# **HTCondor Essentials**

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## Login

To login use ssh protocol through the following command:

> ssh -i <path\_private\_key> <username>@frontend.recas.ba.infn.it

The login occurs in the user home: > pwd /lustrehome/<username>

## How to submit a job in the HTCondor pool

Suppose we want to run the echo command to print on screen the string "Hello World!". To submit a job in HTCondor we need a submit description file, a text file which will describe the job (path of executable, requirements, etc...).

A further explanation about submit description file and its commands is described later.

### Submit description file

```
# This is a comment in the submit file
# file name : submit echo
# universe describes an execution environment. Set universe to vanilla
universe = vanilla
# Path of the executable (it can be a system command, your own application, a
script, etc...)
executable = /bin/echo
# The argument to pass to the executable
arguments = "Hello World!"
# The output of the remote machine running the job will be printed on
echo.out
output = echo.out
error = echo.error
\log = echo.log
request_cpus = 1
rank = Memory
queue
```

Note: if you don't specify request\_cpus, request\_disk, request\_memory in the submit file, the job will run on a default amount of cpus (1), memory and disk space.

To submit the job use condor\_submit passing as an argument the name of the submit file: > condor\_submit submit\_echo -name ettore

## Why the -name<schedd> option?

In order to submit HTCondor job-related commands you need to specify a schedd, hence the -name<schedd> option in the command submission above.

<u>All commands described in this document need the -name ettore option to work except</u> <u>condor\_status.</u>

## Submitting a job

condor\_submit is the program for submitting jobs for execution under HTCondor.

```
> condor_submit <path_submit_file>
```

```
> condor_submit <path_submit_file> -interactive
```

Indicates that the user wants to run an interactive shell on the remote machine that execute the job.

The submit file should look like the following examples:

Submit description file example in order to execute the mathematica application with 1GB of RAM as resource allocation policy:

executable	= mathematica
universe	= vanilla
input	= test.data
output	= loop.out
error	= loop.error
log	= loop.log
request_memory	= 1 GB
initialdir	= run_1
queue	

Submit description file example in order to execute the mathematica application with 24GB of RAM and 8 cores as resource allocation policy:

executable	= mathematica
universe	= vanilla
input	= test.data
output	= loop.out
error	= loop.error
log	= loop.log
request_memory	= 24 GB
request_cpus	= 8
initialdir	= run_1

#### queue

Resources allocation are managed in a hard way. By configuration HTCondor will not allow the job to exceed the requested resources.

Requesting more than one core could lead the job to high waiting time in queue.

## Checking status of submitted jobs

### Getting id and other info about a job

> condor\_q

Displays information about jobs in the HTCondor job queue. For every job is shown:

- <u>id</u>: id of the condor job
- <u>status</u>: I idle (waiting for a machine to execute on), R running, H on hold, S – suspended, C – completed, X – removed, < – transferring input,</li>
   – transferring output
- other info (like runtime, size, priority (PRI), name of the executable (CMD))

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### Displaying running jobs

> condor\_q -run

### Displaying only your jobs

> condor\_q -constraint 'OWNER == "<username>"'

### Displaying jobs on hold

> condor\_q -hold

### Displaying a specific job

> condor\_q <job\_id>

### Why a job won't complete its execution?

> condor\_q -better-analyze <job\_id> Performs a detailed matchmaking analysis to determine how many slots are available to run the requested job.

Checking output of a running job

> condor\_tail <job\_id>
 Displays the last lines of stdout of a running job

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## Managing a job

### Removing a job from the queue

A job can be removed from the queue at any time by using the condor\_rm command.

```
> condor_rm <job_id>
```

## Putting a job on hold

A job can be put on hold state with condor\_hold command. When a job is put on hold, it will not be scheduled to run until is released. If the job is running when condor\_hold is invoked, it will be vacated from the machine it was running on.

```
> condor_hold <job_id>
```

### **Releasing a job**

A job can be released with condor\_release command. When a job is released from hold state, it is returned to idle state, and will be scheduled to run when possible. Only jobs that are on hold can be released.

```
> condor_release <job_id>
```

## Changing the priority of the jobs

The priority of jobs can be changed with condor\_prio command.

The priority of a job can be any integer, with higher numbers corresponding to greater priority. For adjustment of the current priority, + *value* increases the priority by the amount given with *value*. - *value* decreases the priority by the amount given with *value*.

```
> condor_prio -p <+|-value> <job_id>
```

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## Checking pool status

condor\_status is a versatile tool that may be used to monitor and query the HTCondor pool.

Note: condor\_status command doesn't need -name<schedd> option to work.

- > condor\_status -available
   Shows available slots
- > condor\_status -available -autoformat Name Memory Cpus Disk Shows name, memory, cpus, disk space of available slots
- > condor\_status -run Shows slots which are currently running jobs

### Displaying slots running your jobs

```
> condor_status -constraint 'RemoteUser == "<username>@ReCaSCluster"'
```

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## SSH to a running job

To create an ssh session to a running job, type

```
> condor_ssh_to_job -name <schedd> <job_id>
```

replacing <schedd> with the name of the schedd to which the job has been submitted (e.g. ettore), and <job\_id> with the job id. Notice that you must be the owner of the job.

The remote session runs with the same user as the running job, in the folder from which it has been launched. A PID, associated to the job, is provided. To leave the session, type logout. More options can be found through

```
> condor_ssh_to_job -help
```

Further information and some examples on how to use it can be found at this <u>link</u>.

## Submit description file

A submit description file is a text file which contains everything HTCondor needs to know about the job to be submitted such as the name of the executable to run, the initial working directory, command-line arguments, etc...

#### Mandatory commands

#### universe = vanilla

universe defines an HTCondor execution envirorment. Set this command to vanilla.

#### executable = <path\_name>

Path where the executable is located.

queue

This command will send the job to the queue, so it should be the last command in the submit description file.

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#### Really useful commands

input = <path\_name>

This file should contains the keyboard input the program requires (this file is basically stdin). End of line character is equivalent to press ENTER on the keyboard.

output = <path\_name>

This file contains the output the program writes on the remote machine (this file is basically stdout).

error = <path\_name>

This file contains any error messages the program would normally write to the screen (this file is basically stderr).

log = <path\_name>

This file contains info about what happens while the job is running. If this file is specified HTCondor will add a log entry for several event like when the job starts running, migrates to another machine, the job completes.

#### arguments = <arguments list>

List of arguments to be supplied to the executable as part of the command line.

In HTCondor there are two possible formats to specify arguments, known as the old syntax and the new syntax. You can find more details and examples <u>here</u>.

If you type the following command:

> condor\_q <job\_id> -long -autoformat args arguments

depending on which sintax you used, it will be prompted on screen args if you used the old sintax, arguments if you used the new sintax.

#### priority = <+|- value>

Assign a priority to the job. The highest the value, the greater the priority.

Adding requirements to the machines which will execute the job

#### request\_cpus = <num\_cpus>

Requested amount of CPUs to execute the job. If not specified, the number of CPUs for the job is 1. request\_disk = <kilobytes>

The requested amount of disk space in KB requested for this job. If not specified, the job will run on a default amount of disk space.

#### request\_memory = <megabytes>

The requested amount of memory in MB requested to run the job. If non specified, the job will run on a default amount of memory.

#### requirements = <ClassAd expression>

Run the job on the machines that match the ClassAd expression.

rank = <ClassAd expression>

The rank command will assign an order to the machines based on the ClassAd expression and will run the job on the machine with the highest rank. the rank command and requirements commands described above can coexist in the same file: while the requirements commands will exclude a machine which doesn't meet the user criteria from running the job, the rank command will run the job on the best machine, according to the user criteria, currently available.

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#### About requirements and rank

Both requirements and rank need to be valid ClassAd expression. In a ClassAd expression attribute names are case insensitive while string values are always case sensitive. So the following ClassAd expressions are valid:

Requirements = OpSys == "LINUX" && Arch == "INTEL"
requirements = opsys == "LINUX" && arch == "INTEL"
while the following expression is not:
 requirements = opsys == "linux" && arch == "intel"

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## **More Job Examples**

### 1. Multiple submission

The following submit file executes 5 istances of the program sleep; for every run the process id related to the single execution is supplied as argument:

#### Submit description file

universe	= vanilla
executable	= /bin/sleep
arguments	= \$(Process)
sleep	<pre>= sleep.log</pre>
queue 5	

Note: The job id in HTCondor is defined as Cluster.Process. If you submit more than one job from the same submit file each job will share the same cluster id.

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### 2. More about multiple submission

The following submit file executes 3 instances of the program echo and for every run a different string is printed on stdout

#### Submit description file

universe executable output error log	= = =	<pre>vanilla /bin/echo job_\$(Cluster).\$(Process).out job_\$(Cluster).\$(Process).err job_\$(Cluster).log</pre>
arguments queue	=	"String 1"
arguments queue	=	"String 2"
arguments queue	=	"String 3"

For the x run:

- stdout will be sent to job\_idcluster.x.out
- stderr will be sent to job\_idcluster.x.err

### 3. Working with files

Because the pool uses a shared file system you don't have to specify in the submit file the transfer of file to and from the remote machine that execute the job. All you need to do is to make sure that the paths of the files (either absolute or relative) the program needs are valid.

Suppose we want to run a simple bash script that prints on screen the content of a text file:

```
#!/bin/sh
while read line; do
        echo "$line"
done < file.txt</pre>
```

Submit description file

universe	= vanilla
executable	= script.sh
log	= script.log
output	= script.out
queue	

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### 4. Multiple submission and files

Suppose we want to run 2 instances of an executable named myprogram that needs input from stdin, a text file and one argument to work; once its execution is complete, it yields an output file named out.txt

Using the command initial dir allows to specify a different base directory for each job avoiding in this example the overwriting of the output file out.txt

#### Submit description file

universe	= vanilla
executable	= myprogram
log	= myprogram.log
input	= myprogram.in
output	= myprogram.out
error	= myprogram.err
initialdir	= run_1
arguments	= a
queue	
initialdir	= run_2
arguments	= w
queue	

For the x run:

- stdout(stderr) will be sent to run\_x/myprogram.out(run\_x/myprogram.err)
- stdin will be read from run\_x/myprogram.in