down to the section “Request new group”. This should look something like Figure 6.6.2.
2. Fill out the group name. This cannot contain spaces.
3. Put a description of your group in the “Info” field.
4. You will now be a member and moderator of your newly created group.

### 6.6.3 Managing a group

Group moderators can go to <https://account.vscentrum.be/django/group/edit> to manage their group (see Figure 6.6.3). Moderators can invite and remove members. They can also promote other members to moderator and remove other moderators.

### 6.6.4 Inspecting groups

You can get details about the current state of groups on the HPC infrastructure with the following command (example is the name of the group we want to inspect):

Figure 6.1: Joining a group.

The screenshot shows the Vlaams Supercomputer Centrum (VSC) website interface. At the top, there is a navigation bar with the VSC logo and the text "Vlaams Supercomputer Centrum". The navigation bar includes links for "View Account", "Edit Account", "View Groups", "New/Join Group" (which is highlighted in blue), "Edit Group", "New/Join VO", and "Log Out". Below the navigation bar, the main content area has a heading "New/Join Group". A warning message in a grey box states: "⚠ Your institute is Gent, which means all the groups from your institute start with 'g'. Groups starting with any other letter are from other institutes. Join them at your own risk." Under the heading, there is a section titled "Join group" with a sub-instruction: "Select a group to join. The groupmoderator will be sent your message (including your full name and VSC ID) and asked to confirm your request." There is a red asterisk next to the word "Group" indicating it is a required field. A dropdown menu for selecting a group is shown, followed by a "Message" input field and a "Submit" button.

New/Join Group

⚠ Your institute is Gent, which means all the groups from your institute start with 'g'. Groups starting with any other letter are from other institutes. Join them at your own risk.

Join group

Select a group to join. The groupmoderator will be sent your message (including your full name and VSC ID) and asked to confirm your request.

**Group \***

**Message \***

**Submit**

Figure 6.2: Creating a new group.

The screenshot shows the VSC web interface. At the top left is the VSC logo with the text "Vlaams Supercomputer Centrum". Below the logo is a navigation bar with the following items: View Account, Edit Account, View Groups, New/Join Group, Edit Group, New/Join VO, and Log Out. The "New/Join Group" item is highlighted with a yellow underline. The main content area has a blue header "New/Join Group". Below the header is a warning message: "⚠ Your institute is Gent, which means all the groups from your institute start with 'g'. Groups starting with any other letter are from other institutes. Join them at your own risk." In the center, there is a large red text "-- scroll down --". Below this, there is a section titled "Create new group" with a red asterisk next to the input field. A warning message in a grey box says "⚠ We will automatically prepend the letter 'g' to your groupname." There is also an "Info" section with a large empty text area.

Figure 6.3: Creating a new group.

The screenshot shows the Vlaams Supercomputer Centrum (VSC) web interface. At the top, there is a logo for 'VSC' with a stylized blue and grey design, followed by the text 'Vlaams Supercomputer Centrum'. Below the logo is a horizontal navigation bar with the following items: 'View Account', 'Edit Account', 'View Groups', 'New/Join Group', 'Edit Group' (which is highlighted with a yellow background and a small edit icon), 'New/Join VO', and 'Log Out'. The main content area has a light grey background. It starts with a section titled 'Edit group' in blue text. Below this is a section titled 'General information' with a blue horizontal bar underneath. Under 'General information', there are several key-value pairs: 'Group: example', 'Vsc\_id: example', 'Vsc\_id\_number: 1234567', and 'Status: active'. The next section is titled 'Manage members' with a blue horizontal bar underneath. Under 'Manage members', there is a section titled 'Members \*' in red text. A note says 'Remove members by clicking the X in front of their names.' Below this is a text input field containing 'x vsc40000 (John Smith)'. There is also a section titled 'Invited users' with a note 'Invite new accounts by clicking in the field below and start typing their vsc id.' A note at the bottom of the page says 'Selected members are already invited.' and 'Remove invites by clicking the X in front of their names.' Below this is a large empty text input field.

```
$ getent group example
example:*:1234567:vsc40001,vsc40002,vsc40003
```

We can see that the VSC id number is 1234567 and that there are three members in the group: vsc40001, vsc40002 and vsc40003.

## 6.7 Virtual Organisations

A Virtual Organisation (VO) is a special type of group. You can only be a member of one single VO at a time (or not be in a VO at all). Being in a VO allows for larger storage quota to be obtained (but these requests should be well-motivated).

### 6.7.1 Joining an existing VO

1. Get the VO id of the research group you belong to (this id is formed by the letters gvo, followed by 5 digits).
2. Go to <https://account.vscentrum.be/django/vo/join> and fill in the section named “Join VO”. You will be asked to fill in the VO id and a message for the moderator of the VO, where you identify yourself. This should look something like [Figure 6.7.1](#).
3. After clicking the submit button, a message will be sent to the moderator of the VO, who will either approve or deny the request.

### 6.7.2 Creating a new VO

1. Go to <https://account.vscentrum.be/django/vo/new> and scroll down to the section “Request new VO”. This should look something like [Figure 6.7.2](#).
2. Fill why you want to request a VO.
3. Fill out the both the internal and public VO name. These cannot contain spaces, and should be 8-10 characters long. For example, genome25 is a valid VO name.
4. Fill out the rest of the form and press submit. This will send a message to the HPC administrators, who will then either approve or deny the request.
5. If the request is approved, you will now be a member and moderator of your newly created VO.

### 6.7.3 Requesting more storage space

If you’re a moderator of a VO, you can request additional quota for the VO and its members.

1. Go to <https://account.vscentrum.be/django/vo/edit> and scroll down to “Request additional quota”. See [Figure 6.7.3](#) to see how this looks.

Figure 6.4: Joining a VO.

The screenshot shows the Vlaams Supercomputer Centrum (VSC) website interface. At the top, there is a navigation bar with links: View Account, Edit Account, View Groups, New/Join Group, Edit Group, **New/Join VO** (which is highlighted with a yellow background), and Log Out. Below the navigation bar, the main content area has a heading "New/Join VO". Under this heading, there is a sub-section titled "Join VO" with a red asterisk next to it. A descriptive text below says: "Select a vo to join. The vo moderator will be sent your message (including your full name and vscid) and asked to confirm your request." There are two input fields: one for "Group \*" and one for "Message \*". Both fields have red asterisks next to them. A yellow "Submit" button is located at the bottom of these fields. Below the "Join VO" section, there is another section titled "Request new VO" with a red asterisk next to it. A question "Why do you want to request a VO" is followed by a large text input field.

Figure 6.5: Creating a new VO.

The screenshot shows the Vlaams Supercomputer Centrum (VSC) web interface. At the top, there is a logo with the letters 'VSC' and a circular graphic, followed by the text 'Vlaams Supercomputer Centrum'. Below the logo is a navigation bar with the following items:

View Account	Edit Account	View Groups	<b>New/Join Group</b>	Edit Group	New/Join VO	View VO	Edit VO	Reservations	Log Out
--------------	--------------	-------------	-----------------------	------------	-------------	---------	---------	--------------	---------

A red arrow points to the 'New/Join Group' button. Below the navigation bar, the text '--- scroll down ---' is displayed in red. The main content area has a light blue header with the text 'Create new group'. A note below it says: '⚠ We will automatically prepend the letter 'g' to your groupname.' The 'Groupname \*' field is empty. There is a large empty text area labeled 'Info' and a yellow 'Submit' button at the bottom left.

2. Fill out how much *additional* storage you want. In the screenshot below, we're asking for 500 GiB extra space for VSC\_DATA, and for 1 TiB extra space on VSC\_SCRATCH\_KYUKON.
3. Add a comment explaining why you need additional storage space and submit the form.
4. An HPC administrator will review your request and approve or deny it.

Figure 6.6: Requesting additional quota for the VO and its members.

**Edit gvo00020**

**General information**

**VO:** gvo00020  
**Institute:** Gent  
**Vsc\_id:** gvo00020  
**Vsc\_id\_number:** 2640143  
**Status:** active

**--- scroll down ---**

**Request additional quota**

**⚠** Every value entered is an increase to your current quota. Note that we might grant less quota than requested. This is looked at on a case by case basis. The quota is bounded by the available storage space so we can not guarantee you will be able to use all of your quota.

Storage Type	Current Quota (%)	Additional Quota (+)	Unit
VSC_DATA	74.85% (2.59TiB/3.46TiB)	+ 500	GiB
VSC_DATA_SHARED	0.0% (0B/2.0GiB)	+ 0	GiB
VSC_SCRATCH_KYUKON	38.93% (3.71TiB/9.52TiB)	+ 1	TiB
VSC_SCRATCH_PHANPY	22.75% (2.17TiB/9.52TiB)	+ 0	GiB

#### 6.7.4 Setting per-member VO quota

VO moderators can tweak how much of the VO quota each member can use. By default, this is set to 50% for each user, but the moderator can change this: it is possible to give a particular user more than half of the VO quota (for example 80%), or significantly less (for example 10%).

Note that the total percentage can be above 100%: the percentages the moderator allocates per user are *the maximum percentages* of storage users can use.

1. Go to <https://account.vscentrum.be/django/vo/edit> and scroll down to “Manage per-member quota share”. See Figure 6.7.4 to see how this looks.
2. Fill out how much percent of the space you want each user to be able to use. Note that the total can be above 100%. In the screenshot below, there are four users. Alice and Bob can use up to 50% of the space, Carl can use up to 75% of the space, and Dave can only use 10% of the space. So in total, 185% of the space has been assigned, but of course only 100% can actually be used.

Figure 6.7: Setting per-member quota.

User	Current Usage	Assigned Quota (%)
vsc40001 (Alice)	0.00% (3.25MiB/4.76TiB)	50
vsc40002 (Bob)	0.00% (0B/4.76TiB)	50
vsc40003 (Carl)	30.33% (2.17TiB/7.14TiB)	75
vsc40004 (Dave)	0.00% (0B/4.76TiB)	10

### 6.7.5 VO directories

When you're a member of a VO, there will be some additional directories on each of the shared filesystems available:

**VO scratch (\$VSC\_SCRATCH\_VO)** A directory on the shared *scratch* filesystem shared by the members of your VO, where additional storage quota can be provided (see [subsection 6.7.3](#)). You can use this as an alternative to your personal \$VSC\_SCRATCH directory (see [subsection 6.2.4](#)).

**VO data (\$VSC\_DATA\_VO)** A directory on the shared *data* filesystem shared by the members of your VO, where additional storage quota can be provided (see [subsection 6.7.3](#)). You can use this as an alternative to your personal \$VSC\_DATA directory (see [subsection 6.2.3](#)).

If you put \_USER after each of these variable names, you can see your personal folder in these filesystems. For example: \$VSC\_DATA\_VO\_USER is your personal folder in your VO data filesystem (this is equivalent to \$VSC\_DATA\_VO/\$USER), and analogous for \$VSC\_SCRATCH\_VO\_USER

# Chapter 7

## Multi core jobs/Parallel Computing

### 7.1 Why Parallel Programming?

There are two important motivations to engage in parallel programming.

1. Firstly, the need to decrease the time to solution: distributing your code over  $C$  cores holds the promise of speeding up execution times by a factor  $C$ . All modern computers (and probably even your smartphone) are equipped with multi-core processors capable of parallel processing.
2. The second reason is problem size: distributing your code over  $N$  nodes increases the available memory by a factor  $N$ , and thus holds the promise of being able to tackle problems which are  $N$  times bigger.

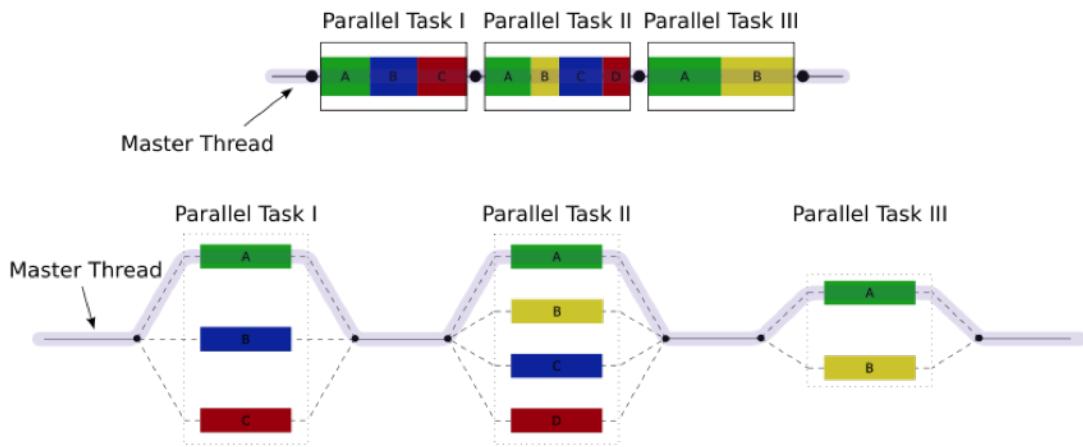
On a desktop computer, this enables a user to run multiple programs and the operating system simultaneously. For scientific computing, this means you have the ability in principle of splitting up your computations into groups and running each group on its own core.

There are multiple different ways to achieve parallel programming. The table below gives a (non-exhaustive) overview of problem independent approaches to parallel programming. In addition there are many problem specific libraries that incorporate parallel capabilities. The next three sections explore some common approaches: (raw) threads, OpenMP and MPI.

Parallel programming approaches		
Tool	Available language bindings	Limitations
Raw threads pthreads, boost:: threading, ...	Threading libraries are available for all common programming languages	Threads are limited to shared memory systems. They are more often used on single node systems rather than for HPC. Thread management is hard.
OpenMP	Fortran/C/C++	Limited to shared memory systems, but large shared memory systems for HPC are not uncommon (e.g., SGI UV). Loops and task can be parallelised by simple insertion of compiler directives. Under the hood threads are used. Hybrid approaches exist which use OpenMP to parallelise the work load on each node and MPI (see below) for communication between nodes.
Lightweight threads with clever scheduling, Intel TBB, Intel Cilk Plus	C/C++	Limited to shared memory systems, but may be combined with MPI. Thread management is taken care of by a very clever scheduler enabling the programmer to focus on parallelisation itself. Hybrid approaches exist which use TBB and/or Cilk Plus to parallelise the work load on each node and MPI (see below) for communication between nodes.
MPI	Fortran/C/C++, Python	Applies to both distributed and shared memory systems. Cooperation between different nodes or cores is managed by explicit calls to library routines handling communication routines.
Global Arrays library	C/C++, Python	Mimics a global address space on distributed memory systems, by distributing arrays over many nodes and one sided communication. This library is used a lot for chemical structure calculation codes and was used in one of the first applications that broke the PetaFlop barrier.
Scoop	Python	Applies to both shared and distributed memory system. Not extremely advanced, but may present a quick road to parallelisation of Python code.

## 7.2 Parallel Computing with threads

Multi-threading is a widespread programming and execution model that allows multiple threads to exist within the context of a single process. These threads share the process' resources, but are able to execute independently. The threaded programming model provides developers with a useful abstraction of concurrent execution. Multi-threading can also be applied to a single process to enable parallel execution on a multiprocessor system.



This advantage of a multithreaded program allows it to operate faster on computer systems that have multiple CPUs or across a cluster of machines — because the threads of the program naturally lend themselves to truly concurrent execution. In such a case, the programmer needs to be careful to avoid race conditions, and other non-intuitive behaviours. In order for data to be correctly manipulated, threads will often need to synchronise in time in order to process the data in the correct order. Threads may also require mutually exclusive operations (often implemented using semaphores) in order to prevent common data from being simultaneously modified, or read while in the process of being modified. Careless use of such primitives can lead to deadlocks.

Threads are a way that a program can spawn concurrent units of processing that can then be delegated by the operating system to multiple processing cores. Clearly the advantage of a multithreaded program (one that uses multiple threads that are assigned to multiple processing cores) is that you can achieve big speedups, as all cores of your CPU (and all CPUs if you have more than one) are used at the same time.

Here is a simple example program that spawns 5 threads, where each one runs a simple function that only prints “Hello from thread”.

Go to the example directory:

```
$ cd ~/examples/Multi-core-jobs-Parallel-Computing
```

Study the example first:

— T\_hello.c —

```

1  /*
2   * VSC      : Flemish Supercomputing Centre
3   * Tutorial : Introduction to HPC
4   * Description: Showcase of working with threads
5   */
6 #include <stdio.h>
7 #include <stdlib.h>
8 #include <pthread.h>
9
10 #define NTHREADS 5
11
12 void *myFun(void **x)
13 {
14     int tid;
15     tid = *(int *) x;
16     printf("Hello from thread %d!\n", tid);
17     return NULL;
18 }
19
20 int main(int argc, char *argv[])
21 {
22     pthread_t threads[NTHREADS];
23     int thread_args[NTHREADS];
24     int rc, i;
25
26     /* spawn the threads */
27     for (i=0; i<NTHREADS; ++i)
28     {
29         thread_args[i] = i;
30         printf("spawning thread %d\n", i);
31         rc = pthread_create(&threads[i], NULL, myFun, (void *) &thread_args[i]);
32     }
33
34     /* wait for threads to finish */
35     for (i=0; i<NTHREADS; ++i) {
36         rc = pthread_join(threads[i], NULL);
37     }
38
39     return 1;
40 }
```

And compile it (whilst including the thread library) and run and test it on the login-node:

```

$ module load GCC
$ gcc -o T_hello T_hello.c -lpthread
$ ./T_hello
spawning thread 0
spawning thread 1
spawning thread 2
Hello from thread 0!
Hello from thread 1!
Hello from thread 2!
spawning thread 3
spawning thread 4
Hello from thread 3!
Hello from thread 4!
```

Now, run it on the cluster and check the output:

```
$ qsub T_hello.pbs
123456
$ more T_hello.pbs.o123456
spawning thread 0
spawning thread 1
spawning thread 2
Hello from thread 0!
Hello from thread 1!
Hello from thread 2!
spawning thread 3
spawning thread 4
Hello from thread 3!
Hello from thread 4!
```

**Tip:** If you plan engaging in parallel programming using threads, this book may prove useful: *Professional Multicore Programming: Design and Implementation for C++ Developers*. Cameron Hughes and Tracey Hughes. Wrox 2008.

## 7.3 Parallel Computing with OpenMP

**OpenMP** is an API that implements a multi-threaded, shared memory form of parallelism. It uses a set of compiler directives (statements that you add to your code and that are recognised by your Fortran/C/C++ compiler if OpenMP is enabled or otherwise ignored) that are incorporated at compile-time to generate a multi-threaded version of your code. You can think of Pthreads (above) as doing multi-threaded programming “by hand”, and OpenMP as a slightly more automated, higher-level API to make your program multithreaded. OpenMP takes care of many of the low-level details that you would normally have to implement yourself, if you were using Pthreads from the ground up.

An important advantage of OpenMP is that, because it uses compiler directives, the original serial version stays intact, and minimal changes (in the form of compiler directives) are necessary to turn a working serial code into a working parallel code.

Here is the general code structure of an OpenMP program:

```
1 #include <omp.h>
2 main () {
3     int var1, var2, var3;
4     // Serial code
5     // Beginning of parallel section. Fork a team of threads.
6     // Specify variable scoping
7
8     #pragma omp parallel private(var1, var2) shared(var3)
9     {
10        // Parallel section executed by all threads
11        // All threads join master thread and disband
12    }
13    // Resume serial code
14 }
```

### 7.3.1 Private versus Shared variables

By using the private() and shared() clauses, you can specify variables within the parallel region as being **shared**, i.e., visible and accessible by all threads simultaneously, or **private**, i.e., private to each thread, meaning each thread will have its own local copy. In the code example below for parallelising a for loop, you can see that we specify the `thread_id` and `nloops` variables as private.

### 7.3.2 Parallelising for loops with OpenMP

Parallelising for loops is really simple (see code below). By default, loop iteration counters in OpenMP loop constructs (in this case the `i` variable) in the for loop are set to private variables.

— omp1.c —

```
1 /*  
2  * VSC      : Flemish Supercomputing Centre  
3  * Tutorial  : Introduction to HPC  
4  * Description: Showcase program for OMP loops  
5  */  
6 /* OpenMP_loop.c */  
7 #include <stdio.h>  
8 #include <omp.h>  
9  
10 int main(int argc, char **argv)  
11 {  
12     int i, thread_id, nloops;  
13  
14 #pragma omp parallel private(thread_id, nloops)  
15 {  
16     nloops = 0;  
17  
18 #pragma omp for  
19     for (i=0; i<1000; ++i)  
20     {  
21         ++nloops;  
22     }  
23     thread_id = omp_get_thread_num();  
24     printf("Thread %d performed %d iterations of the loop.\n", thread_id, nloops );  
25 }  
26  
27 return 0;  
28 }
```

And compile it (whilst including the “openmp” library) and run and test it on the login-node:

```
$ module load GCC
$ gcc -fopenmp -o omp1 omp1.c
$ ./omp1
Thread 6 performed 125 iterations of the loop.
Thread 7 performed 125 iterations of the loop.
Thread 5 performed 125 iterations of the loop.
Thread 4 performed 125 iterations of the loop.
Thread 0 performed 125 iterations of the loop.
Thread 2 performed 125 iterations of the loop.
Thread 3 performed 125 iterations of the loop.
Thread 1 performed 125 iterations of the loop.
```

Now run it in the cluster and check the result again.

```
$ qsub omp1.pbs
$ cat omp1.pbs.o*
Thread 1 performed 125 iterations of the loop.
Thread 4 performed 125 iterations of the loop.
Thread 3 performed 125 iterations of the loop.
Thread 0 performed 125 iterations of the loop.
Thread 5 performed 125 iterations of the loop.
Thread 7 performed 125 iterations of the loop.
Thread 2 performed 125 iterations of the loop.
Thread 6 performed 125 iterations of the loop.
```

### 7.3.3 Critical Code

Using OpenMP you can specify something called a “critical” section of code. This is code that is performed by all threads, but is only performed **one thread at a time** (i.e., in serial). This provides a convenient way of letting you do things like updating a global variable with local results from each thread, and you don’t have to worry about things like other threads writing to that global variable at the same time (a collision).

— omp2.c —

```

1  /*
2   * VSC      : Flemish Supercomputing Centre
3   * Tutorial : Introduction to HPC
4   * Description: OpenMP Test Program
5   */
6 #include <stdio.h>
7 #include <omp.h>
8
9 int main(int argc, char *argv[])
10 {
11     int i, thread_id;
12     int glob_nloops, priv_nloops;
13     glob_nloops = 0;
14
15     // parallelize this chunk of code
16     #pragma omp parallel private(priv_nloops, thread_id)
17     {
18         priv_nloops = 0;
19         thread_id = omp_get_thread_num();
20
21         // parallelize this for loop
22         #pragma omp for
23         for (i=0; i<100000; ++i)
24         {
25             ++priv_nloops;
26         }
27
28         // make this a "critical" code section
29         #pragma omp critical
30         {
31             printf("Thread %d is adding its iterations (%d) to sum (%d), ", thread_id,
32             priv_nloops, glob_nloops);
33             glob_nloops += priv_nloops;
34             printf("total is now %d.\n", glob_nloops);
35         }
36     }
37     printf("Total # loop iterations is %d\n", glob_nloops);
38     return 0;
}

```

And compile it (whilst including the “openmp” library) and run and test it on the login-node:

```

$ module load GCC
$ gcc -fopenmp -o omp2 omp2.c
$ ./omp2
Thread 3 is adding its iterations (12500) to sum (0), total is now 12500.
Thread 7 is adding its iterations (12500) to sum (12500), total is now 25000.
Thread 5 is adding its iterations (12500) to sum (25000), total is now 37500.
Thread 6 is adding its iterations (12500) to sum (37500), total is now 50000.
Thread 2 is adding its iterations (12500) to sum (50000), total is now 62500.
Thread 4 is adding its iterations (12500) to sum (62500), total is now 75000.
Thread 1 is adding its iterations (12500) to sum (75000), total is now 87500.
Thread 0 is adding its iterations (12500) to sum (87500), total is now 100000.
Total # loop iterations is 100000

```

Now run it in the cluster and check the result again.

```
$ qsub omp2.pbs
$ cat omp2.pbs.o*
Thread 2 is adding its iterations (12500) to sum (0), total is now 12500.
Thread 0 is adding its iterations (12500) to sum (12500), total is now 25000.
Thread 1 is adding its iterations (12500) to sum (25000), total is now 37500.
Thread 4 is adding its iterations (12500) to sum (37500), total is now 50000.
Thread 7 is adding its iterations (12500) to sum (50000), total is now 62500.
Thread 3 is adding its iterations (12500) to sum (62500), total is now 75000.
Thread 5 is adding its iterations (12500) to sum (75000), total is now 87500.
Thread 6 is adding its iterations (12500) to sum (87500), total is now 100000.
Total # loop iterations is 100000
```

#### 7.3.4 Reduction

Reduction refers to the process of combining the results of several sub-calculations into a final result. This is a very common paradigm (and indeed the so-called “map-reduce” framework used by Google and others is very popular). Indeed we used this paradigm in the code example above, where we used the “critical code” directive to accomplish this. The map-reduce paradigm is so common that OpenMP has a specific directive that allows you to more easily implement this.

— omp3.c —

```

1  /*
2   * VSC      : Flemish Supercomputing Centre
3   * Tutorial : Introduction to HPC
4   * Description: OpenMP Test Program
5   */
6 #include <stdio.h>
7 #include <omp.h>
8
9 int main(int argc, char *argv[])
10 {
11     int i, thread_id;
12     int glob_nloops, priv_nloops;
13     glob_nloops = 0;
14
15     // parallelize this chunk of code
16 #pragma omp parallel private(priv_nloops, thread_id) reduction(+:glob_nloops)
17 {
18     priv_nloops = 0;
19     thread_id = omp_get_thread_num();
20
21     // parallelize this for loop
22 #pragma omp for
23     for (i=0; i<100000; ++i)
24     {
25         ++priv_nloops;
26     }
27     glob_nloops += priv_nloops;
28 }
29 printf("Total # loop iterations is %d\n", glob_nloops);
30 return 0;
31 }
```

And compile it (whilst including the “*openmp*” library) and run and test it on the login-node:

```

$ module load GCC
$ gcc -fopenmp -o omp3 omp3.c
$ ./omp3
Total # loop iterations is 100000
```

Now run it in the cluster and check the result again.

```

$ qsub omp3.pbs
$ cat omp3.pbs.o*
Total # loop iterations is 100000
```

### 7.3.5 Other OpenMP directives

There are a host of other directives you can issue using OpenMP.

Some other clauses of interest are:

1. barrier: each thread will wait until all threads have reached this point in the code, before

proceeding

2. nowait: threads will not wait until everybody is finished
3. schedule(type, chunk) allows you to specify how tasks are spawned out to threads in a for loop. There are three types of scheduling you can specify
4. if: allows you to parallelise only if a certain condition is met
5. ... and a host of others

**Tip:** If you plan engaging in parallel programming using OpenMP, this book may prove useful: *Using OpenMP - Portable Shared Memory Parallel Programming*. By Barbara Chapman Gabriele Jost and Ruud van der Pas Scientific and Engineering Computation. 2005.

## 7.4 Parallel Computing with MPI

The Message Passing Interface (MPI) is a standard defining core syntax and semantics of library routines that can be used to implement parallel programming in C (and in other languages as well). There are several implementations of MPI such as Open MPI, Intel MPI, M(VA)PICH and LAM/MPI.

In the context of this tutorial, you can think of MPI, in terms of its complexity, scope and control, as sitting in between programming with Pthreads, and using a high-level API such as OpenMP. For a Message Passing Interface (MPI) application, a parallel task usually consists of a single executable running concurrently on multiple processors, with communication between the processes. This is shown in the following diagram:



The process numbers 0, 1 and 2 represent the process rank and have greater or less significance depending on the processing paradigm. At the minimum, Process 0 handles the input/output and determines what other processes are running.

The MPI interface allows you to manage allocation, communication, and synchronisation of a set of processes that are mapped onto multiple nodes, where each node can be a core within a single CPU, or CPUs within a single machine, or even across multiple machines (as long as they are networked together).

One context where MPI shines in particular is the ability to easily take advantage not just of multiple cores on a single machine, but to run programs on clusters of several machines. Even if

you don't have a dedicated cluster, you could still write a program using MPI that could run your program in parallel, across any collection of computers, as long as they are networked together.

Here is a “Hello World” program in MPI written in C. In this example, we send a “Hello” message to each processor, manipulate it trivially, return the results to the main process, and print the messages.

Study the MPI-programme and the PBS-file:

— mpi\_hello.c —

```

1  /*
2   * VSC      : Flemish Supercomputing Centre
3   * Tutorial : Introduction to HPC
4   * Description: "Hello World" MPI Test Program
5   */
6 #include <stdio.h>
7 #include <mpi.h>
8
9 #include <mpi.h>
10 #include <stdio.h>
11 #include <string.h>
12
13 #define BUFSIZE 128
14 #define TAG 0
15
16 int main(int argc, char *argv[])
17 {
18     char idstr[32];
19     char buff[BUFSIZE];
20     int numprocs;
21     int myid;
22     int i;
23     MPI_Status stat;
24     /* MPI programs start with MPI_Init; all 'N' processes exist thereafter */
25     MPI_Init(&argc,&argv);
26     /* find out how big the SPMD world is */
27     MPI_Comm_size(MPI_COMM_WORLD,&numprocs);
28     /* and this processes' rank is */
29     MPI_Comm_rank(MPI_COMM_WORLD,&myid);
30
31     /* At this point, all programs are running equivalently, the rank
32      distinguishes the roles of the programs in the SPMD model, with
33      rank 0 often used specially... */
34     if(myid == 0)
35     {
36         printf("%d: We have %d processors\n", myid, numprocs);
37         for(i=1;i<numprocs;i++)
38         {
39             sprintf(buff, "Hello %d! ", i);
40             MPI_Send(buff, BUFSIZE, MPI_CHAR, i, TAG, MPI_COMM_WORLD);
41         }
42         for(i=1;i<numprocs;i++)
43         {
44             MPI_Recv(buff, BUFSIZE, MPI_CHAR, i, TAG, MPI_COMM_WORLD, &stat);
45             printf("%d: %s\n", myid, buff);
46         }
47     }
48     else
49     {
50         /* receive from rank 0: */
51         MPI_Recv(buff, BUFSIZE, MPI_CHAR, 0, TAG, MPI_COMM_WORLD, &stat);
52         sprintf(idstr, "Processor %d ", myid);
53         strncat(buff, idstr, BUFSIZE-1);
54         strncat(buff, "reporting for duty", BUFSIZE-1);
55         /* send to rank 0: */
56         MPI_Send(buff, BUFSIZE, MPI_CHAR, 0, TAG, MPI_COMM_WORLD);
57     }
58
59     /* MPI programs end with MPI_Finalize; this is a weak synchronization point */
60     MPI_Finalize();
61     return 0;
62 }
```

— mpi\_hello.pbs —

```

1 #!/bin/bash
2
3 #PBS -N mpihello
4 #PBS -l walltime=00:05:00
5
6     # assume a 40 core job
7 #PBS -l nodes=2:ppn=20
8
9     # make sure we are in the right directory in case writing files
10 cd $PBS_O_WORKDIR
11
12     # load the environment
13
14 module load intel
15
16 mpirun ./mpi_hello

```

and compile it:

```

$ module load intel
$ mpiicc -o mpi_hello mpi_hello.c

```

mpiicc is a wrapper of the Intel C++ compiler icc to compile MPI programs (see the chapter on compilation for details).

Run the parallel program:

```

$ qsub mpi_hello.pbs
$ ls -l
total 1024
-rwxrwxr-x 1 vsc40000 8746 Sep 16 14:19 mpi_hello*
-rw-r--r-- 1 vsc40000 1626 Sep 16 14:18 mpi_hello.c
-rw----- 1 vsc40000      0 Sep 16 14:22 mpi_hello.o123456
-rw----- 1 vsc40000   697 Sep 16 14:22 mpi_hello.o123456
-rw-r--r-- 1 vsc40000   304 Sep 16 14:22 mpi_hello.pbs
$ cat mpi_hello.o123456
0: We have 16 processors
0: Hello 1! Processor 1 reporting for duty
0: Hello 2! Processor 2 reporting for duty
0: Hello 3! Processor 3 reporting for duty
0: Hello 4! Processor 4 reporting for duty
0: Hello 5! Processor 5 reporting for duty
0: Hello 6! Processor 6 reporting for duty
0: Hello 7! Processor 7 reporting for duty
0: Hello 8! Processor 8 reporting for duty
0: Hello 9! Processor 9 reporting for duty
0: Hello 10! Processor 10 reporting for duty
0: Hello 11! Processor 11 reporting for duty
0: Hello 12! Processor 12 reporting for duty
0: Hello 13! Processor 13 reporting for duty
0: Hello 14! Processor 14 reporting for duty
0: Hello 15! Processor 15 reporting for duty

```

The runtime environment for the MPI implementation used (often called mpirun or mpiexec)

spawns multiple copies of the program, with the total number of copies determining the number of process *ranks* in MPI\_COMM\_WORLD, which is an opaque descriptor for communication between the set of processes. A single process, multiple data (SPMD = Single Program, Multiple Data) programming model is thereby facilitated, but not required; many MPI implementations allow multiple, different, executables to be started in the same MPI job. Each process has its own rank, the total number of processes in the world, and the ability to communicate between them either with point-to-point (send/receive) communication, or by collective communication among the group. It is enough for MPI to provide an SPMD-style program with MPI\_COMM\_WORLD, its own rank, and the size of the world to allow algorithms to decide what to do. In more realistic situations, I/O is more carefully managed than in this example. MPI does not guarantee how POSIX I/O would actually work on a given system, but it commonly does work, at least from rank 0.

MPI uses the notion of process rather than processor. Program copies are *mapped* to processors by the MPI runtime. In that sense, the parallel machine can map to 1 physical processor, or N where N is the total number of processors available, or something in between. For maximum parallel speedup, more physical processors are used. This example adjusts its behaviour to the size of the world N, so it also seeks to scale to the runtime configuration without compilation for each size variation, although runtime decisions might vary depending on that absolute amount of concurrency available.

**Tip:** mpirun does not always do the optimal core pinning and requires a few extra arguments to be the most efficient possible on a given system. At Ghent we have a wrapper around mpirun called mympirun. See [chapter 24](#) for more information.

You will generally just start an MPI program on the UGent-HPC by using mympirun instead of mpirun -n <nr of cores> <--other settings> <--other optimisations>

**Tip:** If you plan engaging in parallel programming using MPI, this book may prove useful: *Parallel Programming with MPI*. Peter Pacheo. Morgan Kaufmann. 1996.

## Chapter 8

# Using the HPC-UGent web portal

The HPC-UGent web portal provides “one stop shop” for the HPC-UGent infrastructure. It is based on [Open OnDemand](#) (or OoD for short).

Via this web portal you can upload and download files, create, edit, submit, and monitor jobs, run GUI applications, and connect via SSH, all via a standard web browser like Firefox, Chrome or Safari. You do not need to install or configure any client software, and no SSH key is required to connect to your VSC account via this web portal.

To connect to the HPC-UGent infrastructure via the web portal, visit:

<https://login.hpc.ugent.be>

Note that you may only see a “*Submitting...*” message appear for a couple of seconds, which is perfectly normal.

Through this web portal, you can:

- browse through the files & directories in your VSC account, and inspect, manage or change them;
- consult active jobs (across all HPC-UGent Tier-2 clusters);
- submit new jobs to the HPC-UGent Tier-2 clusters, either from existing job scripts or from job templates;
- start an interactive graphical user interface (a desktop environment), either on the login nodes or on a cluster workernode;
- open a terminal session directly in your web browser;

More detailed information is available below, as well as in the [Open OnDemand documentation](#). A walkthrough video is available on YouTube [here](#).

## Pilot access

The HPC-UGent web portal is currently available for all VSC accounts, but there may be a couple of small problems that we still need to be resolved.

If you notice anything that doesn't work as expected or could be improved, please contact [hpc@ugent.be](mailto:hpc@ugent.be).

In addition, during the pilot phase you *must* be connected to the HPC-UGent network (via [VPN](#) if necessary) in order to use the HPC-UGent web portal.

### 8.0.1 Known issues & limitations

**Limited resources** All web portal sessions are currently served through a single separate login node, so the available resources are relatively limited. We will monitor the resources used by the active web portal sessions throughout the pilot phase to evaluate whether more resources are required.

## 8.1 Login

When visiting the HPC-UGent web portal you will be automatically logged in via the VSC accountpage (see also Section [2.2](#)).

### 8.1.1 First login

The first time you visit <https://login.hpc.ugent.be> permission will be requested to let the web portal access some of your personal information (VSC login ID, account status, login shell and institute name), as shown in this screenshot below:

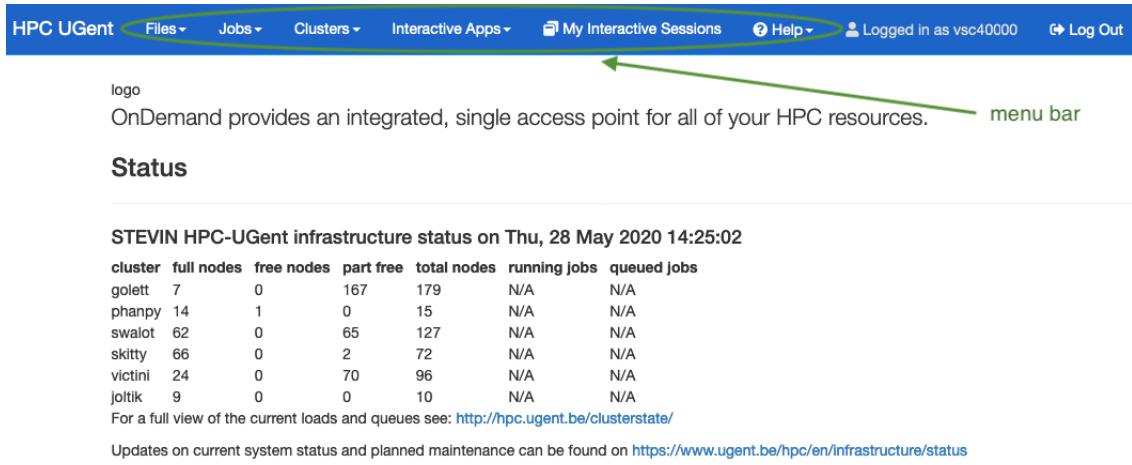


Please click "Authorize" here.

This request will only be made once, you should not see this again afterwards.

## 8.2 Start page

Once logged in, you should see this start page:



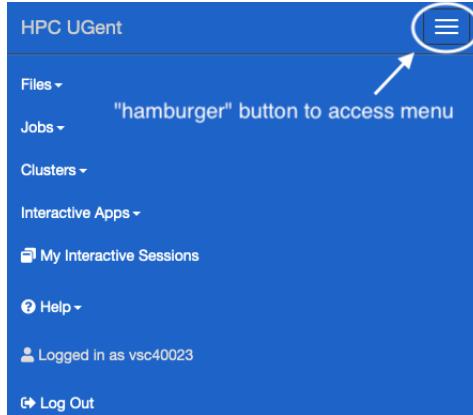
The screenshot shows the HPC-UGent web portal interface. At the top, there is a blue header bar with the "HPC UGent" logo on the left. To the right of the logo is a "File" menu with a green oval around it. Next are "Jobs", "Clusters", "Interactive Apps", and "My Interactive Sessions" menus. A "Help" menu and a user account section ("Logged in as vsc40000" and "Log Out") are on the far right. Below the header, a banner states "OnDemand provides an integrated, single access point for all of your HPC resources." A green arrow points from the "menu bar" label to the top row of buttons. The main content area is titled "Status" and displays the "STEVIN HPC-UGent infrastructure status" for Thursday, May 28, 2020, at 14:25:02. It includes a table of cluster statistics and links to cluster state and system status pages.

cluster	full nodes	free nodes	part free	total nodes	running jobs	queued jobs
golett	7	0	167	179	N/A	N/A
phanpy	14	1	0	15	N/A	N/A
swalot	62	0	65	127	N/A	N/A
skitty	66	0	2	72	N/A	N/A
victini	24	0	70	96	N/A	N/A
joltik	9	0	0	10	N/A	N/A

For a full view of the current loads and queues see: <http://hpc.ugent.be/clusterstate/>  
Updates on current system status and planned maintenance can be found on <https://www.ugent.be/hpc/en/infrastructure/status>

This page includes a menu bar at the top, with buttons on the left providing access to the different features supported by the web portal, as well as a *Help* menu, your VSC account name, and a *Log Out* button on the top right, and the familiar HPC-UGent welcome message with a high-level overview of the HPC-UGent Tier-2 clusters.

If your browser window is too narrow, the menu is available at the top right through the “hamburger” icon:



## 8.3 Features

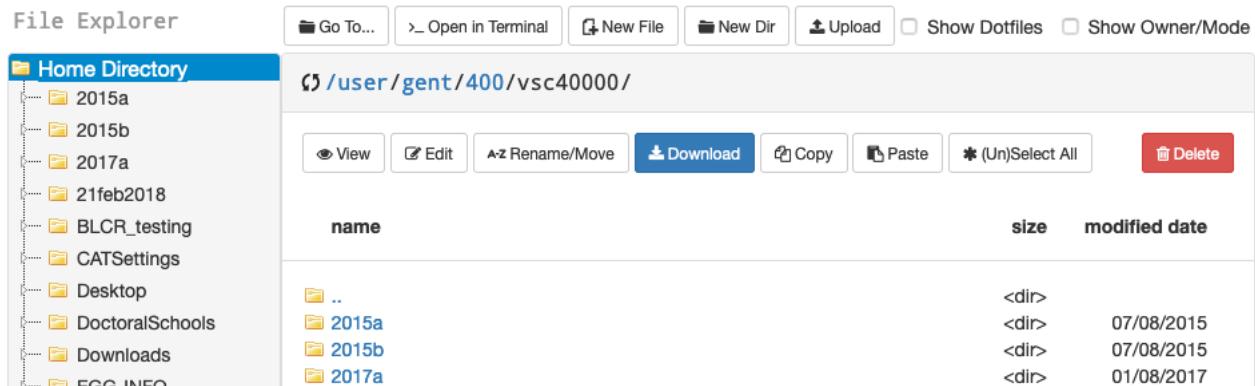
We briefly cover the different features provided by the web portal, going from left to right in the menu bar at the top.

### 8.3.1 File browser

Via the *Files* drop-down menu at the top left, you can browse through the files and directories in your VSC account using an intuitive interface that is similar to a local file browser, and manage, inspect or change them.

The drop-down menu provides short-cuts to the different \$VSC\_\* directories and filesystems

you have access to. Selecting one of the directories will open a new browser tab with the *File Explorer*:



Here you can:

- Click a directory in the tree view on the left to open it;
- Use the buttons on the top to:
  - go to a specific subdirectory by typing in the path (via *Go To...*);
  - open the current directory in a terminal (shell) session (via *Open in Terminal*);
  - create a new file (via *New File*) or subdirectory (via *New Dir*) in the current directory;
  - upload files or directories from your local workstation into your VSC account, in the correct directory (via *Upload*);
  - show hidden files and directories, of which the name starts with a dot (.) (via *Show Dotfiles*);
  - show the owner and permissions in the file listing (via *Show Owner/Mode*);
- Double-click a directory in the file listing to open that directory;
- Select one or more files and/or directories in the file listing, and:
  - use the *View* button to see the contents (use the button at the top right to close the resulting popup window);
  - use the *Edit* button to open a simple file editor in a new browser tab which you can use to make changes to the selected file and save them;
  - use the *Rename/Move* button to rename or move the selected files and/or directories to a different location in your VSC account;
  - use the *Download* button to download the selected files and directories from your VSC account to your local workstation;
  - use the *Copy* button to copy the selected files and/or directories, and then use the *Paste* button to paste them in a different location;
  - use the *(Un)Select All* button to select (or unselect) all files and directories in the current directory;

- use the *Delete* button to (**permanently!**) remove the selected files and directories;

For more information, see also [https://www.osc.edu/resources/online\\_portals/ondemand/file\\_transfer\\_and\\_management](https://www.osc.edu/resources/online_portals/ondemand/file_transfer_and_management).

### 8.3.2 Job management

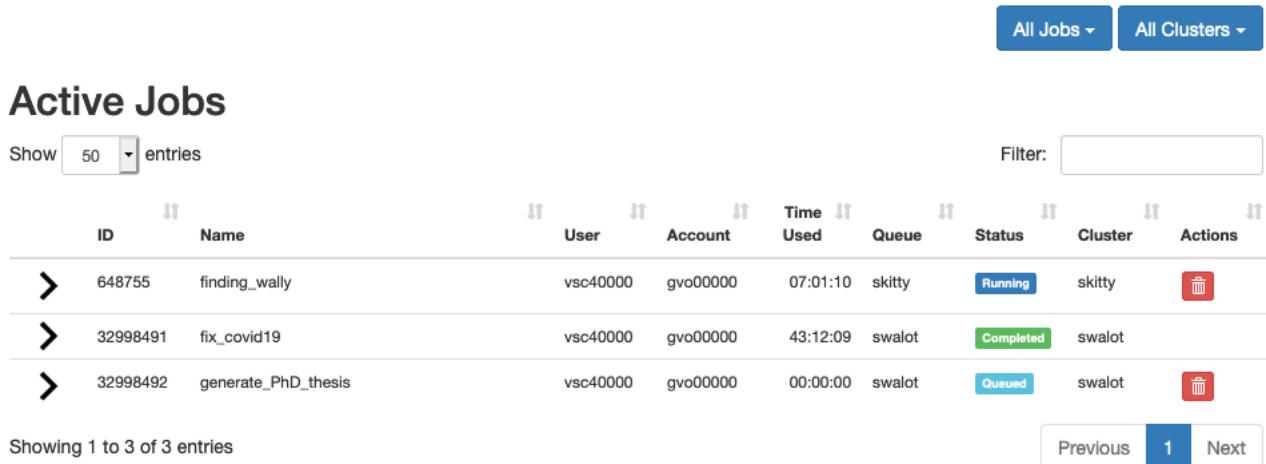
Via the *Jobs* menu item, you can consult your active jobs or submit new jobs using the *Job Composer*.

For more information, see the sections below as well as [https://www.osc.edu/resources/online\\_portals/ondemand/job\\_management](https://www.osc.edu/resources/online_portals/ondemand/job_management).

#### Active jobs

To get an overview of all your currently active jobs, use the *Active Jobs* menu item under *Jobs*.

A new browser tab will be opened that shows all your current queued and/or running jobs:



The screenshot shows a table titled "Active Jobs" with the following data:

ID	Name	User	Account	Time Used	Queue	Status	Cluster	Actions
> 648755	finding_wally	vsc40000	gvo00000	07:01:10	skitty	Running	skitty	
> 32998491	fix_covid19	vsc40000	gvo00000	43:12:09	swalot	Completed	swalot	
> 32998492	generate_PhD_thesis	vsc40000	gvo00000	00:00:00	swalot	Queued	swalot	

Showing 1 to 3 of 3 entries

All Jobs ▾ All Clusters ▾

Filter:

Previous 1 Next

You can control which jobs are shown using the *Filter* input area, or select a particular cluster from the drop-down menu *All Clusters*, both at the top right.

Jobs that are still queued or running can be deleted using the red button on the right.

Completed jobs will also be visible in this interface, but only for a short amount of time after they have stopped running.

For each listed job, you can click on the arrow (>) symbol to get a detailed overview of that job, and get quick access to the corresponding output directory (via the *Open in File Manager* and *Open in Terminal* buttons at the bottom of the detailed overview).

## Job composer

To submit new jobs, you can use the *Job Composer* menu item under *Jobs*. This will open a new browser tab providing an interface to create new jobs:

The screenshot shows a 'Jobs' interface with a 'Job Details' panel on the right and a list of existing jobs on the left.

**Job Details Panel:**

- Job Name:** Simple Multinode MPI Job
- Submit to:** skitty
- Account:** Not specified
- Script location:** /user/gent/400/vsc40023/ondemand/data/sys/myjobs/projects/def
- Script name:** job\_script.sh

**List of Existing Jobs:**

Created	Name	ID	Cluster	Status
May 26, 2020 4:34pm	Simple Multinode MPI Job	skitty		Not Submitted
May 26, 2020 4:34pm	Simple Single Core Job	skitty		Not Submitted
May 26, 2020 4:33pm	(default) Simple Sequential Job	skitty		Not Submitted
October 1, 2019 3:22pm	(default) Simple Sequential Job	victini		Not Submitted

This extensive interface allows you to create jobs from one of the available templates, or by copying an existing job.

You can carefully prepare your job and the corresponding job script via the *Job Options* button and by editing the job script (see lower right).

Don't forget to actually submit your job to the system via the green *Submit* button!

**Job templates** In addition, you can inspect provided job templates, copy them or even create your own templates via the *Templates* button on the top:

## Templates

To create a new job, select a template to copy, fill out the form to the right, and click "Create New Job".

[View Files](#) [Open Terminal](#)

Show 10 entries Search:

Name	Cluster	Source
Simple Multinode MPI Job	Skitty	System Templates
Simple Single Core Job	Skitty	System Templates

Showing 1 to 2 of 2 entries

Create New "Simple Single Core Job"

A very basic template for a small python job

**Job Name:** Simple Single Core Job

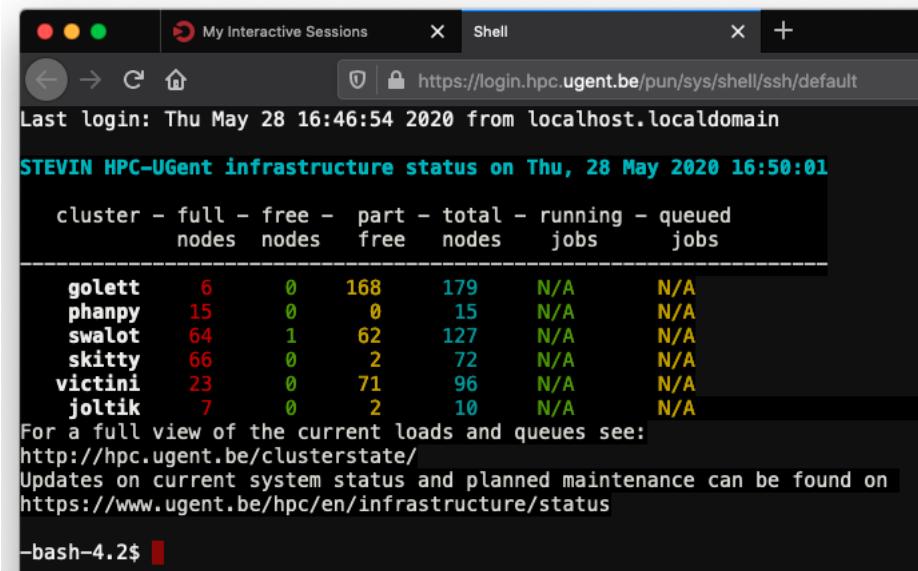
**Cluster:** skitty

**Script Name:** job\_script.sh

[Create New Job](#) [Reset](#)

### 8.3.3 Shell access

Through the *Shell Access* button that is available under the *Clusters* menu item, you can easily open a terminal (shell) session into your VSC account, straight from your browser!



Using this interface requires being familiar with a Linux shell environment (see Appendix C).

To exit the shell session, type `exit` followed by *Enter* and then close the browser tab.

Note that you can not access a shell session after you closed a browser tab, even if you didn't exit the shell session first (unless you use terminal multiplexer tool like `screen` or `tmux`).

### 8.3.4 Interactive applications

#### Graphical desktop environment

To create a graphical desktop environment, use one of the *desktop on ... node* buttons under *Interactive Apps* menu item. For example:

The screenshot shows the 'Interactive Apps' section of a web interface. On the left, a sidebar lists 'Desktops' with several options like 'desktop on golett node', 'desktop on joltik node', etc., and 'desktop on victimi node' which is highlighted with a blue background. Below this are 'Servers' and 'Jupyter Notebook'. The main area is titled 'desktop on victimi node' and contains the following information:

- Description:** This app will launch an interactive desktop on one or more compute nodes. You will have full access to the resources these nodes provide. This is analogous to an interactive batch job.
- Number of hours:** A text input field containing '1'.
- Number of nodes:** A text input field containing '1'.
- Number of cores:** A text input field containing '1'.
- Email Notification:** A checkbox labeled 'I would like to receive an email when the session starts'.
- Launch Button:** A large blue button labeled 'Launch'.

A small note at the bottom states: \* The desktop on victimi node session data for this session can be accessed under the [data root directory](#).

You can either start a desktop environment on a login node for some lightweight tasks, or on a workernode of one of the HPC-UGent Tier-2 clusters if more resources are required. Keep in mind that for desktop sessions on a workernode the regular queueing times are applicable dependent on requested resources.

**Do keep in mind that desktop environments on a cluster workernode are limited to a maximum of 72 hours, just like regular jobs are.**

To access the desktop environment, click the *My Interactive Sessions* menu item at the top, and then use the *Launch desktop on ... node* button if the desktop session is *Running*:

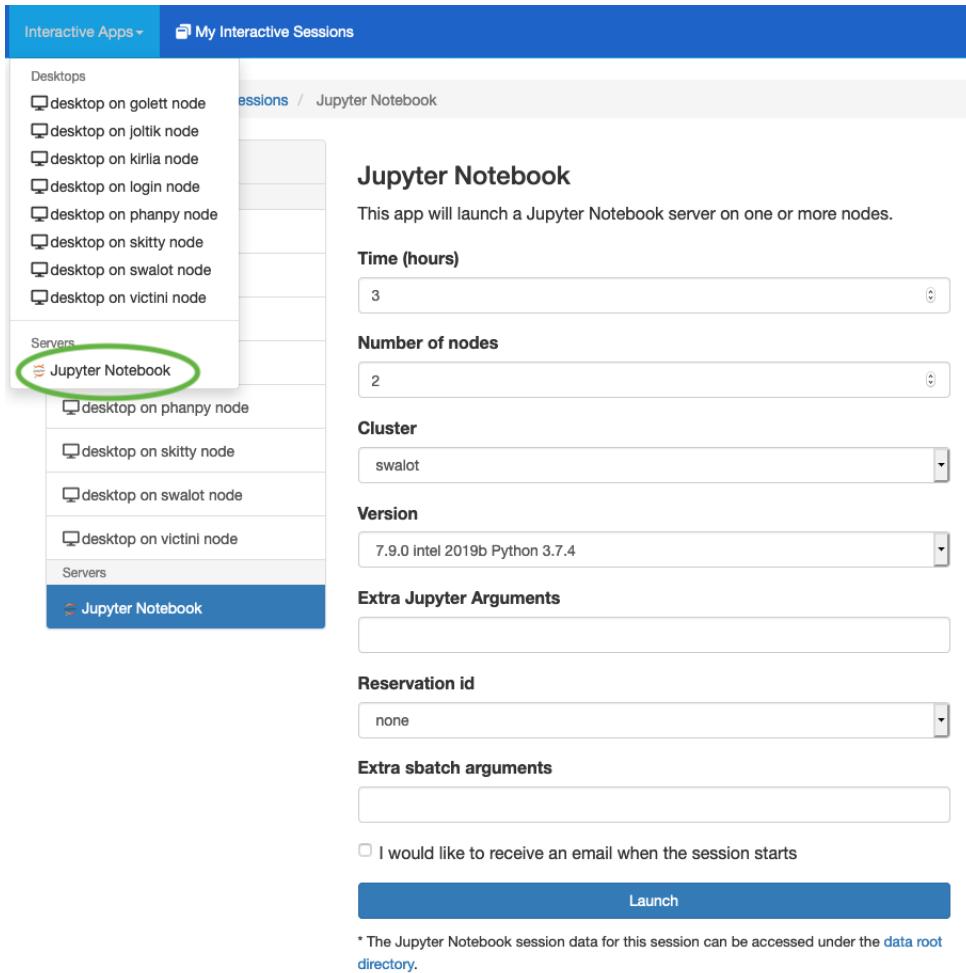
The screenshot shows a running desktop session named 'desktop on victimi node (9525105)'. The session details are as follows:

- Host:** >\_node3209.victini.os
- Created at:** 2020-05-28 16:52:59 CEST
- Time Remaining:** 59 minutes
- Session ID:** 10a86acc-9b81-4f4f-bc6f-89910ffd2489
- Resource Allocation:** 1 node | 1 core | Running

Below these details are two sliders for 'Compression' and 'Image Quality', both set to the middle position. At the bottom are two buttons: 'Launch desktop on victimi node' and 'View Only (Share-able Link)'.

## Jupyter notebook

Through the web portal you can easily start a [Jupyter notebook](#) on a workernode, via the *Jupyter Notebook* button under the *Interactive Apps* menu item.

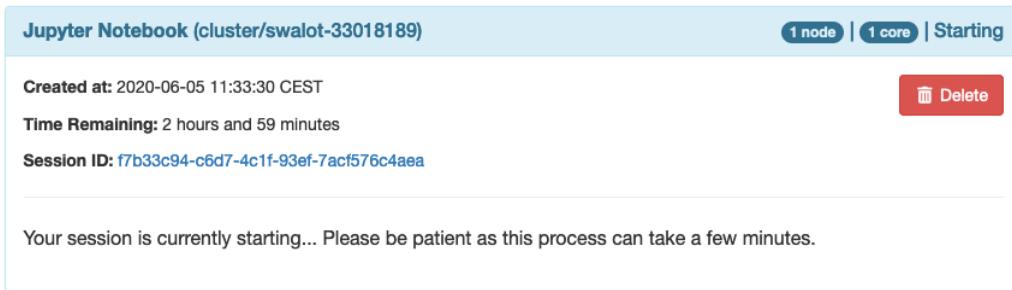


The screenshot shows the 'Interactive Apps' interface. On the left, there's a sidebar with sections for 'Desktops' (listing nodes like golett, joltik, kirila, login, phanpy, skitty, swalot, and victimi) and 'Servers' (listing nodes like phanpy, skitty, swalot, and victimi). The 'Jupyter Notebook' button is located under the 'Servers' section and is circled in green. The main panel shows the 'My Interactive Sessions' dashboard with a breadcrumb trail: 'sessions / Jupyter Notebook'. Below the breadcrumb, the title 'Jupyter Notebook' is displayed, followed by the subtext 'This app will launch a Jupyter Notebook server on one or more nodes.' Configuration fields include 'Time (hours)' set to 3, 'Number of nodes' set to 2, 'Cluster' set to swalot, 'Version' set to 7.9.0 intel 2019b Python 3.7.4, and 'Extra Jupyter Arguments' and 'Extra sbatch arguments' input fields. A checkbox for receiving an email when the session starts is present, and a large blue 'Launch' button is at the bottom.

After starting the Jupyter notebook using the *Launch* button, you will see it being added in state *Queued* in the overview of interactive sessions (see *My Interactive Sessions* menu item):

Jupyter Notebook (cluster/swalot-33018189)		Queued
<b>Created at:</b> 2020-06-05 11:33:30 CEST		
<b>Time Requested:</b> 3 hours		
<b>Session ID:</b> <a href="#">f7b33c94-c6d7-4c1f-93ef-7acf576c4aea</a>		
Please be patient as your job currently sits in queue. The wait time depends on the number of cores as well as time requested.		

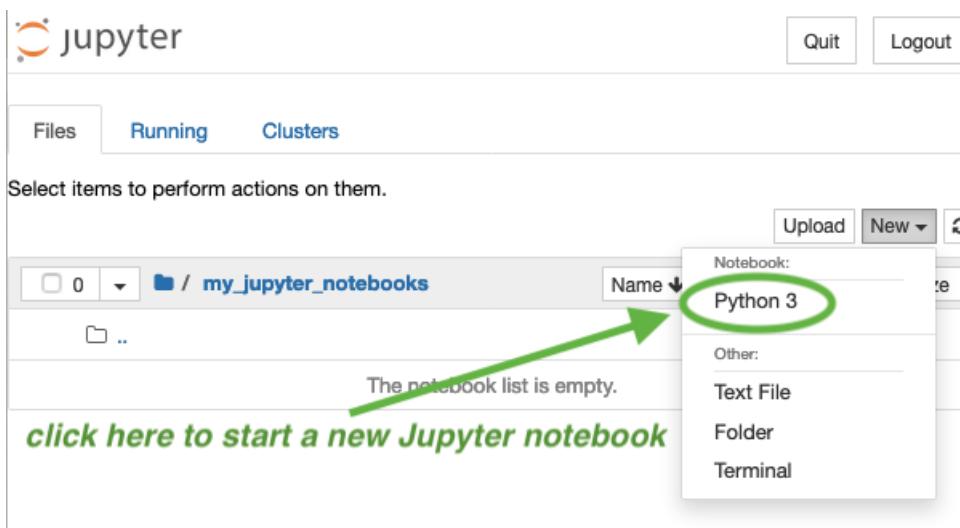
When your job hosting the Jupyter notebook starts running, the status will first change the *Starting*:



and eventually the status will change to *Running*, and you will be able to connect to the Jupyter environment using the blue *Connect to Jupyter* button:



This will launch the Jupyter environment in a new browser tab, where you can open an existing notebook by navigating to the directory where it located and clicking it, or using the *New* menu on the top right:



Here's an example of a Jupyter notebook in action. Note that several non-standard Python packages (like *numpy*, *scipy*, *pandas*, *matplotlib*) are readily available:

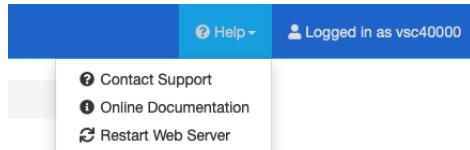
The screenshot shows a Jupyter Notebook interface. At the top, there's a toolbar with a Python logo, a 'Logout' button, and various icons for file operations like save, new, and run. Below the toolbar, the menu bar includes 'Menu', 'Trusted', and 'Python 3'. The main area contains three code cells:

- In [1]:** `import numpy, scipy, matplotlib, pandas`
- In [2]:** `myarray = numpy.array([[1, 2, 3], [4, 5, 6]])  
myarray.shape`
- Out[2]:** `(2, 3)`
- In [3]:** `from scipy.constants import pi`
- Out[3]:** `3.141592653589793`

## 8.4 Restarting your web server in case of problems

In case of problems with the web portal, it could help to restart the web server running in your VSC account.

You can do this via the *Restart Web Server* button under the *Help* menu item:



Of course, this only affects your own web portal session (not those of others).

# Chapter 9

## Troubleshooting

### 9.1 Walltime issues

If you get from your job output an error message similar to this:

```
=>> PBS: job killed: walltime <value in seconds> exceeded limit <value in seconds>
```

This occurs when your job did not complete within the requested walltime. See section [12.1](#) for more information about how to request the walltime. It is recommended to use *checkpointing* if the job requires **72 hours** of walltime or more to be executed.

### 9.2 Out of quota issues

Sometimes a job hangs at some point or it stops writing in the disk. These errors are usually related to the quota usage. You may have reached your quota limit at some storage endpoint. You should move (or remove) the data to a different storage endpoint (or request more quota) to be able to write to the disk and then resubmit the jobs. Another option is to request extra quota for your VO to the VO moderator/s. See section [6.2.1](#) and section [6.2.7](#) for more information about quotas and how to use the storage endpoints in an efficient way.

### 9.3 Issues connecting to login node

If you are confused about the SSH public/private key pair concept, maybe the key/lock analogy in [subsection 2.1.1](#) can help.

If you have errors that look like:

```
vsc40000@login.hpc.ugent.be: Permission denied
```

or you are experiencing problems with connecting, here is a list of things to do that should help:

1. Keep in mind that it can take up to an hour for your VSC account to become active after it has been *approved*; until then, logging in to your VSC account will not work.

2. Make sure you are connecting from an IP address that is allowed to access the VSC login nodes, see section [3.1](#) for more information.
3. Your SSH private key may not be in the default location (`$HOME/.ssh/id_rsa`). There are several ways to deal with this (using one of these is sufficient):
  - (a) Use the `ssh -i` (see section [3.2.1](#)) *OR*;
  - (b) Use `ssh-add` (see section [2.1.4](#)) *OR*;
  - (c) Specify the location of the key in `$HOME/.ssh/config`. You will need to replace the VSC login id in the `User` field with your own:

```
Host hpcugent
  Hostname login.hpc.ugent.be
  IdentityFile /path/to/private/key
  User vsc40000
```

Now you can just connect with `ssh hpcugent`.

4. Please double/triple check your VSC login ID. It should look something like `vsc40000`: the letters vsc, followed by exactly 5 digits. Make sure it's the same one as the one on <https://account.vscentrum.be/>.
5. You previously connected to the HPC from another machine, but now have another machine? Please follow the procedure for adding additional keys in section [2.2.2](#). You may need to wait for 15-20 minutes until the SSH public key(s) you added become active.
6. When using an SSH key in a non-default location, make sure you supply the path of the private key (and not the path of the public key) to `ssh`. `id_rsa.pub` is the usual filename of the public key, `id_rsa` is the usual filename of the private key. (See also section [3.2.1](#))
7. If you have multiple private keys on your machine, please make sure you are using the one that corresponds to (one of) the public key(s) you added on <https://account.vscentrum.be/>.
8. Please do not use someone else's private keys. You must never share your private key, they're called *private* for a good reason.

If you've tried all applicable items above and it doesn't solve your problem, please contact `hpc@ugent.be` and include the following information:

Please add `-vvv` as a flag to `ssh` like:

```
$ ssh -vvv vsc40000@login.hpc.ugent.be
```

and include the output of that command in the message.

## 9.4 Security warning about invalid host key

If you get a warning that looks like the one below, it is possible that someone is trying to intercept the connection between you and the system you are connecting to. Another possibility is that the host key of the system you are connecting to has changed.

```
@@@@@@@@@@@@@@@@@@@WARNING: REMOTE HOST IDENTIFICATION HAS CHANGED!@@@@@@
IT IS POSSIBLE THAT SOMEONE IS DOING SOMETHING NASTY!
Someone could be eavesdropping on you right now (man-in-the-middle attack) !
It is also possible that a host key has just been changed.
The fingerprint for the ECDSA key sent by the remote host is
SHA256:1MNKFTf11T9sm6tTWAo4sn7zyEfiWFLKbk/mLT+7S5s.
Please contact your system administrator.
Add correct host key in ~/.ssh/known_hosts to get rid of this message.
Offending ECDSA key in ~/.ssh/known_hosts:21
ECDSA host key for login.hpc.ugent.be has changed and you have requested strict
    checking.
Host key verification failed.
```

You will need to remove the line it's complaining about (in the example, line 21). To do that, open `~/.ssh/config` in an editor, and remove the line. This results in `ssh` “forgetting” the system you are connecting to.

After you've done that, you'll need to connect to the HPC again. See [section 9.6](#) to verify the fingerprints. **It's important to verify the fingerprints. If they don't match, do not connect and contact `hpc@ugent.be` instead.**

## 9.5 DOS/Windows text format

If you get errors like:

```
$ qsub fibo.pbs
qsub:   script is written in DOS/Windows text format
```

It's probably because you transferred the files from a Windows computer. Please go to the section about `dos2unix` in [chapter 5 of the intro to Linux](#) to fix this error.

## 9.6 Warning message when first connecting to new host

```
$ ssh vsc4000@login.hpc.ugent.be
The authenticity of host login.hpc.ugent.be (<IP-adress>) can't be established.
<algorithm> key fingerprint is <hash>
Are you sure you want to continue connecting (yes/no) ?
```

Now you can check the authenticity by checking if the line that is at the place of the underlined

```
RSA key fingerprint is 2f:0c:f7:76:87:57:f7:5d:2d:7b:d1:a1:e1:86:19:f3
RSA key fingerprint is SHA256:k+eqH4D4mTpJTeeskACyouIWf+60sv1JByxODjvEKE
ECDSA key fingerprint is 13:f0:11:d1:94:cb:ca:e5:ca:82:21:62:ab:9f:3f:c2
ECDSA key fingerprint is SHA256:1MNKFTf11T9sm6tTWAo4sn7zyEfiWFLKbk/mLT+7S5s
ED25519 key fingerprint is fa:23:ab:1f:f0:65:f3:0d:d3:33:ce:7a:f8:f4:fc:2a
ED25519 key fingerprint is SHA256:5hnjlJLolblqkKCmRduiWA21DsxJcSlpVoww0GLlagc
```

If it does, type *yes*. If it doesn't, please contact support: `hpc@ugent.be`.

## 9.7 Memory limits

To avoid jobs allocating too much memory, there are memory limits in place by default. It is possible to specify higher memory limits if your jobs require this.

### 9.7.1 How will I know if memory limits are the cause of my problem?

If your program fails with a memory-related issue, there is a good chance it failed because of the memory limits and you should increase the memory limits for your job.

Examples of these error messages are: `malloc failed`, `Out of memory`, `Could not allocate memory` or in Java: `Could not reserve enough space for object heap`. Your program can also run into a `Segmentation fault` (or `segfault`) or crash due to bus errors.

You can check the amount of virtual memory (in Kb) that is available to you via the `ulimit -v` command *in your job script*.

### 9.7.2 How do I specify the amount of memory I need?

See [subsection 4.6.1](#) to set memory and other requirements, see [section 12.2](#) to finetune the amount of memory you request.

## 9.8 Module conflicts

Modules that are loaded together must use the same toolchain version: it is impossible to load two versions of the same module. In the following example, we try to load a module that uses the `intel-2018a` toolchain together with one that uses the `intel-2017a` toolchain:

```
$ module load Python/2.7.14-intel-2018a
$ module load HMMER/3.1b2-intel-2017a
Lmod has detected the following error: A different version of the 'intel' module is
already loaded (see output of 'ml').
You should load another 'HMMER' module for that is compatible with the currently
loaded version of 'intel'.
Use 'ml avail HMMER' to get an overview of the available versions.

If you don't understand the warning or error, contact the helpdesk at hpc@ugent.be
While processing the following module(s):

Module fullname           Module Filename
-----
HMMER/3.1b2-intel-2017a  /apps/gent/C07/haswell-ib/modules/all/HMMER/3.1b2-intel
-2017a.lua
```

This resulted in an error because we tried to load two different versions of the `intel` module.

To fix this, check if there are other versions of the modules you want to load that have the same version of common dependencies. You can list all versions of a module with `module avail`: for `HMMER`, this command is `module avail HMMER`.

Another common error is:

```
$ module load cluster/skitty
Lmod has detected the following error: A different version of the 'cluster' module
is already loaded (see output of 'ml').

If you don't understand the warning or error, contact the helpdesk at hpc@ugent.be
```

This is because there can only be one `cluster` module active at a time. The correct command is `module swap cluster/skitty`. See also [subsection 4.3.2](#).

## 9.9 Running software that is incompatible with host

When running software provided through modules (see [section 4.1](#)), you may run into errors like:

```
$ module swap cluster/golett

The following have been reloaded with a version change:
 1) cluster/victini => cluster/golett

$ module load Python/2.7.14-intel-2018a
$ python

Please verify that both the operating system and the processor support Intel(R)
  MOVBE, F16C, FMA, BMI, LZCNT and AVX2 instructions.
```

or errors like:

```
$ module swap cluster/golett

The following have been reloaded with a version change:
 1) cluster/victini => cluster/golett

$ module load Python/2.7.14-foss-2018a
$ python
Illegal instruction
```

When we swap to a different cluster, the available modules change so they work for that cluster. That means that if the cluster and the login nodes have a different CPU architecture, software loaded using modules might not work.

If you want to test software on the login nodes, make sure the `cluster/victini` module is loaded (with `module swap cluster/victini`, see [subsection 4.3.2](#)), since the login nodes and `victini` have the same CPU architecture.

If modules are already loaded, and then we swap to a different cluster, all our modules will get reloaded. This means that all current modules will be unloaded and then loaded again, so they'll work on the newly loaded cluster. Here's an example of how that would look like:

```
$ module load Python/2.7.14-intel-2018a
$ module swap cluster/swalot

Due to MODULEPATH changes, the following have been reloaded:
  1) GCCcore/6.4.0          5) Tcl/8.6.8-GCCcore-6.4.0          9)
     iccifort/2018.1.163-GCC-6.4.0-2.28    13) impi/2018.1.163-iccifort-2018.1.163-
     GCC-6.4.0-2.28    17) ncurses/6.0-GCCcore-6.4.0
  2) GMP/6.1.2-GCCcore-6.4.0          6) binutils/2.28-GCCcore-6.4.0          10) ifort
     /2018.1.163-GCC-6.4.0-2.28    14) intel/2018a
     18) zlib/1.2.11-GCCcore-6.4.0
  3) Python/2.7.14-intel-2018a          7) bzip2/1.0.6-GCCcore-6.4.0          11) iimpi
     /2018a          15) libffi/3.2.1-GCCcore-6.4.0
  4) SQLite/3.21.0-GCCcore-6.4.0          8) icc/2018.1.163-GCC-6.4.0-2.28    12) imkl
     /2018.1.163-iimpi-2018a    16) libreadline/7.0-GCCcore-6.4.0

The following have been reloaded with a version change:
  1) cluster/victini => cluster/swalot
```

This might result in the same problems as mentioned above. When swapping to a different cluster, you can run `module purge` to unload all modules to avoid problems (see [subsection 4.1.6](#)).

## Chapter 10

# HPC Policies

Stub chapter

# Chapter 11

## Frequently Asked Questions

### 11.1 When will my job start?

See the explanation about how jobs get prioritized in [subsection 4.3.1](#).

### 11.2 Can I share my account with someone else?

**NO.** You are not allowed to share your VSC account with anyone else, it is strictly personal. See <https://helpdesk.ugent.be/account/en/regels.php>. If you want to share data, there are alternatives (like a shared directories in VO space, see [section 6.7](#)).

### 11.3 Can I share my data with other HPC users?

Yes, you can use the chmod or setfacl commands to change permissions of files so other users can access the data. For example, the following command will enable a user named “otheruser” to read the file named dataset.txt. See

```
$ setfacl -m u:otheruser:r dataset.txt
$ ls -l dataset.txt
-rwxr-x---+ 2 vsc40000 mygroup        40 Apr 12 15:00 dataset.txt
```

For more information about chmod or setfacl, see [the section on chmod in chapter 3 of the Linux intro manual](#).

### 11.4 Can I use multiple different SSH key pairs to connect to my VSC account?

Yes, and this is recommended when working from different computers. Please see [subsection 2.2.2](#) on how to do this.

## **11.5 I want to use software that is not available on the clusters yet**

Please fill out the details about the software and why you need it in this form: <https://www.ugent.be/hpc/en/support/software-installation-request>. When submitting the form, a mail will be sent to hpc@ugent.be containing all the provided information. The HPC team will look into your request as soon as possible and contact you when the installation is done or if further information is required.

## Part II

# Advanced Guide

## Chapter 12

# Fine-tuning Job Specifications

As HPC system administrators, we often observe that the HPC resources are not optimally (or wisely) used. For example, we regularly notice that several cores on a computing node are not utilised, due to the fact that one sequential program uses only one core on the node. Or users run I/O intensive applications on nodes with “slow” network connections.

Users often tend to run their jobs without specifying specific PBS Job parameters. As such, their job will automatically use the default parameters, which are not necessarily (or rarely) the optimal ones. This can slow down the run time of your application, but also block HPC resources for other users.

Specifying the “optimal” Job Parameters requires some knowledge of your application (e.g., how many parallel threads does my application uses, is there a lot of inter-process communication, how much memory does my application need) and also some knowledge about the HPC infrastructure (e.g., what kind of multi-core processors are available, which nodes have InfiniBand).

There are plenty of monitoring tools on Linux available to the user, which are useful to analyse your individual application. The HPC environment as a whole often requires different techniques, metrics and time goals, which are not discussed here. We will focus on tools that can help to optimise your Job Specifications.

Determining the optimal computer resource specifications can be broken down into different parts. The first is actually determining which metrics are needed and then collecting that data from the hosts. Some of the most commonly tracked metrics are CPU usage, memory consumption, network bandwidth, and disk I/O stats. These provide different indications of how well a system is performing, and may indicate where there are potential problems or performance bottlenecks. Once the data have actually been acquired, the second task is analysing the data and adapting your PBS Job Specifications.

Another different task is to monitor the behaviour of an application at run time and detect anomalies or unexpected behaviour. Linux provides a large number of utilities to monitor the performance of its components.

This chapter shows you how to measure:

1. Walltime
2. Memory usage

3. CPU usage
4. Disk (storage) needs
5. Network bottlenecks

First, we allocate a compute node and move to our relevant directory:

```
$ qsub -I  
$ cd ~/examples/Fine-tuning-Job-Specifications
```

## 12.1 Specifying Walltime

One of the most important and also easiest parameters to measure is the duration of your program. This information is needed to specify the *walltime*.

The *time* utility **executes** and **times** your application. You can just add the time command in front of your normal command line, including your command line options. After your executable has finished, **time** writes the total time elapsed, the time consumed by system overhead, and the time used to execute your executable to the standard error stream. The calculated times are reported in seconds.

Test the time command:

```
$ time sleep 75  
real 1m15.005s  
user 0m0.001s  
sys 0m0.002s
```

It is a good practice to correctly estimate and specify the run time (duration) of an application. Of course, a margin of 10% to 20% can be taken to be on the safe side.

It is also wise to check the walltime on different compute nodes or to select the “slowest” compute node for your walltime tests. Your estimate should appropriate in case your application will run on the “slowest” (oldest) compute nodes.

The walltime can be specified in a job scripts as:

```
#PBS -l walltime=3:00:00:00
```

or on the command line

```
$ qsub -l walltime=3:00:00:00
```

It is recommended to always specify the walltime for a job.

## 12.2 Specifying memory requirements

In many situations, it is useful to monitor the amount of memory an application is using. You need this information to determine the characteristics of the required compute node, where that

application should run on. Estimating the amount of memory an application will use during execution is often non-trivial, especially when one uses third-party software.

### 12.2.1 Available Memory on the machine

The first point is to be aware of the available free memory in your computer. The “*free*” command displays the total amount of free and used physical and swap memory in the system, as well as the buffers used by the kernel. We also use the options “-m” to see the results expressed in Mega-Bytes and the “-t” option to get totals.

```
$ free -m -t
              total    used    free   shared  buffers   cached
Mem:        16049     4772   11277       0      107     161
-/+ buffers/cache:    4503   11546
Swap:       16002     4185   11816
Total:     32052     8957   23094
```

Important is to note the total amount of memory available in the machine (i.e., 16 GB in this example) and the amount of used and free memory (i.e., 4.7 GB is used and another 11.2 GB is free here).

It is not a good practice to use swap-space for your computational applications. A lot of “swapping” can increase the execution time of your application tremendously.

### 12.2.2 Checking the memory consumption

To monitor the memory consumption of a running application, you can use the “*top*” or the “*htop*” command.

**top** provides an ongoing look at processor activity in real time. It displays a listing of the most CPU-intensive tasks on the system, and can provide an interactive interface for manipulating processes. It can sort the tasks by memory usage, CPU usage and run time.

**htop** is similar to top, but shows the CPU-utilisation for all the CPUs in the machine and allows to scroll the list vertically and horizontally to see all processes and their full command lines.

```
$ top
$ htop
```

### 12.2.3 Setting the memory parameter

Once you gathered a good idea of the overall memory consumption of your application, you can define it in your job script. It is wise to foresee a margin of about 10%.

Sequential or single-node applications:

The maximum amount of physical memory used by the job can be specified in a job script as:

```
#PBS -l mem=4gb
```

or on the command line

```
$ qsub -l mem=4gb
```

This setting is ignored if the number of nodes is not 1.

Parallel or multi-node applications:

When you are running a parallel application over multiple cores, you can also specify the memory requirements per processor (pmem). This directive specifies the maximum amount of physical memory used by any process in the job.

For example, if the job would run four processes and each would use up to 2 GB (gigabytes) of memory, then the memory directive would read:

```
#PBS -l pmem=2gb
```

or on the command line

```
$ qsub -l pmem=2gb
```

(and of course this would need to be combined with a CPU cores directive such as nodes=1:ppn=4). In this example, you request 8 GB of memory in total on the node.

## 12.3 Specifying processors requirements

Users are encouraged to fully utilise all the available cores on a certain compute node. Once the required numbers of cores and nodes are decently specified, it is also good practice to monitor the CPU utilisation on these cores and to make sure that all the assigned nodes are working at full load.

### 12.3.1 Number of processors

The number of core and nodes that a user shall request fully depends on the architecture of the application. Developers design their applications with a strategy for parallelisation in mind. The application can be designed for a certain fixed number or for a configurable number of nodes and cores. It is wise to target a specific set of compute nodes (e.g., Westmere, Harpertown) for your computing work and then to configure your software to nicely fill up all processors on these compute nodes.

The */proc/cpuinfo* stores info about your CPU architecture like number of CPUs, threads, cores, information about CPU caches, CPU family, model and much more. So, if you want to detect how many cores are available on a specific machine:

```
$ less /proc/cpuinfo
processor      : 0
vendor_id     : GenuineIntel
cpu family    : 6
model         : 23
model name    : Intel(R) Xeon(R) CPU E5420 @ 2.50GHz
stepping       : 10
cpu MHz       : 2500.088
cache size    : 6144 KB
...
...
```

Or if you want to see it in a more readable format, execute:

```
$ grep processor /proc/cpuinfo
processor : 0
processor : 1
processor : 2
processor : 3
processor : 4
processor : 5
processor : 6
processor : 7
```

Remark: Unless you want information of the login nodes, you'll have to issue these commands on one of the workernodes. This is most easily achieved in an interactive job, see the chapter on Running interactive jobs.

In order to specify the number of nodes and the number of processors per node in your job script, use:

```
#PBS -l nodes=N:ppn=M
```

or with equivalent parameters on the command line

```
$ qsub -l nodes=N:ppn=M
```

This specifies the number of nodes (nodes=N) and the number of processors per node (ppn=M) that the job should use. PBS treats a processor core as a processor, so a system with eight cores per compute node can have ppn=8 as its maximum ppn request. You can also use this statement in your job script:

```
#PBS -l nodes=N:ppn=all
```

to request all cores of a node, or

```
#PBS -l nodes=N:ppn=half
```

to request half of them.

Note that unless a job has some inherent parallelism of its own through something like MPI or OpenMP, requesting more than a single processor on a single node is usually wasteful and can impact the job start time.

### 12.3.2 Monitoring the CPU-utilisation

This could also be monitored with the *htop* command:

```
$ htop
```

PID	USER	PRI	NI	VIRT	RES	SHR	S	CPU%	MEM%	TIME+	Command
22350	vsc00000	20	0	1729M	1071M	704	R	98.0	1.7	27:15.59	bwa index
7703	root		0	-20	10.1G	1289M	S	11.0	2.0	36h10:11	/usr/lpp/mmfss/bin
27905	vsc00000	20	0	123M	2800	1556	R	7.0	0.0	0:17.51	htop

The advantage of htop is that it shows you the cpu utilisation for all processors as well as the details per application. A nice exercise is to start 4 instances of the “cpu\_eat” program in 4 different terminals, and inspect the cpu utilisation per processor with monitor and htop.

If ***htop*** reports that your program is taking 75% CPU on a certain processor, it means that 75% of the samples taken by top found your process active on the CPU. The rest of the time your application was in a wait. (It is important to remember that a CPU is a discrete state machine. It really can be at only 100%, executing an instruction, or at 0%, waiting for something to do. There is no such thing as using 45% of a CPU. The CPU percentage is a function of time.) However, it is likely that your application's rest periods include waiting to be dispatched on a CPU and not on external devices. That part of the wait percentage is then very relevant to understanding your overall CPU usage pattern.

### 12.3.3 Fine-tuning your executable and/or job script

It is good practice to perform a number of run time stress tests, and to check the CPU utilisation of your nodes. We (and all other users of the HPC) would appreciate that you use the maximum of the CPU resources that are assigned to you and make sure that there are no CPUs in your node who are not utilised without reasons.

But how can you maximise?

1. Configure your software. (e.g., to exactly use the available amount of processors in a node)
  2. Develop your parallel program in a smart way.
  3. Demand a specific type of compute node (e.g., Harpertown, Westmere), which have a specific number of cores.
  4. Correct your request for CPUs in your job script.

## 12.4 The system load

On top of the CPU utilisation, it is also important to check the **system load**. The system **load** is a measure of the amount of computational work that a computer system performs.

The system load is the number of applications running or waiting to run on the compute node. In a system with for example four CPUs, a load average of 3.61 would indicate that there were, on average, 3.61 processes ready to run, and each one could be scheduled into a CPU.

The load averages differ from CPU percentage in two significant ways:

1. “*load averages*” measure the trend of processes waiting to be run (and not only an instantaneous snapshot, as does CPU percentage); and
2. “*load averages*” include all demand for all resources, e.g., CPU and also I/O and network (and not only how much was active at the time of measurement).

### 12.4.1 Optimal load

What is the “*optimal load*” rule of thumb?

The load averages tell us whether our physical CPUs are over- or under-utilised. The **point of perfect utilisation**, meaning that the CPUs are always busy and, yet, no process ever waits for one, is **the average matching the number of CPUs**. Your load should not exceed the number of cores available. E.g., if there are four CPUs on a machine and the reported one-minute load average is 4.00, the machine has been utilising its processors perfectly for the last 60 seconds. The “100% utilisation” mark is 1.0 on a single-core system, 2.0 on a dual-core, 4.0 on a quad-core, etc. The optimal load shall be between 0.7 and 1.0 per processor.

In general, the intuitive idea of load averages is the higher they rise above the number of processors, the more processes are waiting and doing nothing, and the lower they fall below the number of processors, the more untapped CPU capacity there is.

*Load averages* do include any processes or threads waiting on I/O, networking, databases or anything else not demanding the CPU. This means that the optimal *number of applications* running on a system at the same time, might be more than one per processor.

The “**optimal number of applications**” running on one machine at the same time depends on the type of the applications that you are running.

1. When you are running **computational intensive applications**, one application per processor will generate the optimal load.
2. For **I/O intensive applications** (e.g., applications which perform a lot of disk-I/O), a higher number of applications can generate the optimal load. While some applications are reading or writing data on disks, the processors can serve other applications.

The optimal number of applications on a machine could be empirically calculated by performing a number of stress tests, whilst checking the highest throughput. There is however no manner in the HPC at the moment to specify the maximum number of applications that shall run per core dynamically. The HPC scheduler will not launch more than one process per core.

The manner how the cores are spread out over CPUs does not matter for what regards the load. Two quad-cores perform similar to four dual-cores, and again perform similar to eight single-cores. It's all eight cores for these purposes.

### 12.4.2 Monitoring the load

The **load average** represents the average system load over a period of time. It conventionally appears in the form of three numbers, which represent the system load during the last **one-**, **five-**, and **fifteen-**minute periods.

The **uptime** command will show us the average load

```
$ uptime  
10:14:05 up 86 days, 12:01, 11 users, load average: 0.60, 0.41, 0.41
```

Now, start a few instances of the “*eat\_cpu*” program in the background, and check the effect on the load again:

```
$ ./eat_cpu&  
$ ./eat_cpu&  
$ ./eat_cpu&  
$ uptime  
10:14:42 up 86 days, 12:02, 11 users, load average: 2.60, 0.93, 0.58
```

You can also read it in the **htop** command.

### 12.4.3 Fine-tuning your executable and/or job script

It is good practice to perform a number of run time stress tests, and to check the system load of your nodes. We (and all other users of the HPC) would appreciate that you use the maximum of the CPU resources that are assigned to you and make sure that there are no CPUs in your node who are not utilised without reasons.

But how can you maximise?

1. Profile your software to improve its performance.
2. Configure your software (e.g., to exactly use the available amount of processors in a node).
3. Develop your parallel program in a smart way, so that it fully utilises the available processors.
4. Demand a specific type of compute node (e.g., Harpertown, Westmere), which have a specific number of cores.
5. Correct your request for CPUs in your job script.

And then check again.

## 12.5 Checking File sizes & Disk I/O

### 12.5.1 Monitoring File sizes during execution

Some programs generate intermediate or output files, the size of which may also be a useful metric.

Remember that your available disk space on the HPC online storage is limited, and that you have environment variables which point to these directories available (i.e., `$VSC_DATA`, `$VSC_SCRATCH` and `$VSC_SCRATCH`). On top of those, you can also access some temporary storage (i.e., the `/tmp` directory) on the compute node, which is defined by the `$VSC_SCRATCH_NODE` environment variable.

It is important to be aware of the sizes of the file that will be generated, as the available disk space for each user is limited. We refer to [section 6.5](#) on “Quotas” to check your quota and tools to find which files consumed the “quota”.

Several actions can be taken, to avoid storage problems:

1. Be aware of all the files that are generated by your program. Also check out the hidden files.
2. Check your quota consumption regularly.
3. Clean up your files regularly.
4. First work (i.e., read and write) with your big files in the local `/tmp` directory. Once finished, you can move your files once to the `VSC_DATA` directories.
5. Make sure your programs clean up their temporary files after execution.
6. Move your output results to your own computer regularly.
7. Anyone can request more disk space to the HPC staff, but you will have to duly justify your request.

## 12.6 Specifying network requirements

Users can examine their network activities with the `htop` command. When your processors are 100% busy, but you see a lot of red bars and only limited green bars in the `htop` screen, it is mostly an indication that they loose a lot of time with inter-process communication.

Whenever your application utilises a lot of inter-process communication (as is the case in most parallel programs), we strongly recommend to request nodes with an “InfiniBand” network. The InfiniBand is a specialised high bandwidth, low latency network that enables large parallel jobs to run as efficiently as possible.

The parameter to add in your job script would be:

```
#PBS -l ib
```

If for some other reasons, a user is fine with the gigabit Ethernet network, he can specify:

```
#PBS -l gbe
```

# Chapter 13

## Multi-job submission

A frequent occurring characteristic of scientific computation is their focus on data intensive processing. A typical example is the iterative evaluation of a program over different input parameter values, often referred to as a “*parameter sweep*”. A **Parameter Sweep** runs a job a specified number of times, as if we sweep the parameter values through a user defined range.

Users then often want to submit a large numbers of jobs based on the same job script but with (i) slightly different parameters settings or with (ii) different input files.

These parameter values can have many forms, we can think about a range (e.g., from 1 to 100), or the parameters can be stored line by line in a comma-separated file. The users want to run their job once for each instance of the parameter values.

One option could be to launch a lot of separate individual small jobs (one for each parameter) on the cluster, but this is not a good idea. The cluster scheduler isn’t meant to deal with tons of small jobs. Those huge amounts of small jobs will create a lot of overhead, and can slow down the whole cluster. It would be better to bundle those jobs in larger sets. In TORQUE, an experimental feature known as “*job arrays*” existed to allow the creation of multiple jobs with one *qsub* command, but is was not supported by Moab, the current scheduler.

The “**Worker framework**” has been developed to address this issue.

It can handle many small jobs determined by:

**parameter variations** i.e., many small jobs determined by a specific parameter set which is stored in a .csv (comma separated value) input file.

**job arrays** i.e., each individual job got a unique numeric identifier.

Both use cases often have a common root: the user wants to run a program with a large number of parameter settings, and the program does not allow for aggregation, i.e., it has to be run once for each instance of the parameter values.

However, the Worker Framework’s scope is wider: it can be used for any scenario that can be reduced to a **MapReduce** approach.<sup>1</sup>

---

<sup>1</sup>MapReduce: ‘Map’ refers to the map pattern in which every item in a collection is mapped onto a new value by applying a given function, while “reduce” refers to the reduction pattern which condenses or reduces a collection of previously computed results to a single value.

## 13.1 The worker Framework: Parameter Sweeps

First go to the right directory:

```
$ cd ~/examples/Multi-job-submission/par_sweep
```

Suppose the program the user wishes to run the “*weather*” program, which takes three parameters: a temperature, a pressure and a volume. A typical call of the program looks like:

```
$ ./weather -t 20 -p 1.05 -v 4.3
T: 20  P: 1.05  V: 4.3
```

For the purpose of this exercise, the weather program is just a simple bash script, which prints the 3 variables to the standard output and waits a bit:

weather— par\_sweep/weather —

```
1 #!/bin/bash
2 # Here you could do your calculations
3 echo "T: $2  P: $4  V: $6"
4 sleep 100
```

A job script that would run this as a job for the first parameters (p01) would then look like:

weather\_p01.pbs— par\_sweep/weather\_p01.pbs —

```
1 #!/bin/bash
2
3 #PBS -l nodes=1:ppn=8
4 #PBS -l walltime=01:00:00
5
6 cd $PBS_O_WORKDIR
7 ./weather -t 20 -p 1.05 -v 4.3
```

When submitting this job, the calculation is performed for this particular instance of the parameters, i.e., temperature = 20, pressure = 1.05, and volume = 4.3.

To submit the job, the user would use:

```
$ qsub weather_p01.pbs
```

However, the user wants to run this program for many parameter instances, e.g., he wants to run the program on 100 instances of temperature, pressure and volume. The 100 parameter instances can be stored in a comma separated value file (.csv) that can be generated using a spreadsheet program such as Microsoft Excel or RDBMS or just by hand using any text editor (do **not** use a word processor such as Microsoft Word). The first few lines of the file “*data.csv*” would look like:

```
$ more data.csv
temperature, pressure, volume
293, 1.0e5, 107
294, 1.0e5, 106
295, 1.0e5, 105
296, 1.0e5, 104
297, 1.0e5, 103
...
```

It has to contain the names of the variables on the first line, followed by 100 parameter instances in the current example.

In order to make our PBS generic, the PBS file can be modified as follows:

```
weather.pbs- par_sweep/weather.pbs —
```

```
1 #!/bin/bash
2
3 #PBS -l nodes=1:ppn=8
4 #PBS -l walltime=04:00:00
5
6 cd $PBS_O_WORKDIR
7 ./weather -t $temperature -p $pressure -v $volume
8
9 # # This script is submitted to the cluster with the following 2 commands:
10 # module load worker/1.6.8-intel-2018a
11 # wsub -data data.csv -batch weather.pbs
```

Note that:

1. the parameter values 20, 1.05, 4.3 have been replaced by variables \$temperature, \$pressure and \$volume respectively, which were being specified on the first line of the “*data.csv*” file;
2. the number of processors per node has been increased to 8 (i.e., ppn=1 is replaced by ppn=8);
3. the walltime has been increased to 4 hours (i.e., walltime=00:15:00 is replaced by walltime=04:00:00).

The walltime is calculated as follows: one calculation takes 15 minutes, so 100 calculations take 1500 minutes on one CPU. However, this job will use 8 CPUs, so the 100 calculations will be done in  $1500/8 = 187.5$  minutes, i.e., 4 hours to be on the safe side.

The job can now be submitted as follows (to check which worker module to use, see [subsection 4.1.7](#)):

```
$ module load worker/1.6.8-intel-2018a
$ wsub -batch weather.pbs -data data.csv
total number of work items: 41
123456
```

Note that the PBS file is the value of the -batch option. The weather program will now be run for all 100 parameter instances – 8 concurrently – until all computations are done. A computation for such a parameter instance is called a work item in Worker parlance.

## 13.2 The Worker framework: Job arrays

First go to the right directory:

```
$ cd ~/examples/Multi-job-submission/job_array
```

As a simple example, assume you have a serial program called *myprog* that you want to run on various input files *input[1-100]*.



The following bash script would submit these jobs all one by one:

```

1 #!/bin/bash
2 for i in `seq 1 100`; do
3     qsub -o output $i -i input $i myprog.pbs
4 done

```

This, as said before, could be disturbing for the job scheduler.

Alternatively, TORQUE provides a feature known as *job arrays* which allows the creation of multiple, similar jobs with only **one** **qsub** command. This feature introduced a new job naming convention that allows users either to reference the entire set of jobs as a unit or to reference one particular job from the set.

Under TORQUE, the *-t range* option is used with **qsub** to specify a job array, where *range* is a range of numbers (e.g., *1-100* or *2,4-5,7*).

The details are

1. a job is submitted for each *number* in the range;
2. individuals jobs are referenced as *jobid-number*, and the entire array can be referenced as *jobid* for easy killing etc.; and
3. each jobs has *PBS\_ARRAYID* set to its *number* which allows the script/program to specialise for that job

The job could have been submitted using:

```
$ qsub -t 1-100 my_prog.pbs
```

The effect was that rather than 1 job, the user would actually submit 100 jobs to the queue system. This was a popular feature of TORQUE, but as this technique puts quite a burden on the scheduler, it is not supported by Moab (the current job scheduler).

To support those users who used the feature and since it offers a convenient workflow, the “worker framework” implements the idea of “job arrays” in its own way.

A typical job script for use with job arrays would look like this:

```
job_array.pbs-- job_array/job_array.pbs --
```

```
1 #!/bin/bash -l
2 #PBS -l nodes=1:ppn=1
3 #PBS -l walltime=00:15:00
4 cd $PBS_O_WORKDIR
5 INPUT_FILE="input_${PBS_ARRAYID}.dat"
6 OUTPUT_FILE="output_${PBS_ARRAYID}.dat"
7 my_prog -input ${INPUT_FILE} -output ${OUTPUT_FILE}
```

In our specific example, we have prefabricated 100 input files in the “./input” subdirectory. Each of those files contains a number of parameters for the “test\_set” program, which will perform some tests with those parameters.

Input for the program is stored in files with names such as input\_1.dat, input\_2.dat, …, input\_100.dat in the ./input subdirectory.

```
$ ls ./input
...
$ more ./input/input_99.dat
This is input file \#99
Parameter #1 = 99
Parameter #2 = 25.67
Parameter #3 = Batch
Parameter #4 = 0x562867
```

For the sole purpose of this exercise, we have provided a short “test\_set” program, which reads the “input” files and just copies them into a corresponding output file. We even add a few lines to each output file. The corresponding output computed by our “test\_set” program will be written to the “./output” directory in output\_1.dat, output\_2.dat, …, output\_100.dat. files.

test\_set-job\_array/test\_set —

```

1 #!/bin/bash
2
3 # Check if the output Directory exists
4 if [ ! -d "./output" ] ; then
5     mkdir ./output
6 fi
7
8 # Here you could do your calculations...
9 echo "This is Job_array #" $1
10 echo "Input File : " $3
11 echo "Output File: " $5
12 cat ./input/$3 | sed -e "s/input/output/g" | grep -v "Parameter" > ./output/$5
13 echo "Calculations done, no results" >> ./output/$5

```

Using the “worker framework”, a feature akin to job arrays can be used with minimal modifications to the job script:

test\_set.pbs-job\_array/test\_set.pbs —

```

1 #!/bin/bash -l
2 #PBS -l nodes=1:ppn=8
3 #PBS -l walltime=04:00:00
4 cd ${PBS_O_WORKDIR}
5 INPUT_FILE="input_${PBS_ARRAYID}.dat"
6 OUTPUT_FILE="output_${PBS_ARRAYID}.dat"
7 ./test_set ${PBS_ARRAYID} -input ${INPUT_FILE} -output ${OUTPUT_FILE}

```

Note that

1. the number of CPUs is increased to 8 (ppn=1 is replaced by ppn=8); and
2. the walltime has been modified (walltime=00:15:00 is replaced by walltime=04:00:00).

The job is now submitted as follows:

```

$ module load worker/1.6.8-intel-2018a
$ wsub -t 1-100 -batch test_set.pbs
total number of work items: 100
123456

```

The “*test\_set*” program will now be run for all 100 input files – 8 concurrently – until all computations are done. Again, a computation for an individual input file, or, equivalently, an array id, is called a work item in Worker speak.

Note that in contrast to TORQUE job arrays, a worker job array only submits a single job.

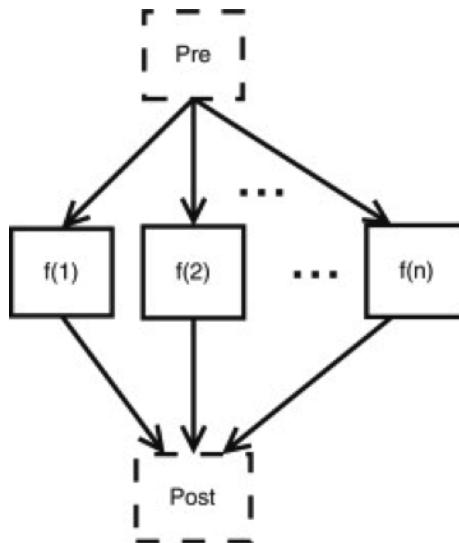
```
$ qstat
Job id      Name      User      Time   Use S Queue
-----
123456  test_set.pbs  vsc40000      0 Q

And you can now check the generated output files:
$ more ./output/output_99.dat
This is output file #99
Calculations done, no results
```

### 13.3 MapReduce: prologues and epilogue

Often, an embarrassingly parallel computation can be abstracted to three simple steps:

1. a preparation phase in which the data is split up into smaller, more manageable chunks;
2. on these chunks, the same algorithm is applied independently (these are the work items); and
3. the results of the computations on those chunks are aggregated into, e.g., a statistical description of some sort.



The Worker framework directly supports this scenario by using a prologue (pre-processing) and an epilogue (post-processing). The former is executed just once before work is started on the work items, the latter is executed just once after the work on all work items has finished. Technically, the master, i.e., the process that is responsible for dispatching work and logging progress, executes the prologue and epilogue.

```
$ cd ~/examples/Multi-job-submission/map_reduce
```

The script “pre.sh” prepares the data by creating 100 different input-files, and the script “post.sh” aggregates (concatenates) the data.

First study the scripts:

pre.sh— map\_reduce/pre.sh —

```

1 #!/bin/bash
2
3 # Check if the input Directory exists
4 if [ ! -d "./input" ] ; then
5     mkdir ./input
6 fi
7
8 # Just generate all dummy input files
9 for i in {1..100} ;
10 do
11     echo "This is input file #$i" > ./input/input_$i.dat
12     echo "Parameter #1 = $i" >> ./input/input_$i.dat
13     echo "Parameter #2 = 25.67" >> ./input/input_$i.dat
14     echo "Parameter #3 = Batch" >> ./input/input_$i.dat
15     echo "Parameter #4 = 0x562867" >> ./input/input_$i.dat
16 done

```

post.sh— map\_reduce/post.sh —

```

1 #!/bin/bash
2
3 # Check if the input Directory exists
4 if [ ! -d "./output" ] ; then
5     echo "The output directory does not exist!"
6     exit
7 fi
8
9 # Just concatenate all output files
10 touch all_output.txt
11 for i in {1..100} ;
12 do
13     cat ./output/output_$i.dat >> all_output.txt
14 done

```

Then one can submit a MapReduce style job as follows:

```

$ wsub -prolog pre.sh -batch test_set.pbs -epilog post.sh -t 1-100
total number of work items: 100
123456
$ cat all_output.txt
...
$ rm -r -f ./output/

```

Note that the time taken for executing the prologue and the epilogue should be added to the job's total walltime.

## 13.4 Some more on the Worker Framework

### 13.4.1 Using Worker efficiently

The “Worker Framework” is implemented using MPI, so it is not restricted to a single compute nodes, it scales well to multiple nodes. However, remember that jobs requesting a large number of nodes typically spend quite some time in the queue.

The “Worker Framework” will be effective when

1. work items, i.e., individual computations, are neither too short, nor too long (i.e., from a few minutes to a few hours); and,
2. when the number of work items is larger than the number of CPUs involved in the job (e.g., more than 30 for 8 CPUs).

### 13.4.2 Monitoring a worker job

Since a Worker job will typically run for several hours, it may be reassuring to monitor its progress. Worker keeps a log of its activity in the directory where the job was submitted. The log’s name is derived from the job’s name and the job’s ID, i.e., it has the form `<jobname>.log<jobid>`. For the running example, this could be `run.pbs.log123456` , assuming the job’s ID is 123456 . To keep an eye on the progress, one can use:

```
$ tail -f run.pbs.log123456
```

Alternatively, `wsummarize`, a Worker command that summarises a log file, can be used:

```
$ watch -n 60 wsummarize run.pbs.log123456
```

This will summarise the log file every 60 seconds.

### 13.4.3 Time limits for work items

Sometimes, the execution of a work item takes long than expected, or worse, some work items get stuck in an infinite loop. This situation is unfortunate, since it implies that work items that could successfully execute are not even started. Again, the Worker framework offers a simple and yet versatile solution. If we want to limit the execution of each work item to at most 20 minutes, this can be accomplished by modifying the script of the running example.

```
1 #!/bin/bash -l
2 #PBS -l nodes=1:ppn=8
3 #PBS -l walltime=04:00:00
4 module load timedrun/1.0
5 cd $PBS_O_WORKDIR
6 timedrun -t 00:20:00 weather -t $temperature -p $pressure -v $volume
```

Note that it is trivial to set individual time constraints for work items by introducing a parameter, and including the values of the latter in the CSV file, along with those for the temperature, pressure and volume.

Also note that “timedrun” is in fact offered in a module of its own, so it can be used outside the Worker framework as well.

#### 13.4.4 Resuming a Worker job

Unfortunately, it is not always easy to estimate the walltime for a job, and consequently, sometimes the latter is underestimated. When using the Worker framework, this implies that not all work items will have been processed. Worker makes it very easy to resume such a job without having to figure out which work items did complete successfully, and which remain to be computed. Suppose the job that did not complete all its work items had ID “445948”.

```
$ wresume -jobid 123456
```

This will submit a new job that will start to work on the work items that were not done yet. Note that it is possible to change almost all job parameters when resuming, specifically the requested resources such as the number of cores and the walltime.

```
$ wresume -l walltime=1:30:00 -jobid 123456
```

Work items may fail to complete successfully for a variety of reasons, e.g., a data file that is missing, a (minor) programming error, etc. Upon resuming a job, the work items that failed are considered to be done, so resuming a job will only execute work items that did not terminate either successfully, or reporting a failure. It is also possible to retry work items that failed (preferably after the glitch why they failed was fixed).

```
$ wresume -jobid 123456 --retry
```

By default, a job’s prologue is not executed when it is resumed, while its epilogue is. “wresume” has options to modify this default behaviour.

#### 13.4.5 Further information

This how-to introduces only Worker’s basic features. The wsub command has some usage information that is printed when the -help option is specified:

```
$ wsub -help
### usage: wsub -batch <batch-file> \
#           [-data <data-files>] \
#           [-prolog <prolog-file>] \
#           [-epilog <epilog-file>] \
#           [-log <log-file>] \
#           [-mpiverbose] \
#           [-dryrun] [-verbose] \
#           [-quiet] [-help] \
#           [-t <array-req>] \
#           [<pbs-qsub-options>]
#
# -batch <batch-file>      : batch file template, containing variables to be
#                             replaced with data from the data file(s) or the
#                             PBS array request option
# -data <data-files>       : comma-separated list of data files (default CSV
#                             files) used to provide the data for the work
#                             items
# -prolog <prolog-file>   : prolog script to be executed before any of the
#                             work items are executed
# -epilog <epilog-file>   : epilog script to be executed after all the work
#                             items are executed
# -mpiverbose              : pass verbose flag to the underlying MPI program
# -verbose                 : feedback information is written to standard error
# -dryrun                  : run without actually submitting the job, useful
# -quiet                   : don't show information
# -help                    : print this help message
# -t <array-req>           : qsub's PBS array request options, e.g., 1-10
# <pbs-qsub-options>      : options passed on to the queue submission
#                           command
```

# Chapter 14

## Compiling and testing your software on the HPC

All nodes in the HPC cluster are running the “CentOS 7.7 (golett, phanpy, skitty, swalot, victimi)” Operating system, which is a specific version of Red Hat Enterprise Linux. This means that all the software programs (executable) that the end-user wants to run on the HPC first must be compiled for CentOS 7.7 (golett, phanpy, skitty, swalot, victimi). It also means that you first have to install all the required external software packages on the HPC.

Most commonly used compilers are already pre-installed on the HPC and can be used straight away. Also many popular external software packages, which are regularly used in the scientific community, are also pre-installed.

### 14.1 Check the pre-installed software on the HPC

In order to check all the available modules and their version numbers, which are pre-installed on the HPC enter:

```
$ module av 2>&1 | more
--- /apps/gent/SL6/sandybridge/modules/all ---
ABAQUS/6.12.1-linux-x86_64
AMOS/3.1.0-ictce-4.0.10
ant/1.9.0-Java-1.7.0_40
ASE/3.6.0.2515-ictce-4.1.13-Python-2.7.3
ASE/3.6.0.2515-ictce-5.5.0-Python-2.7.6
...
```

Or when you want to check whether some specific software, some compiler or some application (e.g., MATLAB) is installed on the HPC.

```
$ module av 2>&1 | grep -i -e "matlab"
MATLAB/2010b
MATLAB/2012b
MATLAB/2013b
```

As you are not aware of the capitals letters in the module name, we looked for a case-insensitive name with the “-i” option.

When your required application is not available on the HPC please contact any HPC member. Be aware of potential “License Costs”. “Open Source” software is often preferred.

## 14.2 Porting your code

To **port** a software-program is to translate it from the operating system in which it was developed (e.g., Windows 7) to another operating system (e.g., Red Hat Enterprise Linux on our HPC) so that it can be used there. Porting implies some degree of effort, but not nearly as much as redeveloping the program in the new environment. It all depends on how “portable” you wrote your code.

In the simplest case the file or files may simply be copied from one machine to the other. However, in many cases the software is installed on a computer in a way, which depends upon its detailed hardware, software, and setup, with device drivers for particular devices, using installed operating system and supporting software components, and using different directories.

In some cases software, usually described as “portable software” is specifically designed to run on different computers with compatible operating systems and processors without any machine-dependent installation; it is sufficient to transfer specified directories and their contents. Hardware- and software-specific information is often stored in configuration files in specified locations (e.g., the registry on machines running MS Windows).

Software, which is not portable in this sense, will have to be transferred with modifications to support the environment on the destination machine.

Whilst programming, it would be wise to stick to certain standards (e.g., ISO/ANSI/POSIX). This will ease the porting of your code to other platforms.

Porting your code to the CentOS 7.7 (golett, phanpy, skitty, swalot, victimi) platform is the responsibility of the end-user.

## 14.3 Compiling and building on the HPC

Compiling refers to the process of translating code written in some programming language, e.g., Fortran, C, or C++, to machine code. Building is similar, but includes gluing together the machine code resulting from different source files into an executable (or library). The text below guides you through some basic problems typical for small software projects. For larger projects it is more appropriate to use makefiles or even an advanced build system like CMake.

All the HPC nodes run the same version of the Operating System, i.e. CentOS 7.7 (golett, phanpy, skitty, swalot, victimi). So, it is sufficient to compile your program on any compute node. Once you have generated an executable with your compiler, this executable should be able to run on any other compute-node.

A typical process looks like:

1. Copy your software to the login-node of the HPC
2. Start an interactive session on a compute node;

3. Compile it;
4. Test it locally;
5. Generate your job scripts;
6. Test it on the HPC
7. Run it (in parallel);

We assume you've copied your software to the HPC. The next step is to request your private compute node.

```
$ qsub -I
qsub: waiting for job 123456 to start
```

#### 14.3.1 Compiling a sequential program in C

Go to the examples for [chapter 14](#) and load the foss module:

```
$ cd ~/examples/Compiling-and-testing-your-software-on-the-HPC
$ module load foss
```

We now list the directory and explore the contents of the “hello.c” program:

```
$ ls -l
total 512
-rw-r--r-- 1 vsc40000 214 Sep 16 09:42 hello.c
-rw-r--r-- 1 vsc40000 130 Sep 16 11:39 hello.pbs*
-rw-r--r-- 1 vsc40000 359 Sep 16 13:55 mpihello.c
-rw-r--r-- 1 vsc40000 304 Sep 16 13:55 mpihello.pbs
```

— hello.c —

```
1  /*
2   * VSC          : Flemish Supercomputing Centre
3   * Tutorial     : Introduction to HPC
4   * Description: Print 500 numbers, whilst waiting 1 second in between
5   */
6  #include "stdio.h"
7  int main( int argc, char *argv[] )
8  {
9     int i;
10    for (i=0; i<500; i++)
11    {
12        printf("Hello #%d\n", i);
13        fflush(stdout);
14        sleep(1);
15    }
16 }
```

The “hello.c” program is a simple source file, written in C. It'll print 500 times “Hello #<num>”, and waits one second between 2 printouts.

We first need to compile this C-file into an executable with the gcc-compiler.

First, check the command line options for “*gcc*” (*GNU C-Compiler*), then we compile and list the contents of the directory again:

```
$ gcc -help
$ gcc -o hello hello.c
$ ls -l
total 512
-rwxrwxr-x 1 vsc40000 7116 Sep 16 11:43 hello*
-rw-r--r-- 1 vsc40000 214 Sep 16 09:42 hello.c
-rwxr-xr-x 1 vsc40000 130 Sep 16 11:39 hello.pbs*
```

A new file “hello” has been created. Note that this file has “execute” rights, i.e., it is an executable. More often than not, calling *gcc* – or any other compiler for that matter – will provide you with a list of errors and warnings referring to mistakes the programmer made, such as typos, syntax errors. You will have to correct them first in order to make the code compile. Warnings pinpoint less crucial issues that may relate to performance problems, using unsafe or obsolete language features, etc. It is good practice to remove all warnings from a compilation process, even if they seem unimportant so that a code change that produces a warning does not go unnoticed.

Let’s test this program on the local compute node, which is at your disposal after the “qsub -I” command:

```
$ ./hello
Hello #0
Hello #1
Hello #2
Hello #3
Hello #4
...
```

It seems to work, now run it on the HPC

```
$ qsub hello.pbs
```

### 14.3.2 Compiling a parallel program in C/MPI

```
$ cd ~/examples/Compiling-and-testing-your-software-on-the-HPC
```

List the directory and explore the contents of the “*mpihello.c*” program:

```
$ ls -l
total 512
total 512
-rw-r--r-- 1 vsc40000 214 Sep 16 09:42 hello.c
-rw-r--r-- 1 vsc40000 130 Sep 16 11:39 hello.pbs*
-rw-r--r-- 1 vsc40000 359 Sep 16 13:55 mpihello.c
-rw-r--r-- 1 vsc40000 304 Sep 16 13:55 mpihello.pbs
```

— mpihello.c —

```

1  /*
2   * VSC      : Flemish Supercomputing Centre
3   * Tutorial : Introduction to HPC
4   * Description: Example program, to compile with MPI
5   */
6 #include <stdio.h>
7 #include <mpi.h>
8
9 main(int argc, char **argv)
10 {
11     int node, i, j;
12     float f;
13
14     MPI_Init(&argc,&argv);
15     MPI_Comm_rank(MPI_COMM_WORLD, &node);
16
17     printf("Hello World from Node %d.\n", node);
18     for (i=0; i<=100000; i++)
19         f=i*2.718281828*i+i+i*3.141592654;
20
21     MPI_Finalize();
22 }
```

The “mpihello.c” program is a simple source file, written in C with MPI library calls.

Then, check the command line options for “*mpicc*” (*GNU C-Compiler with MPI extensions*), then we compile and list the contents of the directory again:

```

$ mpicc -help
$ mpicc -o mpihello mpihello.c
$ ls -l
```

A new file “hello” has been created. Note that this program has “execute” rights.

Let’s test this program on the “login” node first:

```

$ ./mpihello
Hello World from Node 0.
```

It seems to work, now run it on the HPC.

```

$ qsub mpihello.pbs
```

### 14.3.3 Compiling a parallel program in Intel Parallel Studio Cluster Edition

We will now compile the same program, but using the Intel Parallel Studio Cluster Edition compilers. We stay in the examples directory for this chapter:

```

$ cd ~/examples/Compiling-and-testing-your-software-on-the-HPC
```

We will compile this C/MPI -file into an executable with the Intel Parallel Studio Cluster Edition. First, clear the modules (purge) and then load the latest “intel” module:

```
$ module purge
$ module load intel
```

Then, compile and list the contents of the directory again. The Intel equivalent of mpicc is mpiicc.

```
$ mpiicc -o mpihello mpihello.c
$ ls -l
```

Note that the old “mpihello” file has been overwritten. Let’s test this program on the “login” node first:

```
$ ./mpihello
Hello World from Node 0.
```

It seems to work, now run it on the HPC.

```
$ qsub mpihello.pbs
```

Note: The AUGent only has a license for the Intel Parallel Studio Cluster Edition for a fixed number of users. As such, it might happen that you have to wait a few minutes before a floating license becomes available for your use.

Note: The Intel Parallel Studio Cluster Edition contains equivalent compilers for all GNU compilers. Hereafter the overview for C, C++ and Fortran compilers.

	<b>Sequential Program</b>		<b>Parallel Program (with MPI)</b>	
	<b>GNU</b>	<b>Intel</b>	<b>GNU</b>	<b>Intel</b>
<b>C</b>	gcc	icc	mpicc	mpiicc
<b>C++</b>	g++	icpc	mpicxx	mpiicpc
<b>Fortran</b>	gfortran	ifort	mpif90	mpiifort

# Chapter 15

## Checkpointing

### 15.1 Why checkpointing?

If you want to run jobs that require wall time than the maximum wall time per job and/or want to avoid you lose work because of power outages or system crashes, you need to resort to checkpointing.

### 15.2 What is checkpointing?

Checkpointing allows for running jobs that run for weeks or months, by splitting the job into smaller parts (called subjobs) which are executed consecutively. Each time a subjob is running out of requested wall time, a snapshot of the application memory (and much more) is taken and stored, after which a subsequent subjob will pick up the checkpoint and continue.

### 15.3 How to use checkpointing?

Using checkpointing is very simple: just use `csub` instead of `qsub` to submit a job.

The `csub` command creates a wrapper around your job script, to take care of all the checkpointing stuff.

In practice, you (usually) don't need to adjust anything, except for the command used to submit your job.

Checkpointing does not require any changes to the application you are running, and should support most software.

### 15.4 Usage and parameters

An overview of the usage and various command line parameters is given here.

### 15.4.1 Submitting a job

Typically, a job script is submitted with checkpointing support enabled by running:

```
csub -s job_script.sh
```

The `-s` flag specifies the job script to run.

### 15.4.2 Caveat: don't create local directories

One important caveat is that the job script (or the applications run in the script) should *not* create its own local temporary directories, because those will not (always) be restored when the job is restarted from checkpoint.

### 15.4.3 PBS directives

Most PBS directives (`#PBS ...` specified in the job script will be ignored. There are a few exceptions however, i.e., `# PBS -N <name>` (job name) and all `-l` directives (`# PBS -l`), e.g., `nodes`, `ppn`, `vmem` (virtual memory limit), etc. Controlling other job parameters (like requested walltime per sub-job) should be specified on the `csub` command line.

### 15.4.4 Getting help

Help on the various command line parameters supported by `csub` can be obtained using `-h` or `--help`.

### 15.4.5 Local files (`-pre` / `-post`)

The `--pre` and `--post` parameters control whether local files are copied or not. The job submitted using `csub` is (by default) run on the local storage provided by a particular workernode. Thus, no changes will be made to the files on the shared storage.

If the job script needs (local) access to the files of the directory where `csub` is executed, `--pre` flag should be used. This will copy all the files in the job script directory to the location where the job script will execute.

If the output of the job (`stdout/stderr`) that was run, or additional output files created by the job in its working directory are required, the `--post` flag should be used. This will copy the entire job working directory to the location where `csub` was executed, in a directory named `result.<jobname>`. An alternative is to copy the interesting files to the shared storage at the end of the job script.

### 15.4.6 Running on shared storage (`-shared`)

If the job needs to be run on the shared storage, `--shared` should be specified. You should enable this option by default, because it makes the execution of the underlying `csub` script more robust: it doesn't have to copy from/to the local storage on the workernode. When enabled, the

job will be run in a subdirectory of \$VSC\_SCRATCH/chkpt. All files produced by the job will be in \$VSC\_SCRATCH/chkpt/<jobid>/ while the job is running.

Note that if files in the directory where the job script is located are required to run the job, you should also use --pre.

#### 15.4.7 Job wall time (**-job\_time**, **-chkpt\_time**)

To specify the requested wall time per subjob, use the --job-time parameter. The default setting is 10 hours per (sub)job. Lowering this will result in more frequent checkpointing, and thus more (sub)jobs.

To specify the time that is reserved for checkpointing the job, use --chkpt\_time. By default, this is set to 15 minutes which should be enough for most applications/jobs. *Don't change this unless you really need to.*

The total requested wall time per subjob is the sum of both job\_time and chkpt\_time.

If you would like to time how long the job executes, just prepend the main command in your job script with the time command time, e.g.:

```
time main_command
```

The real time will not make sense, as it will also include the time passed between two checkpointed subjobs. However, the user time should give a good indication of the actual time it took to run your command, even if multiple checkpoints were performed.

#### 15.4.8 Resuming from last checkpoint (**-resume**)

The --resume option allows you to resume a job from the last available checkpoint in case something went wrong (e.g., accidentally deleting a (sub)job using qdel, a power outage or other system failure, ...).

Specify the job name as returned after submission (and as listed in \$VSC\_SCRATCH/chkpt). The full job name consists of the specified job name (or the script name if no job name was specified), a timestamp and two random characters at the end, for example my\_job\_name.20200102\_133755.Hk or script.sh.20200102\_133755.Hk.

Note: When resuming from checkpoint, you can change the wall time resources for your job using the --job\_time and --chkpt\_time options. This should allow you to continue from the last checkpoint in case your job crashed due to an excessively long checkpointing time.

In case resuming fails for you, please contact hpc@ugent.be, and include the output of the csub --resume command in your message.

## 15.5 Additional options

### 15.5.1 Array jobs (**-t**)

csub has support for checkpointing array jobs with the **-t <spec>** flag on the csub command line. This behaves the same as qsub, see [section 13.2](#).

### 15.5.2 Pro/epilogue mimicking (**-no\_mimic\_pro\_epi**)

The option **--no\_mimic\_pro\_epi** disables the workaround currently required to resolve a permissions problem when using actual Torque prologue/epilogue scripts. Don't use this option unless you really know what you are doing.

### 15.5.3 Cleanup checkpoints (**-cleanup\_after\_restart**)

Specifying this option will make the wrapper script remove the checkpoint files after a successful job restart. This may be desirable in cause you are short on storage space.

Note that we don't recommend setting this option, because this way you won't be able to resume from the last checkpoint when something goes wrong. It may also prevent the wrapper script from reattempting to resubmit a new job in case an infrequent known failure occurs. So, don't set this unless you really need to.

### 15.5.4 No cleanup after job completion (**-no\_cleanup\_chkpt**)

Specifying this option will prevent the wrapper script from cleaning up the checkpoints and related information once the job has finished. This may be useful for debugging, since this also preserves the `stdout/stderr` of the wrapper script.

*Don't set this unless you know what you are doing.*

# Chapter 16

## Program examples

Go to our examples:

```
$ cd ~/examples/Program-examples
```

Here, we just have put together a number of examples for your convenience. We did an effort to put comments inside the source files, so the source code files are (should be) self-explanatory.

1. 01\_Python
2. 02\_C\_C++
3. 03\_Matlab
4. 04\_MPI\_C
5. 05a\_OMP\_C
6. 05b\_OMP\_FORTRAN
7. 06\_NWChem
8. 07\_Wien2k
9. 08\_Gaussian
10. 09\_Fortran
11. 10\_PQS

The above 2 OMP directories contain the following examples:

---

<b>C Files</b>	<b>Fortran Files</b>	<b>Description</b>
omp_hello.c	omp_hello.f	Hello world
omp_workshare1.c	omp_workshare1.f	Loop work-sharing
omp_workshare2.c	omp_workshare2.f	Sections work-sharing
omp_reduction.c	omp_reduction.f	Combined parallel loop reduction
omp_orphan.c	omp_orphan.f	Orphaned parallel loop reduction
omp_mm.c	omp_mm.f	Matrix multiply
omp_getEnvInfo.c	omp_getEnvInfo.f	Get and print environment information
omp_bug1.c omp_bug1fix.c omp_bug2.c omp_bug3.c omp_bug4.c omp_bug4fix omp_bug5.c omp_bug5fix.c omp_bug6.c	omp_bug1.f omp_bug1fix.f omp_bug2.f omp_bug3.f omp_bug4.f omp_bug4fix omp_bug5.f omp_bug5fix.f omp_bug6.f	Programs with bugs and their solution

Compile by any of the following commands:

<b>C:</b>	icc -openmp omp_hello.c -o hello pgcc -mp omp_hello.c -o hello gcc -fopenmp omp_hello.c -o hello
<b>Fortran:</b>	ifort -openmp omp_hello.f -o hello pgf90 -mp omp_hello.f -o hello gfortran -fopenmp omp_hello.f -o hello

Be invited to explore the examples.

# Chapter 17

## Job script examples

### 17.1 Single-core job

Here's an example of a single-core job script:

— single\_core.sh —

```
1 #!/bin/bash
2 #PBS -N count_example          ## job name
3 #PBS -l nodes=1:ppn=1          ## single-node job, single core
4 #PBS -l walltime=2:00:00       ## max. 2h of wall time
5 module load Python/3.6.4-intel-2018a
6 # copy input data from location where job was submitted from
7 cp $PBS_O_WORKDIR/input.txt $TMPDIR
8 # go to temporary working directory (on local disk) & run
9 cd $TMPDIR
10 python -c "print(len(open('input.txt').read()))" > output.txt
11 # copy back output data, ensure unique filename using $PBS_JOBID
12 cp output.txt $VSC_DATA/output_${PBS_JOBID}.txt
```

1. Using #PBS header lines, we specify the resource requirements for the job, see [Appendix B](#) for a list of these options
2. A module for Python 3.6 is loaded, see also [section 4.1](#)
3. We stage the data in: the file `input.txt` is copied into the “working” directory, see [chapter 6](#)
4. The main part of the script runs a small Python program that counts the number of characters in the provided input file `input.txt`
5. We stage the results out: the output file `output.txt` is copied from the “working directory” (`$TMPDIR`) to a unique directory in `$VSC_DATA`. For a list of possible storage locations, see [subsection 6.2.1](#).

## 17.2 Multi-core job

Here's an example of a multi-core job script that uses mympirun:

— multi\_core.sh —

```

1 #!/bin/bash
2 #PBS -N mpi_hello          ## job name
3 #PBS -l nodes=2:ppn=all     ## 2 nodes, all cores per node
4 #PBS -l walltime=2:00:00    ## max. 2h of wall time
5 module load intel/2017b
6 module load vsc-mympirun    ## We don't use a version here, this is on purpose
7 # go to working directory, compile and run MPI hello world
8 cd $PBS_O_WORKDIR
9 mpicc mpi_hello.c -o mpi_hello
10 mympirun ./mpi_hello

```

An example MPI hello world program can be downloaded from [https://github.com/hpcugent/vsc-mympirun/blob/master/testscripts/mpi\\_helloworld.c](https://github.com/hpcugent/vsc-mympirun/blob/master/testscripts/mpi_helloworld.c).

## 17.3 Running a command with a maximum time limit

If you want to run a job, but you are not sure it will finish before the job runs out of walltime and you want to copy data back before, you have to stop the main command before the walltime runs out and copy the data back.

This can be done with the `timeout` command. This command sets a limit of time a program can run for, and when this limit is exceeded, it kills the program. Here's an example job script using `timeout`:

— timeout.sh —

```

1 #!/bin/bash
2 #PBS -N timeout_example
3 #PBS -l nodes=1:ppn=1      ## single-node job, single core
4 #PBS -l walltime=2:00:00   ## max. 2h of wall time
5
6 # go to temporary working directory (on local disk)
7 cd $TMPDIR
8 # This command will take too long (1400 minutes is longer than our walltime)
9 # $PBS_O_WORKDIR/example_program.sh 1400 output.txt
10
11 # So we put it after a timeout command
12 # We have a total of 120 minutes (2 x 60) and we instruct the script to run for
13 # 100 minutes, but timeout after 90 minute,
14 # so we have 30 minutes left to copy files back. This should
15 # be more than enough.
16 timeout -s SIGKILL 90m $PBS_O_WORKDIR/example_program.sh 100 output.txt
17 # copy back output data, ensure unique filename using $PBS_JOBID
18 cp output.txt $VSC_DATA/output_${PBS_JOBID}.txt

```

The example program used in this script is a dummy script that simply sleeps a specified amount of minutes:

— example\_program.sh —

```
1 #!/bin/bash
2 # This is an example program
3 # It takes two arguments: a number of times to loop and a file to write to
4 # In total, it will run for (the number of times to loop) minutes
5
6 if [ $# -ne 2 ]; then
7     echo "Usage: ./example_program amount filename" && exit 1
8 fi
9
10 for ((i = 0; i < $1; i++ )); do
11     echo "${i} => $(date)" >> $2
12     sleep 60
13 done
```

# Chapter 18

## Best Practices

### 18.1 General Best Practices

1. Before starting you should always check:
  - Are there any errors in the script?
  - Are the required modules loaded?
  - Is the correct executable used?
2. Check your computer requirements upfront, and request the correct resources in your batch job script.
  - Number of requested cores
  - Amount of requested memory
  - Requested network type
3. Check your jobs at runtime. You could login to the node and check the proper execution of your jobs with, e.g., `top` or `vmstat`. Alternatively you could run an interactive job (`qsub -I`).
4. Try to benchmark the software for scaling issues when using MPI or for I/O issues.
5. Use the scratch file system (`$VSC_SCRATCH_NODE`, which is mapped to the local `/tmp`) whenever possible. Local disk I/O is always much faster as it does not have to use the network.
6. When your job starts, it will log on to the compute node(s) and start executing the commands in the job script. It will start in your home directory `$VSC_HOME`, so going to the current directory with `cd $PBS_O_WORKDIR` is the first thing which needs to be done. You will have your default environment, so don't forget to load the software with `module load`.
7. Submit your job and wait (be patient) ...
8. Submit small jobs by grouping them together. See [chapter 13](#) for how this is done.

9. The runtime is limited by the maximum walltime of the queues. For longer walltimes, use checkpointing.
10. Requesting many processors could imply long queue times. It's advised to only request the resources you'll be able to use.
11. For all multi-node jobs, please use a cluster that has an "InfiniBand" interconnect network.
12. And above all, do not hesitate to contact the HPC staff at hpc@ugent.be. We're here to help you.

# Chapter 19

## Graphical applications with VNC

VNC is still available at UGent site but we encourage our users to replace VNC by X2Go client. Please see [chapter 20](#) for more information.

Virtual Network Computing is a graphical desktop sharing system that enables you to interact with graphical software running on the HPC infrastructure from your own computer.

Please carefully follow the instructions below, since the procedure to connect to a VNC server running on the HPC infrastructure is not trivial, due to security constraints.

### 19.1 Starting a VNC server

First login on the login node (see [section 3.2](#)), then start vncserver with:

```
$ vncserver -geometry 1920x1080 -localhost
You will require a password to access your desktops.

Password:<enter a secure password>
Verify:<enter the same password>
Would you like to enter a view-only password (y/n)? n
A view-only password is not used

New 'gligar04.gastly.os:6 (vsc40000)' desktop is gligar04.gastly.os:6

Creating default startup script /user/home/gent/vsc400/vsc40000/.vnc/xstartup
Creating default config /user/home/gent/vsc400/vsc40000/.vnc/config
Starting applications specified in /user/home/gent/vsc400/vsc40000/.vnc/xstartup
Log file is /user/home/gent/vsc400/vsc40000/.vnc/gligar04.gastly.os:6.log
```

**When prompted for a password, make sure to enter a secure password: if someone can guess your password, they will be able to do anything with your account you can!**

Note down the details in bold: the hostname (in the example: gligar04.gastly.os) and the (partial) port number (in the example: 6).

It's important to remember that VNC sessions are permanent. They survive network problems

and (unintended) connection loss. This means you can logout and go home without a problem (like the terminal equivalent screen or tmux). This also means you don't have to start vncserver each time you want to connect.

## 19.2 List running VNC servers

You can get a list of running VNC servers on a node with

```
$ vncserver -list
TigerVNC server sessions:

X DISPLAY #      PROCESS ID
:6              30713
```

This only displays the running VNC servers on **the login node you run the command on**.

To see what login nodes you are running a VNC server on, you can run the `ls .vnc/*.pid` command in your home directory: the files shown have the hostname of the login node in the filename:

```
$ cd $HOME
$ ls .vnc/*.pid
.vnc/gligar04.gastly.os:6.pid
.vnc/gligar05.gastly.os:8.pid
```

This shows that there is a VNC server running on `gligar04.gastly.os` on port 5906 and another one running `gligar05.gastly.os` on port 5908 (see also [subsection 19.3.1](#)).

## 19.3 Connecting to a VNC server

The VNC server runs on a **specific login node** (in the example above, on `gligar04.gastly.os`).

In order to access your VNC server, you will need to set up an SSH tunnel from your workstation to this login node (see [subsection 19.3.3](#)).

Login nodes are rebooted from time to time. You can check that the VNC server is still running in the same node by executing `vncserver -list` (see also [section 19.2](#)). If you get an empty list, it means that there is no VNC server running on the login node.

**To set up the SSH tunnel required to connect to your VNC server, you will need to port forward the VNC port to your workstation.**

The *host* is `localhost`, which means “your own computer”: we set up an SSH tunnel that connects the VNC port on the login node to the same port on your local computer.

### 19.3.1 Determining the source/destination port

The *destination port* is the port on which the VNC server is running (on the login node), which is **the sum of 5900 and the partial port number** we noted down earlier (6); in the running example, that is 5906.

The *source port* is the port you will be connecting to with your VNC client on your workstation. Although you can use any (free) port for this, we strongly recommend to use the **same value as the destination port**.

So, in our running example, both the source and destination ports are 5906.

### 19.3.2 Picking an intermediate port to connect to the right login node

In general, you have no control over which login node you will be on when setting up the SSH tunnel from your workstation to `login.hpc.ugent.be` (see [subsection 19.3.3](#)).

If the login node you end up on is a different one than the one where your VNC server is running (i.e., `glicher05.gastly.os` rather than `glicher04.gastly.os` in our running example), you need to create a **second SSH tunnel** on the login node you are connected to, in order to "patch through" to the correct port on the login node where your VNC server is running.

In the remainder of these instructions, we will assume that we are indeed connected to a different login node. Following these instructions should always work, even if you happen to be connected to the correct login node.

To set up the second SSH tunnel, you need to **pick an (unused) port on the login node you are connected to**, which will be used as an *intermediate* port.

Now we have a chicken-egg situation: you need to pick a port before setting up the SSH tunnel from your workstation to `glicher04.gastly.os`, but only after starting the SSH tunnel will you be able to determine whether the port you picked is actually free or not...

In practice, if you **pick a random number between 10000 and 30000**, you have a good chance that the port will not be used yet.

We will proceed with 12345 as intermediate port, but **you should pick another value that other people are not likely to pick**. If you need some inspiration, run the following command on a Linux server (for example on a login node): `echo $RANDOM` (but do not use a value lower than 1025).

### 19.3.3 Setting up the SSH tunnel(s)

#### Setting up the first SSH tunnel from your workstation to `login.hpc.ugent.be`

First, we will set up the SSH tunnel from our workstation to `login.hpc.ugent.be`.

Use the settings specified in the sections above:

- *source port*: the port on which the VNC server is running (see [subsection 19.3.1](#));
- *destination host*: `localhost`;
- *destination port*: use the intermediate port you picked (see [subsection 19.3.2](#))

Execute the following command to set up the SSH tunnel.

```
$ ssh -L 5906:localhost:12345 vsc40000@login.hpc.ugent.be
```

Replace the source port (**5906**, destination port (**12345**) and the user ID (**vsc40000**) with your own!

With this, we have forwarded port 5906 on our workstation to port 12345 on the login node we are connected to.

Again, do *not* use **12345** as destination port, as this port will most likely be used by somebody else already; replace it with a port number you picked yourself, which is unlikely to be used already (see [subsection 19.3.2](#)).

### Checking whether the intermediate port is available

Before continuing, it's good to check whether the intermediate port that you have picked is actually still available (see [subsection 19.3.2](#)).

You can check using the following command (do not forget to replace **12345** the value you picked for your intermediate port):

```
$ netstat -an | grep -i listen | grep tcp | grep 12345
```

If you see no matching lines, then the port you picked is still available, and you can continue.

If you see one or more matching lines as shown below, you must disconnect the first SSH tunnel, pick a different intermediate port, and set up the first SSH tunnel again using the new value.

```
$ netstat -an | grep -i listen | grep tcp | grep 12345
tcp 0 0 0.0.0.0:12345 0.0.0.0:*
tcp6 0 0 ::::12345 ::::* LISTEN
$
```

### Setting up the second SSH tunnel to the correct login node

In the session on the login node you created by setting up an SSH tunnel from your workstation to `login.hpc.ugent.be`, you now need to set up the second SSH tunnel to "patch through" to the login node where your VNC server is running (`gligar04.gastly.os` in our running example, see [section 19.1](#)).

To do this, run the following command:

```
$ ssh -L 12345:localhost:5906 gligar04.gastly.os
$ hostname
gligar04.gastly.os
```

With this, we are forwarding port 12345 on the login node we are connected to (which is referred to as `localhost`) through to port 5906 on our target login node (`gligar04.gastly.os`).

Combined with the first SSH tunnel, port 5906 on our workstation is now connected to port 5906 on the login node where our VNC server is running (via the intermediate port 12345 on

the login node we ended up one with the first SSH tunnel).

**Do not forget to change the intermediate port (12345), destination port (5906), and hostname of the login node (`gligar04.gastly.os`) in the command shown above!**

As shown above, you can check again using the `hostname` command whether you are indeed connected to the right login node. If so, you can go ahead and connect to your VNC server (see subsection 19.3.4).

#### 19.3.4 Connecting using a VNC client

Download and setup a VNC client. A good choice is `tigervnc`. You can start it with the `vncviewer` command.

Now start your VNC client and connect to `localhost:5906`. **Make sure you replace the port number 5906 with your own destination port** (see subsection 19.3.1).

When prompted for a password, use the password you used to setup the VNC server.

When prompted for default or empty panel, choose default.

If you have an empty panel, you can reset your settings with the following commands:

```
$ xfce4-panel -quit ; pkill xfconfd  
$ mkdir ~/.oldxfcesettings  
$ mv ~/.config/xfce4 ~/.oldxfcesettings  
$ xfce4-panel
```

### 19.4 Stopping the VNC server

The VNC server can be killed by running

```
vncserver -kill :6
```

where 6 is the port number we noted down earlier. If you forgot, you can get it with `vncserver -list` (see section 19.2).

### 19.5 I forgot the password, what now?

You can reset the password by first stopping the VNC server (see section 19.4), then removing the `.vnc/passwd` file (with `rm .vnc/passwd`) and then starting the VNC server again (see section 19.1).

# Chapter 20

## Graphical applications with X2Go

X2Go is a graphical desktop software for Linux similar to VNC but with extra advantages. It does not require to execute a server in the login node and it is possible to setup a SSH proxy to connect to an specific login node. It can also be used to access Windows, Linux and macOS desktops. X2Go provides several advantages such:

1. A graphical remote desktop that works well over low bandwidth connections.
2. Copy/paste support from client to server and vice-versa.
3. File sharing from client to server.
4. Support for sound.
5. Printer sharing from client to server.
6. The ability to access single applications by specifying the name of the desired executable like a terminal or an internet browser.

### 20.1 Install X2Go client

X2Go is available for several operating systems. You can download the latest client from <https://wiki.x2go.org/doku.php/doc:installation:x2goclient>.

X2Go requires a valid private SSH key to connect to the login node, this is described in [subsection 2.1.1](#). This section also describes how to use X2Go client with a SSH agent. The SSH agent setup is optional but it is the easiest way to connect to the login nodes using several SSH keys and applications. Please see [subsection 2.1.4](#) if you want to know how to setup an SSH agent in your system.

### 20.2 Create a new X2Go session

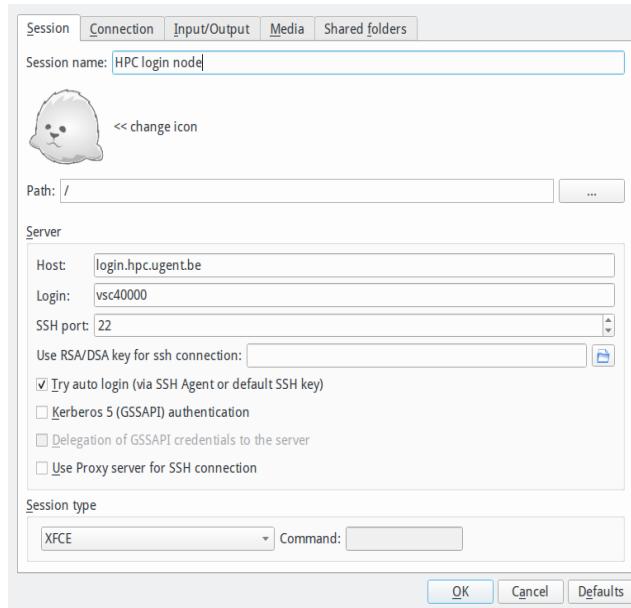
After the X2Go client installation just start the client. When you launch the client for the first time, it will start the new session dialogue automatically.

There are two ways to connect to the login node:

- *Option A:* A direct connection to “***login.hpc.ugent.be***”. This is the simpler option, the system will decide which login node to use based on a load-balancing algorithm.
- *Option B:* You can use the node “***login.hpc.ugent.be***” as SSH proxy to connect to a specific login node. Use this option if you want to resume an old X2Go session.

### 20.2.1 Option A: direct connection

This is the easier way to setup X2Go, a direct connection to the login node.

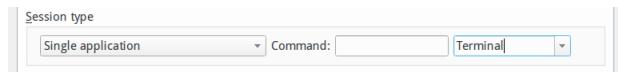


1. Include a session name. This will help you to identify the session if you have more than one, you can choose any name (in our example “HPC login node“).
2. Set the login hostname (In our case: “***login.hpc.ugent.be***”)
3. Set the Login name. In the example is “**vsc40000**” but you must change it by your current VSC account.
4. Set the SSH port (22 by default).
5. Skip this step if you are using an SSH agent (see [section 20.1](#)). If not add your SSH private key into “Use RSA/DSA key..” field. In this case:
  - (a) Click on the “Use RSA/DSA..” folder icon. This will open a file browser.
6. Check “Try autologin” option.



- (b) You should look for your **private** SSH key generated in [subsection 2.1.3](#). This file has been stored in the directory “**~/.ssh/**” (by default “**id\_rsa**”).

7. Choose Session type to **Xfce**. Only the **Xfce** desktop is available for the moment. It is also possible to choose single applications instead of a full desktop, like the **Terminal** or **Internet browser** (you can change this option later directly from the X2Go session tab if you want).
- (a) **[optional]:** Set a single application like **Terminal** instead of **Xfce** desktop.

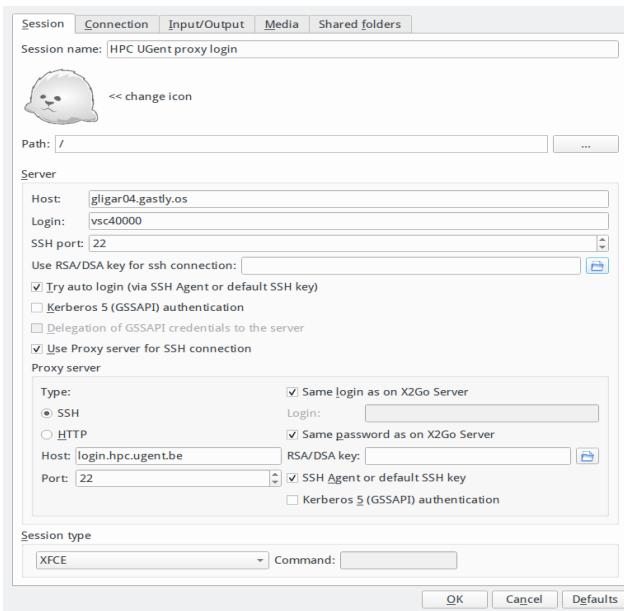


8. **[optional]:** Change the session icon.

9. Click the **OK** button after these changes.

### 20.2.2 Option B: use the login node as SSH proxy

This option is useful if you want to resume a previous session or if you want to set explicitly the login node to use. In this case you should include a few more options. Use the same **Option A** setup but with these changes:



1. Include a session name. This will help you to identify the session if you have more than one (in our example “HPC UGent proxy login”).
2. Set the login hostname. This is the login node that you want to use at the end (In our case: “*gligar04.gastly.os*”)
3. Set “Use Proxy server..” to enable the proxy. Within “Proxy section” set also these options:
  - (a) Set Type “SSH”, “Same login”, “Same Password” and “SSH agent” options.
  - (b) Set Host to “*login.hpc.ugent.be*” within “Proxy Server” section as well.

- (c) Skip this step if you are using an SSH agent (see [section 20.1](#)). Add your **private** SSH key within “RSA/DSA key” field within “Proxy Server” as you did for the server configuration (The “RSA/DSA key” field must be set in both sections)



- (d) Click the **OK** button after these changes.

## 20.3 Connect to your X2Go session

Just click on any session that you already have to start/resume any session. It will take a few seconds to open the session the first time. It is possible to terminate a session if you logout from the current open session or if you click on the “shutdown” button from X2Go. If you want to suspend your session to continue working with it later just click on the “pause” icon.



X2Go will keep the session open for you (but only if the login node is not rebooted).

## 20.4 Resume a previous session

If you want to re-connect to the same login node, or resume a previous session, you should know which login node were used at first place. You can get this information before logging out from your X2Go session. Just open a terminal and execute:

```
$ hostname
```



This will give you the full login name (like “*gligar04.gastly.os*” but the hostname in your situation may be slightly different). You should set the same name to resume the session the next time. Just add this full hostname into “login hostname” section in your X2Go session (see [subsection 20.2.2](#)).

# Chapter 21

## HPC-UGent GPGPU cluster

### 21.1 Submitting jobs

To submit jobs to the HPC-UGent GPU cluster nicknamed `joltik`, first use:

```
$ module swap cluster/joltik
```

Then use the familiar `qsub`, `qstat`, etc. commands, taking into account the guidelines outlined in section [21.3](#).

#### 21.1.1 Interactive jobs

To interactively experiment with GPUs, you can submit an interactive job using `qsub -I` (and request one or more GPUs, see section [21.3](#)).

Note that due to a bug in Slurm you will currently not be able to be able to interactively use MPI software that requires access to the GPUs. If you need this, please contact use via `hpc@ugent.be`.

### 21.2 Hardware

See <https://www.ugent.be/hpc/en/infrastructure/overzicht.htm>.

### 21.3 Requesting (GPU) resources

There are 2 main ways to ask for GPUs as part of a job:

- Either as a node property (similar to the number of cores per node specified via `ppn`) using `-l nodes=X:ppn=Y:gpus=Z` (where the `ppn=Y` is optional), or as a separate resource request (similar to the amount of memory) via `-l gpus=Z`. Both notations give exactly the same result. The `-l gpus=Z` is convenient if you only need one node and you are fine with the default number of cores per GPU. The `-l nodes=...:gpus=Z` notation is

required if you want to run with full control or in multinode cases like MPI jobs. If you do not specify the number of GPUs by just using `-l gpus`, you get by default 1 GPU.

- As a resource of its own, via `--gpus X`. In this case however, you are *not* guaranteed that the GPUs are on the same node, so your script or code must be able to deal with this.

Some background:

- The GPUs are constrained to the jobs (like the CPU cores), but do not run in so-called “exclusive” mode.
- The GPUs run with the so-called “persistence daemon”, so the GPUs is not re-initialised between jobs.

## 21.4 Attention points

Some important attention points:

- For MPI jobs, we recommend the (new) wrapper `mypmirun` from the `vsc-mympirun` module (`pmi` is the background mechanism to start the MPI tasks, and is different from the usual `mpirun` that is used by the `mympirun` wrapper). At some later point, we *might* promote the `mypmirun` tool or rename it, to avoid the confusion in the naming).
- Sharing GPUs requires MPS. The Slurm built-in MPS does not really do what you want, so we will provide integration with `mypmirun` and `wurker`.
- For parallel work, we are working on a `wurker` wrapper from the `vsc-mympirun` module that supports GPU placement and MPS, without any limitations wrt the requested resources (i.e. also support the case where GPUs are spread heterogenous over nodes from using the `--gpus Z` option).
- Both `mypmirun` and `wurker` will try to do the most optimised placement of cores and tasks, and will provide 1 (optimal) GPU per task/MPI rank, and set one so-called *visible device* (i.e. `CUDA_VISIBLE_DEVICES` only has 1 ID). The actual devices are not constrained to the ranks, so you can access all devices requested in the job. *We know that at this moment, this is not working properly, but we are working on this. We advise against trying to fix this yourself.*

## 21.5 Software with GPU support

Use `module avail` to check for centrally installed software.

The subsections below only cover a couple of installed software packages, more are available.

### 21.5.1 GROMACS

Please consult `module avail GROMACS` for a list of installed versions.

### 21.5.2 Horovod

Horovod can be used for (multi-node) multi-GPU TensorFlow/PyTorch calculations.

Please consult module avail Horovod for a list of installed versions.

Horovod supports TensorFlow, Keras, PyTorch and MxNet (see <https://github.com/horovod/horovod#id9>), but should be run as an MPI application with mypmirun. (Horovod also provides its own wrapper horovodrun, not sure if it handles placement and others correctly).

At least for simple TensorFlow benchmarks, it looks like Horovod is a bit faster than usual autodetect multi-GPU TensorFlow without horovod, but it comes at the cost of the code modifications to use horovod.

### 21.5.3 PyTorch

Please consult module avail PyTorch for a list of installed versions.

### 21.5.4 TensorFlow

Please consult module avail TensorFlow for a list of installed versions.

**Note:** for running TensorFlow calculations on multiple GPUs and/or on more than one workernode, use **Horovod**, see section [21.5.2](#).

#### Example TensorFlow job script

— TensorFlow\_GPU\_joltik.sh —

```
1 #!/bin/bash
2 #PBS -l walltime=1:0:0
3 #PBS -l nodes=1:ppn=32,gpus=4
4
5 module load TensorFlow/1.14.0-fosscuda-2019.08-Python-3.7.2
6
7 cd $PBS_O_WORKDIR
8 python example.py
```

## 21.6 Getting help

In case of questions or problems, please contact the UGent HPC team via hpc@ugent.be, and clearly indicate that your question relates to the joltik cluster by adding [joltik] in the email subject.

## Part III

# Software-specific Best Practices

# Chapter 22

## MATLAB

### 22.1 Why is the MATLAB compiler required?

The main reason behind this alternative way of using MATLAB is licensing: only a limited number of MATLAB sessions can be active at the same time. However, once the MATLAB program is compiled using the MATLAB compiler, the resulting stand-alone executable can be run without needing to contact the license server.

Note that a license is required for the MATLAB Compiler, see <https://nl.mathworks.com/help/compiler/index.html>. If the `mcc` command is provided by the MATLAB installation you are using, the MATLAB compiler can be used as explained below.

Only a limited amount of MATLAB sessions can be active at the same time because there are only a limited amount of MATLAB research licenses available on the UGent MATLAB license server. If each job would need a license, licenses would quickly run out.

### 22.2 How to compile MATLAB code

Compiling MATLAB code can only be done from the login nodes, because only login nodes can access the MATLAB license server, workernodes on clusters can not.

To access the MATLAB compiler, the MATLAB module should be loaded first. Make sure you are using the same MATLAB version to compile and to run the compiled MATLAB program.

```
$ module avail MATLAB
-----/apps/gent/victini/modules/all-----
    MATLAB/2016b      MATLAB/2017b      MATLAB/2018a (D)
$ module load MATLAB/2018a
```

After loading the MATLAB module, the `mcc` command can be used. To get help on `mcc`, you can run `mcc -?`.

To compile a standalone application, the `-m` flag is used (the `-v` flag means verbose output). To show how `mcc` can be used, we use the `magicsquare` example that comes with MATLAB.

First, we copy the `magicsquare.m` example that comes with MATLAB to `example.m`:

```
$ cp $EBROOTMATLAB/extern/examples/compiler/magicsquare.m example.m
```

To compile a MATLAB program, use `mcc -mv`:

```
$ mcc -mv example.m
Opening log file: /user/home/gent/vsc400/vsc40000/java.log.34090
Compiler version: 6.6 (R2018a)
Dependency analysis by REQUIREMENTS.
Parsing file "/user/home/gent/vsc400/vsc40000/example.m"
    (Referenced from: "Compiler Command Line").
Deleting 0 temporary MEX authorization files.
Generating file "/user/home/gent/vsc400/vsc40000/readme.txt".
Generating file "run\_example.sh".
```

### 22.2.1 Libraries

To compile a MATLAB program that *needs a library*, you can use the `-I library_path` flag. This will tell the compiler to also look for files in `library_path`.

It's also possible to use the `-a path` flag. That will result in all files under the `path` getting added to the final executable.

For example, the command `mcc -mv example.m -I examplelib -a datafiles` will compile `example.m` with the MATLAB files in `examplelib`, and will include all files in the `datafiles` directory in the binary it produces.

### 22.2.2 Memory issues during compilation

If you are seeing Java memory issues during the compilation of your MATLAB program on the login nodes, consider tweaking the default maximum heap size (128M) of Java using the `_JAVA_OPTIONS` environment variable with:

```
$ export _JAVA_OPTIONS="-Xmx64M"
```

The MATLAB compiler spawns multiple Java processes, and because of the default memory limits that are in effect on the login nodes, this might lead to a crash of the compiler if it's trying to create too many Java processes. If we lower the heap size, more Java processes will be able to fit in memory.

Another possible issue is that the heap size is too small. This could result in errors like:

```
Error: Out of memory
```

A possible solution to this is by setting the maximum heap size to be bigger:

```
$ export _JAVA_OPTIONS="-Xmx512M"
```

## 22.3 Multithreading

MATLAB can only use the cores in a single workernode (unless the Distributed Computing toolbox is used, see <https://nl.mathworks.com/products/distriben.html>).

The amount of workers used by MATLAB for the parallel toolbox can be controlled via the `parpool` function: `parpool(16)` will use 16 workers. It's best to specify the amount of workers, because otherwise you might not harness the full compute power available (if you have too few workers), or you might negatively impact performance (if you have too much workers). By default, MATLAB uses a fixed number of workers (12).

You should use a number of workers that is equal to the number of cores you requested when submitting your job script (the `ppn` value, see [subsection 4.6.1](#)). You can determine the right number of workers to use via the following code snippet in your MATLAB program:

— parpool.m —

```
1 % specify the right number of workers (as many as there are cores available in the
   job) when creating the parpool
2 c = parcluster('local')
3 pool = parpool(c.NumWorkers)
```

See also [the parpool documentation](#).

## 22.4 Java output logs

Each time MATLAB is executed, it generates a Java log file in the users home directory. The output log directory can be changed using:

```
$ MATLAB_LOG_DIR=<OUTPUT_DIR>
```

where `<OUTPUT_DIR>` is the name of the desired output directory. To create and use a temporary directory for these logs:

```
# create unique temporary directory in $TMPDIR (or /tmp/$USER if $TMPDIR is not
   defined)
# instruct MATLAB to use this directory for log files by setting $MATLAB_LOG_DIR
$ export MATLAB_LOG_DIR=$(mktemp -d -p $TMPDIR:-/tmp/$USER)
```

```
$ rm -rf $MATLAB_LOG_DIR
```

## 22.5 Cache location

When running, MATLAB will use a cache for performance reasons. This location and size of this cache can be changed trough the `MCR_CACHE_ROOT` and `MCR_CACHE_SIZE` environment variables.

The snippet below would set the maximum cache size to 1024MB and the location to `/tmp/`

testdirectory.

```
$ export MATLAB_CACHE_ROOT=/tmp/testdirectory
$ export MATLAB_CACHE_SIZE=1024M
```

So when MATLAB is running, it can fill up to 1024MB of cache in /tmp/testdirectory.

## 22.6 MATLAB job script

All of the tweaks needed to get MATLAB working have been implemented in an example job script. This job script is also available on the HPC.

— jobscript.sh —

```
1 #!/bin/bash
2 #PBS -l nodes=1:ppn=1
3 #PBS -l walltime=1:0:0
4 #
5 # Example (single-core) MATLAB job script
6 # see http://hpcugent.github.io/vsc_user_docs/
7 #
8
9 # make sure the MATLAB version matches with the one used to compile the MATLAB
10 # program!
11 module load MATLAB/2018a
12
13 # use temporary directory (not $HOME) for (mostly useless) MATLAB log files
14 # subdir in $TMPDIR (if defined, or /tmp otherwise)
15 export MATLAB_LOG_DIR=$(mktemp -d -p ${TMPDIR:-/tmp})
16
17 # configure MATLAB Compiler Runtime cache location & size (1GB)
18 # use a temporary directory in /dev/shm (i.e. in memory) for performance reasons
19 export MCR_CACHE_ROOT=$(mktemp -d -p /dev/shm)
20 export MCR_CACHE_SIZE=1024MB
21
22 # change to directory where job script was submitted from
23 cd $PBS_O_WORKDIR
24
25 # run compiled example MATLAB program 'example', provide '5' as input argument to
26 # the program
# $EBROOTMATLAB points to MATLAB installation directory
./run_example.sh $EBROOTMATLAB 5
```

# Chapter 23

# OpenFOAM

In this chapter, we outline best practices for using the centrally provided OpenFOAM installations on the VSC HPC infrastructure.

## 23.1 Different OpenFOAM releases

There are currently three different sets of versions of OpenFOAM available, each with its own versioning scheme:

- OpenFOAM versions released via <http://openfoam.com>: v3.0+, v1706
  - see also <http://openfoam.com/history/>
- OpenFOAM versions released via <https://openfoam.org>: v4.1, v5.0
  - see also <https://openfoam.org/download/history/>
- OpenFOAM versions released via <http://wikki.gridcore.se/foam-extend>: v3.1

Make sure you know which flavor of OpenFOAM you want to use, since there are important differences between the different versions w.r.t. features. If the OpenFOAM version you need is not available yet, see [section 11.5](#).

## 23.2 Documentation & training material

The best practices outlined here focus specifically on the use of OpenFOAM on the VSC HPC infrastructure. As such, they are intended to augment the existing OpenFOAM documentation rather than replace it. For more general information on using OpenFOAM, please refer to:

- OpenFOAM websites:
  - <https://openfoam.com>

- <https://openfoam.org>
- <http://wikki.gridcore.se/foam-extend>
- OpenFOAM user guides:
  - <https://www.openfoam.com/documentation/user-guide>
  - <https://cfd.direct/openfoam/user-guide/>
- OpenFOAM C++ source code guide: <https://cpp.openfoam.org>
- tutorials: <https://wiki.openfoam.com/Tutorials>
- recordings of "Introduction to OpenFOAM" training session at UGent (May 2016):  
<https://www.youtube.com/playlist?list=PLqjhJj6bcnY9RoIgzeF6xDh5L9bbeK3BL>

Other useful OpenFOAM documentation:

- [https://github.com/ParticulateFlow/OSCCAR-doc/blob/master/openFoamUserManual\\_PFM.pdf](https://github.com/ParticulateFlow/OSCCAR-doc/blob/master/openFoamUserManual_PFM.pdf)
- <http://www.dicat.unige.it/guerrero/openfoam.html>

## 23.3 Preparing the environment

To prepare the environment of your shell session or job for using OpenFOAM, there are a couple of things to take into account.

### 23.3.1 Picking and loading an OpenFOAM module

First of all, you need to pick and load one of the available OpenFOAM modules. To get an overview of the available modules, run ‘module avail OpenFOAM’. For example:

```
$ module avail OpenFOAM
-----
/apps/gent/C07/sandybridge/modules/all -----
OpenFOAM/v1712-foss-2017b    OpenFOAM/4.1-intel-2017a
OpenFOAM/v1712-intel-2017b   OpenFOAM/5.0-intel-2017a
OpenFOAM/2.2.2-intel-2017a   OpenFOAM/5.0-intel-2017b
OpenFOAM/2.2.2-intel-2018a   OpenFOAM/5.0-20180108-foss-2018a
OpenFOAM/2.3.1-intel-2017a   OpenFOAM/5.0-20180108-intel-2017b
OpenFOAM/2.4.0-intel-2017a   OpenFOAM/5.0-20180108-intel-2018a
OpenFOAM/3.0.1-intel-2016b   OpenFOAM/6-intel-2018a          (D)
OpenFOAM/4.0-intel-2016b
```

To pick a module, take into account the differences between the different OpenFOAM versions w.r.t. features and API (see also [section 23.1](#)). If multiple modules are available that fulfill your requirements, give preference to those providing a more recent OpenFOAM version, and to the ones that were installed with a more recent compiler toolchain; for example, prefer a module that includes intel-2020b in its name over one that includes intel-2020a.

To prepare your environment for using OpenFOAM, load the OpenFOAM module you have picked;

```
$ module load OpenFOAM/4.1-intel-2017a
```

### 23.3.2 Sourcing the `$FOAM_BASH` script

OpenFOAM provides a script that you should source to further prepare the environment. This script will define some additional environment variables that are required to use OpenFOAM. The OpenFOAM modules define an environment variable named `FOAM_BASH` that specifies the location to this script. Assuming you are using `bash` in your shell session or job script, you should always run the following command after loading an OpenFOAM module:

```
$ source $FOAM_BASH
```

### 23.3.3 Defining utility functions used in tutorial cases

If you would like to use the `getApplication`, `runApplication`, `runParallel`, `cloneCase` and/or `compileApplication` functions that are used in OpenFOAM tutorials, you also need to source the `RunFunctions` script:

```
$ source $WM_PROJECT_DIR/bin/tools/RunFunctions
```

Note that this needs to be done **after** sourcing `$FOAM_BASH` to make sure `$WM_PROJECT_DIR` is defined.

### 23.3.4 Dealing with floating-point errors

If you are seeing Floating Point Exception errors, you can undefine the `$FOAM_SIGFPE` environment variable that is defined by the `$FOAM_BASH` script as follows:

```
$ unset $FOAM_SIGFPE
```

Note that this only prevents OpenFOAM from propagating floating point exceptions, which then results in terminating the simulation. However, it does not prevent that illegal operations (like a division by zero) are being executed; if NaN values appear in your results, floating point errors are occurring.

As such, **you should *not* use this in production runs**. Instead, you should track down the root cause of the floating point errors, and try to prevent them from occurring at all.

## 23.4 OpenFOAM workflow

The general workflow for OpenFOAM consists of multiple steps. Prior to running the actual simulation, some *pre-processing* needs to be done:

- generate the mesh;
- decompose the domain into subdomains using `decomposePar` (only for parallel OpenFOAM simulations);

After running the simulation, some *post-processing* steps are typically performed:

- reassemble the decomposed domain using `reconstructPar` (only for parallel OpenFOAM simulations, and optional since some postprocessing can also be done on decomposed cases);
- evaluate or further process the simulation results, either visually using ParaView (for example, via the `paraFoam` tool; use `paraFoam -builtin` for decomposed cases) or using command-line tools like `postProcess`; see also <https://cfd.direct/openfoam/user-guide/postprocessing>.

Depending on the size of the domain and the desired format of the results, these pre- and post-processing steps can be run either before/after the job running the actual simulation, either on the HPC infrastructure or elsewhere, or as a part of the job that runs the OpenFOAM simulation itself.

Do make sure you are using the same OpenFOAM version in each of the steps. Meshing can be done sequentially (i.e., on a single core) using for example `blockMesh`, or in parallel using more advanced meshing tools like `snappyHexMesh`, which is highly recommended for large cases. For more details, see <https://cfd.direct/openfoam/user-guide/mesh/>.

One important aspect to keep in mind for ‘offline’ pre-processing is that the domain decomposition needs to match the number of processor cores that are used for the actual simulation, see also [subsection 23.5.3](#).

For post-processing you can either download the simulation results to a local workstation, or do the post-processing (interactively) on the HPC infrastructure, for example on the login nodes or using an interactive session on a workernode. This may be interesting to avoid the overhead of downloading the results locally.

## 23.5 Running OpenFOAM in parallel

For general information on running OpenFOAM in parallel, see <https://cfd.direct/openfoam/user-guide/running-applications-parallel/>.

### 23.5.1 The `-parallel` option

When running OpenFOAM in parallel, **do not forget to specify the `-parallel` option**, to avoid running the same OpenFOAM simulation  $N$  times, rather than running it once using  $N$  processor cores.

You can check whether OpenFOAM was run in parallel in the output of the main command: the OpenFOAM header text should only be included *once* in the output, and it should specify a value different than ‘1’ in the `nProcs` field. Note that most pre- and post-processing utilities like `blockMesh`, `decomposePar` and `reconstructPar` can not be run in parallel.

### 23.5.2 Using `mympirun`

It is highly recommended to use the `mympirun` command when running parallel OpenFOAM simulations rather than the standard `mpirun` command; see [chapter 24](#) for more information on

mympirun.

See [section 24.1](#) for how to get started with mympirun.

To pass down the environment variables required to run OpenFOAM (which were defined by the \$FOAM\_BASH script, see [section 23.3](#)) to each of the MPI processes used in a parallel OpenFOAM execution, the \$MYMPIRUN\_VARIABLESPREFIX environment variable must be defined as follows, prior to running the OpenFOAM simulation with mympirun:

```
$ export MYMPIRUN_VARIABLESPREFIX=WM_PROJECT,FOAM,MPI
```

Whenever you are instructed to use a command like `mpirun -np <N> ...`, use `mympirun ...` instead; mympirun will automatically detect the number of processor cores that are available (see also [section 24.2](#)).

### 23.5.3 Domain decomposition and number of processor cores

To run OpenFOAM in parallel, you must decompose the domain into multiple subdomains. Each subdomain will be processed by OpenFOAM on one processor core.

Since mympirun will automatically use all available cores, you need to make sure that the number of subdomains matches the number of processor cores that will be used by mympirun. If not, you may run into an error message like:

```
number of processor directories = 4 is not equal to the number of processors = 16
```

In this case, the case was decomposed in 4 subdomains, while the OpenFOAM simulation was started with 16 processes through mympirun. To match the number of subdomains and the number of processor cores used by mympirun, you should either:

- adjust the value for `numberOfSubdomains` in `system/decomposeParDict` (and adjust the value for `n` accordingly in the domain decomposition coefficients), and run `decomposePar` again; or
- submit your job requesting exactly the same number of processor cores as there are subdomains (see the `processor*` directories that were created by `decomposePar`)

See [section 24.2](#) to control the number of process mympirun will start.

This is interesting if you require more memory per core than is available by default. Note that the decomposition method being used (which is specified in `system/decomposeParDict`) has significant impact on the performance of a parallel OpenFOAM simulation. Good decomposition methods (like `metis` or `scotch`) try to limit communication overhead by minimising the number of processor boundaries.

To visualise the processor domains, use the following command:

```
$ mympirun foamToVTK -parallel -constant -time 0 -excludePatches '(".*.")'
```

and then load the VTK files generated in the VTK folder into ParaView.

## 23.6 Running OpenFOAM on a shared filesystem

OpenFOAM is known to significantly stress shared filesystems, since a lot of (small) files are generated during an OpenFOAM simulation. Shared filesystems are typically optimised for dealing with (a small number of) large files, and are usually a poor match for workloads that involve a (very) large number of small files (see also [http://www.prace-ri.eu/IMG/pdf/IO-profiling\\_with\\_Darshan-2.pdf](http://www.prace-ri.eu/IMG/pdf/IO-profiling_with_Darshan-2.pdf)).

Take into account the following guidelines for your OpenFOAM jobs, which all relate to input parameters for the OpenFOAM simulation that you can specify in `system/controlDict` (see also <https://cfd.direct/openfoam/user-guide/controlDict>).

- instruct OpenFOAM to write out results at a reasonable frequency, **certainly not for every single time step**; you can control this using the `writeControl`, `writeInterval`, etc. keywords;
- consider only retaining results for the last couple of time steps, see the `purgeWrite` keyword;
- consider writing results for only part of the domain (e.g., a line or plane) rather than the entire domain;
- if you do not plan to change the parameters of the OpenFOAM simulation while it is running, set `runTimeModifiable` to **false** to avoid that OpenFOAM re-reads each of the `system/*Dict` files at every time step;
- if the results per individual time step are large, consider setting `writeCompression` to `true`;

For modest OpenFOAM simulations where a single workernode suffices, consider using the local disk of the workernode as working directory (accessible via `$VSC_SCRATCH_NODE`), rather than the shared `$VSC_SCRATCH` filesystem. **Certainly do not use a subdirectory in `$VSC_HOME` or `$VSC_DATA` as working directory for OpenFOAM simulations**, since these shared filesystems are too slow for these type of workloads.

For large parallel OpenFOAM simulations on the UGent Tier-2 clusters, consider using the alternative shared scratch filesystem `$VSC_SCRATCH_PHANPY` (see [subsection 6.2.1](#)).

These guidelines are especially important for large-scale OpenFOAM simulations that involve more than a couple of dozen of processor cores.

## 23.7 Using own solvers with OpenFOAM

See <https://cfd.direct/openfoam/user-guide/compiling-applications/>.

## 23.8 Example OpenFOAM job script

Example job script for damBreak OpenFOAM tutorial (see also <https://cfd.direct/openfoam/user-guide/dambreak>):

## — OpenFOAM\_damBreak.sh —

```
1 #!/bin/bash
2 #PBS -l walltime=1:0:0
3 #PBS -l nodes=1:ppn=4
4 # check for more recent OpenFOAM modules with 'module avail OpenFOAM'
5 module load OpenFOAM/6-intel-2018a
6 source $FOAM_BASH
7 # purposely not specifying a particular version to use most recent mympirun
8 module load vsc-mympirun
9 # let mympirun pass down relevant environment variables to MPI processes
10 export MYMPIRUN_VARIABLESPREFIX=WM_PROJECT,FOAM,MPI
11 # set up working directory
12 # (uncomment one line defining $WORKDIR below)
13 #export WORKDIR=$VSC_SCRATCH/$PBS_JOBID # for small multi-node jobs
14 #export WORKDIR=$VSC_SCRATCH_PHANPY/$PBS_JOBID # for large multi-node jobs
15 export WORKDIR=$VSC_SCRATCH_NODE/$PBS_JOBID # for single-node jobs
16 mkdir -p $WORKDIR
17 # damBreak tutorial, see also https://cfd.direct/openfoam/user-guide/dambreak
18 cp -r $FOAM_TUTORIALS/multiphase/interFoam/laminar/damBreak/damBreak $WORKDIR
19 cd $WORKDIR/damBreak
20 echo "working directory: $PWD"
21 # pre-processing: generate mesh
22 echo "start blockMesh: $(date)"
23 blockMesh &> blockMesh.out
24 # pre-processing: decompose domain for parallel processing
25 echo "start decomposePar: $(date)"
26 decomposePar &> decomposePar.out
27 # run OpenFOAM simulation in parallel
28 # note:
29 # * the -parallel option is strictly required to actually run in parallel!
30 # without it, the simulation is run N times on a single core...
31 # * mympirun will use all available cores in the job by default,
32 # you need to make sure this matches the number of subdomains!
33 echo "start interFoam: $(date)"
34 mympirun --output=interFoam.out interFoam -parallel
35 # post-processing: reassemble decomposed domain
36 echo "start reconstructPar: $(date)"
37 reconstructPar &> reconstructPar.out
38 # copy back results, i.e. all time step directories: 0, 0.05, ..., 1.0 and inputs
39 export RESULTS_DIR=$VSC_DATA/results/$PBS_JOBID
40 mkdir -p $RESULTS_DIR
41 cp -a *.out [0-9.]* constant system $RESULTS_DIR
42 echo "results copied to $RESULTS_DIR at $(date)"
43 # clean up working directory
44 cd $HOME
45 rm -rf $WORKDIR
```

# Chapter 24

## Mympirun

mympirun is a tool to make it easier for users of HPC clusters to run MPI programs with good performance. We strongly recommend to use mympirun instead of impirun.

In this chapter, we give a high-level overview. For a more detailed description of all options, see the [vsc-mympirun README](#).

### 24.1 Basic usage

Before using mympirun, we first need to load its module:

```
$ module load vsc-mympirun
```

As an exception, we don't specify a version here. The reason is that we want to ensure that the latest version of the mympirun script is always used, since it may include important bug fixes or improvements.

The most basic form of using mympirun is `mympirun [mympirun options] your_program [your_program options]`.

For example, to run a program named `example` and give it a single argument (5), we can run it with `mympirun example 5`.

### 24.2 Controlling number of processes

There are four options you can choose from to control the number of processes mympirun will start. In the following example, the program `mpi_hello` prints a single line: Hello world from processor <node> ... (the sourcecode of `mpi_hello` is [available in the vsc-mympirun repository](#)).

By default, mympirun starts one process per *core* on every node you assigned. So if you assigned 2 nodes with 16 cores each, mympirun will start  $2 \cdot 16 = 32$  test processes in total.

### 24.2.1 --hybrid/-h

This is the most commonly used option for controlling the number of processing.

The --hybrid option requires a positive number. This number specifies the number of processes started on each available physical *node*. It will ignore the number of available *cores* per node.

```
$ echo $PBS_NUM_NODES
2
$ mympirun -hybrid 2 ./mpi_hello
Hello world from processor node2400.golett.os, rank 1 out of 4 processors
Hello world from processor node2401.golett.os, rank 3 out of 4 processors
Hello world from processor node2401.golett.os, rank 2 out of 4 processors
Hello world from processor node2400.golett.os, rank 0 out of 4 processors
```

### 24.2.2 Other options

There's also --universe, which sets the exact amount of processes started by mympirun; --double, which uses double the amount of processes it normally would; and --multi that does the same as --double, but takes a multiplier (instead of the implied factor 2 with --double).

See [vsc-mympirun README](#) for a detailed explanation of these options.

## 24.3 Dry run

You can do a so-called “dry run”, which doesn't have any side-effects, but just prints the command that mympirun would execute. You enable this with the --dry-run flag:

```
$ mympirun --dry-run ./mpi_hello
mpirun ... -genv I_MPI_FABRICS shm:dapl ... -np 16 ... ./mpi_hello
```

## 24.4 FAQ

### 24.4.1 mympirun seems to ignore its arguments

For example, we have a simple script (`./hello.sh`):

```
1 #!/bin/bash
2 echo "hello world"
```

And we run it like `mympirun ./hello.sh --output output.txt`.

To our surprise, this doesn't output to the file `output.txt`, but to standard out! This is because mympirun expects the program name and the arguments of the program to be its last arguments. Here, the `--output output.txt` arguments are passed to `./hello.sh` instead of to mympirun. The correct way to run it is:

```
$ mympirun --output output.txt ./hello.sh
```

#### **24.4.2 I have other problems/questions**

Please don't hesitate to contact hpc@ugent.be.

# Chapter 25

## Singularity

### 25.1 What is Singularity?

Singularity is an open-source computer program that performs operating-system-level virtualization (also known as containerisation).

One of the main uses of Singularity is to bring containers and reproducibility to scientific computing and the high-performance computing (HPC) world. Using Singularity containers, developers can work in reproducible environments of their choosing and design, and these complete environments can easily be copied and executed on other platforms.

For more general information about the use of Singularity, please see the official documentation at <https://www.sylabs.io/docs/>.

This documentation only covers aspects of using Singularity on the UGent-HPC infrastructure.

### 25.2 Restrictions on image location

Some restrictions have been put in place on the use of Singularity. This is mainly done for performance reasons and to avoid that the use of Singularity impacts other users on the system.

The Singularity image file must be located on either one of the scratch filesystems, the local disk of the workernode you are using or /dev/shm. The centrally provided `singularity` command will refuse to run using images that are located elsewhere, in particular on the \$VSC\_HOME, /apps or \$VSC\_DATA filesystems.

In addition, this implies that running containers images provided via a URL (e.g., `shub://...` or `docker://...`) will not work.

If these limitations are a problem for you, please let us know via `hpc@ugent.be`.

## 25.3 Available filesystems

All HPC-UGent shared filesystems will be readily available in a Singularity container, including the home, data and scratch filesystems, and they will be accessible via the familiar \$VSC\_HOME, \$VSC\_DATA\* and \$VSC\_SCRATCH\* environment variables.

## 25.4 Singularity Images

### 25.4.1 Creating Singularity images

Creating new Singularity images or converting Docker images requires admin privileges, which is obviously not available on the UGent-HPC infrastructure.

As an alternative, you can either:

- install Singularity on a local Linux system you have administrator privileges on, create your Singularity images there and upload them to the UGent-HPC infrastructure
- create Singularity images via Singularity Hub (<https://www.singularity-hub.org/>), and download them on the UGent-HPC infrastructure

We strongly recommend the use of Singularity Hub, see <https://singularity-hub.org/> for more information.

### 25.4.2 Converting Docker images

For more information on converting existing Docker images to Singularity images, see [https://www.sylabs.io/guides/3.4/user-guide/singularity\\_and\\_docker.html](https://www.sylabs.io/guides/3.4/user-guide/singularity_and_docker.html). Note that this can also be done via Singularity Hub, see <https://singularity-hub.org/>.

## 25.5 Execute our own script within our container

Copy testing image from /apps/gent/tutorials/Singularity to \$VSC\_SCRATCH:

```
$ cp /apps/gent/tutorials/Singularity/CentOS7_EasyBuild.img $VSC_SCRATCH/singularity
```

Create a job script like:

```
1 #!/bin/sh
2
3 #PBS -o singularity.output
4 #PBS -e singularity.error
5 #PBS -l nodes=1:ppn=1
6 #PBS -l walltime=12:00:00
7
8
9 singularity exec $VSC_SCRATCH/singularity/CentOS7_EasyBuild.img ~/my_script.sh
```

Create an example myscript.sh:

```
1 #!/bin/bash
2
3 # prime factors
4 factor 1234567
```

## 25.6 Tensorflow example

We already have a Tensorflow example image, but you can also convert the Docker image (see <https://hub.docker.com/r/tensorflow/tensorflow>) to a Singularity image yourself

Copy testing image from /apps/gent/tutorials to \$VSC\_SCRATCH:

```
$ cp /apps/gent/tutorials/Singularity/Ubuntu14.04_tensorflow.img $VSC_SCRATCH
```

```
1 #!/bin/sh
2 #
3 #
4 #PBS -o tensorflow.output
5 #PBS -e tensorflow.error
6 #PBS -l nodes=1:ppn=4
7 #PBS -l walltime=12:00:00
8 #
9
10 singularity exec $VSC_SCRATCH/Ubuntu14.04_tensorflow.img python ~/linear_regression.py
```

You can download linear\_regression.py from [the official Tensorflow repository](#).

## 25.7 MPI example

It is also possible to execute MPI jobs within a container, but the following requirements apply:

- Mellanox IB libraries must be available from the container (install the infiniband-diags, libmlx5-1 and libmlx4-1 OS packages)
- Use modules within the container (install the environment-modules or lmod package in your container)
- Load the required module(s) before singularity execution.
- Set C\_INCLUDE\_PATH variable in your container if it is required during compilation time (`export C_INCLUDE_PATH=/usr/include/x86_64-linux-gnu/:$C_INCLUDE_PATH` for Debian flavours)

Copy the testing image from /apps/gent/tutorials/Singularity to \$VSC\_SCRATCH

```
$ cp /apps/gent/tutorials/Singularity/Debian8_UgentMPI.img $VSC_SCRATCH/singularity
```

For example to compile an [MPI example](#):

```
$ module load intel
$ singularity shell $VSC_SCRATCH/singularity/Debian8_UGentMPI.img
$ export LANG=C
$ export C_INCLUDE_PATH=/usr/include/x86_64-linux-gnu/:$C_INCLUDE_PATH
$ mpicc ompi/examples/ring_c.c -o ring_debian
$ exit
```

Example MPI job script:

```
1 #!/bin/sh
2
3 #PBS -N mpi
4 #PBS -o singularitympi.output
5 #PBS -e singularitympi.error
6 #PBS -l nodes=2:ppn=15
7 #PBS -l walltime=12:00:00
8
9 module load intel vsc-mympirun
10 mympirun --impi-fallback singularity exec $VSC_SCRATCH/singularity/Debian8_UGentMPI.
     img ~/ring_debian
```

# Chapter 26

## SCOOP

SCOOP (Scalable COncurrent Operations in Python) is a distributed task module allowing concurrent parallel programming on various environments, from heterogeneous grids to supercomputers. It is an alternative to the worker framework, see [chapter 13](#).

It can be used for projects that require lots of (small) tasks to be executed.

The `myscoop` script makes it very easy to use SCOOP, even in a multi-node setup.

### 26.1 Loading the module

Before using `myscoop`, you first need to load the `vsc-mympirun-scoop` module. We don't specify a version here (this is an exception, for most other modules you should, see [subsection 4.1.7](#)) because newer versions might include important bug fixes or performance improvements.

```
$ module load vsc-mympirun-scoop
```

### 26.2 Write a worker script

A Python worker script implements both the main program, and (typically) the small task function that needs to be executed a large amount of times.

This is done using the functionality provided by the `scoop` Python module, for example `futures.map` (see also <https://scoop.readthedocs.org/>).

First, the necessary imports need to be specified:

```
1 import sys
2 from scoop import futures
```

A Python function must be implemented for the core task, for example to compute the square of a number:

```
1 def square(x):
2     return x*x
```

The main function then applies this simple function to a range of values specified as an argument. Note that it should be guarded by a conditional (`if __name__ == "__main__"`) to make sure it is only executed when executing the script (and not when importing from it):

```

1 if __name__ == "__main__":
2
3     # obtain n from first command line argument
4     n = int(sys.argv[1])
5
6     # compute the square of the first n numbers, in parallel using SCOOP
7     # functionality
8     squares = futures.map(square, range(n))    # note: returns an iterator
9
10    print("First %d squares: %s" % (n, list(squares)))

```

## 26.3 Executing the program

To execute the Python script implementing the task and main function in a SCOOP environment, specify to the `python` command to use the `scoop` module:

```
$ python -m scoop squares.py 10000
```

## 26.4 Using myscoop

To execute the SCOOP program in an multi-node environment, where workers are spread across multiple physical systems, simply use `myscoop`: just specify the name of the Python module in which the SCOOP program is implemented, and specify further arguments on the command line.

You will need to make sure that the path to where the Python module is located is listed in `$PYTHONPATH`.

This is an example of a complete job script executing the SCOOP program in parallel in a multi-node job (i.e., 2 nodes with 8 cores each):

— squares\_jobscript.pbs —

```
1 #!/bin/bash
2
3 #PBS -l nodes=2:ppn=8
4
5 module load vsc-mympirun-scoop
6
7 # change to directory where job was submitted from
8 cd $PBS_O_WORKDIR
9
10 # assume squares.py is in current directory
11 export PYTHONPATH=.:$PYTHONPATH
12
13 # compute first 10k squares, in parallel on available cores
14 myscoop --scoop-module=squares 10000
```

Note that you don't need to specify how many workers need to be used; the myscoop command figures this out by itself. This is because myscoop is a wrapper around mympirun (see [chapter 24](#)). In this example, 16 workers (one per available core) will be execute the 10000 tasks one by one until all squares are computed.

To run the same command on the local system (e.g., a login node for testing), add the `--sched=local` option to myscoop.

## 26.5 Example: calculating $\pi$

A more practical example of a worker script is one to compute  $\pi$  using a Monte-Carlo method (see also <https://scoop.readthedocs.org/en/0.6/examples.html#computation-of>).

The `test` function implements a tiny task that is be executed `tries` number of times by each worker. Afterwards, the number of successful tests is determined using the Python `sum` function, and an approximate value of  $\pi$  is computed and returned by `calcPi` so the main function can print it out.

— picalc.py —

```

1  from math import hypot
2  from random import random
3  from scoop import futures
4
5  NAME = 'SCOOP_piCalc'
6
7  # A range is used in this function for python3. If you are using python2,
8  # an xrange might be more efficient.
9  try:
10     range_fn = xrange
11 except:
12     range_fn = range
13
14
15 def test(tries):
16     return sum(hypot(random(), random()) < 1 for i in range_fn(tries))
17
18 # Calculates pi with a Monte-Carlo method. This function calls the function
19 # test "n" times with an argument of "t". Scoop dispatches these
20 # functions interactively accross the available resources.
21 def calcPi(workers, tries):
22     expr = futures.map(test, [tries] * workers)
23     piValue = 4. * sum(expr) / float(workers * tries)
24     return piValue
25
26
27 if __name__ == '__main__':
28     import sys
29     nr_batches = 3000
30     batch_size = 5000
31
32     # Program name and two arguments
33     if len(sys.argv) == 3:
34         try:
35             nr_batches = int(sys.argv[1])
36             batch_size = int(sys.argv[2])
37         except ValueError as ex:
38             sys.stderr.write("ERROR: Two integers expected as arguments: %s\n" % ex)
39             sys.exit(1)
40     elif len(sys.argv) != 1:
41         sys.stderr.write("ERROR: Expects either zero or two integers as arguments.\n")
42         sys.exit(1)
43
44     print("PI=%f (in nr_batches=%d,batch_size=%d)" % (calcPi(nr_batches, batch_size),
45 , nr_batches, batch_size))

```

— picalc\_job\_script.pbs —

```
1 #!/bin/bash
2 #PBS -l nodes=2:ppn=16
3
4 module load vsc-mympirun-scoop
5
6 # change to directory where job was submitted from
7 cd $PBS_O_WORKDIR
8
9 # assume picalc.py is in current directory
10 export PYTHONPATH=.:$PYTHONPATH
11
12 # run 10k batches/workers with a batch size of 5000
13 myscoop --scoop-module=picalc 10000 5000
```

# Chapter 27

## Easybuild

### 27.1 What is Easybuild?

You can use EasyBuild to build and install supported software in your own VSC account, rather than requesting a central installation by the HPC support team.

EasyBuild (<https://easybuilders.github.io/easybuild>) is the software build and installation framework that was created by the HPC-UGent team, and has recently been picked up by HPC sites around the world. It allows you to manage (scientific) software on High Performance Computing (HPC) systems in an efficient way.

### 27.2 When should I use Easybuild?

For general software installation requests, please see [section 11.5](#). However, there might be reasons to install the software yourself:

- applying custom patches to the software that only you or your group are using
- evaluating new software versions prior to requesting a central software installation
- installing (very) old software versions that are no longer eligible for central installation (on new clusters)

### 27.3 Configuring EasyBuild

Before you use EasyBuild, you need to configure it:

#### 27.3.1 Path to sources

This is where EasyBuild can find software sources:

```
$ export EASYBUILD_SOURCEPATH=$VSC_DATA/easybuild/sources:/apps/gent/source
```

- the first directory `$VSC_DATA/easybuild/sources` is where EasyBuild will (try to) automatically download sources if they’re not available yet
- `/apps/gent/source` is the central “cache” for already downloaded sources, and will be considered by EasyBuild before downloading anything

### 27.3.2 Build directory

This directory is where EasyBuild will build software in. To have good performance, this needs to be on a fast filesystem.

```
$ export EASYBUILD_BUILDPATH=${TMPDIR:-/tmp/$USER}
```

On cluster nodes, you can use the fast, in-memory `/dev/shm/$USER` location as a build directory.

### 27.3.3 Software install location

This is where EasyBuild will install the software (and accompanying modules) to.

For example, to let it use `$VSC_DATA/easybuild`, use:

```
$ export EASYBUILD_INSTALLPATH=$VSC_DATA/easybuild/$VSC_OS_LOCAL/
$VSC_ARCH_LOCAL$VSC_ARCH_SUFFIX
```

Using the `$VSC_OS_LOCAL`, `$VSC_ARCH` and `$VSC_ARCH_SUFFIX` environment variables ensures that your install software to a location that is specific to the cluster you are building for.

Make sure you **do not build software on the login nodes**, since the loaded `cluster` module determines the location of the installed software. Software built on the login nodes may not work on the cluster you want to use the software on (see also [section 9.9](#)).

To share custom software installations with members of your VO, replace `$VSC_DATA` with `$VSC_DATA_VO` in the example above.

## 27.4 Using EasyBuild

Before using EasyBuild, you first need to load the EasyBuild module. We don’t specify a version here (this is an exception, for most other modules you should, see [subsection 4.1.7](#)) because newer versions might include important bug fixes.

```
module load EasyBuild
```

### 27.4.1 Installing supported software

EasyBuild provides a large collection of readily available software versions, combined with a particular toolchain version. Use the `--search` (or `-S`) functionality to see which different ‘easycon-

figs' (build recipes, see [http://easybuild.readthedocs.org/en/latest/Concepts\\_and\\_Terminology.html#easyconfig-files](http://easybuild.readthedocs.org/en/latest/Concepts_and_Terminology.html#easyconfig-files)) are available:

```
$ eb -S example-1.2
CFGS1=/apps/gent/C07/sandybridge/software/EasyBuild/3.6.2/lib/python2.7/site-
    packages/easybuild_easyconfigs-3.6.2-py2.7.egg/easybuild/easyconfigs
* $CFGS1/e/example/example-1.2.1-foss-2020a.eb
* $CFGS1/e/example/example-1.2.3-foss-2020b.eb
* $CFGS1/e/example/example-1.2.5-intel-2020a.eb
```

For readily available easyconfigs, just specify the name of the easyconfig file to build and install the corresponding software package:

```
$ eb example-1.2.1-foss-2020a.eb --robot
```

#### 27.4.2 Installing variants on supported software

To install small variants on supported software, e.g., a different software version, or using a different compiler toolchain, use the corresponding `--try-X` options:

To try to install `example v1.2.6`, based on the easyconfig file for `example v1.2.5`:

```
$ eb example-1.2.5-intel-2020a.eb --try-software-version=1.2.6
```

To try to install `example v1.2.5` with a different compiler toolchain:

```
$ eb example-1.2.5-intel-2020a.eb --robot --try-toolchain=intel,2020b
```

#### 27.4.3 Install other software

To install other, not yet supported, software, you will need to provide the required easyconfig files yourself. See [https://easybuild.readthedocs.org/en/latest/Writing\\_easyconfig\\_files.html](https://easybuild.readthedocs.org/en/latest/Writing_easyconfig_files.html) for more information.

### 27.5 Using the installed modules

To use the modules you installed with EasyBuild, extend `$MODULEPATH` to make them accessible for loading:

```
$ module use $EASYBUILD_INSTALLPATH/modules/all
```

It makes sense to put this `module use` command and all `export` commands in your `.bashrc` login script. That way you don't have to type these commands every time you want to use EasyBuild or you want to load modules generated with EasyBuild. See also [the section on `.bashrc` in the “Beyond the basics” chapter of the intro to Linux](#).

# Chapter 28

## Hanythingondemand (HOD)

Hanythingondemand (or HOD for short) is a tool to run a Hadoop (Yarn) cluster on a traditional HPC system.

### 28.1 Documentation

The official documentation for HOD version 3.0.0 and newer is available at <https://hod.readthedocs.org/en/latest/>. The slides of the 2016 HOD training session are available at [http://users.ugent.be/~kehorte/hod\\_20161024.pdf](http://users.ugent.be/~kehorte/hod_20161024.pdf).

This chapter only covers how HOD is installed on the UGent-HPC infrastructure.

### 28.2 Using HOD

Before using HOD, you first need to load the `hod` module. We don't specify a version here (this is an exception, for most other modules you should, see subsection 4.1.7) because newer versions might include important bug fixes.

```
$ module load hod
```

#### 28.2.1 Compatibility with login nodes

The `hod` modules are constructed such that they can be used on the UGent-HPC login nodes, regardless of which `cluster` module is loaded (this is not the case for software installed via modules in general, see section 9.9).

As such, you should experience no problems if you swap to a different cluster module before loading the `hod` module and subsequently running `|hod|`.

For example, this will work as expected:

```
$ module swap cluster/skitty
$ module load hod
$ hod
hanythingondemand - Run services within an HPC cluster
usage: hod <subcommand> [subcommand options]
Available subcommands (one of these must be specified!):
  batch           Submit a job to spawn a cluster on a PBS job controller, run a
  job script, and tear down the cluster when it's done
  clean           Remove stale cluster info.
...
...
```

Note that also modules named hanythingondemand/\* are available. These should however not be used directly, since they may not be compatible with the login nodes (depending on which cluster they were installed for).

### 28.2.2 Standard HOD configuration

The `hod` module will also put a basic configuration in place for HOD, by defining a couple of `$HOD_*` environment variables:

```
$ module load hod
$ env | grep HOD | sort
HOD_BATCH_HOD_MODULE=hanythingondemand/3.2.2-intel-2016b-Python-2.7.12
HOD_BATCH_WORKDIR=$VSC_SCRATCH/hod
HOD_CREATE_HOD_MODULE=hanythingondemand/3.2.2-intel-2016b-Python-2.7.12
HOD_CREATE_WORKDIR=$VSC_SCRATCH/hod
```

By defining these environment variables, we avoid that you have to specify `--hod-module` and `--workdir` when using `hod batch` or `hod create`, since they are strictly required.

If you want to use a different parent working directory for HOD, it suffices to either redefine `$HOD_BATCH_WORKDIR` and `$HOD_CREATE_WORKDIR`, or to specify `--workdir` (which will override the corresponding environment variable).

Changing the HOD module that is used by the HOD backend (i.e., using `--hod-module` or redefining `$HOD_*_HOD_MODULE`) is strongly discouraged.

### 28.2.3 Cleaning up

After HOD clusters terminate, their local working directory and cluster information is typically not cleaned up automatically (for example, because the job hosting an interactive HOD cluster submitted via `hod create` runs out of walltime).

These HOD clusters will still show up in the output of `hod list`, and will be marked as `<job-not-found>`.

You should occasionally clean this up using `hod clean`:

```
$ module list
Currently Loaded Modulefiles:
 1) cluster/victini(default)    2) pbs_python/4.6.0          3) vsc-base/2.4.2
    4) hod/3.0.0-cli

$ hod list
Cluster label   Job ID           State
Hosts
example1         123456        <job-not-found> <none>

$ hod clean
Removed cluster localworkdir directory /user/scratch/gent/vsc400/vsc40000/hod/hod/
123456 for cluster labeled example1
Removed cluster info directory /user/home/gent/vsc400/vsc40000/.config/hod.d/
wordcount for cluster labeled example1

$ module swap cluster/skitty
$ hod list
Cluster label   Job ID           State           Hosts
example2         98765.master19.skitty.gent.vsc  <job-not-found> <none>

$ hod clean
Removed cluster localworkdir directory /user/scratch/gent/vsc400/vsc40000/hod/hod/
/98765.master19.skitty.gent.vsc for cluster labeled example2
Removed cluster info directory /user/home/gent/vsc400/vsc40000/.config/hod.d/
wordcount for cluster labeled example2
```

Note that **only HOD clusters that were submitted to the currently loaded `cluster` module will be cleaned up.**

## 28.3 Getting help

If you have any questions, or are experiencing problems using HOD, you have a couple of options:

- Subscribe to the HOD mailing list via <https://lists.ugent.be/wws/info/hod>, and contact the HOD users and developers at `hod@lists.ugent.be`.
- Contact the UGent HPC team via `hpc@ugent.be`
- Open an issue in the hanythingondemand GitHub repository, via <https://github.com/hpcugent/hanythingondemand/issues>.

## Appendix A

# HPC Quick Reference Guide

Remember to substitute the usernames, login nodes, file names, ... for your own.

Login	
Login	ssh vsc40000@login.hpc.ugent.be
Where am I?	hostname
Copy to HPC	scp foo.txt vsc40000@login.hpc.ugent.be:
Copy from HPC	scp vsc40000@login.hpc.ugent.be:foo.txt .
Setup ftp session	sftp vsc40000@login.hpc.ugent.be

Modules	
List all available modules	module avail
List loaded modules	module list
Load module	module load example
Unload module	module unload example
Unload all modules	module purge
Help on use of module	module help

Jobs	
Submit job with job script script.pbs	qsub script.pbs
Status of job with ID 12345	qstat 12345
Show compute node of job with ID 12345	qstat -n 12345
Delete job with ID 12345	qdel 12345
Status of all your jobs	qstat
Detailed status of your jobs + a list nodes they are running on	qstat -na
Submit Interactive job	qsub -I

Disk quota	
Check your disk quota	See <a href="https://account.vscentrum.be">https://account.vscentrum.be</a>
Disk usage in current directory (.)	du -h .

<b>Worker Framework</b>	
Load worker module	module load worker/1.6.8-intel-2018a Don't forget to specify a version. To list available versions, use module avail worker/
Submit parameter sweep	wsub -batch weather.pbs -data data.csv
Submit job array	wsub -t 1-100 -batch test_set.pbs
Submit job array with prolog and epilog	wsub -prolog pre.sh -batch test_set.pbs -epilog post.sh -t 1-100

## Appendix B

# TORQUE options

### B.1 TORQUE Submission Flags: common and useful directives

Below is a list of the most common and useful directives.

Option	System type	Description
-k	All	Send “stdout” and/or “stderr” to your home directory when the job runs <b>#PBS -k o or #PBS -k e or #PBS -koe</b>
-l	All	Precedes a resource request, e.g., processors, wallclock
-M	All	Send an e-mail messages to an alternative e-mail address <b>#PBS -M me@mymail.be</b>
-m	All	Send an e-mail address when a job begins execution and/or ends or aborts <b>#PBS -m b or #PBS -m be or #PBS -m ba</b>
mem	Shared Memory	Specifies the amount of memory you need for a job. <b>#PBS -l mem=80gb</b>
mpiprocs	Clusters	Number of processes per node on a cluster. This should equal number of processors on a node in most cases. <b>#PBS -l mpiprocs=4</b>
-N	All	Give your job a unique name <b>#PBS -N galaxies1234</b>
-ncpus	Shared Memory	The number of processors to use for a shared memory job. <b>#PBS ncpus=4</b>
-r	All	Control whether or not jobs should automatically re-run from the start if the system crashes or is rebooted. Users with check points might not wish this to happen. <b>#PBS -r n</b> <b>#PBS -r y</b>
select	Clusters	Number of compute nodes to use. Usually combined with the mpiprocs directive <b>#PBS -l select=2</b>

-V	All	Make sure that the environment in which the job <b>runs</b> is the same as the environment in which it was <b>submitted</b> . <b>#PBS -V</b>
Walltime	All	The maximum time a job can run before being stopped. If not used a default of a few minutes is used. Use this flag to prevent jobs that go bad running for hundreds of hours. Format is HH:MM:SS <b>#PBS -l walltime=12:00:00</b>

## B.2 Environment Variables in Batch Job Scripts

TORQUE-related environment variables in batch job scripts.

```
1 # Using PBS - Environment Variables:
2 # When a batch job starts execution, a number of environment variables are
3 # predefined, which include:
4 #
5 #      Variables defined on the execution host.
6 #      Variables exported from the submission host with
7 #          -v (selected variables) and -V (all variables).
8 #      Variables defined by PBS.
9 #
10 # The following reflect the environment where the user ran qsub:
11 # PBS_O_HOST      The host where you ran the qsub command.
12 # PBS_O_LOGNAME  Your user ID where you ran qsub.
13 # PBS_O_HOME     Your home directory where you ran qsub.
14 # PBS_O_WORKDIR  The working directory where you ran qsub.
15 #
16 # These reflect the environment where the job is executing:
17 # PBS_ENVIRONMENT Set to PBS_BATCH to indicate the job is a batch job,
18 #                  or to PBS_INTERACTIVE to indicate the job is a PBS interactive job.
19 # PBS_O_QUEUE    The original queue you submitted to.
20 # PBS_QUEUE     The queue the job is executing from.
21 # PBS_JOBID     The job's PBS identifier.
22 # PBS_JOBNAME   The job's name.
```

**IMPORTANT!!** All PBS directives MUST come before the first line of executable code in your script, otherwise they will be ignored.

When a batch job is started, a number of environment variables are created that can be used in the batch job script. A few of the most commonly used variables are described here.

Variable	Description
PBS_ENVIRONMENT	set to PBS_BATCH to indicate that the job is a batch job; otherwise, set to PBS_INTERACTIVE to indicate that the job is a PBS interactive job.
PBS_JOBID	the job identifier assigned to the job by the batch system. This is the same number you see when you do <i>qstat</i> .
PBS_JOBNAME	the job name supplied by the user

PBS_NODEFILE	the name of the file that contains the list of the nodes assigned to the job . Useful for Parallel jobs if you want to refer the node, count the node etc.
PBS_QUEUE	the name of the queue from which the job is executed
PBS_O_HOME	value of the HOME variable in the environment in which <i>qsub</i> was executed
PBS_O_LANG	value of the LANG variable in the environment in which <i>qsub</i> was executed
PBS_O_LOGNAME	value of the LOGNAME variable in the environment in which <i>qsub</i> was executed
PBS_O_PATH	value of the PATH variable in the environment in which <i>qsub</i> was executed
PBS_O_MAIL	value of the MAIL variable in the environment in which <i>qsub</i> was executed
PBS_O_SHELL	value of the SHELL variable in the environment in which <i>qsub</i> was executed
PBS_O_TZ	value of the TZ variable in the environment in which <i>qsub</i> was executed
PBS_O_HOST	the name of the host upon which the <i>qsub</i> command is running
PBS_O_QUEUE	the name of the original queue to which the job was submitted
PBS_O_WORKDIR	the absolute path of the current working directory of the <i>qsub</i> command. This is the most useful. Use it in every job script. The first thing you do is, cd \$PBS_O_WORKDIR after defining the resource list. This is because, pbs throw you to your \$HOME directory.
PBS_O_NODENUM	node offset number
PBS_O_VNODENUM	vnode offset number
PBS_VERSION	Version Number of TORQUE, e.g., TORQUE-2.5.1
PBS_MOMPORT	active port for mom daemon
PBS_TASKNUM	number of tasks requested
PBS_JOBCOOKIE	job cookie
PBS_SERVER	Server Running TORQUE

# Appendix C

## Useful Linux Commands

### C.1 Basic Linux Usage

All the HPC clusters run some variant of the “Red Hat Enterprise Linux” operating system. This means that, when you connect to one of them, you get a command line interface, which looks something like this:

```
vsc40000@ln01[203] $
```

When you see this, we also say you are inside a “shell”. The shell will accept your commands, and execute them.

ls	Shows you a list of files in the current directory
cd	Change current working directory
rm	Remove file or directory
nano	Text editor
echo	Prints its parameters to the screen

Most commands will accept or even need parameters, which are placed after the command, separated by spaces. A simple example with the “echo” command:

```
$ echo This is a test  
This is a test
```

Important here is the “\$” sign in front of the first line. This should not be typed, but is a convention meaning “the rest of this line should be typed at your shell prompt”. The lines not starting with the “\$” sign are usually the feedback or output from the command.

More commands will be used in the rest of this text, and will be explained then if necessary. If not, you can usually get more information about a command, say the item or command “ls”, by trying either of the following:

```
$ ls --help  
$ man ls  
$ info ls
```

(You can exit the last two “manuals” by using the “q” key.) For more exhaustive tutorials about Linux usage, please refer to the following sites: <http://www.linux.org/lessons/>

[http://linux.about.com/od/nwb\\_guide/a/gdenwb06.htm](http://linux.about.com/od/nwb_guide/a/gdenwb06.htm)

## C.2 How to get started with shell scripts

In a shell script, you will put the commands you would normally type at your shell prompt in the same order. This will enable you to execute all those commands at any time by only issuing one command: starting the script.

Scripts are basically non-compiled pieces of code: they are just text files. Since they don't contain machine code, they are executed by what is called a "parser" or an "interpreter". This is another program that understands the command in the script, and converts them to machine code. There are many kinds of scripting languages, including Perl and Python.

Another very common scripting language is shell scripting. In a shell script, you will put the commands you would normally type at your shell prompt in the same order. This will enable you to execute all those commands at any time by only issuing one command: starting the script.

Typically in the following examples they'll have on each line the next command to be executed although it is possible to put multiple commands on one line. A very simple example of a script may be:

```
1 echo "Hello! This is my hostname:"  
2 hostname
```

You can type both lines at your shell prompt, and the result will be the following:

```
$ echo "Hello! This is my hostname:"  
Hello! This is my hostname:  
$ hostname  
gligar04.gastly.os
```

Suppose we want to call this script "foo". You open a new file for editing, and name it "foo", and edit it with your favourite editor

```
$ nano foo
```

or use the following commands:

```
$ echo "echo Hello! This is my hostname:" > foo  
$ echo hostname >> foo
```

The easiest ways to run a script is by starting the interpreter and pass the script as parameter. In case of our script, the interpreter may either be "sh" or "bash" (which are the same on the cluster). So start the script:

```
$ bash foo  
Hello! This is my hostname:  
gligar04.gastly.os
```

Congratulations, you just created and started your first shell script!

A more advanced way of executing your shell scripts is by making them executable by their own, so without invoking the interpreter manually. The system can not automatically detect which

interpreter you want, so you need to tell this in some way. The easiest way is by using the so called “shebang” notation, explicitly created for this function: you put the following line on top of your shell script “#!/path/to/your/interpreter”.

You can find this path with the “which” command. In our case, since we use bash as an interpreter, we get the following path:

```
$ which bash  
/bin/bash
```

We edit our script and change it with this information:

```
1 #!/bin/bash  
2 echo "Hello! This is my hostname:  
3 hostname
```

Note that the “shebang” must be the first line of your script! Now the operating system knows which program should be started to run the script.

Finally, we tell the operating system that this script is now executable. For this we change its file attributes:

```
$ chmod +x foo
```

Now you can start your script by simply executing it:

```
$ ./foo  
Hello! This is my hostname:  
gligar04.gastly.os
```

The same technique can be used for all other scripting languages, like Perl and Python.

Most scripting languages understand that lines beginning with “#” are comments, and should be ignored. If the language you want to use does not ignore these lines, you may get strange results . . .

## C.3 Linux Quick reference Guide

### C.3.1 Archive Commands

tar	An archiving program designed to store and extract files from an archive known as a tar file.
tar -cvf foo.tar foo/	compress the contents of foo folder to foo.tar
tar -xvf foo.tar	extract foo.tar
tar -xvzf foo.tar.gz	extract gzipped foo.tar.gz

### C.3.2 Basic Commands

ls	Shows you a list of files in the current directory
cd	Change the current directory
rm	Remove file or directory
mv	Move file or directory
echo	Display a line or text
pwd	Print working directory
mkdir	Create directories
rmdir	Remove directories

### C.3.3 Editor

emacs	
nano	Nano's ANOther editor, an enhanced free Pico clone
vi	A programmers text editor

### C.3.4 File Commands

cat	Read one or more files and print them to standard output
cmp	Compare two files byte by byte
cp	Copy files from a source to the same or different target(s)
du	Estimate disk usage of each file and recursively for directories
find	Search for files in directory hierarchy
grep	Print lines matching a pattern
ls	List directory contents
mv	Move file to different targets
rm	Remove files
sort	Sort lines of text files
wc	Print the number of new lines, words, and bytes in files

### C.3.5 Help Commands

man	Displays the manual page of a command with its name, synopsis, description, author, copyright etc.
-----	--

### C.3.6 Network Commands

hostname	show or set the system's host name
ifconfig	Display the current configuration of the network interface. It is also useful to get the information about IP address, subnet mask, set remote IP address, netmask etc.
ping	send ICMP ECHO_REQUEST to network hosts, you will get back ICMP packet if the host responds. This command is useful when you are in a doubt whether your computer is connected or not.

### C.3.7 Other Commands

logname	Print user's login name
quota	Display disk usage and limits
which	Returns the pathnames of the files that would be executed in the current environment
whoami	Displays the login name of the current effective user

### C.3.8 Process Commands

&	In order to execute a command in the background, place an ampersand (&) on the command line at the end of the command. A user job number (placed in brackets) and a system process number are displayed. A system process number is the number by which the system identifies the job whereas a user job number is the number by which the user identifies the job
at	executes commands at a specified time
bg	Places a suspended job in the background
crontab	crontab is a file which contains the schedule of entries to run at specified times
fg	A process running in the background will be processed in the foreground
jobs	Lists the jobs being run in the background
kill	Cancels a job running in the background, it takes argument either the user job number or the system process number
ps	Reports a snapshot of the current processes
top	Display Linux tasks

### C.3.9 User Account Commands

chmod	Modify properties for users
chown	Change file owner and group