UPPMAX Introduction

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What is UPPMAX what it provides

Projects at UPPMAX

How to access UPPMAX

Jobs and queuing systems

How to use the resources of UPPMAX

How to use the resources of UPPMAX in a good way!
Efficiency!!!

Uppsala Multidisciplinary Center for Advanced Computational Science

http://www.uppmax.uu.se

2 (3) computer clusters

- **Rackham**: ~ 500 nodes à 20 cores (128, 256 & 1024 GB RAM)
  + Snowy (old Milou): ~ 200 nodes à 16 cores (128, 256 & 512 GB RAM)
- **Bianca**: 200 nodes à 16 cores (128, 256 & 512 GB RAM) - virtual cluster

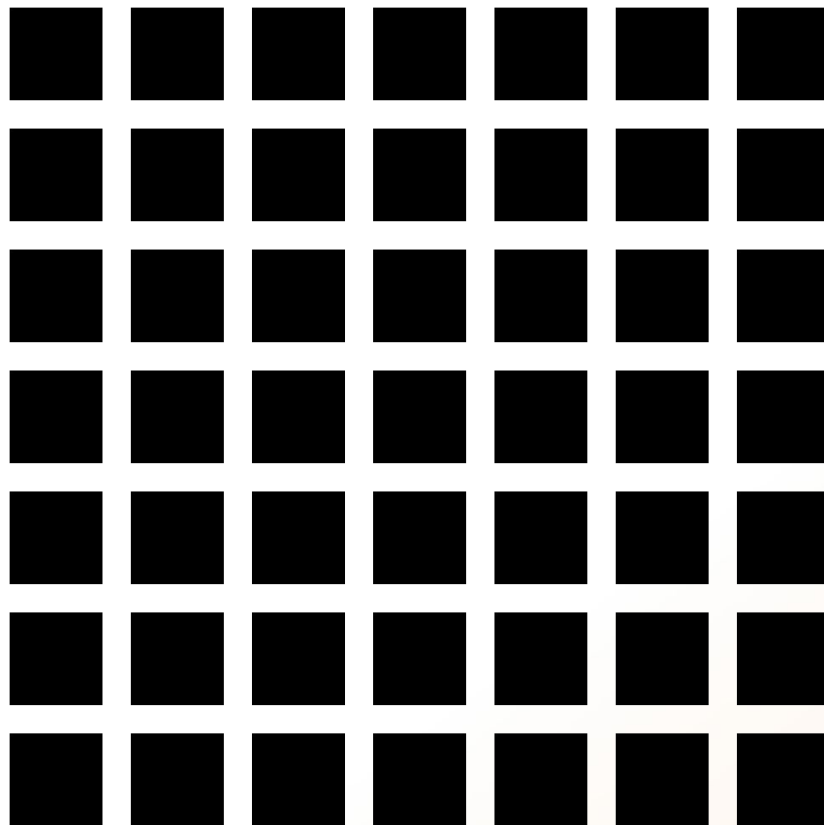>12 PB fast parallel **storage**

Bioinformatics **software**

The basic structure of supercomputer

node = computer

Login nodes
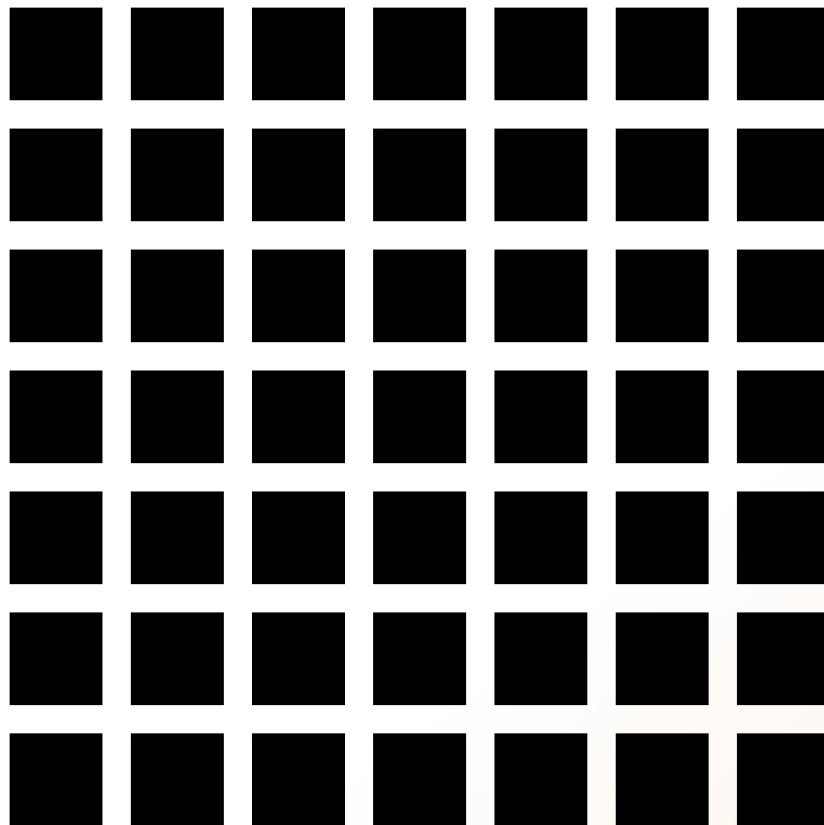
The basic structure of supercomputer

Calculation nodes

Login nodes

The basic structure of supercomputer

Calculation nodes

Storage

Login nodes

SciLifeLab
UPPSALA

Calculation nodes
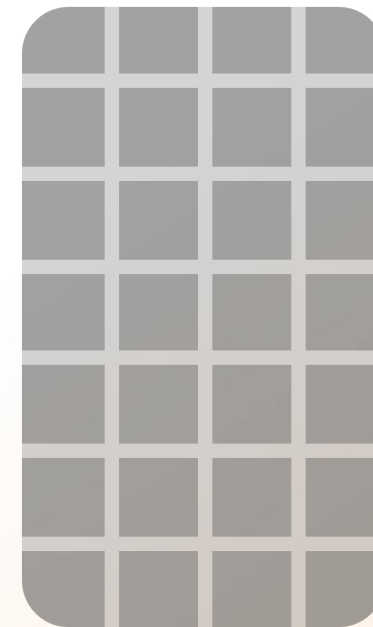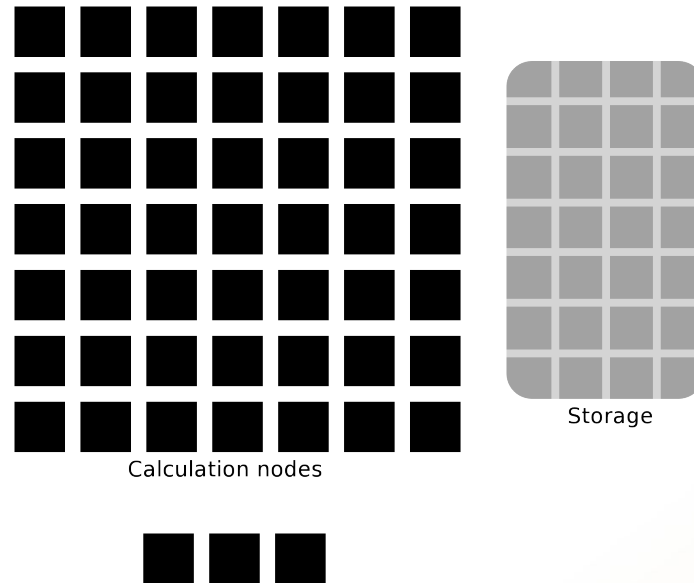
Storage

UPPMAX provides

Compute and **Storage**

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                                        Efficiency!!!

UPPMAX provides its resources via

projects

your project

Storage

Calculation nodes
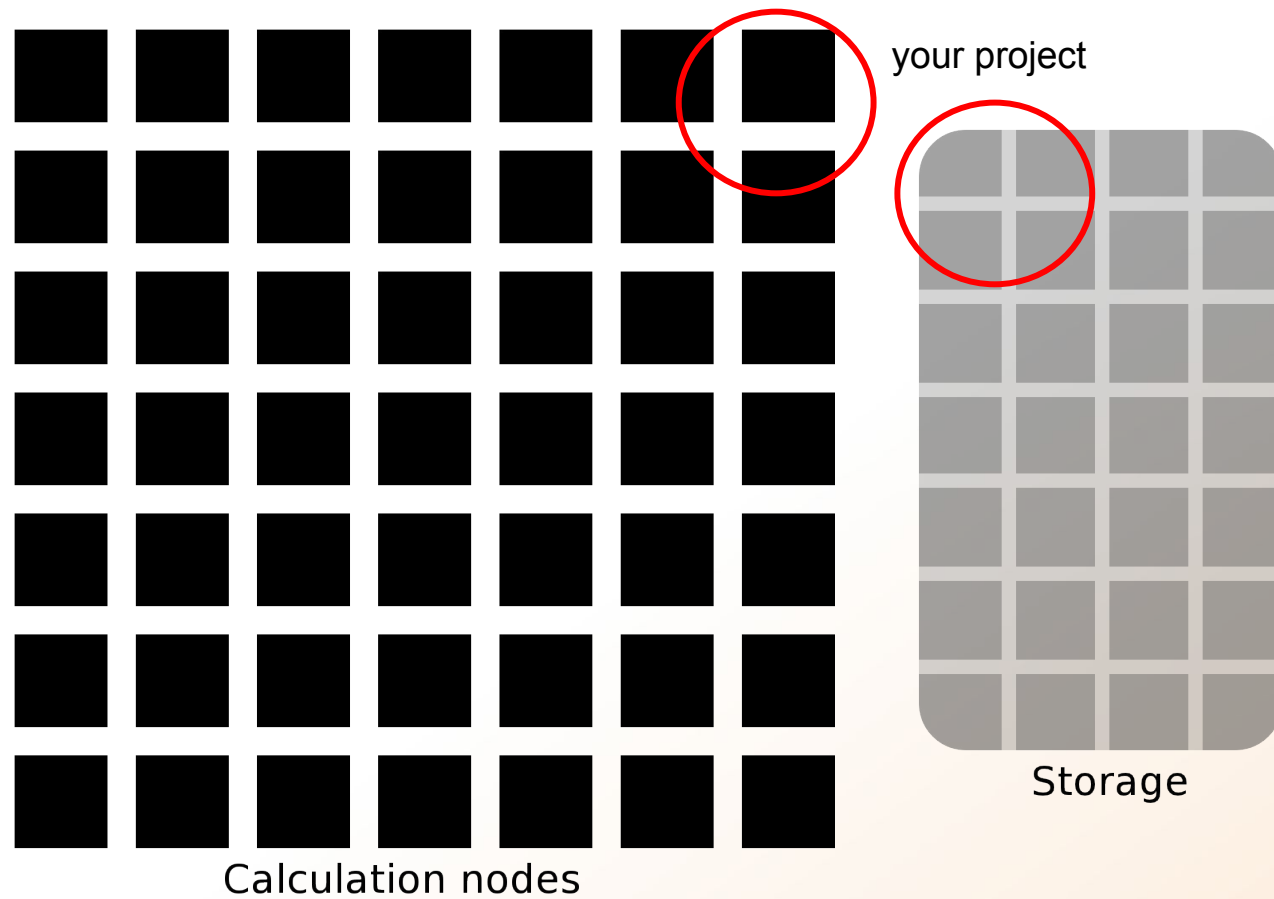
Resources:

compute
(core-hours/month)

storage
(GB)

Two separate projects:

<u>SNIC project</u>:
   cluster **Rackham**
      2000 - 100 000+ core-hours/month
      128 GB

<u>Uppstore Storage project</u>:
   storage system **CREX**
      1 - 100+ TB

← → C 🔒 Uppsala universitet [SE] | https://supr.snic.se/round/

SNIC SUPR

| Admin | User |

Start / **Rounds**

Rounds

Start
Proposals
  g2018002
  SNIC 2017/1-504
  g2017029
Rounds
Projects
  SNIC 2017/7-274
  sllstore2017094
  sllstore2017027
  g2018002
  SNIC 2017/13-23
  SNIC 2017/13-6
Groups
  UPPMAXStaff
Accounts
Personal Information
Support
Logout

Logged in as:
Valentin Georgiev
(valentin.georgiev@icm.uu.se)

Open for Proposals

SNIC Rounds	Deadline
SNAC Medium, 2018	—
SNAC Small C3SE, 2018	—
SNAC Small HPC2N, 2018	—
SNAC Small Lunarc, 2018	—
SNAC Small NSC, 2018	—
SNAC Small UPPMAX, 2018	—
SNIC Science Cloud 2018	—
SNAC Medium Swestore 2018	—
SNAC Small Swestore 2018	—
DCS 2018	—
SNIC SENS Medium 2018	—
SNIC SENS Small 2018	—

Projects

Start / Rounds / **SNAC Small UPPMAX, 2018**

SNAC Small UPPMAX, 2018

This Round is Open for Proposals

This round is for compute resources on Rackham. All research areas are welcome. Projects with a large storage requirement are prioritised on Rackham.
More information about this round is available at http://snic.se/allocations/small-allocations/.

This round is open for proposals until 2019-01-01 00:00.

Create New Proposal for SNAC Small UPPMAX, 2018 | View Committee Overview

Resources

	Resource	Centre	Available	Capacity Unit	Note
▶	Crex 1	UPPMAX	500	GiB	
▶	Rackham	UPPMAX	1 000	x 1000 core-h/month	

Click the ▶ to show more information about the resource.

Sidebar

Admin | User

Start
Proposals
  g2018002
  SNIC 2017/1-504
  g2017029
Rounds
Projects
  SNIC 2017/7-274
  sllstore2017094
  sllstore2017027
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What is UPPMAX what it provides

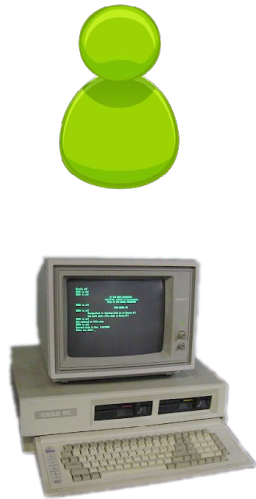**Projects at UPPMAX**

How to access UPPMAX

Jobs and queuing systems

How to use the resources of UPPMAX

How to use the resources of UPPMAX in a good way!
Efficiency!!!

SSH to a cluster

ssh -Y *your_username@cluster_name*.uppmax.uu.se

How to access UPPMAX

SSH to Rackham

```
[VG-MBP:~ valentingeorgiev$ ssh -Y valent@rackham.uppmax.uu.se
Last login: Sun Oct 22 10:14:21 2017 from host-95-195-196-83.mobileonline.telia.com
  _   _ ____ ____ __  __     _    __  __
 | | | |  _ \|  _ \|  \/  |  / \   \ \/ /     | System:    rackham1
 | | | | |_) | |_) | |\/| | / _ \   \  /      | User:      valent
 | |_| |  __/|  __/| |  | |/ ___ \  /  \      | Jobs:      0 running
  \___/|_|   |_|   |_|  |_/_/   \_\/_/\_\     | Queue:     0 pending


#############################################################################################

        User Guides: http://www.uppmax.uu.se/support/user-guides
        FAQ: http://www.uppmax.uu.se/support/faq

        Write to support@uppmax.uu.se, if you have questions or comments.


[valent@rackham1 ~]$
```

SSH

Local
computer

Login
nodes

Computation
nodes

Local
computer

ssh

Login
nodes

Computation
nodes

Login nodes

use them to access UPPMAX
never use them to run **jobs**
don't even use them to do "quick stuff"

Calculation nodes

do your work here - testing and running

Calculation nodes

not accessible directly
SLURM (queueing system) gives you access

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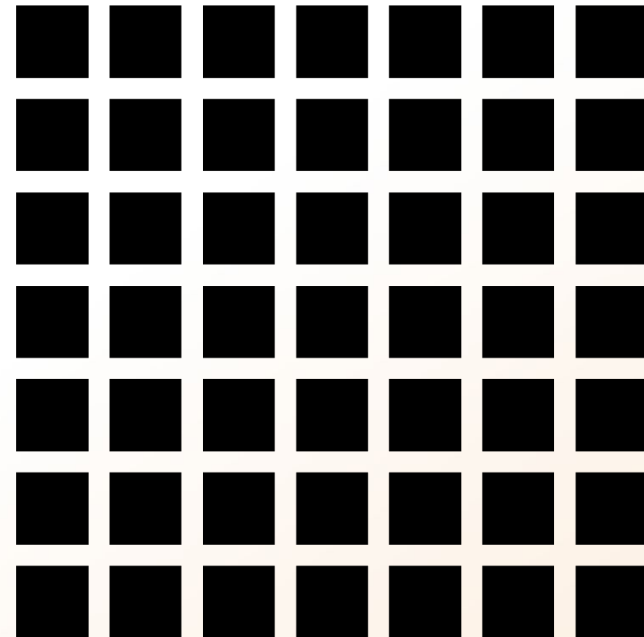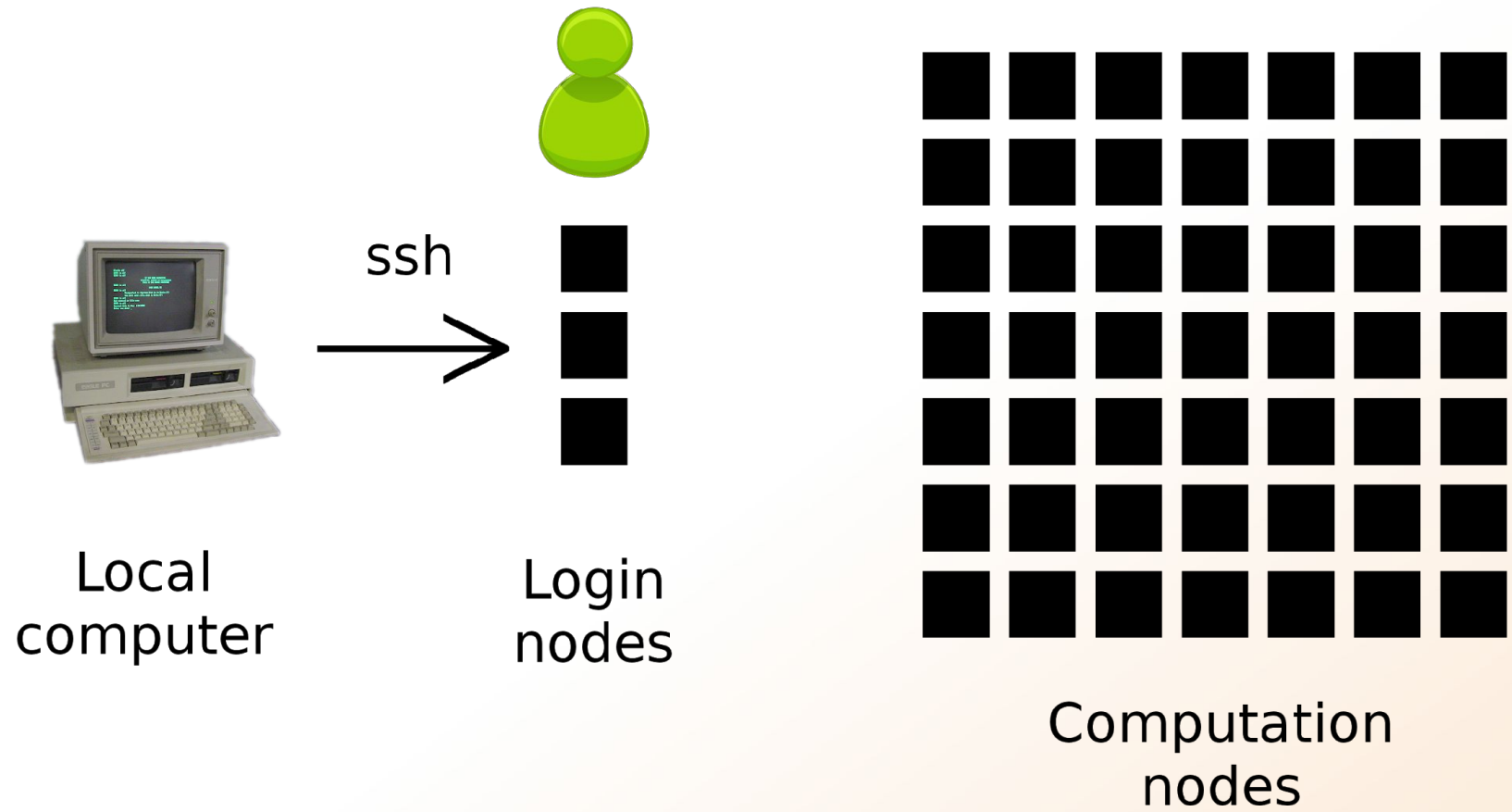   **Efficiency!!!**

Job (computing)

From Wikipedia, the free encyclopedia

For other uses, see Job (Unix) and Job stream.

In computing, a **job** is a unit of work or unit of execution (that performs said work). A component of a job (as a unit of work) is called a *task* or a *step* (if sequential, as in a job stream). As a unit of execution, a job may be concretely identified with a single process, which may in turn have subprocesses (child processes; the process corresponding to the job being the parent process) which perform the tasks or steps that comprise the work of the job; or with a process group; or with an abstract reference to a process or process group, as in Unix job control.

Read/open files

Do something with the data

Print/save output

Read/open files

Do something with the data

Print/save output

The basic structure of a supercomputer

Parallel computing!!!
   Not one super fast
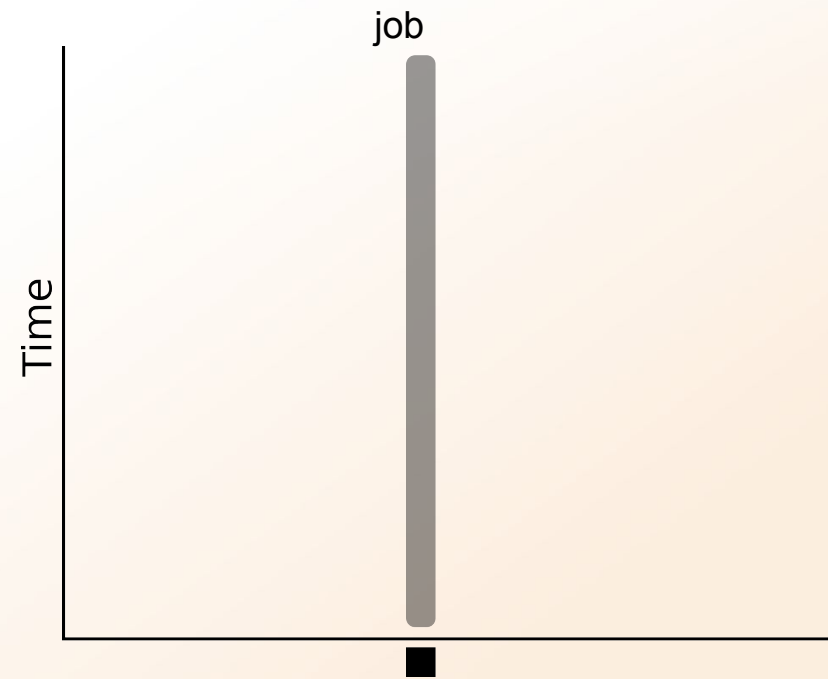
The basic structure of a supercomputer

Parallel computing!!!
    Not one super fast

More users than nodes
Need for a queue

nodes - hundreds
users - thousands
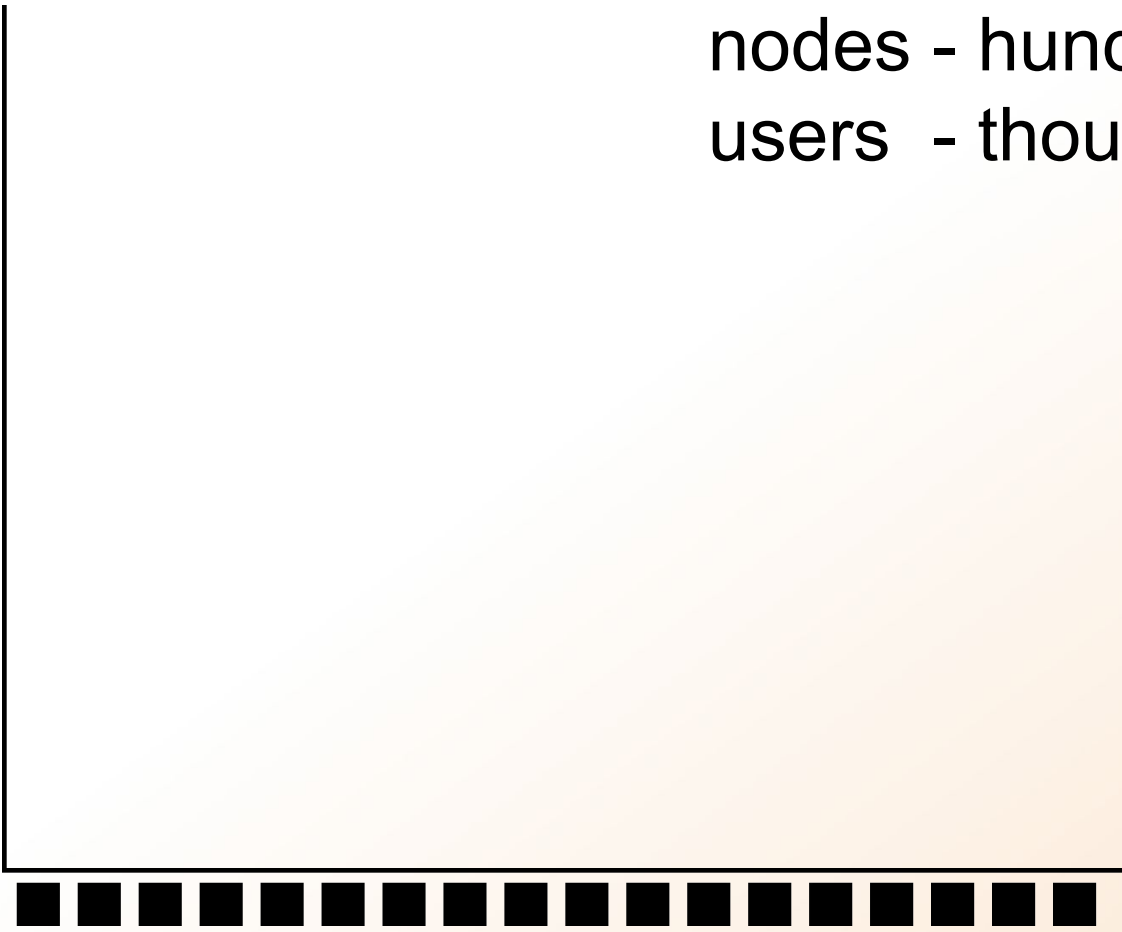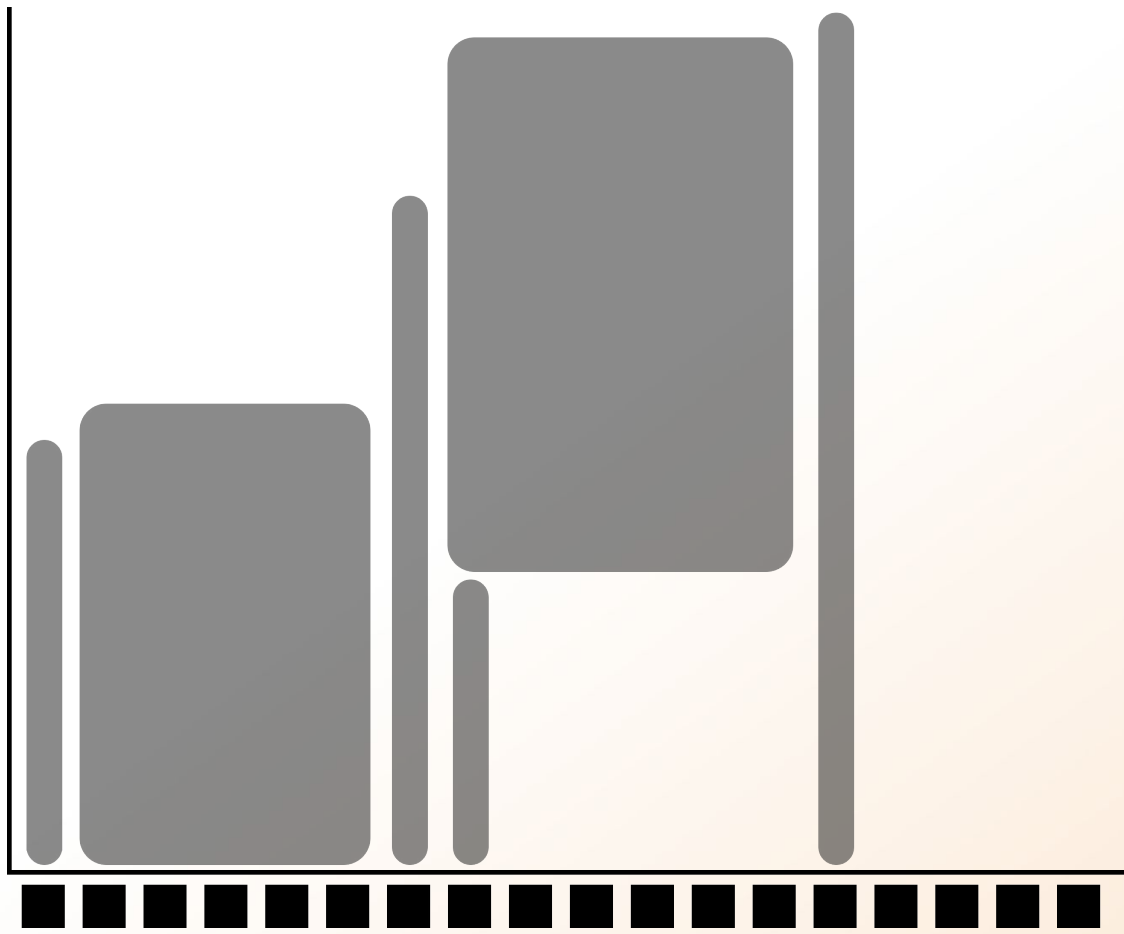
More users than nodes

Need for a queue

More users than nodes
Need for a queue

Added job

More users than nodes
Need for a queue

Added job
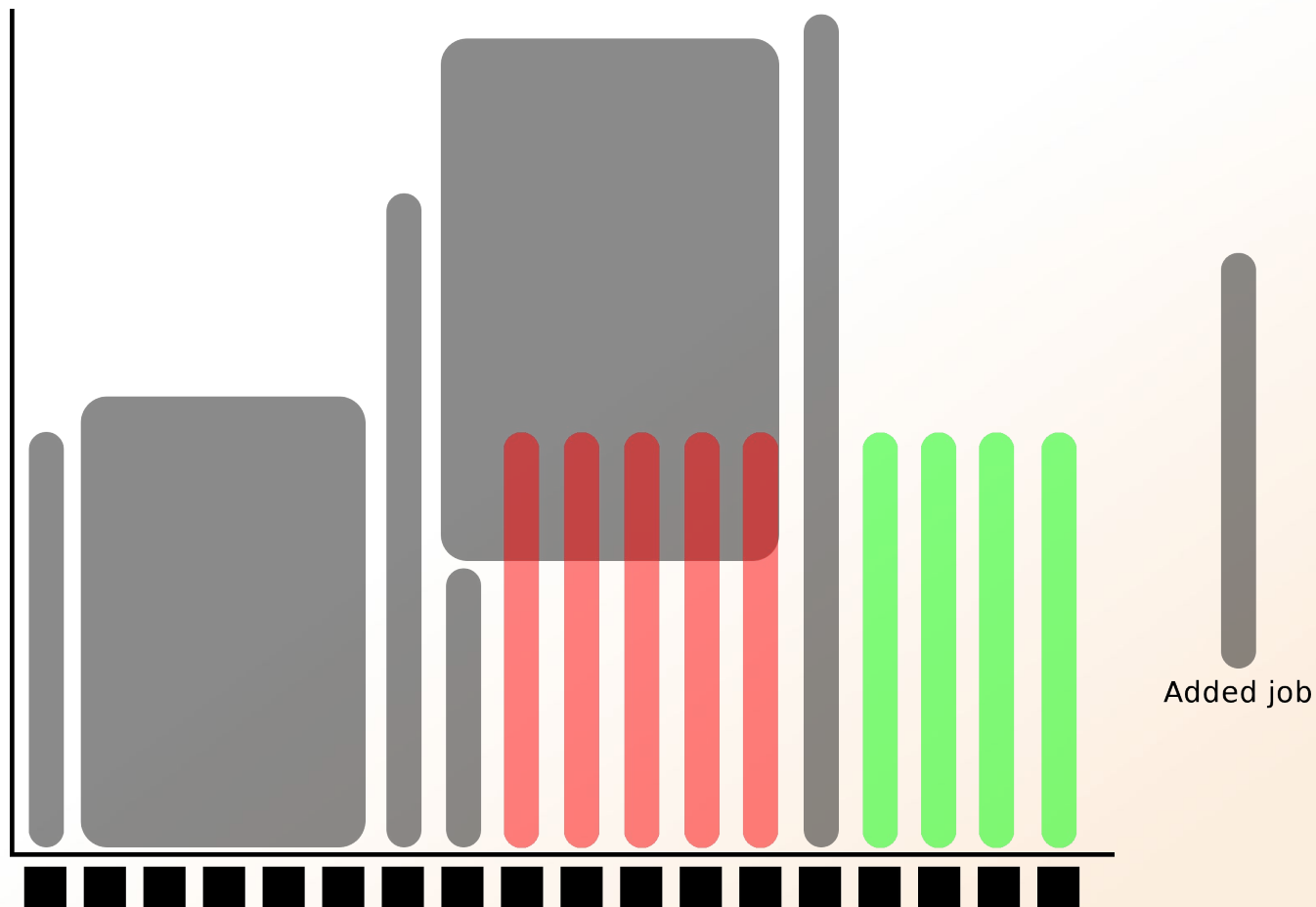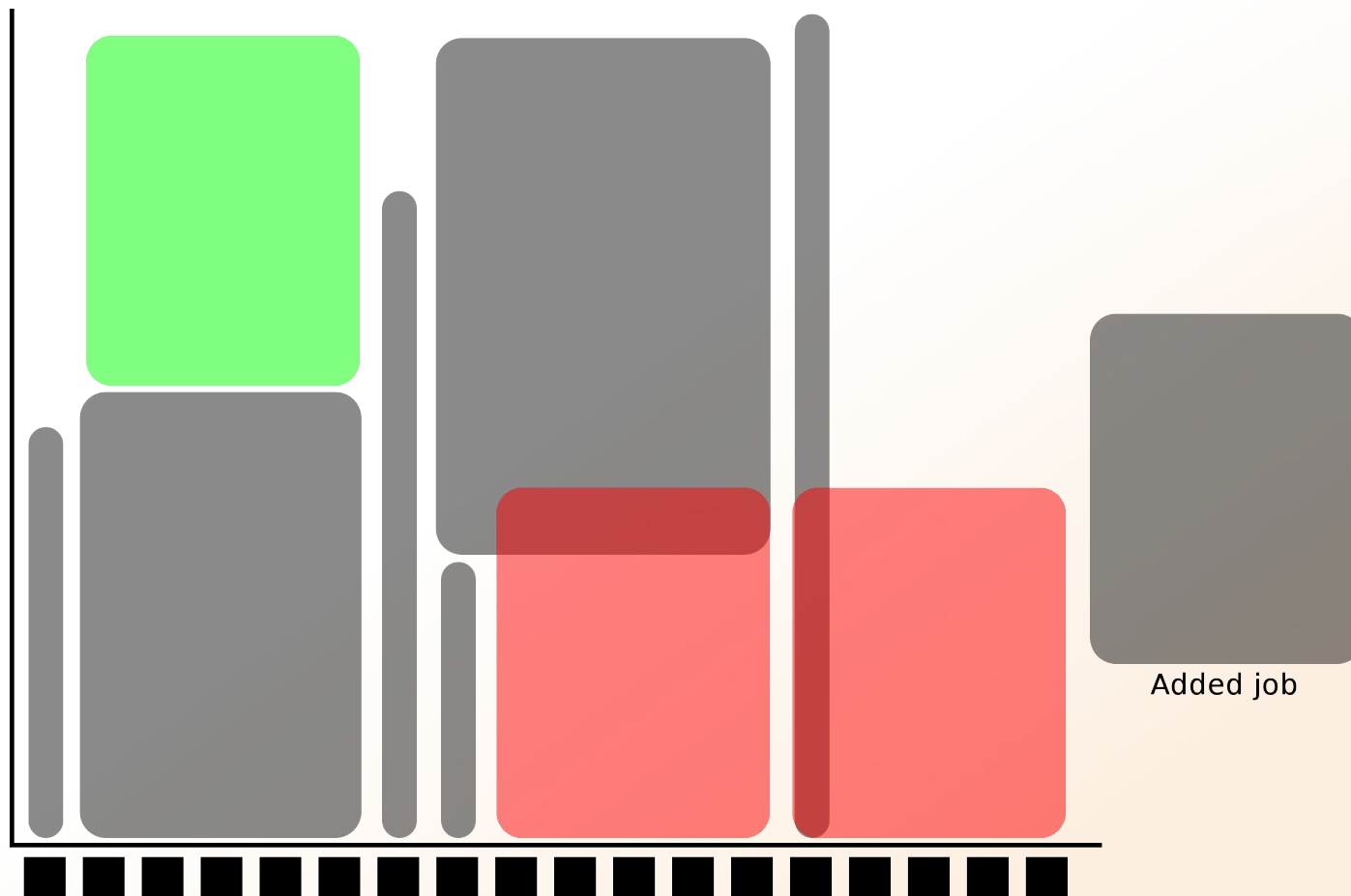
**workload manager
job queue
batch queue
job scheduler**

SLURM (Simple Linux Utility for Resource Management)
free and open source

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How to use the resources of UPPMAX

How to use the resources of UPPMAX in a good way!
Efficiency!!!

1) Ask for resource and run jobs manually

For testing, possibly small jobs, specific programs needing user input while running

2)Write a script and submit it to SLURM

Submits an automated job to the job queue, runs when it's your turn

1) Ask for resource and run jobs manually

submit a request for resources

$\downarrow$

ssh to a calculation node

$\downarrow$

run programs

1) Ask for resource and run jobs manually

salloc -A g2019011 -p core -n 1 -t 00:05:00

salloc - command
mandatory job parameters:
-A   - project ID (who "pays")
-p   - node or core (the type of resource)
-n   - number of nodes/cores
-t   - time

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-A   this course project g2019011
         you have to be a member

-p   1 node = 20 cores
         1 hour walltime = 20 core-hours

-n   number of cores (default value = 1)
-N   number of nodes

-t   format - hh:mm:ss
         default value= 7-00:00:00
jobs killed when time limit reaches - always overestimate ~ 50%

Information about your jobs

squeue -u <user>

```
[valent@milou2 valent]$ squeue -u valent
          JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
       11334919      core       sh   valent  R       0:11      1 m164
```

SSH to a calculation node (from a login node)

ssh -Y *<node_name>*

```
[[valent@milou2 valent]$ salloc -A b2015245 -p core -n 1 -t 00:05:00 &
[2] 10994
[valent@milou2 valent]$ salloc: Granted job allocation 11334919

[valent@milou2 valent]$ squeue -u valent
          JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
       11334919      core       sh   valent  R       0:11      1 m164
[[valent@milou2 valent]$ ssh -Y m164

  _   _ ____  ____  __  __  _   __  __
 | | | |  _ \|  _ \|  \/  | / \  \ \/ /    | System:   m164
 | | | | |_) | |_) | |\/| |/ _ \  \  /     | User:     valent
 | |_| |  __/|  __/| |  | / ___ \ /  \     | Jobs:     1 running
  \___/|_|   |_|   |_|  |_/_/   \_\/_/\_\   | Queue:    0 pending

################################################################################

        User Guides: http://www.uppmax.uu.se/support/user-guides
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[valent@m164 ~]$ █
```

SciLifeLab UPPSALA

SLURM

ssh

ssh

Local
computer

Login
nodes

Computation
nodes

1a) Ask for node/core and run jobs manually

Interactive - books a node and connects you to it

interactive -A g2019011 -p core -n 1 -t 00:05:00

```
  _   _ ___  ___  __  __    _    __  __          | System:   m1
 | | | |  _ \|  _ \|  \/  |  / \   \ \/ /         | User:     valent
 | | | | |_) | |_) | |\/| | / _ \   \  /          | Jobs:     1 running
 | |_| |  __/|  __/| |  | |/ ___ \  /  \          | Queue:    0 pending
  \___/|_|   |_|   |_|  |_/_/   \_\/_/\_\         |

###################################################################################

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[valent@m1 valent]$ █
```

2)Write a script and submit it to SLURM

put all commands in a text file - script

tell SLURM to run the script
(use the same job parameters)

2)Write a script and submit it to SLURM

put all commands in a text file - script

```
#! /bin/bash -l
#SBATCH -A g2012157
#SBATCH -p core
#SBATCH -J Template_script
#SBATCH -t 08:00:00
```

job parameters

```
# go to some directory
cd ~/glob

# do something
echo Hello world!
```

tasks to be done

2) Write a script and submit it to SLURM

put all commands in a text file - script

```
#! /bin/bash -l
#SBATCH -A g2012157
#SBATCH -p node
#SBATCH -J Template_script
#SBATCH -t 08:00:00
```

```
# go to the correct directory
cd /home/dahlo/glob/work/uppmaxScripts/misc

# run tophat on the data, using 8 cores
tophat -p 8 /bubo/proj/g2012157/indexes/bowtie/hg19 tophat/input/ad12.fq
```

2)Write a script and submit it to SLURM

tell SLURM to run the script
(use the same job parameters)

sbatch test.sbatch

2)Write a script and submit it to SLURM

tell SLURM to run the script
(use the same job parameters)

sbatch test.sbatch

sbatch - command
test.sbatch - name of the script file

2)Write a script and submit it to SLURM

tell SLURM to run the script
(use the same job parameters)

sbatch -A g2019011 -p core -n 1 -t 00:05:00 test.sbatch

SLURM Output

Prints to a file instead of terminal
    slurm-<job id>.out

```
[valent@milou2 temp]$ ll
total 32
-rw-rw-r-- 1 valent valent 209 Oct 22 13:34 test.sbatch
[valent@milou2 temp]$ sbatch test.sbatch
Submitted batch job 11334939
[valent@milou2 temp]$ ll
total 64
-rw-rw-r-- 1 valent valent  31 Oct 22 13:35 slurm-11334939.out
-rw-rw-r-- 1 valent valent 209 Oct 22 13:34 test.sbatch
[valent@milou2 temp]$ cat slurm-11334939.out
this goes to slurm-<jobID>.out
[valent@milou2 temp]$ cat test.sbatch
#!/bin/bash -l

#SBATCH -A b2015245
#SBATCH -p core
#SBATCH -n 1
#SBATCH -t 00:05:00


# go to dir work
cd ~/work
# do something useless
echo "this goes to slurm-<jobID>.out"
echo "Hello, world!" > hello.txt
[valent@milou2 temp]$
```

Shows information about your jobs

squeue -u <user>

```
[valent@milou2 temp]$ sbatch test.sbatch
Submitted batch job 11334948
[valent@milou2 temp]$ squeue -u valent
         JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
      11334948      core test.sba   valent CG       0:01      1 m200
```

jobinfo -u <user>

SLURM user guide
go to http://www.uppmax.uu.se/
click User Guides (left-hand side menu)
click Slurm user guide

or just google "uppmax slurm user guide"

link:
http://www.uppmax.uu.se/support/user-guides/slurm-user-guide/

100+ programs installed

Managed by a 'module system'
    Installed, but hidden
    Manually loaded before use

module avail - Lists all available modules
module load <module name> - Loads the module
module unload <module name> - Unloads the module
module list - Lists loaded modules
module spider <word> - Searches all modules after 'word'

Most bioinfo programs hidden under bioinfo-tools
    Load bioinfo-tools first, then program module

```
[dahlo@kalkyl3 work]$ module load cufflinks/1.2.1
ModuleCmd_Load.c(200):ERROR:105: Unable to locate a modulefile for 'cufflinks/1.2.1'
[dahlo@kalkyl3 work]$ module load bioinfo-tools
[dahlo@kalkyl3 work]$ module load cufflinks/1.2.1
[dahlo@kalkyl3 work]$
```

or

```
[dahlo@kalkyl3 work]$ module load samtools
ModuleCmd_Load.c(200):ERROR:105: Unable to locate a modulefile for 'samtools'
[dahlo@kalkyl3 work]$ module load bioinfo-tools samtools
[dahlo@kalkyl3 work]$
```

```
[dahlo@kalkyl4 work]$ module load bioinfo-tools
[dahlo@kalkyl4 work]$ module avail

------------------------------ /bubo/sw/mf/kalkyl/bioinfo-tools/alignment ------------------------------
MUMmer/3.22(default)          blast/2.2.24(default)        maq/0.7.1(default)
anfo/0.97                     blast/2.2.24+                mosaik-aligner/1.0.1388(default)
anfo/0.98(default)            blast/2.2.25                 mosaik-aligner/1.1.0021
blast/2.2.15                  blat/34                      mpiblast/1.6.0(default)
blast/2.2.18                  bwa/0.5.8a                   splitseek/1.3.2
blast/2.2.23                  bwa/0.5.9                    splitseek/1.3.4(default)
blast/2.2.23+                 hmmer/3.0

------------------------------ /bubo/sw/mf/kalkyl/bioinfo-tools/assembly ------------------------------
Ray/0.0.4           abyss/1.2.4            abyss/1.3.0            velvet/1.0.03(default)
Ray/0.0.7(default)  abyss/1.2.5(default)  abyss/1.3.2            velvet/1.1.04
Ray/1.6.1           abyss/1.2.7           mira/3.0.0             velvet/1.1.04_K101
abyss/1.2.3         abyss/1.2.7-maxk96    mira/3.2.0(default)    velvet/1.1.07

------------------------------ /bubo/sw/mf/kalkyl/bioinfo-tools/misc ------------------------------
BclConverter/1.7.1                  freebayes/0.8.9           samtools/0.1.12-10(default)
BioPerl/1.6.1                       freebayes/0.9.4           samtools/0.1.16
BioPerl/1.6.1_PERL5.10.1(default)   gcta/0.92.0               samtools/0.1.18
BioPerl/1.6.1_PERL5.12.3            gcta/0.92.6               samtools/0.1.7a
FastQC/0.6.1                        genometools/1.3.5(default) samtools/0.1.8
FastQC/0.7.2(default)               htseq/0.4.6               samtools/0.1.9
Fastx/0.0.13(default)               htseq/0.5.1               snpEff/2.0.3
IGV/1.5.51                          matrix2png/1.2.1          trinity/2011-05-13
biopython/1.56                      picard/1.40               trinity/2011-10-29
cellprofiler/20111024               picard/1.41
emmax/beta-07Mar2010                plink/1.07

------------------------------ /bubo/sw/mf/kalkyl/bioinfo-tools/phylogeny ------------------------------
concaterpillar/1.4     garli/2.0          raxml/7.0.4(default)  raxml/7.2.8
garli/0.96b8(default)  mrbayes/3.1.2-mpi  raxml/7.2.7

------------------------------ /bubo/sw/mf/kalkyl/bioinfo-tools/pipelines ------------------------------
ab_wtp/1.1(default)        cufflinks/0.9.2        cufflinks/1.1.0        tophat/1.2.0
bowtie/0.12.6(default)     cufflinks/0.9.3        cufflinks/1.2.1        tophat/1.3.3
```

UPPMAX Commands

uquota

```
[dahlo@biologin work]$ uquota
Your File Area              Usage (GB)   Quota Limit (GB)   Over Quota   Grace Time
----------------           ----------   ----------------   ----------   ----------
dahlo glob                        196               2048                         -
dahlo home                          4                 32                         -
/proj/b2010015                    229                256                         -
/proj/b2010015/nobackup             0                512                         -
/proj/b2010033                    132               6348                         -
/proj/b2010033/nobackup            27                512                         -
```

UPPMAX Commands

projinfo

```
[dahlo@kalkyl4 work]$ projinfo
(Counting the number of core hours used since 2012-08-19/00:00:00 until now.)

Project          Used[h]   Current allocation [h/month]
    User
------------------------------------------------------------
b2010015         1257.20              2000
    ameur        1257.20


------------------------------------------------------------
b2010069            0.00              2000


------------------------------------------------------------
b2010074          110.98              2000
    dahlo           1.01
    seba          109.97


------------------------------------------------------------
b2012044            0.00              2000


------------------------------------------------------------
g2012005            0.00              2000


------------------------------------------------------------
g2012083            0.00              2000


------------------------------------------------------------
g2012157            0.12              2000
    dahlo           0.12

[dahlo@kalkyl4 work]$
```
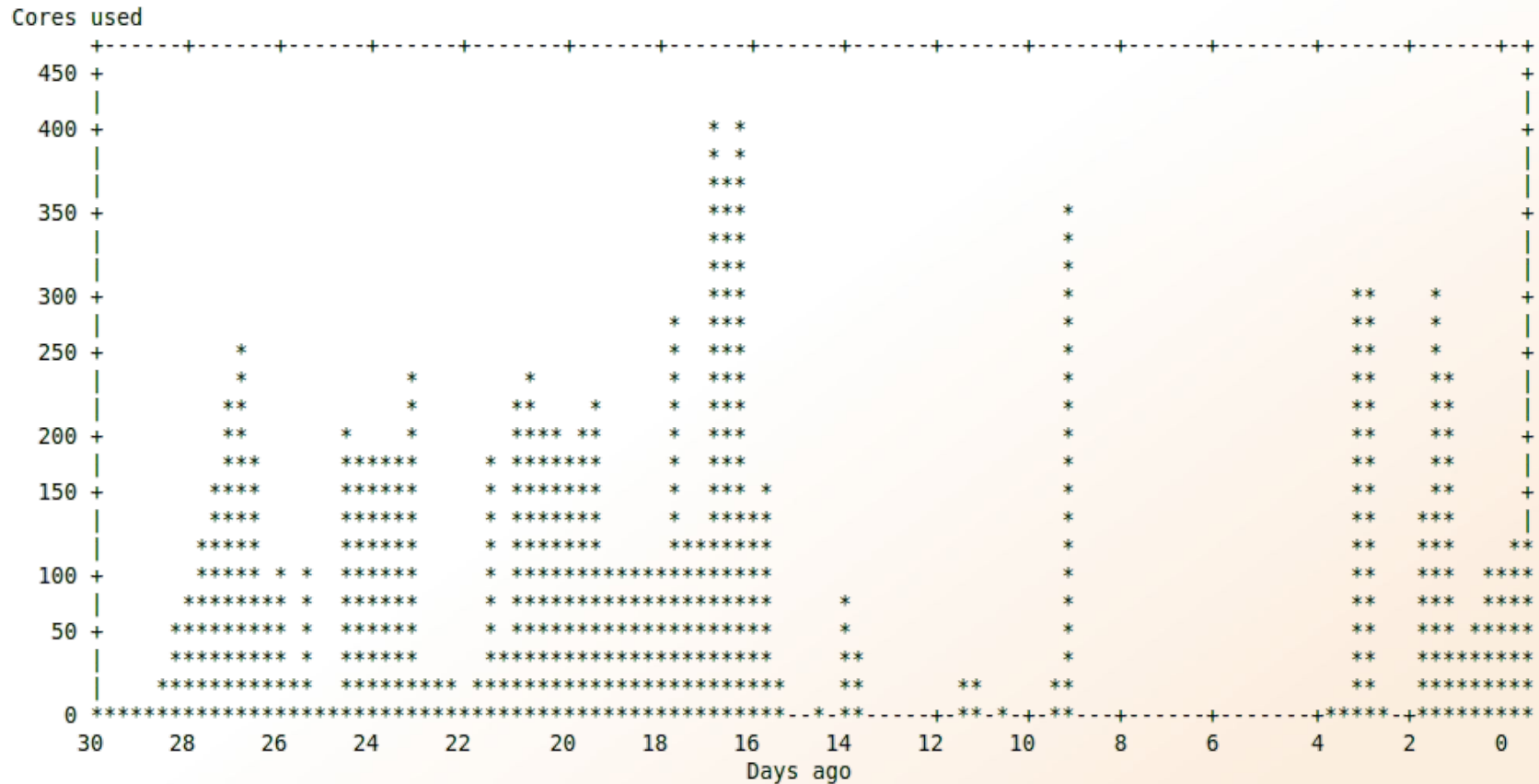
UPPMAX Commands

projplot -A <proj-id>   (-h for more options)

[dahlo@biologin slurm-usage]$

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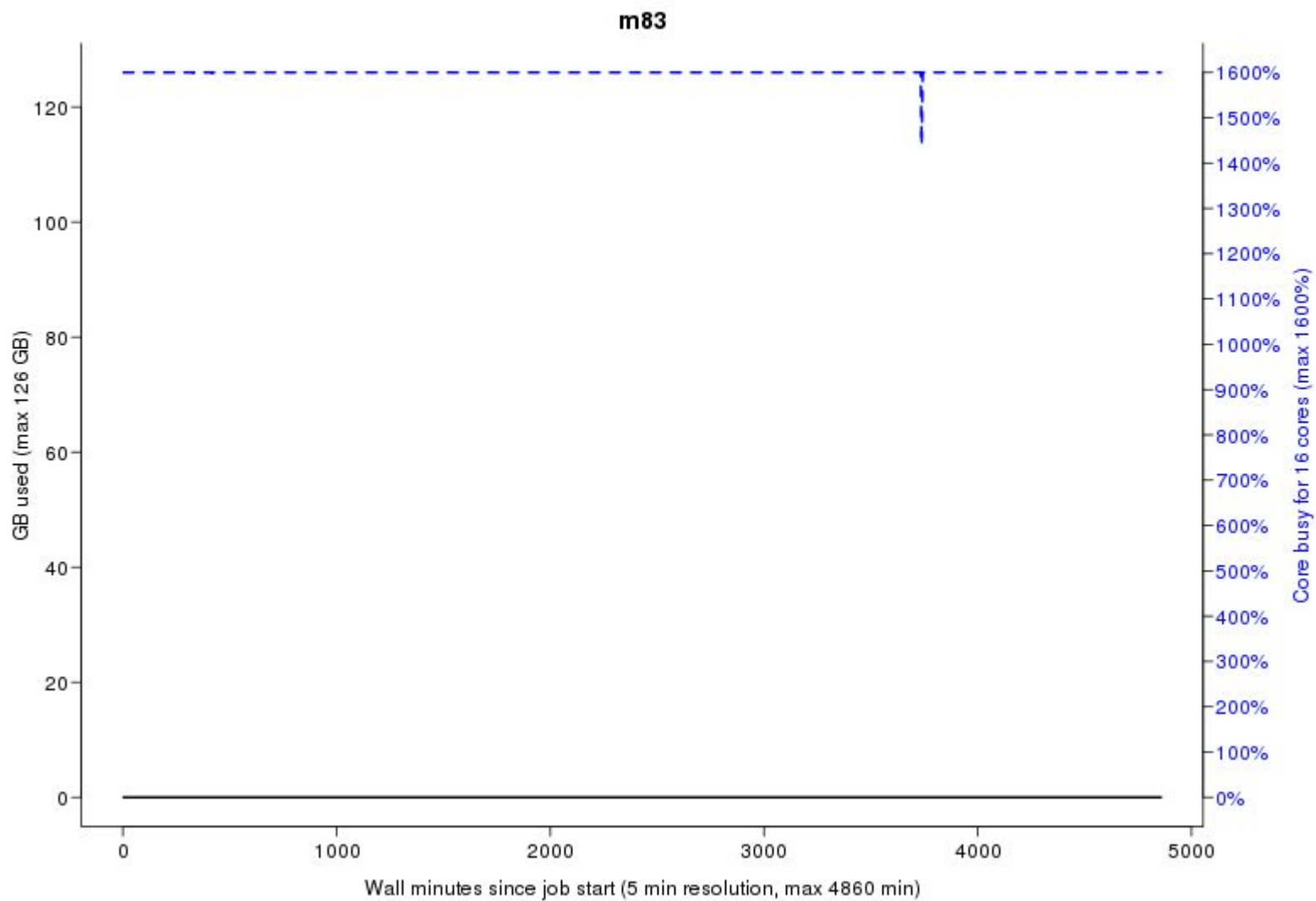
How to use the resources of UPPMAX in a good way!
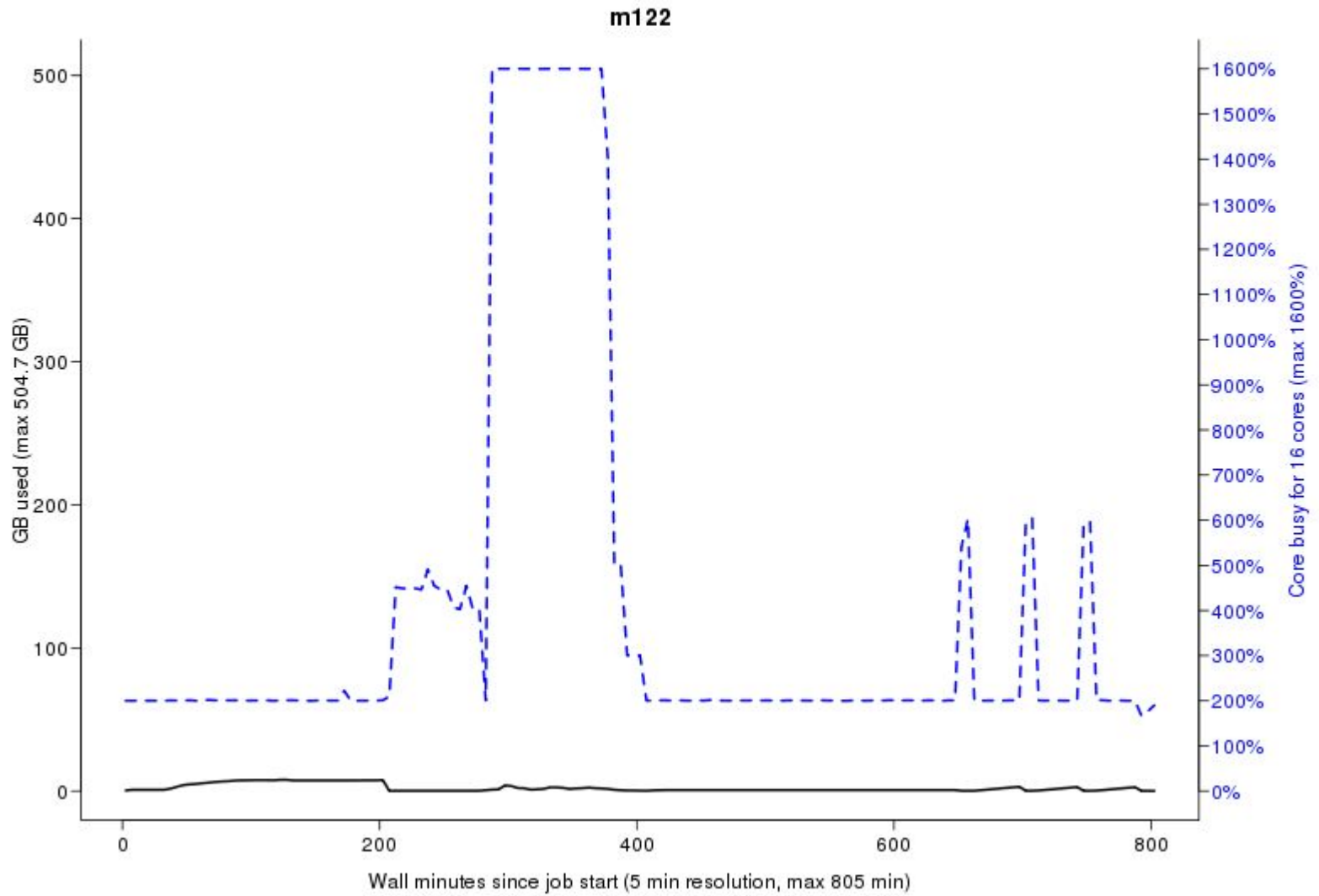Efficiency!!!

Plot efficiency
jobstats -p -A <projid>

2719328 on 'milou' end: 2014-09-09T08:26:34 runtime: 03-08:59:53

Flags: mem_underused:126:0

m83

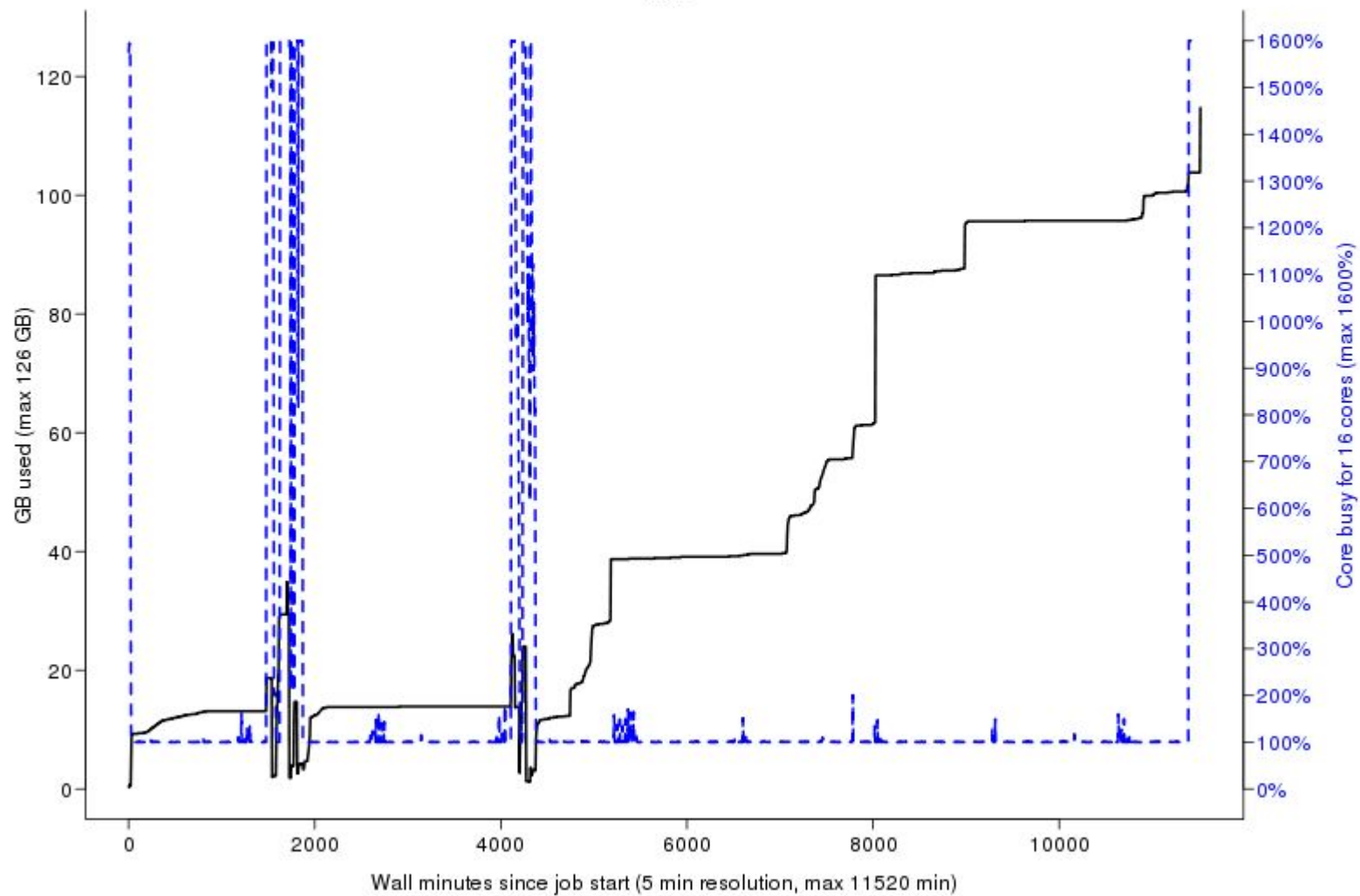# 2934193 on 'milou' end: 2014-09-26T01:40:23 runtime: 13:30:23

m122

2799665 on 'milou' end: 2014-09-18T07:36:54 runtime: 07-23:56:23

Flags: none

m26

Wall minutes since job start (5 min resolution, max 11520 min)

Take-home messages

- The difference between **user account** and **project**
- **Login nodes** are not for running jobs
- SLURM gives you access to the **compute nodes** when you specify a project that you are member of
- Use **interactive** for quick jobs and for testing
- Do not ask for more cores/nodes than your job can actually use
- A job script usually consists of:
    - Job settings (-A, -p, -n, -t)
    - Modules to be loaded
    - Bash code to perform actions
    - Run a program, or multiple programs

Laboratory time! (again)