i-Trop cluster Slurm Initiation

www.southgreen.fr

https://southgreenplatform.github.io/trainings

i-Trop presentation

Emmanuelle Beyne
20% ETP

Aurore COMTE
20% ETP

Bruno GRANOUILLAC
50% ETP

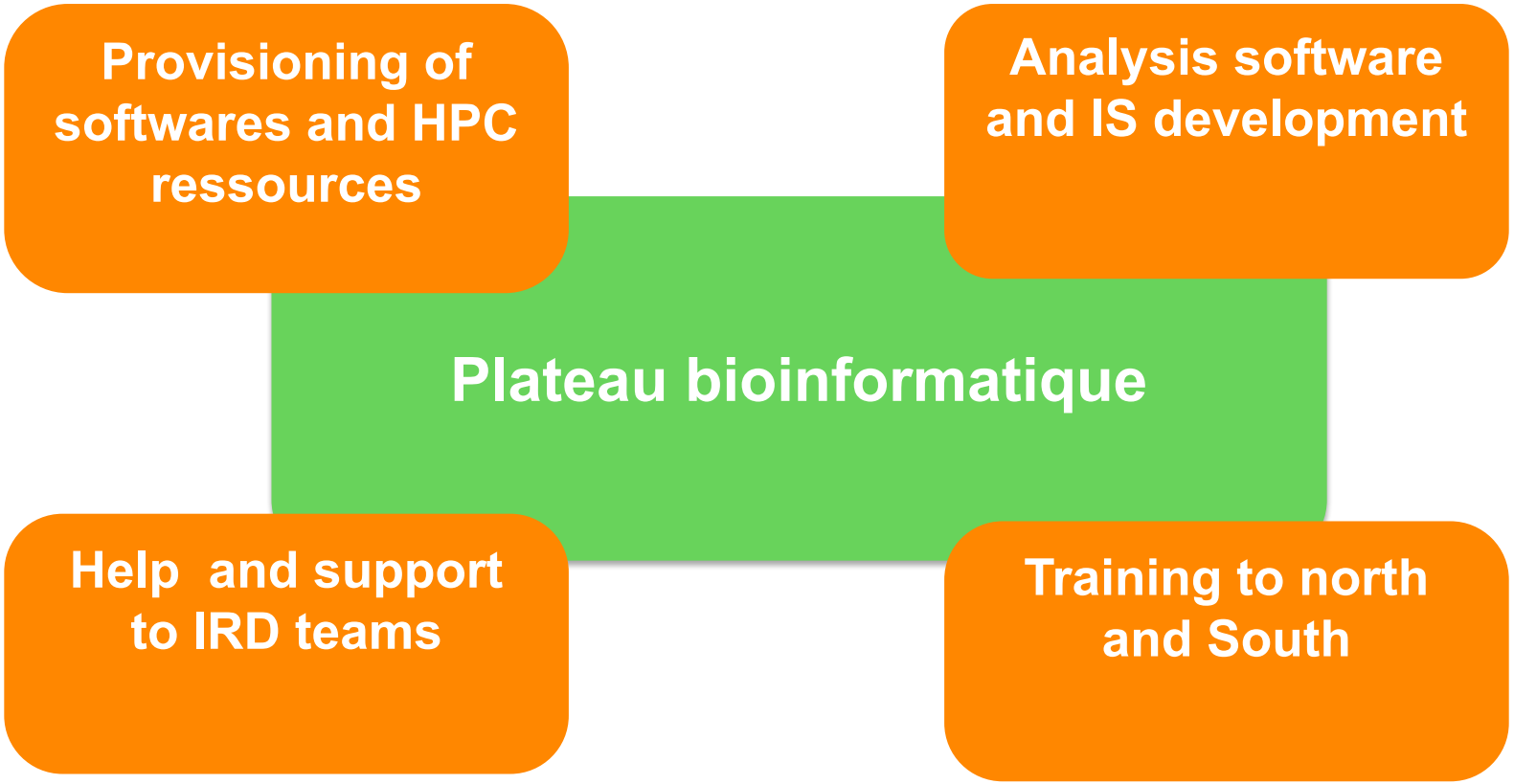
Valérie NOEL
25% ETP

Julie ORJUELA-BOUNIOL
25% ETP

Ndomassi TANDO
100% ETP

Christine TRANCHANT-DUBREUIL
20% ETP

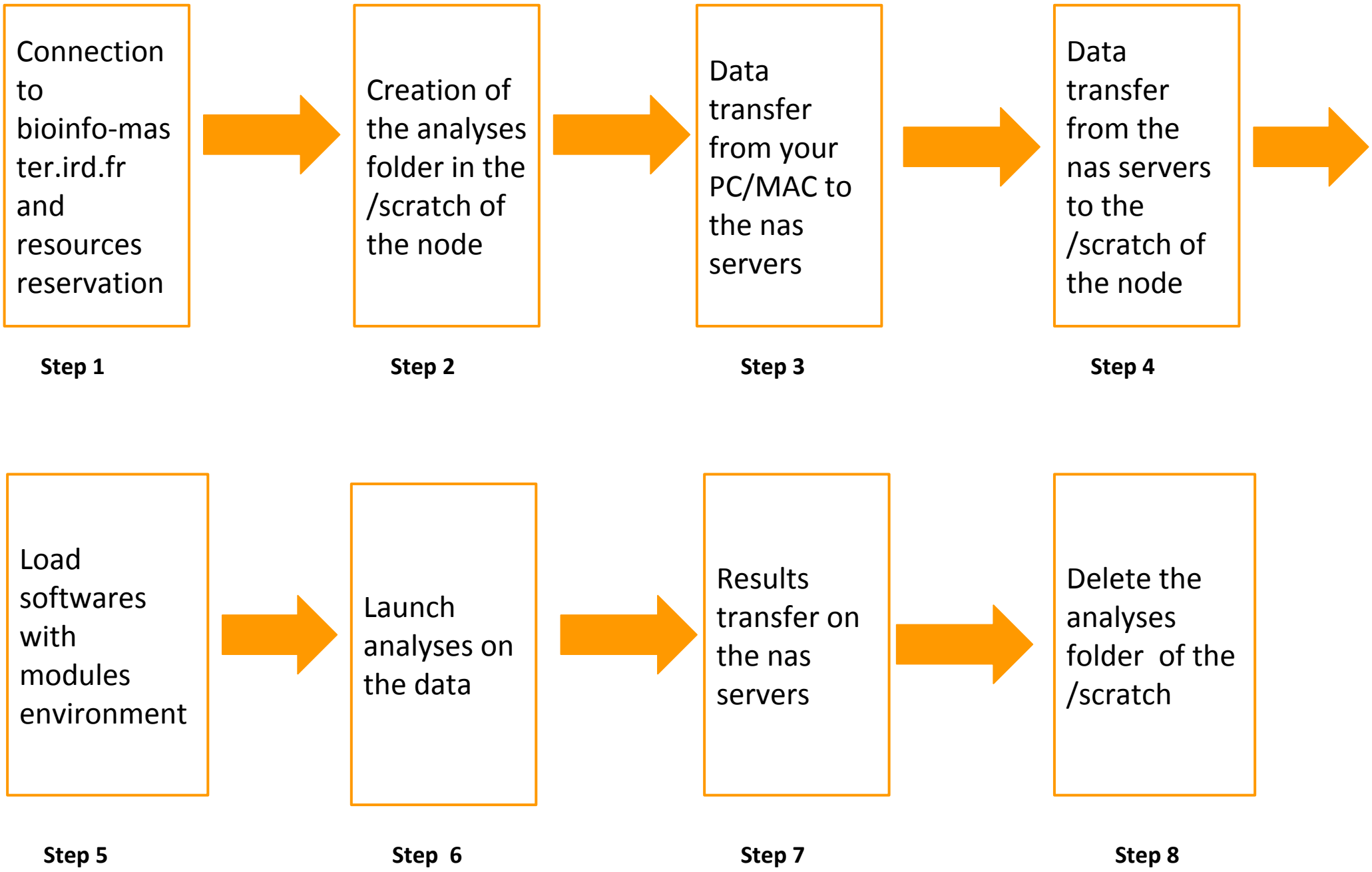
i-Trop Presentation



Demandes/incidents/Howtos

- Request forms: https://itrop-glpi.ird.fr/plugins/formcreator/front/formlist.php
  - Accounts
  - Softwares
  - Projects
- Incidents: contact bioinfo@ird.fr
- Howtos: https://southgreenplatform.github.io/trainings/hpc/hpcHowto/
- Slurm Tutorials: https://southgreenplatform.github.io/tutorials//cluster-itrop/Slurm/

Analyses steps of the cluster



Practice

Step 1: Connection, sinfo

1

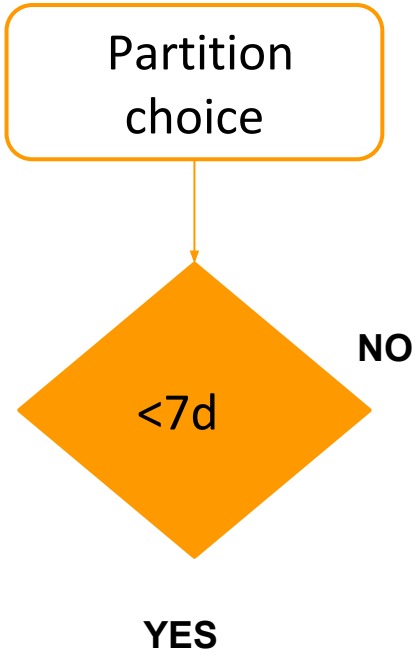
Go to the Practice 1 and 2 *of github*

Partitions

Partitions	Use	RAM on nodes	Core on nodes
short	Short Jobs < 1 day (higher priority, interactive jobs)	48 to 64 GB	12 cores
normal	Short Jobs max 7 days	64 Go to 96 GB	12 to 24 cores
long	45 days >long jobs > 7 days	48 GB	12 to 24 cores
highmem	Jobs with more memory needs	144 GB	12 to 24 cores
supermem	Jobs with much more memory needs	1TB	40 cores
gpu	Need for analyses on GPU cores	192GB	24 cpus and 8 GPUs cores

*Request to do with arguments

How do I choose the partition?



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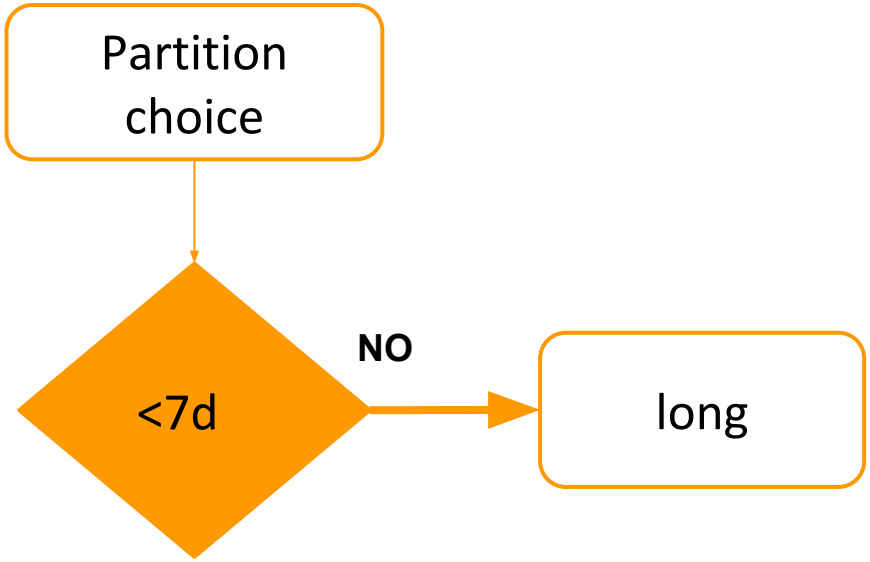

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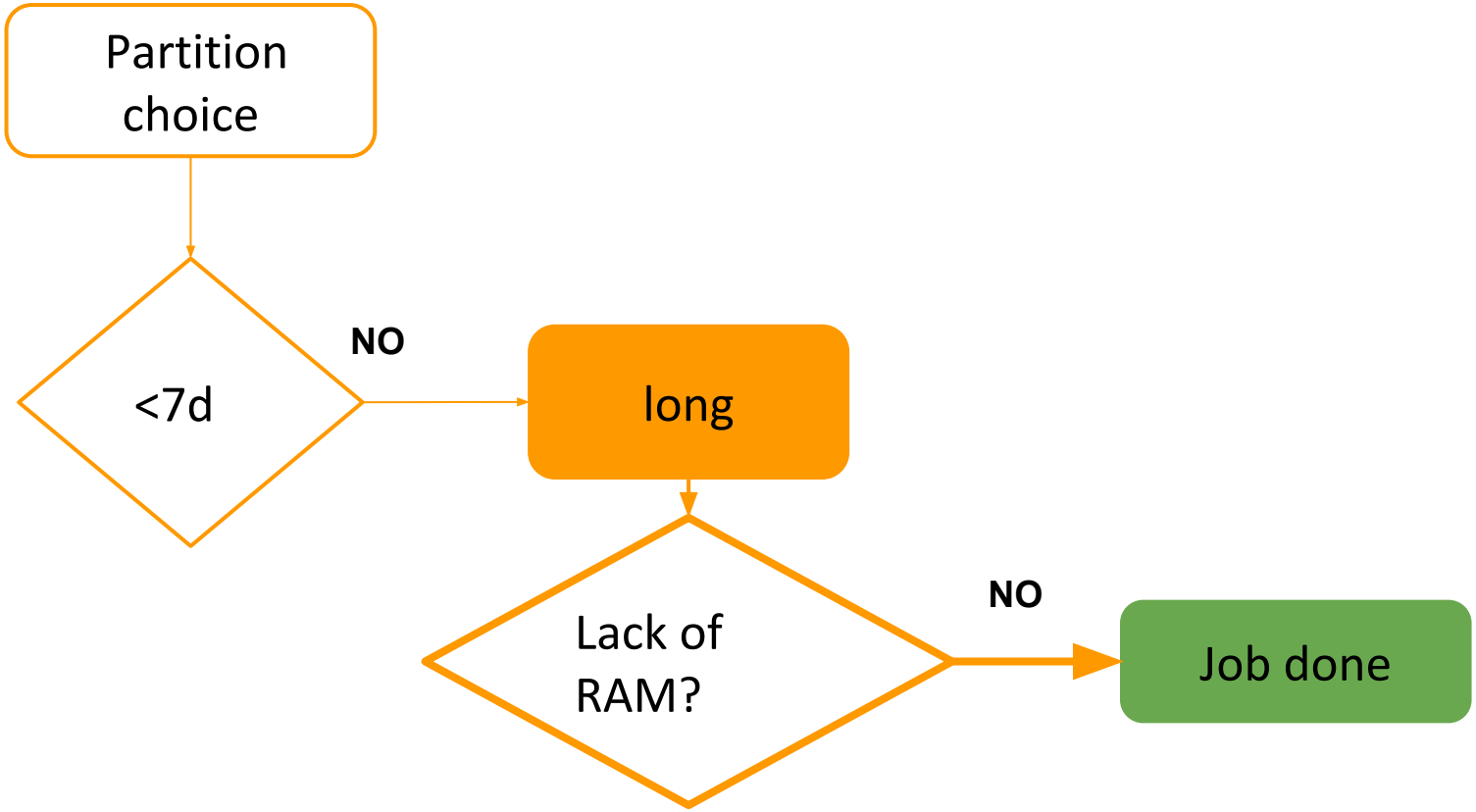

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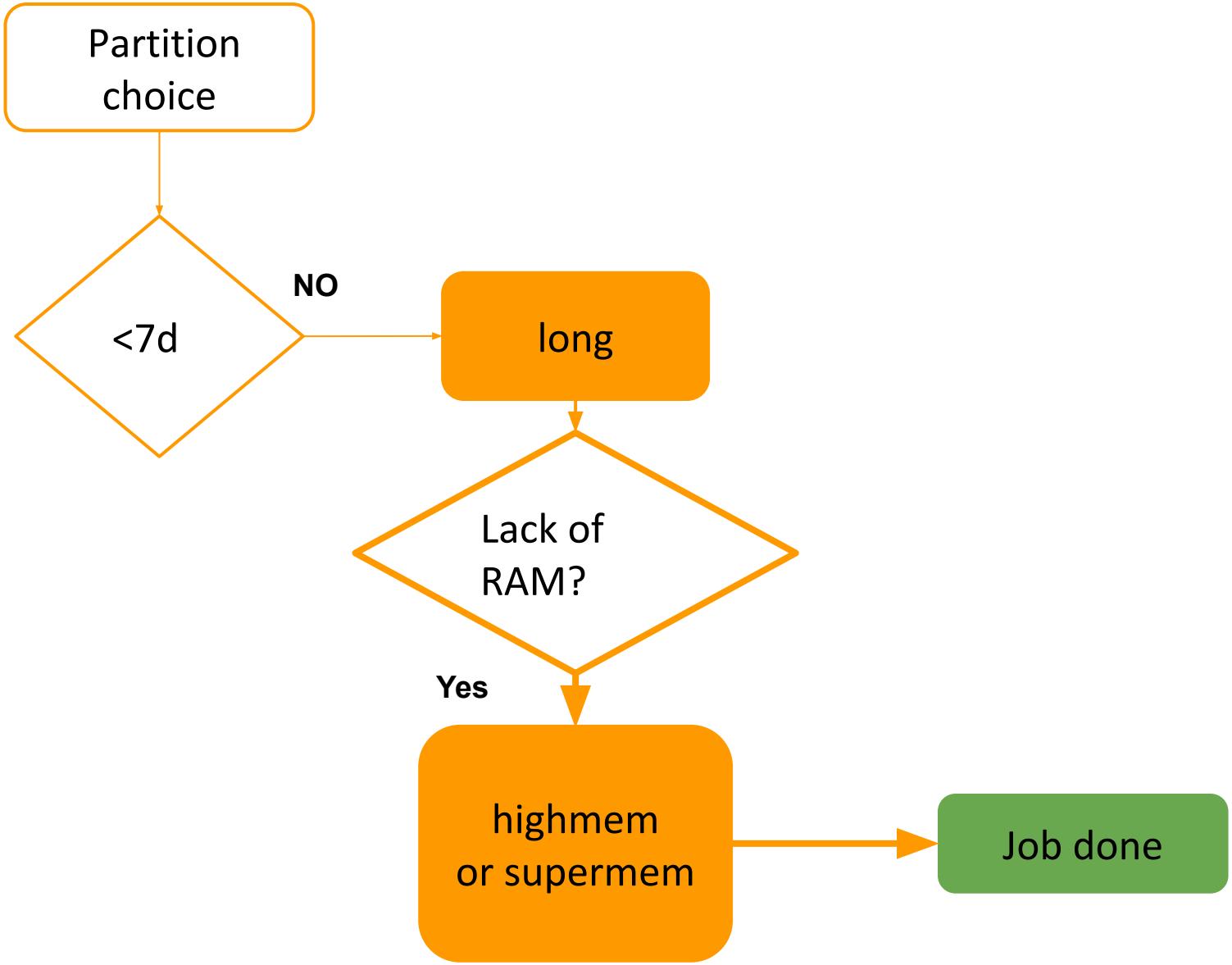

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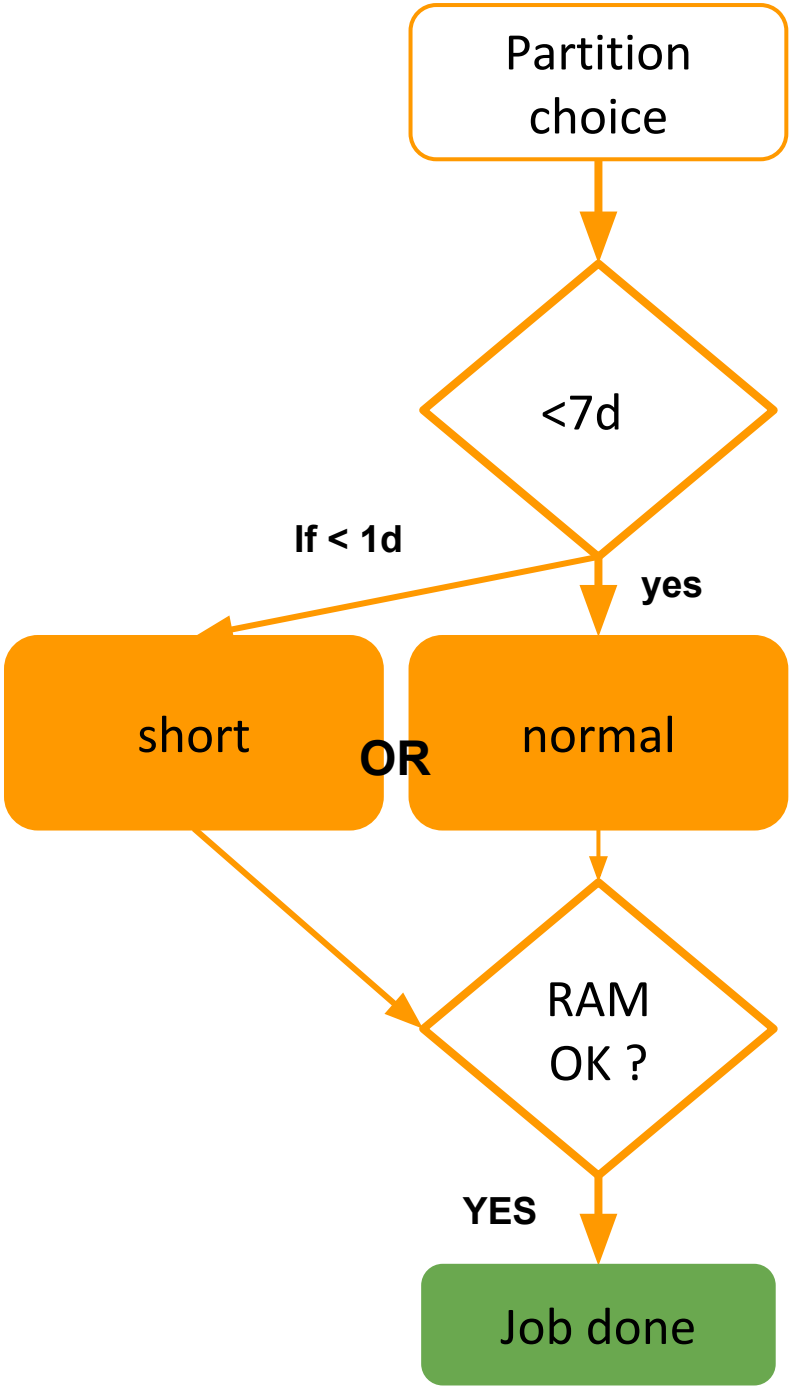
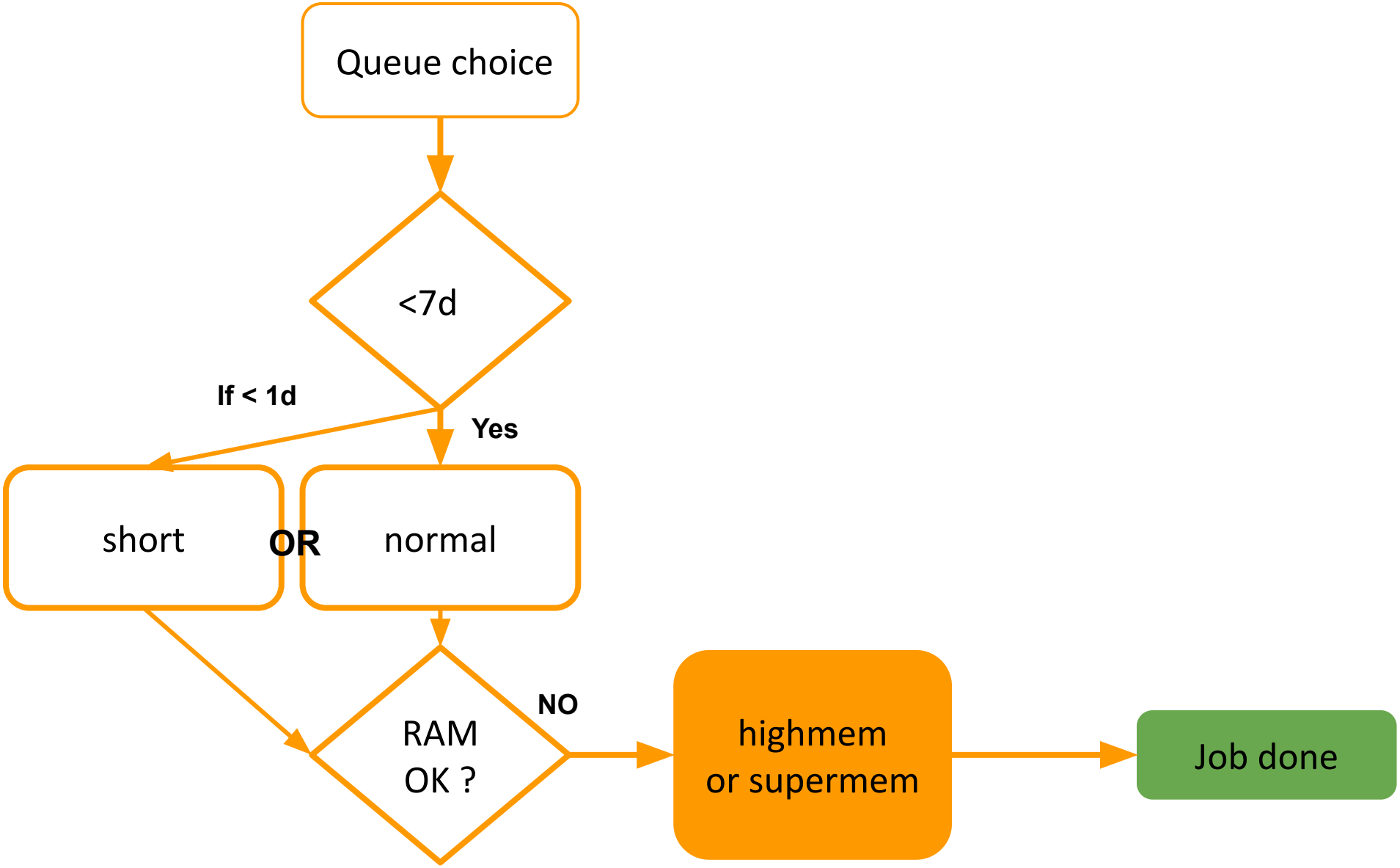
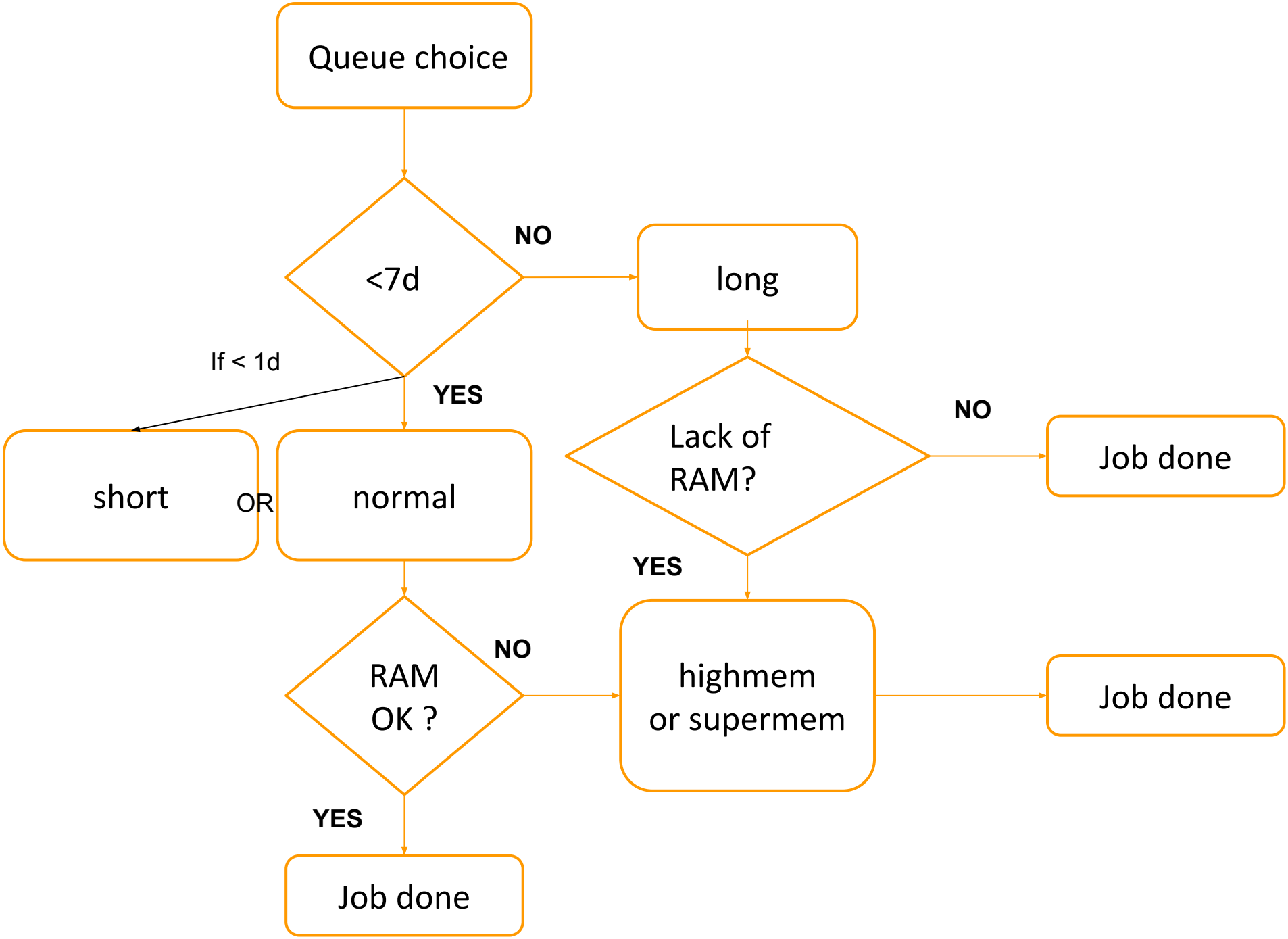


How do I choose the queue?



How do I choose the queue?

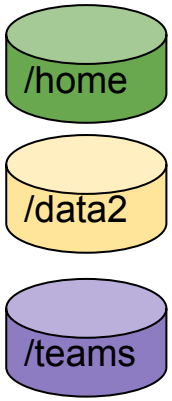


Particular case : gpu partition

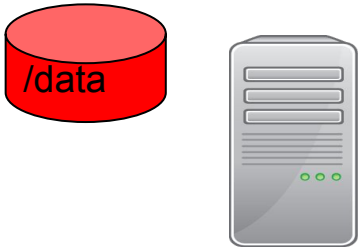
- Partition to work on GPUs processors : basecalling, MiniOn etc..
- Restricted access to gpu_account group
- Request access with arguments to do here:

  https://itrop-glpi.ird.fr/plugins/formcreator/front/formlist.php

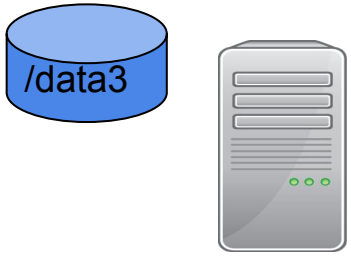
cluster i-Trop disk partitions



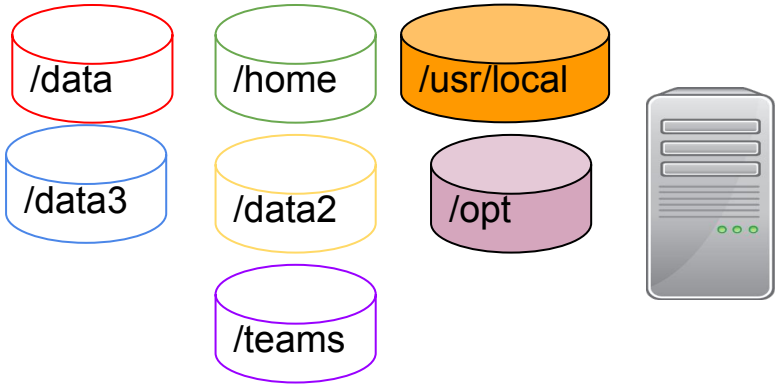
bioinfo-nas.ird.fr



bioinfo-nas2.ird.fr

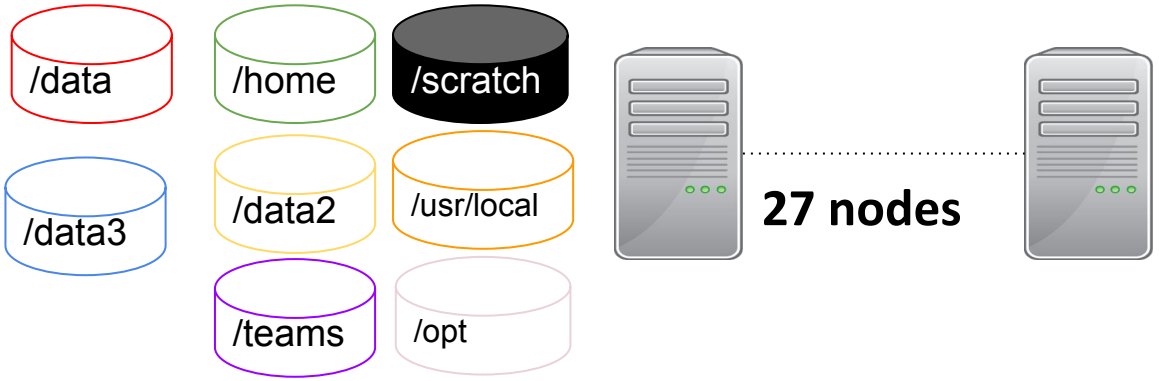


bioinfo-nas3.ird.fr



bioinfo-master.ird.fr

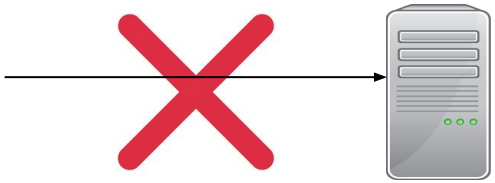
Virtual links to the other servers partitions



27 nodes

Data transfer on i-Trop cluster

PC/MAC



direct transfer
via filezilla
forbidden

bioinfo-master.ird.fr
91.203.34.148

Practice

Step 3 and 4: scp to nodes

4

Go to the Practice4 *of the github*

Module Environment

- Allow to choose the version of software you want to use

- 2 types of softwares :
  bioinfo : includes all the bioinformatics softwares (example BEAST)
  system : includes all the system softwares(example JAVA)

- Overcome the environment variables

Module Environment

➢ 5 types of commands :

- See the available modules :

  module avail

- Obtain infos on a particular module:

  module whatis + module name

- Load a module :

  module load + modulename

- List the loaded module :

  module list

- Unload a module :

  module unload + modulename

- Unload all the modules :

  module purge

Practice

Step 5: module environment

5

Go to the Practice5 *of the github*

Launch a command from the prompt

- Load the software version to launch
- Launch the data analysis

```
$~ command <options> <arguments>
```

With *command*: the command to launch

Launch a command line job

- Execute a bash command via srun
- Launch the command from a node
- We use:

$~ **srun** <options> <*command*>

With *command*: the command to launch

Practice

Step6: launch the analysis

6

Go to the Practice6 *of the github*

Main Slurm commands

Commande	Description	Exemple
srun --time=0X:00 --pty bash -i	Interactive way to connect to a node for X minutes	srun --time=02:00:00 --pty bash -i Connection for 2h
salloc --time=0X:00	Allocate one or several nodes for a later use	salloc -N 2 --p short --time=05:00
sbatch	Launch a analyses in background via a script	sbatch script.sh
sinfo	Informations on partitions	sinfo
scancel	Job deletion	scancel 1029
squeue	Infos on all jobs	squeue -u tando
scontrol show job <job_id>	Infos on the active job <job_id>	scontrol show job 1029

More infos here : https://southgreenplatform.github.io/tutorials//cluster-itrop/Slurm/#part-2

Options of sbatch, srun, salloc commands

Options	Description	Exemple
--job-name=<name>	Name the job	sbatch --job-name=tando_blast
-p **<**partition>	Choose a partition	sbatch -p highmem
--nodelist=<nodeX>	Choose a particular node	sbatch -p normal --nodelist=node14
-n <nb_tasks>	Launch several instance of a command	srun -n 4
-c <nb_cpu_per_task>	Allocate the number of cpus per task	srun -n 4 -c 2 hostname
--mail-user=<emailaddress>	Send a email	sbatch --mail-user=ndomassi.tando@ird.fr
--mail-type=<event>	Send a email when : END: end of the job FAIL: abortion BEGIN: beginning of job ALL: all events	sbatch ---mail-type=BEGIN
--workdir=[dir_name]	Precise the working directory	sbatch s--workdir=/scratch/tando script.sh

Practice

Step 7: Retrieve the results

7

Go to the Practice7 *of the github*

Delete results from scratchs

- Scratch= temporary spaces
- Verify that the copy is OK before
- Use rm command

```
cd /scratch
rm -rf nom_rep
```

Practice

Step8: Data deletion

8

Go to the Practice8 *of the github*

Scripts to visualize/delete données temporary data

- Scripts location: /opt/scripts/scratch-scripts
- Visualize data on scratchs: scratch_use.sh

```
sh /opt/scripts/scratch-scripts/scratch_use.sh
```

- Delete data on scratchs: clean_scratch.sh

```
sh /opt/scripts/scratch-scripts/clean_scratch.sh
```

LAUNCH A JOB

Advantages

- Scheduler choose resources automatically
- Use up to 24 cores at the same time
- Possibility to configure this choice
- Jobs launch in background

→ possibility to turn off your PC/MAC

→ automatic results retrieving

Launch a batch job

- Execute a script via rm
- Use:

```
$~ sbatch script.sh
```

with script.sh : the name of the script

Options of sbatch, srun, salloc commands

Options	Description	Exemple
--job-name=<name>	Name the job	sbatch --job-name=tando_blast
-p **<**partition>	Choose a partition	sbatch -p highmem
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-c <nb_cpu_per_task>	Allocate the number of cpus per task	srun -n 4 -c 2 hostname
--mail-user=<emailaddress>	Send a email	sbatch --mail-user=ndomassi.tando@ird.fr
--mail-type=<event>	Send a email when : END: end of the job FAIL: abortion BEGIN: beginning of job ALL: all events	Sbatch ---mail-type=BEGIN
--workdir=[dir_name]	Precise the working directory	sbatch s--workdir=/scratch/tando script.sh

Bash scripts syntax

First part of the script (in green): sge execution options with the key word #SBATCH

```
#!/bin/bash

###### Configuration SLURM#####################################
## Name of the job:
#SBATCH --job-name=test
## Name of the output file:
#SBATCH --output=res.txt
## Number of tasks
#SBATCH --ntasks=1
## Execution Time Limit
#SBATCH --time=10:00
#############################################################
```

Bash scripts syntax

In the 2nd part of the script: the command to execute

```
###############Partie exécution des commandes ###################

nom_variable1=”valeur_variable1”
nom_variable2=”valeur_variable2”

sleep 30
hostname
```

Practice

Launch a script with Slurm

9

Go to the Practice9 of the github

Satisfaction survey

Thank you to fill up the form at this URL:

https://itrop-survey.ird.fr/index.php/562934?lang=fr

Citations

If you use i-Trop Bioinformatics resources.

Thank you for citing with:

“The authors acknowledge the IRD itrop HPC (South Green Platform) at IRD montpellier
for providing HPC resources that have contributed to the research results reported within this paper.
URL: https://bioinfo.ird.fr/- http://www.southgreen.fr”

Projects

- Include a budget for bioinformatics resources in your answer to projects funding

- A need in hard drives, renewal machinesetc…

- Available quotations

- Contact bioinfo@ird.fr : help, needs definition, quotations...

Thank you for your attention !