

HPC in Life Sciences

Erica Bianco, PhD
Computational Scientist @ HPCNow!

Why use an HPC?

The key goal is to solve the problems faster.

- Speed → Split the work between several processors : the program will run N-ish times faster by using N processors.
- Volume → large data analyses
- Cost → faster results, reduced wet lab analyses
- Efficiency and convenience → shared resources used 24/7, no need to use all resources of your own PC

Why use an HPC?

The key goal is to solve

- Speed → Split the work across many processors.
- Volume → large data sets
- Cost → faster results
- Efficiency and convenience

Because life is short.



es faster by using N

ources of your own PC

Main Use Cases for HPC

Clustered (Tightly coupled)

- Fluid dynamics
- Weather forecasting
- Materials simulations
- Crash simulations

- Seismic processing
- Metagenomics
- Astrophysics
- Deep learning

Modest IO requirements

Heavy IO requirements

- Risk simulations
- Molecular modeling
- Contextual search
- Logistics simulations

- Animation and VFX
- Semiconductor verification
- Image processing/GIS
- Genomics

Distributed/Grid (Loosely coupled)

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Distributed/Grid (Loosely coupled)

Table 1 High-performance computing architectures: advantages and drawbacks

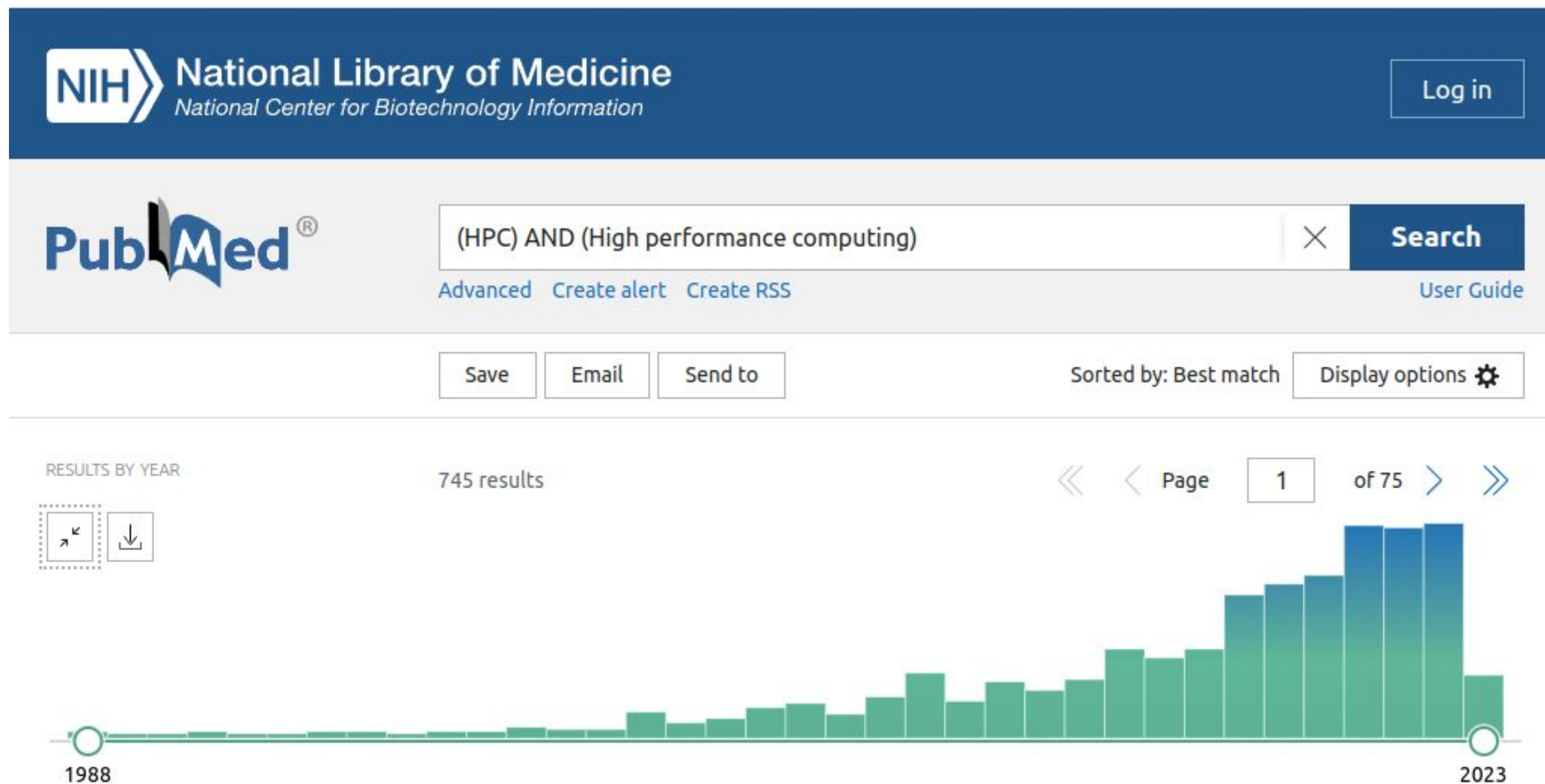
HPC type	Architecture	Advantages	Drawbacks	Computing paradigm
Computer cluster	Set of interconnected computers controlled by a centralized scheduler	Require minimal changes to the existing source code of CPU programs, with the exception of possible modifications necessary for message passing	Expensive, characterized by relevant energy consumption and requires maintenance	Multiple Instruction Multiple Data
Grid computing	Set of geographically distributed and logically organized (heterogeneous) computing resources	Require minimal changes to the existing source code of CPU programs, with the exception of possible modifications necessary for message passing	Generally based on ‘volunteering’: computer owners donate resources (e.g. computing power, storage) to a specific project; no guarantee about the availability of remote computers: some allocated tasks could never be processed and need to be reassigned; remote computers might not be completely trustworthy	Multiple Instruction Multiple Data
Cloud computing	Pool of computation resources (e.g. computers, storage) offered by private companies, attainable on demand and ubiquitously over the Internet	Mitigate some problems like the costs of the infrastructure and its maintenance	Data are stored on servers owned by private companies; issues of privacy, potential piracy, espionage, international legal conflicts, continuity of the service (e.g. owing to some malfunctioning, DDoS attacks, or Internet connection problems)	Multiple Instruction Multiple Data
GPU - Graphics Processing Units	Dedicated parallel co-processor, formerly devoted to real-time rendering of computer graphics, nowadays present in every common computer	High number of programmable computing units allow the execution of thousands simultaneous threads. Availability of high-performance local memories	Based on a modified SIMD computing paradigm: conditional branches imply serialization of threads’ execution. GPU’s peculiar architecture generally requires code rewriting and algorithms redesign	Same Instruction Multiple Data (although temporary divergence is allowed)
MIC - Many Integrated Cores	Dedicated parallel co-processor installable in common desktop computers, workstations and servers	Similar to GPUs but based on the conventional x86 instructions set: existing CPU code, in principle, might be ported without any modification. All cores are independent	Fewer cores with respect to latest GPUs. To achieve GPU-like performances, modification of existing CPU code to exploit vector instructions are required	Multiple Instruction Multiple Data
FPGA - Field Programmable Gates Arrays	Integrated circuits containing an array of programmable logic blocks	Able to implement a digital circuit, which directly performs purpose-specific tasks (unlike general-purpose software tools). Such tasks are executed on a dedicated hardware without any computational overhead (e.g. those related to the operating system)	Generally programmed using a descriptive language (e.g. VHDL, Verilog [18]), which can be cumbersome. Debugging using digital circuits simulators might be complicated and not realistic. Experience with circuit design optimization might be necessary to execute tasks using the highest clock frequency	Dedicated hardware

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HPC in Life Sciences recent papers :

Queried NCBI PubMed on April 11, 2023



HPC in Life Sciences recent papers



[Brief Bioinform.](#), 2017 Sep; 18(5): 870–885.
Published online 2016 Jul 7. doi: [10.1093/bib/bbw058](#)

Graphics processing units in bioinformatics, computational biology and systems biology

Is high performance computing a requirement for novel drug discovery and how will this impact academic efforts?

Savins Puertas-Martín , Antonio J. Banegas-Luna , Juana L. Redondo , Pilar M. Ortigosa , Olha C. Pages 981-985 | Received 16 Oct 2019, Accepted 17 Apr 2020
 [https://doi.org/10.1080/17445019.2020.1811744](#)

[Open Access](#) | [Published: 03 May 2018](#)

Towards Portable Large-Scale High-Performance Computing

[Yuankai Huo](#) , [Justin Blaber](#), [Stephen M. Damon](#), [Brian D. Boyd](#), [Shun-Wei Parvathaneni](#), [Camilo Bermudez Noguera](#), [Shikha Chaganti](#), [Vishwesh Narayan Greer](#), [Ilwac Landman](#)
[J Med Libr Assoc.](#) 2018 Oct; 106(4): 494–495.
Published online 2018 Oct 1. doi: [10.5195/jmla.2018.512](#)

High-performance computing service for bioinformatics

[Jean-Paul Courneya](#)

Bioinformationist, Health Sciences and Human Services Library, University of Alberta

[Alexa Mayo](#), AHIP

Associate Director for Services, Health Sciences and Human Services Library, University of Alberta
T6G 2G1, Edmonton, Alberta, Canada
T21201

PMCID: PMC6188000 [Open Access](#) [Article](#)

High Performance Computing PP-Distance Algorithms to Generate X-ray Spectra from 3D Models

by César González ^{1,*} Simone Balocco ² Jaume Bosch ³ Juan Miguel de Haro ³ Maurizio Paolini ⁴,
 Antonio Filgueras ³ Carlos Álvarez ³ and Ramon Pons ^{1,*}

- ¹ Institut de Química Avançada de Catalunya (IQAC-CSIC), 08034 Barcelona, Spain
 - ² Department of Mathematics and Informatics, Universitat de Barcelona, 08007 Barcelona, Spain
 - ³ Barcelona Supercomputing Center (BSC), 08034 Barcelona, Spain
 - ⁴ INTEL, 20090 Assago, Italy
- * Authors to whom correspondence should be addressed.

[tps://doi.org/10.3390/ijms231911408](https://doi.org/10.3390/ijms231911408)

20 September 2022 / Accepted: 22 September 2022 / Published: 27 September 2022

Exscalate4CoV: Innovative High Performing Computing (HPC) Strategies to Tackle Pandemic Crisis

by Andrea R. Beccari ¹ and Giulio Vistoli ^{2,*}

- ¹ EXSCALATE, Dompé Farmaceutici S.p.A., Via Tommaso De Amicis 95, I-80131 Napoli, Italy
 - ² Dipartimento di Scienze Farmaceutiche, Università degli Studi di Milano, Via Mangiagalli 25, I-20133 Milano, Italy
- * Author to whom correspondence should be addressed.

Hyperparameter Tuning with Imbalanced Learning for Alzheimer's Disease Data

by Fan Zhang ^{1,2,*} Melissa Petersen ^{1,2} Leigh Johnson ^{1,3} James Hall ^{1,2} and
 Sid E. O'Bryant ^{1,2}

- ¹ Institute for Translational Research, University of North Texas Health Science Center, Fort Worth, TX 76107, USA
 - ² Department of Family Medicine, University of North Texas Health Science Center, Fort Worth, TX 76107, USA
 - ³ Department of Pharmacology and Neuroscience, University of North Texas Health Science Center, Fort Worth, TX 76107, USA
- * Author to whom correspondence should be addressed.

[Appl. Sci.](#) **2022**, *12*(13), 6670; <https://doi.org/10.3390/app12136670>

[Biocomputing](#) **2023**, pp. 541-545 (2022)

HIGH-PERFORMANCE COMPUTING MEETS HIGH-PERFORMANCE MEDICINE

Anurag Verma, Jennifer Huffman, Ali Torkamani, and Ravi Madduri

https://doi.org/10.1142/9789811270611_0050 | Cited by: 0

Editorial | [Published: 18 July 2018](#)

Special Issue on High Performance Computing in Bio-medical Informatics

[Luping Zhou](#), [Islem Rekik](#), [Chenggang Yan](#) & [Guorong Wu](#)

[Neuroinformatics](#) **16**, 283 (2018) | [Cite this article](#)

2370 Accesses | 2 Citations | [Metrics](#)

Research | [Open Access](#) | [Published: 16 December 2022](#)

Profiling the BLAST bioinformatics application for load balancing on high-performance computing clusters

[Trinity Cheng](#), [Pei-Ju Chin](#), [Kenny Cha](#), [Nicholas Petrick](#) & [Mike Mikailov](#)

[BMC Bioinformatics](#) **23**, Article number: 544 (2022) | [Cite this article](#)

987 Accesses | 4 Altmetric | [Metrics](#)



[Biol Methods Protoc.](#) 2022; 7(1): bpac032.

Published online 2022 Nov 15. doi: [10.1093/biomethods/bpac032](#)

PMCID: PMC9767868

PMID: [36561335](#)

Teaching computational genomics and bioinformatics on a high performance computing cluster—a primer

[Arun Sethuraman](#)

High-Performance Computing in Cardiovascular Medicine of Multi-Dimensional Data Analysis-Driven Modeling and Simulation

re, Shinichi Goto

Cardiovascular dynamics, Artificial intelligence, Neural network, Machine learning

High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE

[Guy Baele](#) , [Daniel L. Ayres](#), [Andrew Rambaut](#), [Marc A. Suchard](#) & [Philippe Lemey](#)

[Open Access](#) |

[Open Access](#) | [First Online: 06 July 2019](#)

Accesses | 4 Citations | 8 Altmetric

Part of the [Methods in Molecular Biology](#) book series (MIMB, volume 1910)

Some topics covered and tools used

- protein folding
- drugs design
- genomics
 - WGS
 - RNAseq
 - proteome
 - metabolome
- ecology
- large datasets
- precision medicine
- ML / AI
- simulations
- [AlphaFold](#)
- [Nextflow](#) - workflow managers
- CI/CD
- containers
- Quantum computing is coming
- cloud vs on-prem
- [GPU](#)
- Future directions in [HPC](#)
- [Heroes](#)

A person wearing glasses and a dark shirt is standing in a server room, looking down at a laptop. The room is filled with rows of server racks, and the lighting is dim with blue highlights from the equipment.

How to run 4*100k simulations in few days

And what happens when you accidentally delete $\frac{1}{4}$ of your temporary results

<https://doi.org/10.1093/molbev/msaa156>

Run 4*100k simulations in few days

- when to make the job start (waiting in the queue)
- "auto"launching launcher and set a waiting time
- Keep working on the cluster while simulating and fairplay
- Control in real time how much memory your job is using


```
wflow_fsc_cluster.sh (ebianco on marvin.s.upf.edu /gpfs42/robbyfs/homes/users/ebianco/SCRIPTS) - gedit
Open ▾ [icon] Save

1 #!/bin/bash
2 #mar 17 abr 2018 10:43:18 CEST
3 #script to:
4 # (1) run fastsimcoal simulation
5 # (2) send the script to convert apr file to vcf individually
6 #      (or in blocks defined by variable $rep, default is rep=10 )
7 #to launch it
8 # sbatch -t 30-00 -x mr-01-[01-02] -J fsc.$model ~/SCRIPTS/wflow_fsc_cluster.sh $model
9 # squeue -o "%.18i %.9P %.8j %.8T %.10M " -u ebianco
10
11 #SBATCH -o fsc.%j.out
12 #SBATCH -e fsc.%j.err
13 #SBATCH --job-name=fsc
14 #SBATCH --cpus-per-task=12
15 #SBATCH --partition=normal
16 #SBATCH --mem-per-cpu=4g
17 #SBATCH --mail-type=all
18 # SBATCH --mail-type=fail
19
20 module load fastsimcoal2/2.6.0.3
21
22 model=$1
23
24 SCRIPTF="/homes/users/ebianco/SCRIPTS"
25
26 #check if variables are set correctly
27 if [[ ! $model ]]
28 then
29 echo -e "ERROR: model is not specified. \nScript must be run as \nsbatch wflow_fsc.sh \"$model\" \"$numsim\" \"$numsamp\" \"$rep[optional]\""
30 exit 1
31 fi
32
33 #run fastsimcoal after checking if model files are present in running folder
34 # if [[ -a $model.tpl && -a $model.est ]]
35 # then
36 time fsc26 -t $model.tpl -n 15 -e $model.est -E 25000 -q -c 12
37
38 rm -f $model/sust.*.out|
39 # else
40 # echo "ERROR: no $model.tpl or $model.est file in running folder."
41 # exit 1
42 # fi
43
44 exit 0
```

When to make a job start (waiting in the queue)

```
sbatch --dependency=after:$j launcher_sust.sh $model $m
```


When to make a job start (waiting in the queue)

sbatch --dependency=after:\$j launcher_sust.sh \$model \$m

-d, --dependency=<dependency_list>

Defer the start of this job until the specified dependencies have been satisfied completed. <dependency_list> is of the form <type:job_id[:job_id][,type:job_id[:job_id]]> or <type:job_id[:job_id][?type:job_id[:job_id]]>. All dependencies must be satisfied if the "," separator is used. Any dependency may be satisfied if the "?" separator is used. Many jobs can share the same dependency and these jobs may even belong to different users. The value may be changed after job submission using the scontrol command. Once a job dependency fails due to the termination state of a preceding job, the dependent job will never be run, even if the preceding job is requeued and has a different termination state in a subsequent execution.

after:job_id[:jobid...]

This job can begin execution after the specified jobs have begun execution.

afterany:job_id[:jobid...]

This job can begin execution after the specified jobs have terminated.

afterburstbuffer:job_id[:jobid...]

This job can begin execution after the specified jobs have terminated and any associated burst buffer stage out operations have completed.

aftercorr:job_id[:jobid...]

A task of this job array can begin execution after the corresponding task ID in the specified job has completed successfully (ran to completion with an exit code of zero).

afternotok:job_id[:jobid...]

This job can begin execution after the specified jobs have terminated in some failed state (non-zero exit code, node failure, timed out, etc).

afterok:job_id[:jobid...]

This job can begin execution after the specified jobs have successfully executed (ran to completion with an exit code of zero).

expand:job_id

Resources allocated to this job should be used to expand the specified job. The job to expand must share the same QOS (Quality of Service) and partition. Gang scheduling of resources in the partition is also not supported.

singleton

This job can begin execution after any previously launched jobs sharing the same job name and user have terminated.

"Auto"launching launcher and set a waiting time

```
sbatch --begin=now+5minutes launcher_sust.sh $model $m
```


"Auto"launching launcher and set a waiting time

```
sbatch --begin=now+5minutes launcher_sust.sh $model $m
```

--begin=<time>

Submit the batch script to the Slurm controller immediately, like normal, but tell the controller to defer the allocation of the job until the specified time.

Time may be of the form *HH:MM:SS* to run a job at a specific time of day (seconds are optional). (If that time is already past, the next day is assumed.) You may also specify *midnight*, *noon*, *fika* (3 PM) or *teatime* (4 PM) and you can have a time-of-day suffixed with *AM* or *PM* for running in the morning or the evening. You can also say what day the job will be run, by specifying a date of the form *MMDDYY* or *MM/DD/YY YYYY-MM-DD*. Combine date and time using the following format *YYYY-MM-DD[THH:MM[:SS]]*. You can also give times like *now + count time-units*, where the time-units can be *seconds* (default), *minutes*, *hours*, *days*, or *weeks* and you can tell Slurm to run the job today with the keyword *today* and to run the job tomorrow with the keyword *tomorrow*. The value may be changed after job submission using the **scontrol** command. For example:

```
--begin=16:00
--begin=now+1hour
--begin=now+60          (seconds by default)
--begin=2010-01-20T12:34:00
```

Notes on date/time specifications:

- Although the 'seconds' field of the HH:MM:SS time specification is allowed by the code, note that the poll time of the Slurm scheduler is not precise enough to guarantee dispatch of the job on the exact second. The job will be eligible to start on the next poll following the specified time. The exact poll interval depends on the Slurm scheduler (e.g., 60 seconds with the default sched/builtin).
- If no time (HH:MM:SS) is specified, the default is (00:00:00).
- If a date is specified without a year (e.g., MM/DD) then the current year is assumed, unless the combination of MM/DD and HH:MM:SS has already passed for that year, in which case the next year is used.

Keep working on the cluster while simulating and fairplay

```
sbatch -x mr-01-[01-02] --time=30 --array=0-9 -J sust.${m}.${model} \
```

```
~/SCRIPTS/wflow_sust_cluster.sh $model $mult
```


Keep working on the cluster while simulating and fairplay

```
sbatch -x mr-01-[01-02] --time=30 --array=0-9 -J sust.${m}.${model} \
```

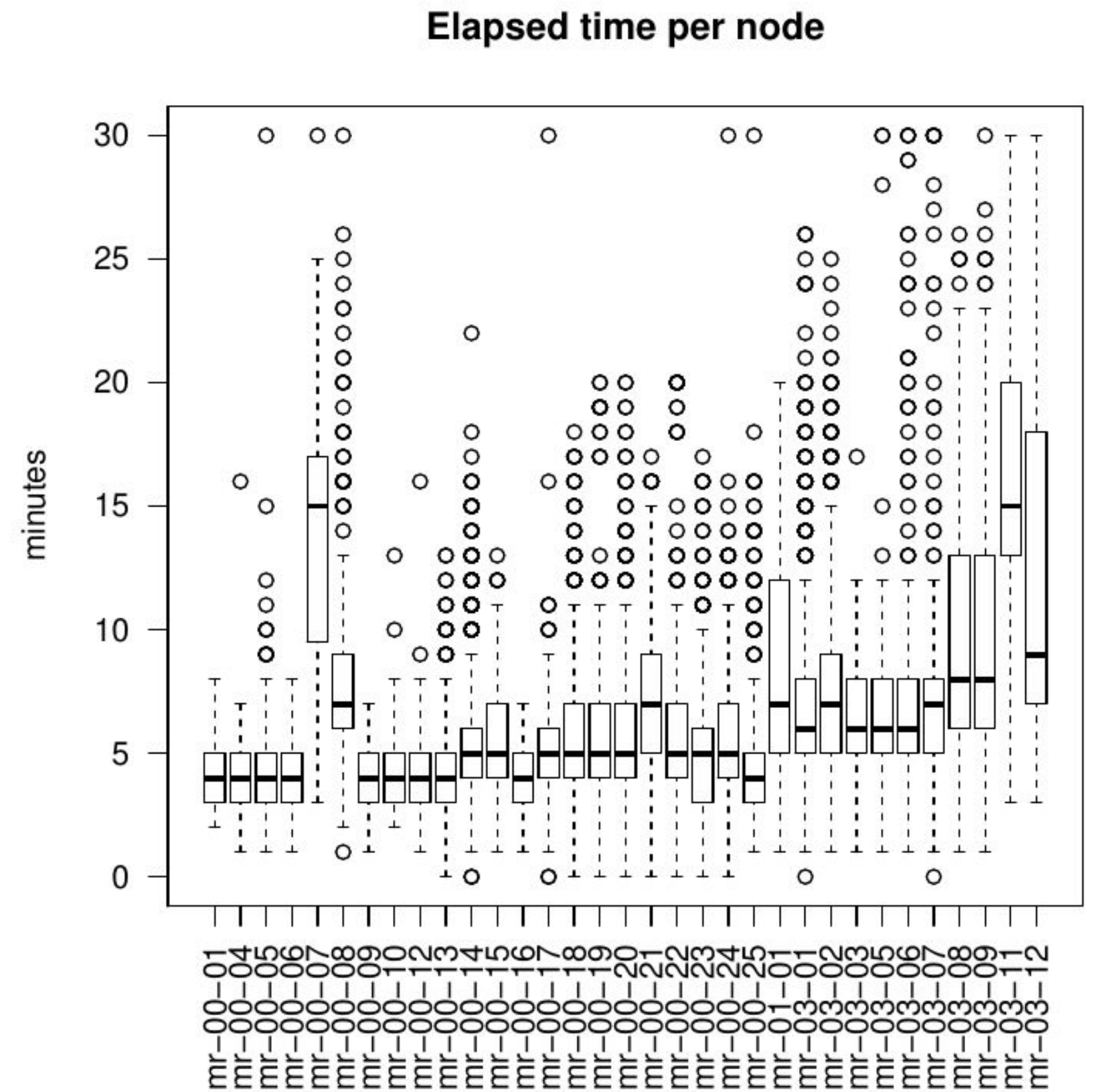
```
~/SCRIPTS/wflow_sust_cluster.sh $model $mult
```

-t, --time=<time>

Set a limit on the total run time of the job allocation. If the requested time limit exceeds the partition's time limit, the job will be left in a PENDING state (possibly indefinitely). The default time limit is the partition's default time limit. When the time limit is reached, each task in each job step is sent SIGTERM followed by SIGKILL. The interval between signals is specified by the Slurm configuration parameter **KillWait**. The **OverTimeLimit** configuration parameter may permit the job to run longer than scheduled. Time resolution is one minute and second values are rounded up to the next minute.

A time limit of zero requests that no time limit be imposed. Acceptable time formats include "minutes", "minutes:seconds", "hours:minutes:seconds", "days-hours", "days-hours:minutes" and "days-hours:minutes:seconds".

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Keep working on the cluster while simulating and fairplay

```
sbatch -x mr-01-[01-02] --time=30 --array=0-9 -J sust.${m}.${model} \
```

```
~/SCRIPTS/wflow_sust_cluster.sh $model $mult
```

-x, --exclude=<node name list>

Explicitly exclude certain nodes from the resources granted to the job.

-w, --nodelist=<node name list>

Request a specific list of hosts. The job will contain *all* of these hosts and possibly additional hosts as needed to satisfy resource requirements. The list may be specified as a comma-separated list of hosts, a range of hosts (host[1-5,7,...] for example), or a filename. The host list will be assumed to be a filename if it contains a "/" character. If you specify a minimum node or processor count larger than can be satisfied by the supplied host list, additional resources will be allocated on other nodes as needed. Duplicate node names in the list will be ignored. The order of the node names in the list is not important; the node names will be sorted by Slurm.

Job array: Keep working on the cluster while simulating and fairplay

```
sbatch -x mr-01-[01-02] --time=30 --array=0-9 -J sust.${m}.${model} \
```

```
~/SCRIPTS/wflow_sust_cluster.sh $model $mult
```

-a, --array=<indexes>

Submit a job array, multiple jobs to be executed with identical parameters. The *indexes* specification identifies what array index values should be used. Multiple values may be specified using a comma separated list and/or a range of values with a "-" separator. For example, "--array=0-15" or "--array=0,6,16-32". A step function can also be specified with a suffix containing a colon and number. For example, "--array=0-15:4" is equivalent to "--array=0,4,8,12". A maximum number of simultaneously running tasks from the job array may be specified using a "%" separator. For example "--array=0-15%4" will limit the number of simultaneously running tasks from this job array to 4. The minimum index value is 0. the maximum value is one less than the configuration parameter MaxArraySize. NOTE: currently, federated job arrays only run on the local cluster.

Job array: Keep working on the cluster while simulating and fairplay

```
sbatch -x mr-01-[01-02] --time=30 --array=0-9 -J sust.${m}.${model} \
```

```
~/SCRIPTS/wflow_sust_cluster.sh $model $mult
```

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Keep working on the cluster while simulating

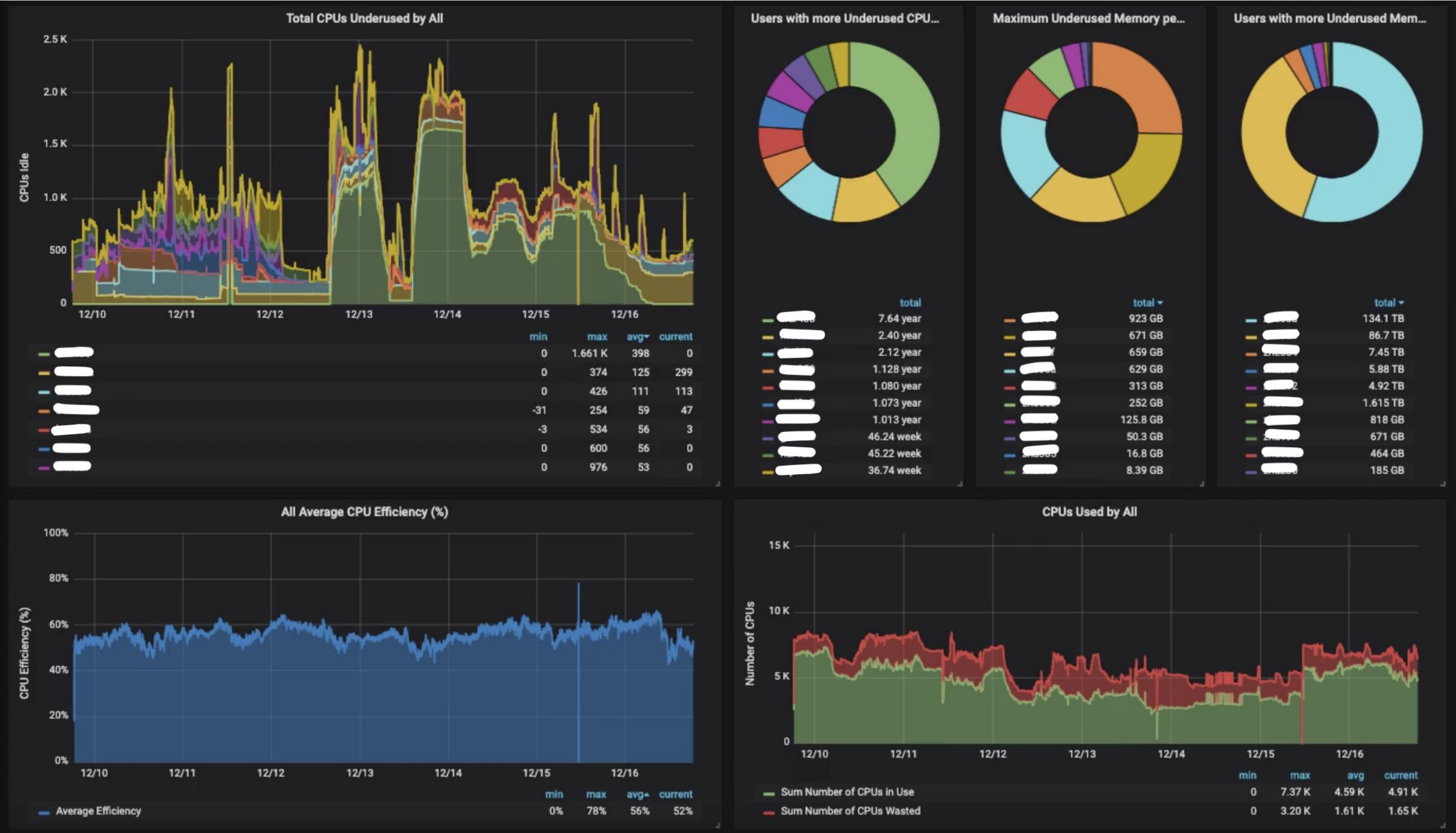
```
sbatch -x mr-01-[01-02] --time=30 --array=0-9 -J sust.${m}.${model} \
```

```
~/SCRIPTS/wflow_sust_cluster.sh $model $mult
```



```
wflow_sust_cluster.sh (ebianco on marvin.s.upf.edu /gpfs42/robbyfs/hc)
Open [x] Save
1 #!/bin/bash
2 #SBATCH -o sust.%j.out
3 #SBATCH --job-name=sust
4 #SBATCH --cpus-per-task=1
5 #SBATCH --partition=normal
6 #SBATCH --mem-per-cpu=10G
7 #SBATCH --mail-type=end
8 #SBATCH --mail-type=fail
9
10
11 ss="${SLURM_ARRAY_TASK_ID}"
12 ss=$((ss+1))
13 mult=$2
14 s=$((ss+mult))
15 model=${1}
16
17 cd /gpfs42/robbyfs/scratch/lab_dcomas/ebianco/DEMO/$model
18
19 outname=${model}_${s}
20
21 if [ ! $outname ]
22 then
23 echo "WARNING: no outname specified, exit."
24 exit 1
25 fi
26
27 echo "Converting $outname"
28
29 rm -fr $outname/
30
31 mkdir $outname
32 cd $outname
33
34 python ~/SCRIPTS/arp2selink_cluster.py $outname 15
35
36 bash wflow_${outname}.sh
37
38 exit 0
39
40 #####
41
42
sh Tab Width: 8 Ln 21, Col 18 INS
```


Control in real time how much memory your job is using - job monitoring tool



Control in real time how much memory your job is using - without job monitoring tool

- scontrol show jobid \$JOBID
- queue -t R -u \$USER → to see in which node your job is running
- interactive -m 1 -w <node>
- top

```
ebianco@marvin:/homes/users/ebianco/DEMO/POSTPR/p-values
top - 10:06:33 up 13 days, 19:57, 0 users, load average: 11.06, 10.83, 10.27
Tasks: 425 total, 8 running, 417 sleeping, 0 stopped, 0 zombie
%Cpu(s): 34.5 us, 0.1 sy, 0.0 ni, 65.4 id, 0.0 wa, 0.0 hi, 0.0 si, 0.0 st
KiB Mem : 26385593+total, 21930035+free, 42007624 used, 2547968 buff/cache
KiB Swap: 8388604 total, 8384696 free, 3908 used. 22034067+avail Mem

  PID USER      PR  NI    VIRT    RES    SHR  S  %CPU  %MEM    TIME+  COMMAND
115251 ebianco   20   0  5768200    5.4g   4528 R  100.0   2.1   25:23.98 R
170308 mbogaer+  20   0  3546604    3.4g   1920 R  100.0   1.3  12879:46 i_baypass
 60456 asantini  20   0   938912  921208   1968 R  100.0   0.3   542:59.64 hgs
105448 adedios   20   0   14.6g    3.0g  13940 S  100.0   1.2   47:46.60 java
112066 ebianco   20   0  5743200    5.3g   4704 R  100.0   2.1   31:53.20 R
123451 ebianco   20   0  5287080    4.9g   4664 R  100.0   2.0    7:50.24 R
133028 xfarre    20   0   180312   33656    884 R  100.0   0.0   1185:34 codeml
147993 sdeb      20   0  3356648  471444  117792 S  100.0   0.2   2334:13 MATLAB
148257 sdeb      20   0  3291112  474312  117724 S  100.0   0.2   2334:09 MATLAB
148376 sdeb      20   0  3356648  435040  117716 S  100.0   0.2   2334:05 MATLAB
165293 xfarre    20   0  2050016    1.0g   10588 R  100.0   0.4   1124:13 python
 13469 root       0  -20   28.9g   12.7g  611168 S    0.7   5.1  108:34.38 mmfsd
127293 ebianco   20   0   172572    2716    1668 R    0.7   0.0    0:00.12 top
  1297 root      20   0    13216     752     604 S    0.3   0.0    3:43.33 rngd
  2149 root      20   0   384544    1912    1356 S    0.3   0.0    1:31.44 dsm_ism_srvmgrd
    1 root      20   0   193432     6388    2612 S    0.0   0.0    8:28.13 systemd
    2 root      20   0         0         0         0 S    0.0   0.0    0:00.54 kthreadd
    3 root      20   0         0         0         0 S    0.0   0.0    0:04.75 ksoftirqd/0
    5 root       0  -20         0         0         0 S    0.0   0.0    0:00.04 kworker/0:0H
    8 root      rt    0         0         0         0 S    0.0   0.0    0:00.71 migration/0
    9 root      20   0         0         0         0 S    0.0   0.0    0:00.00 rcu_bh
   10 root      20   0         0         0         0 S    0.0   0.0   9:48.37 rcu_sched
   11 root       0  -20         0         0         0 S    0.0   0.0    0:00.00 lru-add-drain
```


In conclusion:

- All disciplines in Life Science can benefit from HPC
- Work smarter: use your resources at their best performance
 - reduce analysis time,
 - reduce costs,
 - reduce wetlab tests
- Be fair, and FAIR (Findability, Accessibility, Interoperability, and Reuse)
 - document and comment all your codes! (It's for your own benefit)



Questions?

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