

# HTCondor@IAC User's Manual

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## Contents

|          |   |           |
|----------|---|-----------|
| <b>1</b> | <b>Introduction</b>   | <b>3</b>  |
| 1.1      | What is HTCondor? . . . . .   | 3         |
| 1.2      | How can HTCondor help me? . . . . .   | 3         |
| 1.3      | How <b>powerful</b> is HTCondor? . . . . .  | 3         |
| 1.4      | Which machines are part of HTCondor? . . . . .  | 3         |
| 1.5      | How can I use HTCondor? . . . . .   | 4         |
| 1.6      | Where will my application run? . . . . .  | 4         |
| 1.7      | Basic HTCondor workflow . . . . .   | 4         |
| 1.8      | Acknowledging HTCondor in publications . . . . .  | 7         |
| 1.9      | Further information and support . . . . .   | 7         |
| <b>2</b> | <b>Submit files</b>   | <b>7</b>  |
| 2.1      | Introduction . . . . .  | 7         |
| 2.2      | <i>Submit files</i> syntax . . . . .  | 7         |
| 2.2.1    | Comments . . . . .  | 7         |
| 2.2.2    | Variables and macros . . . . .  | 7         |
| 2.2.3    | Submit commands . . . . .   | 8         |
| 2.3      | Examples . . . . .  | 9         |
| 2.3.1    | HTCondor <i>Hello World!</i> . . . . .  | 9         |
| 2.3.2    | Similar jobs with one <b>Queue</b> command . . . . .  | 9         |
| <b>3</b> | <b>Main HTCondor commands</b>   | <b>9</b>  |
| 3.1      | Checking pool status . . . . .  | 10        |
| 3.2      | Submitting jobs . . . . .   | 10        |
| 3.3      | Checking and managing submitted jobs . . . . .  | 10        |
| 3.4      | Getting info from logs . . . . .  | 12        |
| 3.5      | Other commands . . . . .  | 12        |
| <b>4</b> | <b>Submit files (HowTo)</b>   | <b>12</b> |
| 4.1      | How to . . . add requirements on the target machines where my jobs will be run? . . . . .     | 12        |
| 4.2      | How to . . . add preferences on the target machines where my jobs will be run? . . . . .      | 13        |
| 4.3      | How to . . . get/set environment variables? . . . . .   | 13        |
| 4.4      | How to . . . control HTCondor notifications? . . . . .  | 13        |
| 4.5      | How to . . . run some shell commands/scripts/programs before/after our application? . . . . . | 13        |
| 4.6      | How to . . . specify the priority of your jobs? . . . . .                                     | 14        |
| 4.7      | How to . . . deal with jobs that fail? . . . . .  | 14        |
| 4.8      | How to . . . limit the number of concurrent running jobs? . . . . .                           | 16        |
| 4.9      | How to . . . do some complex operations in my submit file? . . . . .                          | 16        |
| 4.10     | How to . . . work with nested loops? . . . . .  | 17        |
| 4.11     | How to . . . program my jobs to begin at a predefined time? . . . . .                         | 17        |
| 4.12     | How to . . . run jobs that have dependencies among them? . . . . .                            | 18        |
| 4.13     | How to . . . know the attributes of the machines where our jobs are run? . . . . .            | 18        |

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|          |  |           |
|----------|--|-----------|
| <b>5</b> | <b>FAQs</b>  | <b>18</b> |
| 5.1      | General Information  | 18        |
| 5.1.1    | What is Condor? How can Condor help me? Who can use it? Who could help me if I have any problems?                                      | 18        |
| 5.1.2    | How does Condor work? My machine is in "Owner/Unclaimed/Claimed" state, what does it mean?   | 18        |
| 5.1.3    | Sometimes Condor runs jobs on my computer when I am working on it, can I avoid that?   | 19        |
| 5.1.4    | I am using Condor, should I add an acknowledgement text in my publications?  | 19        |
| 5.2      | Preparing and submitting your jobs   | 19        |
| 5.2.1    | I have developed a program, do I need to make any modification to run it with Condor?  | 19        |
| 5.2.2    | How do I run my application with Condor? (submitting jobs to queue)  | 20        |
| 5.2.3    | How do I check the Condor queue and my submitted jobs?   | 20        |
| 5.2.4    | Where should I put my input files so that Condor will be able to find them?  | 21        |
| 5.2.5    | If Condor runs my program on different machines, how I can get my output files?  | 21        |
| 5.2.6    | Can I tell Condor to use a different directory for input/output files?   | 22        |
| 5.2.7    | I would like to use a loop to send my jobs with different arguments... can I do that?  | 22        |
| 5.2.8    | Do I need to rename my input/output files to work with Condor?   | 22        |
| 5.2.9    | Should I delete temporary files?   | 23        |
| 5.2.10   | What are the technical specifications of machines running Condor? Can I restrict and/or prioritize those specifications in my jobs?    | 23        |
| 5.2.11   | How can I get/set environment variables when running with Condor (python and other programs may need them)?                            | 23        |
| 5.2.12   | Can I change my jobs attributes after submitting them?   | 24        |
| 5.3      | Having some troubles with your jobs  | 24        |
| 5.3.1    | I cannot submit jobs, what is wrong?   | 24        |
| 5.3.2    | How can I check that my program is running fine? Can I access to the input/output files in the remote machine?                         | 24        |
| 5.3.3    | My submitted jobs are always in Idle status, why do they never run (and what about users' priority)?                                   | 25        |
| 5.3.4    | Condor have problems with input and/or output files... are my paths wrong?   | 25        |
| 5.3.5    | My jobs are 'on hold' status and never finish, what does it mean?  | 25        |
| 5.3.6    | Condor is copying unwanted files to my machine, how can I avoid that?  | 25        |
| 5.3.7    | Some of my jobs are failing due to wrong inputs, can I fix that problem and then run again only those jobs that failed?                | 26        |
| 5.3.8    | Some of my jobs randomly fail (or I know they will fail in some specific machines)... how can I prevent that?                          | 27        |
| 5.3.9    | I want to repeat (resubmit) ONLY some of my jobs, is that possible?  | 28        |
| 5.3.10   | I see that my jobs complete after being running for N+X minutes/hours, when they only need N to finish. Is that normal?                | 28        |
| 5.3.11   | I have submitted jobs that need some hours to finish. They have been running for days and just few have finished... what is happening? | 28        |
| 5.3.12   | Some of my python programs work fine, but other fail...  | 29        |
| 5.3.13   | I receive an error when running HTCondor jobs that use python and matplotlib...  | 29        |
| 5.3.14   | I would like to get more information about the execution, is there an easy way to see the logs created by Condor?                      | 29        |
| 5.4      | Special needs  | 30        |
| 5.4.1    | I am running many jobs, but some are more important than others, how can I prioritize them?  | 30        |
| 5.4.2    | I am receiving hundreds of emails from Condor, can I stop that?  | 30        |
| 5.4.3    | What happens with my IDL or Matlab jobs that require licences to run?  | 30        |
| 5.4.4    | I need to run some commands or scripts before/after my executable, is that possible?   | 30        |
| 5.4.5    | Is it possible to limit the maximum number of concurrent running jobs?   | 30        |
| 5.4.6    | I need to do some complex operations in my submit file, is that possible?  | 30        |
| 5.4.7    | I would like to submit my jobs now, but they should run at a programmed time, can I do that?   | 31        |
| 5.4.8    | Jobs leave the queue after finishing. If something went wrong... could they be held or automatically re-executed instead?              | 31        |
| 5.4.9    | I have a fault tolerant application, can I save the state and restore it when executing with Condor?                                   | 31        |
| 5.4.10   | My jobs have some dependencies, is it possible to specify that?  | 31        |
| 5.5      | More info  | 31        |
| 5.5.1    | My question is not in this list or I need further information, where can I find it?  | 31        |

|          |  |           |
|----------|--|-----------|
| <b>6</b> | <b>HTCondor and IDL</b>  | <b>31</b> |
| 6.1      | Submitting a job to HTCondor using the IDL Virtual Machine (for the impatient) | 32        |
| 6.2      | How is it all done?  | 33        |

This documentation, together with example submit files and other material can be found in the HTCondor@IAC repository.

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## 1 Introduction

If you have no experience with HTCondor, we recommend that you contact us before running any job so we can give you a quick introduction (bear in mind that you will be using other users' computers and there are some basic guidelines that you must follow to avoid disturbing them).

### 1.1 What is HTCondor?

At the IAC we have several Supercomputing resources that allow you to obtain your computational results in much less time and/or work with much more complex problems. One of them is HTCondor, a High Throughput Computing (HTC) system. The underlying idea is quite simple (and powerful): let's use idle machines to perform computations while their owners are away. So, in a nutshell, HTCondor is an application that is installed in our PCs to make it possible to run a large number of yours and others' computations at a time in different machines when they are not being used, achieving a better utilization of our resources. A more detailed overview of HTCondor is available at the official documentation.

### 1.2 How can HTCondor help me?

HTCondor is very useful when you have an application that has to run a large number of times over different input data. For instance, suppose you have a program that carry out some calculations taking an image file as input. Let's say that the processing time is about one hour per image and you want to process 250 images. Then you can use your own machine and process all images one by one, and wait more than 10 days to get all results, or you can use HTCondor to process each image in different computers and hopefully get all results in one hour, or maybe two or four, but for sure less than 10 days. And HTCondor will do all the work for you: it will copy the input files to the remote machines, execute your program there with different inputs and bring back the results to your machine when they are complete.

### 1.3 How powerful is HTCondor?

HTCondor calls a *slot* the unit that executes a job, typically a CPU or a core if the CPU has several of them. Right now we have over 1000 slots that might execute applications submitted via HTCondor. It means that everyday more than 24000 hours could be available to run HTCondor jobs, close to 3 years of computation in a single day! Obviously, this is the theoretical maximum if no one were using their computers and all slots were idle, but the number of actual available slots could be around 400 during office hours and around 700 at nights and weekends.

You can see real-time **HTCondor@IAC statistics** (global and per user) here. Figure 1 is an example showing the global usage where *Owner* represents *slots* that are being used outside of HTCondor. The remaining *slots* are available to HTCondor, but if there are no eligible jobs to run, those slots will be in *CPUsNotInUse* state. Those *slots* that are actually being used by HTCondor are those in the *CPUsInUse* state.

### 1.4 Which machines are part of HTCondor?

HTCondor is installed in a number of *burros* (High Performance Linux PCs) and desktop PCs at the IAC Headquarters in La Laguna.

Regarding their hardware specifications, they are rather heterogeneous and their availability and specifications change from time to time. You can check which machines make up the HTCondor@IAC pool at any given time in the HTCondor Ganglia webpage.

Regarding their software specifications, at present all machines are running Ubuntu 18.04 and the installed software should be also more or less the same in every machine (see the software supported by the SIE), which makes it easy to run almost every application in any machine.

Detailed information about each machine can be obtained with the command `condor_status` (see Section 3.1).

HTCondor provides a simple mechanism by which you can specify a set of requirements for the machines where you want your application to run, for example: memory per slot, OS version, etc. (see Section 2).

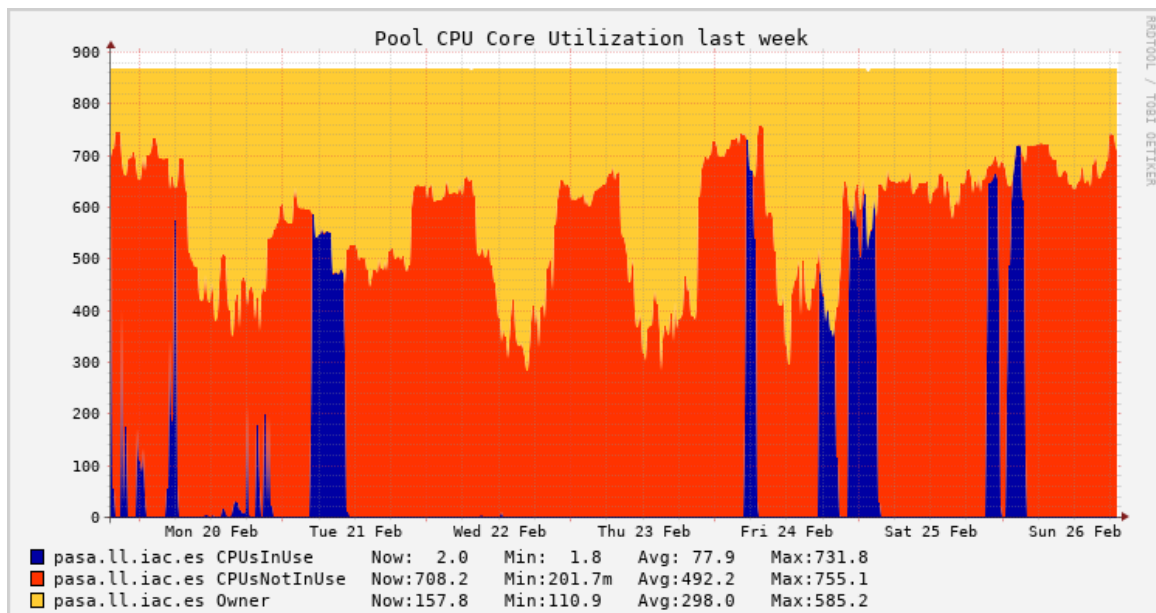


Figure 1: Weekly global usage

## 1.5 How can I use HTCondor?

If you have an account in the IAC network, then you can use HTCondor.

HTCondor is a batch-processing system (i.e. non-interactive), so you submit jobs to the HTCondor queue with the `condor_submit` command, and providing a text submission file, where you specify the executable file, its arguments, inputs and outputs, etc. (see Section 3.2).

You do not need to prepare or compile your programs in any special way to run them, and almost all programming languages should be suitable (shell scripts, Python, Perl, C, Fortran, IDL, etc.). Sometimes a few minor modifications may be needed in order to specify arguments and the locations of inputs or outputs.

## 1.6 Where will my application run?

When you submit jobs to the HTCondor queue, HTCondor uses its allocation algorithm to send and execute your jobs on those idle slots that satisfy your requirements. Idle slots are those located in machines where there has been no keyboard/mouse activity for a long time and the computer load is low enough to ensure that there is no interference with the owner's processes.

While HTCondor is running its jobs, it also keeps checking that the owner is not using the machine. If HTCondor detects any activity in the computer (for instance, keyboard activity), then it will suspend all its jobs and wait a little while to see whether the machine gets idle again so as to resume the jobs. If the machine does not become idle in a short time, HTCondor will *vacate* it, interrupting all HTCondor jobs and sending them to other available slots in any other idle machine.

HTCondor will repeat this process until all jobs are done, optionally sending notifications via email when they are finished or if any errors show up.

## 1.7 Basic HTCondor workflow

The basic workflow with HTCondor will include four steps: checking the HTCondor pool status, submitting a job, checking and managing the submitted job, and getting information from the logs. Commands and examples for these phases are given with further details in the following sections, but here we present a very basic example to **Quick Start** you.

- **Checking the HTCondor pool status**

You can use the command `condor_status`, to quickly check the status of the HTCondor pool:

```
[angelv@denso ~]$ condor_status -compact
```

| Machine           | Platform     | Slots | Cpus | Gpus | TotalGb | FreeCpu | FreeGb | CpuLoad | ST |
|-------------------|--------------|-------|------|------|---------|---------|--------|---------|----|
| cruise.dyn.iac.es | x64/Ubuntu18 | _     | 4    |      | 7.64    | 1       | 1.91   | 0.00    | Oi |
| dama.ll.iac.es    | x64/Ubuntu18 | _     | 40   |      | 754.54  | 1       | 18.86  | 0.00    | Ui |
| [...]             |              |       |      |      |         |         |        |         |    |
| villa.dyn.iac.es  | x64/Ubuntu18 | _     | 16   |      | 187.58  | 1       | 11.72  | 0.00    | Oi |

|   |              |     |   |       |   |      |      |    |
|---|--------------|-----|---|-------|---|------|------|----|
| virus.dyn.iac.es  | x64/Ubuntu18 | _   | 8 | 62.73 | 1 | 7.84 | 0.02 | 0i |
| Total Owner Claimed Unclaimed Matched Preempting Backfill Drain |              |     |   |       |   |      |      |    |
| x64/Ubuntu18  | 868          | 318 | 2 | 548   | 0 | 0    | 0    | 0  |
| Total   | 868          | 318 | 2 | 548   | 0 | 0    | 0    | 0  |

- **Submitting a job**

In order to ask HTCondor to run your application you will need:

- **your application**

For example, given the following basic C code (`simple.c`):

```
#include <stdio.h>

main(int argc, char **argv)
{
    int sleep_time;
    int input;
    int failure;

    if (argc != 3) {
        printf("Usage: _simple_<sleep-time>_<integer>\n");
        failure = 1;
    } else {
        sleep_time = atoi(argv[1]);
        input      = atoi(argv[2]);

        printf("Thinking_really_hard_for_%d_seconds...\n", sleep_time);
        sleep(sleep_time);
        printf("We_calculated:_%d\n", input * 2);
        failure = 0;
    }
    return failure;
}
```

You would compile it as usual:

```
gcc -o simple simple.c
```

- **a submit file**

The submit file is a plain text file that specifies the name of your executable (`simple`), how many jobs to submit (`Queue 100`), etc.

```
Executable = simple
Arguments  = 400 10
Log        = simple.log
Output     = simple.$(Process).out
Error      = simple.$(Process).error

Queue 100
```

- **the condor\_submit command**

Using the *submit file* as an argument to the command `condor_submit` you instruct HTCondor to start executing your job in the HTCondor Pool.

```
[angely@denso ~]$ condor_submit test.condor
Submitting job(s).....
100 job(s) submitted to cluster 4.
```

- **Checking the progress of the submitted jobs**

The basic command to check on the progress of your jobs is `condor_q`. In the following example we can see that all the 100 jobs submitted above are successfully running:

```
[angelv@denso ~]$ condor_q

-- Schedd: denso.ll.iac.es : <161.72.216.13:9618?... @ 02/27/23 09:27:40
OWNER  BATCH_NAME   SUBMITTED   DONE    RUN    IDLE  TOTAL JOB_IDS
angelv ID: 4        2/27 09:24    _      100     _     100 4.0-99

Total for query: 100 jobs; 0 completed, 0 removed, 0 idle, 100 running, 0 held, 0 suspended
Total for angelv: 100 jobs; 0 completed, 0 removed, 0 idle, 100 running, 0 held, 0 suspended
Total for all users: 100 jobs; 0 completed, 0 removed, 0 idle, 100 running, 0 held, 0 suspended
```

- **Getting information from the logs**

If everything goes well, when the jobs finish, any output files created by your application will be, by default, copied back to the directory whence you submitted your job.

At the same time, you can instruct HTCondor to save to files any output that your application produces. In the example above, the *standard output* generated by each job is written to a file called `simple.$(Process).out`, where `$(Process)` will be automatically substituted by HTCondor by the number of each job (in this case, given that we submitted 100 jobs, the numbers will go from 0 to 99). For example, the file `simple.0.out` could read:

```
[angelv@denso ~]$ cat simple.0.out
Thinking really hard for 400 seconds...
We calculated: 20
```

Also, a global log of the steps taken by HTCondor to execute your jobs can be generated (in the example above called `simple.log`). This log will give you details of when each job was submitted, when it started executing, whether it was evicted or had any other problems, etc. In this example, the file `simple.log` could read:

```
[angelv@denso ~]$ cat simple.log
000 (004.000.000) 2023-02-27 09:24:41 Job submitted from host: <161.72.216.13:9618?addrs=161.72.216.13-9618
...
000 (004.001.000) 2023-02-27 09:24:41 Job submitted from host: <161.72.216.13:9618?addrs=161.72.216.13-9618
...
000 (004.002.000) 2023-02-27 09:24:41 Job submitted from host: <161.72.216.13:9618?addrs=161.72.216.13-9618
[...]

040 (004.002.000) 2023-02-27 09:24:47 Started transferring input files
    Transferring to host: <161.72.216.8:9618?addrs=161.72.216.8-9618+[2001-720-1610-50d8-21e-4fff-feba-
...
040 (004.003.000) 2023-02-27 09:24:47 Started transferring input files
    Transferring to host: <161.72.216.8:9618?addrs=161.72.216.8-9618+[2001-720-1610-50d8-21e-4fff-feba-
[...]

001 (004.002.000) 2023-02-27 09:24:48 Job executing on host: <161.72.216.8:9618?addrs=161.72.216.8-9618+[20
...
001 (004.003.000) 2023-02-27 09:24:48 Job executing on host: <161.72.216.8:9618?addrs=161.72.216.8-9618+[20
[...]

005 (004.040.000) 2023-02-27 09:31:45 Job terminated.
    (1) Normal termination (return value 0)
        Usr 0 00:00:00, Sys 0 00:00:00 - Run Remote Usage
        Usr 0 00:00:00, Sys 0 00:00:00 - Run Local Usage
        Usr 0 00:00:00, Sys 0 00:00:00 - Total Remote Usage
        Usr 0 00:00:00, Sys 0 00:00:00 - Total Local Usage
    58 - Run Bytes Sent By Job
    8432 - Run Bytes Received By Job
    58 - Total Bytes Sent By Job
    8432 - Total Bytes Received By Job
    Partitionable Resources :    Usage  Request Allocated
        Cpus                :         0         1         1
        Disk (KB)           :        24        10 207282725
        Memory (MB)         :         0         1        4024

    Job terminated of its own accord at 2023-02-27T09:31:44Z with exit-code 0.
```

## 1.8 Acknowledging HTCondor in publications

It is important that you acknowledge HTCondor in any publication of your work where you have used HTCondor (and we would be grateful if you could send us the details of the published paper). This will help us to improve the visibility of the HTCondor@IAC facility and ensure that it is available at the IAC for the foreseeable future. Although there is no standard acknowledgment format, we suggest the following:

This paper made use of the IAC Supercomputing facility HTCondor (<http://research.cs.wisc.edu/htcondor/>), partly financed by the Ministry of Economy and Competitiveness with FEDER funds, code IACA13-3E-2493.

## 1.9 Further information and support

This manual is only a brief introduction to all HTCondor has to offer. For detailed and complete information, check the official HTCondor v10.0 Manual.

If you need help or you are having any kind of issues related to HTCondor, the SIE gives direct support to IAC's users who want to use HTCondor: we will not code your whole application, but we will help and advise you on how to get the most out of HTCondor.

If you want to stay informed about HTCondor@IAC updates, tips, etc. there is a low traffic mailing list (send us an e-mail if you want to subscribe to it).

## 2 Submit files

### 2.1 Introduction

*HTCondor Submit Description Files*, or simply *Submit files*, are arguably the cornerstone of your interaction with HTCondor, since you use them to specify how to execute your application with HTCondor, by providing a number of parameters like the name of your executable, its arguments, inputs and outputs, requirements, etc.

In section 1.7 we saw a very simple *submit file*. Depending on your needs, that might be enough, but HTCondor offers many options and a rich syntax for writing *submit files*, which will be useful in more advanced cases. In this section we will cover the features needed in some of the most typical scenarios.

Before submitting your jobs, perform always some simple tests in order to make sure that both your submit file and program will work in a proper way. Also, `condor_submit -dry-run` can help you to debug your jobs and make sure they will work as expected.

### 2.2 *Submit files* syntax

HTCondor *submit files* can include comments, variables, macros, commands, etc. Here we will describe the most important syntax components. For a more detailed description you can check the official documentation (Submitting a Job, `condor_submit`).

#### 2.2.1 Comments

Blank lines and lines beginning with a pound sign (#) character are ignored by the submit description file parser.

#### 2.2.2 Variables and macros

You can define your own variables, and there are also many predefined variables and macros that you can use in *submit files*.

- To **define a variable**, just choose a valid name (names are case-insensitive) and assign a value to it, like `N = 4`, `Name = "example"`
- To **get the value** of a variable, use next syntax: `$(varName)` (both the \$ symbol and the parentheses () are mandatory).
- There are several special **automatic variables** defined. The most useful one is `$(Process)*` or `$(ProcId)`, that will contain the Process ID of each job (if you submit N jobs, the value of `$(Process)` will be 0 for the first job and N-1 in the last job). This variable is like an **iteration counter** and you can use it to specify different inputs, outputs, arguments, etc. for each job. There are some **other automatic variables**, like `$(Cluster)` or `$(ClusterId)` that stores the ID of each submission, `$(Item)`, `$(ItemIndex)`, `$(Step)`, `$(Row)`, etc.
- There are several **pre-defined Function Macros**. Their syntax is `$FuncName(varName)` and they can perform some operations on variable `varName` like evaluating expressions and type conversions, selecting a value from a list according an index, getting random numbers, string operations, filenames processing, setting environment variables, etc.
- You can do **basic operations** with variables, like `B = $(A) + 1`, etc. To get the expression evaluated, you may need to use function macros like `$INT(B)`, `$REAL(B)`, etc.

### 2.2.3 Submit commands

The commands which can appear in the submit description file are numerous (see submit description file commands), but in most situations you will only need a few of them. Here we present the most common ones (*commands are case-insensitive*):

- **Mandatory commands**

- **executable** location of the executable file (you can use an absolute path, one relative to the directory where you do the submission or to another directory specified with **initialdir**). You should specify **only the executable** and not other things like arguments, etc., since there are specific commands for that.
- **queue** this command will send your job(s) to the queue, so it should be the last command in your submit file. With it you can specify the number of jobs to submit, but you can also use it to specify variables, iterations over other commands, files to be processed, list of arguments, etc.

- **Highly recommended commands**

- **output** it will copy the standard output printed on the screen (**stdout**) of the remote machines when executing your program to the local file you specify here. In order to generate a different output file for each job, the filename should include variables, like **\$(Process)** (and perhaps also **\$(Cluster)**).
- **error** the same as previous command, but for standard error output (**stderr**).
- **log** file to keep track of the progress of your submission (very useful to debug problems with your job(s). It is advisable to keep just one log file for all jobs belonging to the same submission, so a filename with a name like **log.\$(Cluster)** is recommended.
- **universe** your job(s) **execution environment**. By default, the simplest one (**vanilla**) will be chosen, but for more advanced users, other **universe** might be necessary. See Choosing an HTCondor Universe.

- **Useful commands for application Input/Output**

- **arguments** used to specify options and flags for your executable file (as if it executed in the command line).
- **should\_transfer\_files** assign YES in order to activate HTCondor's file transfer system (needed when working with files).
- **transfer\_input\_files** a comma-separated list of files (with absolute or relative paths) used to specify where the needed input files are located. HTCondor will copy all the files (together with the executable) to the root directory of a virtual location on the remote machine. A directory name with a trailing / character will copy only the contents of the directory. Without the trailing / the directory itself and its contents will be copied.
- **transfer\_output\_files** a comma-separated list of result files to be copied back to our machine. If this command is omitted, HTCondor will automatically copy all files that have been created or modified on the remote machine. Sometimes omitting this command is useful, but other times our program creates many temporary or useless files and we only want to get the ones we specify with this command.
- Other commands for input/output files:
  - \* **transfer\_output\_remaps** it changes the name of the output files when copying them to your machine (useful when output files have the same name, so including a variable part, e.g. **\$(Process)**, will avoid overwritten them).
  - \* **initialdir** used to specify the base directory for input and output files (if it includes a variable part (like **\$(Process)**), a different base directory can be used for each job).
  - \* **input** if your program needs some data from keyboard, you can write it down in a file (as when using **stdin** redirection in the command line with **<**).
  - \* **transfer\_executable** by default **True**. Useful to set it to **False** when the executable is a system command or a program that is installed in all machines, so copying it is not needed.

- **Other useful commands**

- **request\_memory**, **request\_disk** to request machines with at least a certain amount of total RAM memory or free disk space
- **requirements** a very useful command to register any special needs for a job (for example, if you need to avoid certain machines, or you need machines with a given OS, etc.)
- **rank** you can specify some values or combination of them (total memory, free disk space, MIPS, etc.) and HTCondor will choose the best machines for your jobs according to your specifications, where the higher the value, the better (this command is used to specify preferences, not requirements)
- **getenv** (*default: False*) if set to **True**, the job will run with the same environment variables as when the job was submitted. If **False** the jobs will have no preset environment variables.
- **environment** list of environment variables to set for the job
- **nice\_user** (*default: False*) if set to **True** the jobs will be executed with very low priority.
- **priority** assign a priority for your jobs (the higher the value, the higher the priority).



- `concurrency_limits` to limit the maximum number of your jobs that could be executed at the same time (for example if the program needs a licence and only a limited number of them is available).
- `include : <myfile>` to include commands from an external file. It is also possible to include the output of external scripts that will be executed at submission time, adding a pipe symbol after the file: `=include : <myscript.sh> | =`
- `+PreCmd`, `+PreArguments`, `+PostCmd`, `+PostArguments` commands to specify scripts to run before and/or after your executable (to convert, decompress, etc. your inputs and outputs if needed, or for debugging)
- `notify_user`, `notification` commands to request a notification (an email) when your jobs begin, fail and/or finish

## 2.3 Examples

All the submit files in this section can be found in the `examples` directory of the HTCondor@IAC repository.

### 2.3.1 HTCondor *Hello World!*

This example (directory `hello_world`) was the basis for the introductory section 1.7. The commands used were already introduced in section 2.2.3. For convenience we repeat below the *submit file* (`simple.submit`):

```
Executable = simple
Arguments  = 400 10
Log        = simple.log
Output     = simple.$(Process).out
Error      = simple.$(Process).error

Queue 100
```

This example simply defines:

- the executable to run (`simple`), here to be compiled from source code `simple.c`
- the arguments to pass to the executable
- the log file (one file for the log of the 100 submitted jobs)
- the output files (since we use `$(Process)`, one file will be used for each job: `simple.0.out`, `simple.1.out`, etc.)
- the error files (similar to the output files above)
- the `Queue` command, specifying that we want to run 100 jobs (the variable `$(Process)` will have the range `[0:99]`)

### 2.3.2 Similar jobs with one Queue command

The example in the previous section 2.3.1 used the variable `$(Process)` to identify the different jobs in a single run. Sometimes this is enough, but not always. Say you have 100 images to process and your executable takes the filename of the image as an argument. If you were going to use the same method as above, you would need to rename your files to something like `image00.jpg`, `image01.jpg`, etc. or some other similar idea, in order to relate each image with each of the possible values of `$(Process)`.

Luckily, the `queue` command has a powerful syntax that makes this unnecessary. Here we only present one example, but in the official HTCondor documentation you can check the full syntax and further examples.

This example (directory `queue_similar`) shows how to use `queue [...] matching` command to process a number of files having the extension `.txt`, without the need to rename the filenames, and without the need to specify the exact number of jobs to submit. The *submit file* (`simple.submit`) is very simple:

```
Executable = process.sh
Arguments  = $(txtfile)
Log        = queue.log
Output     = queue.$(txtfile).out
Error      = queue.$(txtfile).error

transfer_input_files = $(txtfile)

queue txtfile matching files *.txt
```

## 3 Main HTCondor commands

HTCondor provides around 100 commands (see the Command Reference Manual), but you will only need a few of them for most of you work with HTCondor. In this section we introduce the most common ones, grouped according to the four common tasks introduced in section 1.7: Checking pool status (3.1), Submitting jobs (3.2), Checking and managing submitted jobs (3.3) and Getting info from logs (3.4). For each command we also give a list of some of their most useful options (but note that you can also get full details about each command by executing `man condor_<cmd>` in your shell).

### 3.1 Checking pool status

- **condor\_status** List slots in the HTCCondor pool and their status: **Owner** (used by owner), **Claimed** (used by HTCCondor), **Unclaimed** (available to be used by HTCCondor), etc.
  - **-avail** List those slots that are not busy and could run HTCCondor jobs at this moment
  - **-submitters** Show information about the current general status, like number of running, idle and held jobs (and submitters)
  - **-run** List slots that are currently running jobs and show related information (owner of each job, machine where it was submitted from, etc.)
  - **-compact** Compact list, with one line per machine instead of per slot
  - **-state -total** List a summary according to the state of each slot
  - **-master** List machines, but just their names (status and slots are not shown)
  - **-server** List attributes of slots, such as memory, disk, load, flops, etc.
  - **-sort Memory** Sort slots by Memory, you can try also with other attributes
  - **-af <attr1> <attr2> <...>** List specific attributes of slots, using autoformat (new version, very powerful)
  - **-format <fmt> <attr>** List attributes using the specified format (old version). For instance, next command will show the name of each slot and the disk space: `condor_status -format "%s\t " Name -format "%d KB\n" Disk`
  - **<machine>** Show the status of a specific machine
  - **<machine> -long** Show the complete "ClassAd" of a machine (its specifications). We can use these specifications to add restrictions in the submit file so we can control which machines we want to use.
  - **-constraint <constraint>** Only Show slots that satisfy the constraint. I.e: `condor_status -constraint 'Memory > 1536'` will only show slots with more than 1.5GB of RAM per slot.

### 3.2 Submitting jobs

- **condor\_submit <submit\_file>** Submit jobs to the HTCCondor queue according to the information specified in `submit_file`. Visit the **submit file page** to see some examples of these files. There are also some FAQs related to the submit file.
  - **-dry-run <dest\_file>** this option parses the submit file and saves all the related info (name and locations of input and output files after expanding all variables, value of requirements, etc.) to `<dest_file>`, but jobs are **not** submitted. Using this option is highly recommended when debugging or before the actual submission if you have made some modifications in your submit file and you are not sure whether they will work.
  - **'var=value'** add or modify variable(s) at submission time, without changing the submit file. For instance, if you are using `queue $(N)` in your submit file, then `condor_submit <submit_file> 'N = 10'` will submit 10 jobs. You can specify several pairs of **var=value**.
  - **-append <command>** add submit commands at submission time, without changing the submit file. You can add more than one command using several times **-append**.

When submitted, each job is identified by a pair of numbers **X.Y**, like 345.32. The first number (**X**) is the **cluster id**: every submission gets a different cluster id, that is shared by all jobs belonging to the same submission. The second number (**Y**) is the **process id**: if you submitted N jobs, then this id will go from 0 for the first job to N-1 for the last one. For instance, if you submit a file specifying 4 jobs and HTCCondor assign id 523 to that cluster, then the ids of your jobs will be 523.0, 523.1, 523.2 and 523.3 (you can get these ids and more info using `condor_q` command).

Before submitting your jobs, always do some simple tests in order to make sure that both your submit file and program work in a proper way: if you are going to submit hundreds of jobs and each job takes several hours to finish, before doing that try with just a few jobs and change the input data in order to let them finish in minutes. Then check the results to see if everything went fine before submitting the real jobs. Bear in mind that submitting untested files and/or jobs may cause a waste of time and resources if they fail, and also your priority will be lower in following submissions.

### 3.3 Checking and managing submitted jobs

Each machine manages its own HTCCondor queue, so it has information only about those jobs that were submitted on it (and no information about any other jobs you may have submitted on other machines). Most of the commands explained in this section get information asking only the local queue, which means that you will only see those jobs that you have submitted on that specific machine. If you submit jobs from different machines, and later you want to check, hold, release, remove, etc. those jobs, you may need to connect to each one of those machines where you have submitted jobs from, or, when possible, use the commands with extra options to communicate with other machines.

- **condor\_q** Show my jobs that have been submitted in this machine. By default you will see the ID of the job(**clusterID.processID**), the owner, submitting time, run time, status, priority, size and command. **STATUS** can be: **I**:idle (waiting for a machine to execute on); **R**: running; **H**: on hold (there was an error, waiting for user's action); **S**: suspended; **C**: completed; **X**: removed; **<**: transferring input; and **>**: transferring output. HTCondor will, by default, show only your jobs. If you want to use all users' submitted jobs, you can use the option **-allusers**
  - **-global** Show my jobs submitted in any machine, not only the current one
  - **-nobatch** Starting in version HTCondor 8.6.0 installed in January 2017, data is displayed in a compact mode (one line per cluster). With this option output will be displayed in the old format (one line per process)
  - **-wide** Do not truncate long lines. You can also use **-wide:<n>** to truncate lines to fit **n** columns
  - **-analyze <job\_id>** Analyse a specific job and show the reason why it is in its current state (useful for those jobs in Idle status: Condor will show us how many slots match our restrictions and may give us suggestion)
  - **-better-analyze <job\_id>** Analyse a specific job and show the reason why it is in its current state, giving extended info
  - **-long <job\_id>** Show all information related to that job
  - **-run** Show your running jobs and related info, like how much time they have been running, in which machine, etc.
  - **-currentrun** Show the consumed time on the current run, the cumulative time from last executions will not be used (you can combine also with **-run** flag to see only the running processes at the moment)
  - **-hold** Show only jobs in the "on hold" state and the reason for that. Held jobs are those that got an error so they could not finish. An action from the user is expected to solve the problem, and then he should use the **condor\_release** command in order to check the job again
  - **-af <attr1> <attr2> <...>** List specific attributes of jobs, using autoformat
  - **-global -submitter <user>** Show all jobs from user **<user>** in all machines.
- **condor\_tail <job\_id>** Display on screen the last lines of the **stdout** (screen) of a running job on a remote machine. You can use this command to check whether your job is working fine, you can also visualize errors (**stderr**) or output files created by your program (see also CondorFAQs#ssh). Useful options:
  - **-f** Do not stop displaying the content, it will be displayed until interrupted with **Ctrl+C**
  - **-no-stdout -stderr** Show the content of **stderr** instead of **stdout**
  - **-no-stdout <output\_file>** Show the content of an output file (**output\_file** has to be listed in the **transfer\_output\_files** command in the submit file).
- **condor\_release <job\_id>** Release a specific held job in the queue. Useful options:
  - **<cluster\_id>** Instead of giving a **<job\_id>**, you can specify just the **<cluster\_id>** in order to release all held jobs of a specific submission
  - **-constraint <constraint>** Release all my held jobs that satisfy the constraint
  - **-all** Release all my held jobs
  - **Note:** Jobs with "on hold" state are those that HTCondor was not able

to properly execute, usually due to problems with executable, paths, etc. If you can solve the problems changing the input files and/or the executable, then you can use **condor\_release** command to run again your program since it will send again all files to the remote machines. If you need to change the submit file to solve the problems, then **condor\_release** will NOT work because it will not evaluate again the submit file. In that case you can use **condor\_qedit** (see the HOWTOs.CondorFAQs#ch<sub>submit</sub>) or cancel all held jobs and re-submit them again-]
- **condor\_hold <job\_id>** Put jobs into the hold state. It could be useful when you detect that there are some problems with your input data (see CondorFAQs#bad<sub>inputs</sub> for more info), you are running out of disk space for outputs, etc. With this command you can delay the execution of your jobs holding them, and, after solving the problems, assign them the idle status using **condor\_release**, so they will be executed again. Useful options:
  - **<cluster\_id>** Instead of giving a **<job\_id>**, you can specify just the **<cluster\_id>** in order to hold all jobs of a specific submission
  - **-constraint <constraint>** Hold all jobs that satisfy the constraint
  - **-all** Hold all my jobs from the queue
- **condor\_rm <job\_id>** Remove a specific job from the queue (it will be removed even if it is running). Jobs are only removed from the current machine, so if you submitted jobs from different machines, you need to remove your jobs from each of them. Useful options:
  - **<cluster\_id>** Instead of giving a **<job\_id>**, you can specify just the **<cluster\_id>** in order to remove all jobs of a specific submission
  - **-constraint <constraint>** Remove all jobs that satisfy the constraint

- `-all` Remove all my jobs from the queue
- `-forcex <job_id>` It could happen that after removing jobs, they don't disappear from the queue as expected, but they just change status to **X**. That's normal since HTCondor may need to do some extra operations. If jobs stay with 'X' status a very long time, you can force their elimination adding `-forcex` option. For instance: `condor_rm -forcex -all`.
- `condor_prio` Set the priority of my jobs. A user can only change the priority of her own jobs, to specify which ones she would like to run first (the higher the number, the bigger the priority). Priority could be absolute or relative, use `man condor_prio` for further information
- `condor_ssh_to_job <job_id>` Create an ssh session to a running job in a remote machine. You can use this command to check whether the execution is going fine, download/upload inputs or outputs, etc. More information about this command is available in `CondorFAQs#ssh`.

### 3.4 Getting info from logs

- `=*condor_userlog <file.log>=*` Show and summarize job statistics from the job log files (those created when using `log` command in the submit file)
- `*condor_history*` Show all completed jobs to date (it has to be run in the ~~{same machine}~~ where the submission was done). Useful options:
  - `-userlog <file.log>` list basic information registered in the log files (use `condor_logview <file.log>` to see information in graphic mode)
  - `-long XXX.YYY -af LastRemoteHost` show machine where job XXX.YYY was executed
  - `-constraint <constraint>` Only show jobs that satisfy the constraint. I.e: `condor_history -constraint 'RemoveReason!=UNDEFINED'`: show your jobs that were removed before completion
- `condor_logview <file.log>` This is not an original HTCondor command, we have created this link to the script that allows you to display graphical information contained in the log of your executions.
- There is also an online tool to analyze your log files and get more information: HTCondor Log Analyzer (<http://condorlog.cse.nd.edu/>).

### 3.5 Other commands

- `condor_userprio` Show active HTCondor users' priority. Lower values means higher priority where 0.5 is the highest. Use `condor_userprio -allusers` to see all users' priority, you can also add flags `-priority` and/or `-usage` to get detailed information
- `condor_qedit` use this command to modify the attributes of a job placed on the queue. This may be useful when you need to change some of the parameters specified in the submit file without re-submitting jobs (see `HOWTOs.CondorFAQs#chsubmit`).
- `condor_submit_dag <dag_file>` Submit a DAG file, used to describe jobs with dependencies. Visit the `CondorHowTo#howto_dag` section for more info and examples.
- `condor_version` Print the version of HTCondor.
- If you want some general information about HTCondor queue, the pool of machines, where jobs have been executed on, etc., you can try our online stats about HTCondor: [http://carlota:81/condor\\_stats/](http://carlota:81/condor_stats/) and <http://nectarino/>.

## 4 Submit files (HowTo)

HTCondor has a huge set of commands that should cover most possible scenarios. It is impossible to describe here all of them, but you can read the official documentation to get further information (there are many of these commands at the `condor_submit` page. Just to complement **some of the previous examples**, we will mention here a few useful commands that can be added to the submit file when needed. You can also find more details about these and other commands at the **FAQs** page.

### 4.1 How to ... add requirements on the target machines where my jobs will be run?

If your program has some limitations (memory, disk, libraries, etc.) and cannot run in all machines, you can use `requirements` command to tell HTCondor what those limitations are so it can execute your jobs only on machines that satisfy those requirements. If you try next command `condor_status -long <your_machine>` in your shell, it will list all the parameters that HTCondor has about each slot of your machine, and most of those parameters can be used to add requirements. Conditions and expressions could be as complex as needed, there is a number of **operators, predefined functions, etc.** that can be used. For memory, disk and CPUs you can also use `request_memory`, `request_disk` and `request_cpus`, respectively.

For example, if your program needs at least 1.5 GB of RAM and 5 GB of free space in disk, and due to library dependencies it can only run on machines with Linux Fedora17 or above, add next commands in your submit file:

```
request_disk = 5 GB request_memory = 1.5 GB requirements = (UtsnameSysname = "Linux") && (OpSysName = "Fedora") && (OpSysMajorVer >= 17)
```

Be careful when specifying the values since the default unit for `request_disk` is KB and MB for `request_memory`. It is much better to always specify the unit (KB or K, MB or M, GB or G, TB or T).

**Caution!:** Be careful when choosing your restrictions, using them will reduce the amount of available slots for your jobs so it will be more difficult to execute them. Also check that you are asking for restrictions that can be satisfied by our current machines, or your jobs will stay always in idle status (you can check the reasons why a job is idle using `condor_q -analyze <job.id>`). Before adding a requirement, always check if there are enough slots that satisfy it. For instance, to see which slots satisfy the requirements of this example, use next command (you can add flag `-avail` to see only the slots that could execute your job at this moment):

```
[...]$ condor_status -constraint '(UtsnameSysname = "Linux") && (OpSysName = "Fedora") && (OpSysMajorVer >= 17) && (Memory > 1536) && (Disk >= 5120000)'
```

If you already know which machines are not able to run your application, you can force HTCondor to avoid them... or the opposite: run your application only on some machines (see [HOWTOs.#howtofailing](#) where this is explained).

## 4.2 How to ... add preferences on the target machines where my jobs will be run?

Preferences are similar to requirements, but they do not limit the machines (you can use both preferences and requirements in the same submit file). HTCondor will try to satisfy your preferences when possible, assigning a rank to the available machines and choosing those with higher value. For example, we would like to use slots with at least 4GB of RAM if they are available and the more available disk space, the better. Then commands to add should be the following ones:

```
Rank = Disk && (Memory >= 4096)
```

Rank is evaluated as a float point expression, and always higher values are the better ones. Then, you can do arithmetic operations to emphasize some parameters. For example, the first expression will consider the floating point speed but will give more importance to run on machines with my same Operating System, while the second expression will choose machines with higher values of RAM, and those with also more than 100GB of disk will have 200 extra "points":

```
Rank = kflops + (1000000 * (TARGET.OpSysAndVer = MY.OpSysAndVer)) =Rank = Memory + (200 * (Disk >= 102400))
```

## 4.3 How to ... get/set environment variables?

If your application needs them, use the `getenv` command and HTCondor will create a copy of your environment variables {at the submitting time} so they will be available for your program on the target machine. Also you can create/modify environment variables if needed with the `environment` command. The environment variables can be also used in the submit file using the `ENV` command.

For example, add next commands if you want that your executable can access your environment at the submitting time, then set variables called `working_dir` and `data_dir` pointing to some directories, and finally create a macro called `home_dir` that contains your home directory to be used in your submit file:

```
getenv = True environment = "working_dir=/path/to/some/place data_dir=/path/to/data" home_dir = $ENV(HOME)
```

If you want to run your python program using HTCondor, you might need to define some environment variables, please, read this FAQ [HOWTOs.CondorFAQs#python-fedora](#).

## 4.4 How to ... control HTCondor notifications?

If you are submitting a large set of jobs, receiving notifications from all of them can be annoying. You can set the email address and the type of the notifications that you want to receive. For example, to send notifications to `someaddress@iac.es` only in case of errors, use following commands:

```
notify_user = someaddress@iac.es notification = Error
```

`notify_user` changes the email address used to send notifications, if you need to add more addresses, you can use `email_attributes` command. With `notification` command we tell HTCondor when it should send those notifications, it could be set to `Never`, `Complete`, `Error` or `Always`; we recommend you use `Error`.

## 4.5 How to ... run some shell commands/scripts/programs before/after our application?

If your application needs some pre- or post-processing, you can use `+PreCmd` and `+PostCmd` commands to run it before and after your main executable, respectively. For example, these commands may be useful if you need to rename or move input or output files before or after the execution. You can also use them for debugging purpose, for instance, use `tree` command to check where the input/output files are located:

```
+PreCmd = "tree" +PreArguments = "-o treebefore.$(Cluster).$(Process).txt" +PostCmd = "mypostscript.sh" +PostArguments = "-g"
```

```
should_transfer_files = YES transfer_input_files = mypostscript.sh, /usr/bin/tree transfer_output_files = treebefore.$(Cluster).$(Process).txt
```

Remember that you have to add those scripts/programs to the list of files to be copied with `transfer_input_files` command, and also check that your submit file contains the following command: `should_transfer_files = YES`. When using a shell command (like `tree`), you can get its location using the command `which`. For instance, which `tree` will show `/usr/bin/tree`, this is the path you should add to `transfer_input_files` command.

## 4.6 How to ... specify the priority of your jobs?

HTCondor uses two different types of priorities: **job priority** (which of your jobs will run first) and **users priority** (which users will run their jobs and how many of them).

```
[+*Job priority*+]
```

If some of your jobs/clusters are more important than others and you want to execute them first, you can use the `priority` command to assign them a priority (the higher the value, the higher priority). For instance, if you want to execute first the last jobs of a cluster (reverse order), you can use next

```
command: priority = $(Process)
```

Remember that after submitting your jobs, you can set or change their priority using the shell command `condor_prio`.

```
[+*Users priority*+]
```

Whenever your jobs are being executed, your user priority is decreased (the more jobs are executed, the faster you lose priority). Users with best priority will run more jobs and they will begin sooner, so if your jobs are not so important or the queue is empty, you can use `nice_user` command to run them without wasting your priority. If you set this command to `True`, your jobs will be executed by a "fake user" with very low priority, so you will save your real priority (but it is likely your jobs will not be executed unless the queue is almost empty).

```
nice_user = True
```

Those jobs will be run with user `nice-user.<your_user>` and they will not change your user's priority (you can use shell command `condor_userprio -allusers` to see your and other users' priority).

Remember that using `condor_qedit` command you can change the attributes of your jobs after submitting them (see this FAQ [HOWTOs.CondorFAQs#ch\\_submit](#)). We can use this command to change the status of `NiceUser` attribute depending on how many slots are free (if there are many free slots, then we can set our jobs as "nice" to run them without affecting our priority, or the opposite, setting `NiceUser` to `false` when there are no free slots). For instance, use next commands to set all jobs belonging to Cluster ID 1234:

```
[...]$ condor_q 1234 -af ProcId NiceUser "#Check current status" 0 false 1 false ...
```

```
[...]$ condor_qedit 1234 NiceUser True Set attribute "NiceUser".
```

```
[...]$ condor_q 1234 -af ProcId NiceUser "#Check current status" 0 true 1 true ...
```

If user priority is a critical factor to you, you may want to periodically check the queue to change the `NiceUser` attribute according to the current status, setting it to `True` when you are the only active user or there is a large number of available slots, and set it to `False` when there are more active users or a few available slots. In order to simplify this process, we have developed a script that automatically performs those operations, you only need to specify your username or a particular `clusterID` (and optionally a minimum number of available slots) and it will change the `NiceUser` attribute to save your real priority as much as possible. You can copy the script from `/net/vial/scratch/adorta/htcondor_files/htcondor_niceuser.sh` and use it (or modify it) whenever you want. You can even periodically execute it using `crontab` (but please, do NOT run it too often to avoid overloading the system, every 30 or 60 minutes is fine). Run it with no arguments to get the description and syntax.

**Notes:**

- You can use `condor_qedit *-constraint* ...` to change the attributes of only some of your jobs.
- Condor can evaluate the attributes only when jobs begin to run, so new values may not affect the currently running jobs at the time of using `condor_qedit`, but they will be valid in jobs that begin to run after using the command.

## 4.7 How to ... deal with jobs that fail?

Sometimes jobs fail because there are problems when executing your program. It could happen that the problem is not in your program, but in the machine that executed it (a missing or misconfigured application, a library with a different version from the one you need, etc.). Then you should identify those problematic machines and use `requirements` commands in your submit file in order to block them, as is explained in this FAQ [HOWTOs.CondorFAQs#blackholes](#). For example, to block machines with names `piston` and `loro` use only one of the next commands (both are equivalent):

```
requirements = ((UtsnameNodename ! "piston") && (UtsnameNodename ! "loro")) requirements = *!*=stringListMember=(UtsnameNodename, "piston,loro")
```

You can also block all machines that satisfy a pattern. For instance, to avoid executing your jobs on those machines with names beginning with "k", "c" and "l", add next lines (you can specify more complex patterns using the **predefined functions and macros**:

```
letter = substr=(toLower(Target.Machine),0,1) =requirements = *!*=stringListMember=$(letter), "k,c,l")
```

Sometimes it is better to specify a list of machines where your application can run (and avoid any other that is not in that list). For that purpose, just use previous expressions after negating them with an "exclamation mark" "!" (or remove it if they were already negated).

After avoiding machines that are not able to run your program, you should submit again your jobs. But, please, execute **{only}** those jobs that failed (check this FAQ [CondorFAQs#repeat](#) to see how), do not execute again jobs that were already correctly executed to avoid wasting time and resources. For instance, add next command to only execute jobs with Process ID 0, 13, 25 and those from 37 to 44:

```
noop_job = *!*=( stringListMember="(Process)", "0,13,25")|(((Process) >= 37) && ((Process) <= 44)) )
```

**Note:** `noop_job` will "not" execute those jobs where the condition is `True`. Therefore, if you want to specify a list of jobs "to be executed", you need to "negate" your expression adding an exclamation mark at the beginning: `noop_job = *!(...)`. On the other hand, if you want to specify a list of jobs that should "not" be executed, then use the expression without negating it.

Jobs that are not executed may stay in the queue with `Complete` status (when using `condor_q` you will see that `ST` column is `C`). To remove all `C` jobs from the queue, try next command in your shell (use the second one to remove `{only}` `Complete` jobs that belongs to cluster `XXX`):

```
condor_rm -constraint 'JobStatus = 4' =condor_rm -constraint 'JobStatus = 4 && clusterID = XXX'
```

Also, it could be interesting to avoid the **black holes**: suppose that each of your jobs needs hours to finish, but they fail in an specific machine after a few minutes of execution time. That means that machine will be idle every few minutes, ready to accept another of your jobs, that will also fail, and this process may repeat again and again... sometimes a failing machine could even execute almost all your jobs... That is known as "black hole". To avoid it, we can force HTCondor to change machines when sending jobs. For that purpose add these lines to your submit file:

```
"#Avoid black holes: send to different machines" job_machine_attrs = Machine job_machine_attrs_history_length = 5 requirements = $(requirements) && (target.machine ! MachineAttrMachine1) && (target.machine ! MachineAttrMachine2)
```

When there are problems with your jobs, you should receive an email with an error and some related information (if it was not disabled using `notification` command as explained above) and the job will leave the queue. You can change this behavior with `on_exit_hold` and/or `on_exit_remove` commands, forcing HTCondor to keep that job in the queue with status "on hold" or even as "idle" so it will be executed again:

```
(:table border=1 cellpadding=5 cellspacing=0 width=70% align=center:)(:cell align=center valign=middle:) Command (:cell align=center valign=middle:) * True * (:cell align=center valign=middle:) * False * (:cellnr align=center valign=middle:) on_exit_hold (:cell align=center valign=middle:) Stay in the queue with "on hold" status (:cell align=center valign=middle:) Leave the queue (:cellnr align=center valign=middle:) on_exit_remove (:cell align=center valign=middle:) Leave the queue (:cell align=center valign=middle:) Stay in the queue with "idle" status (it can be executed again) (:tableend:) \$\
```

Last commands will be evaluated when jobs are ready to exit the queue, but you can force a periodic evaluation (using a configurable time) with commands like `periodic_hold`, `periodic_remove`, `periodic_release`, etc., and then decide if you want to hold/remove/release them according to your conditions. There are also some other commands to add a "reason" and/or a "subcode" when holding/removing/releasing these jobs. On the other hand, you can force your jobs to exit the queue when they satisfy a given condition using `noop_job`, or they stay in the queue even after their completion using `leave_in_queue` command (those jobs will stay in the queue with `Complete` status till you remove them using shell command `condor_rm`).

In the [http://research.cs.wisc.edu/htcondor/manual/v8.6/condor\\_submit.html#condor-submit-on-exit-hold](http://research.cs.wisc.edu/htcondor/manual/v8.6/condor_submit.html#condor-submit-on-exit-hold) official HTCondor documentation there are some examples about how to use these commands (all valid `JobStatus` could be displayed using shell command: `condor_q -help status`):

- With the next command, if the job exits after less than an hour (3600 seconds), it will be placed on hold and an e-mail notification sent, instead of being allowed to leave the queue:

```
on_exit_hold = ((CurrentTime - JobStartDate) < 3600)
```

- Next expression lets the job leave the queue if the job was not killed by a signal or if it was killed by a signal other than 11, representing segmentation fault in this example. So, if it exited due to signal 11, it will stay in the job queue. In any other case of the job exiting, the job will leave the queue as it normally would have done.

```
on_exit_remove = ((ExitBySignal = False) || (ExitSignal ! 11))
```

- With next command, if the job was killed by a signal or exited with a non-zero exit status, HTCondor would leave the job in the queue to run again:

```
on_exit_remove = ((ExitBySignal = False) && (ExitCode = 0))
```

- Use the following command to hold jobs that have been executing (`JobStatus = 2=`) for more than 2 hours (by default, all periodic checks are performed every 5 minutes. Please, contact us if you want a shorter period):

```
periodic_hold = ((JobStatus == 2) && (time() - EnteredCurrentStatus) > 7200)
```

- The following command is used to remove all "completed" (`JobStatus = 4=`) jobs 15 minutes after their completion:

```
periodic_remove = ((JobStatus == 4) && (time() - EnteredCurrentStatus) > 900)
```

- Next command will assign again the "idle" status to "on hold" (`JobStatus = 5=`) jobs 30 min. after they were held:

```
periodic_release = ((JobStatus == 5) && (time() - EnteredCurrentStatus) > 1800)
```

**[-IMPORTANT:** `periodic_release` command is useful when your program is correct, but it fails in specific machines and gets the "on hold" status. If that happens, this command will allow HTCondor to periodically release those jobs so they can be executed on other machines. But ~~{use this command with caution}~~: if there are problems in your program and/or data, then your application could be indefinitely held and released, what means a big waste of resources (CPU time, network used in file transferring, etc.) and inconveniences for other users, be careful! (you can always remove your jobs using `condor_rm` command in your shell).-]

When using `periodic_remove` or `periodic_hold` HTCondor submit commands, running jobs that satisfy the condition(s) will be killed and all files on remote machines will be deleted. Sometimes you want to get some of the output files that have been created on the remote machine, maybe your program is a simulation that does not converge for some sets

of inputs so it never ends, but it still produces valid data and you want to get the output files. In those cases, do not use the mentioned submit commands because you will lose the output files, and use instead utilities like `timeout` in order to limit the time that your application can be running. When using this linux command, you specify the maximum time your program can run, and once it reaches that limit, it will be automatically killed. Then HTCondor will detect your program has finished and it will copy back the output files to your machine as you specified. Next example will show how to limit the execution of your program up to 30 minutes:

```
"# Some common commands above..." ...
"# Max running time (in seconds)" MAXTIME = 30 * 60
"# Your executable and arguments" MYEXEC = your_exec MYARGS = "your_arg1 your_arg2"
"# If your executable is not a system command, do not forget to transfer it!" transfer_input_files = your_inputs,$(MYEXEC)
"# By default all new and modified files will be copied. Uncomment next line to indicate only specific output files"
"#=transfer_output_files = your_outputs"
executable = /bin/timeout "# Since timeout is a system command, we do not need to copy it to remote machines"
transfer_executable = False arguments = "$INT(MAXTIME) $(MYEXEC) $(MYARGS)"
queue ...
```

## 4.8 How to ... limit the number of concurrent running jobs?

There are some situations where it could be interesting to limit the number of jobs that can concurrently run. For instance, when your application needs licenses to run and few of them are available, or when your jobs access a shared resource (like directly reading/writing files located at `scratch`, too many concurrent access could produce locks and a considerable slowdown in your and others' computer performance).

To deal with these situations, HTCondor is able to manage limits and apply them to running job. Different kinds of limits can be defined in the "negotiator" (the machine that decides which job will run on which slot), but, unfortunately, you cannot change its configuration (for obvious security reasons, only administrators can do that). If you want to use a limit, you can contact us so we will configure it, but there is an easier way to use this feature without changing the configuration: we have set a high default value (1000 units) for any undefined limit, so you only need to use a limit not defined yet and adjust the number of consumed units per job. For example, suppose that you would like to limit your concurrent running jobs to 20: then you only need to specify that every job consumes 50 units of that limit ( $1000 / 20 = 50$ ). In this way no more than 20 jobs could concurrently run.

The command used to specify limits is `concurrency_limits = XXX:YYY`, where `XXX` is the name of the limit and `YYY` is the number of units that each job uses. You can use any name for the limit, but it should be unique, so we recommend you include your username in it.

- For instance, if your username is `jsmith` and you want to specify a limit of 12 running job ( $1000 / 12 \approx 83$  units/job), just add next line to your submit file:  
`concurrency_limits = jsmith:83`
- Previous command will affect all your jobs that use that limit, even in different submissions. If you want to set limits that are only applied to each submission, you can use a combination of your username and the cluster ID in the name of the limit:  
`concurrency_limits = jsmith$(Cluster):83`
- If you need it, you can use several limits and specify them in the same command line, using "commas" to build the list of limits and consumed units per job. For instance, next line will limit to 12 the number of running jobs in this submission and to 25 ( $1000 / 25 = 40$ ) the number of your total running jobs where the common limit `jsmith_total` has been used:  
`concurrency_limits = jsmith$(Cluster):83,jsmith_total:40`
- If you are executing jobs with **IDL without the IDL Virtual Machine**, then each job will be using one license. Since the total amount of licenses is limited, you must add next line in your submit file:  
`concurrency_limits = idl:40`

Limits can be changed after jobs are submitted using `condor_qedit` command. For instance, we want to change the limit that we have previously set to `jsmith:83` (12 concurrent jobs) to `jsmith:50` (20 concurrent jobs) in all jobs belonging to Cluster with ID 1234. Then use next commands:

```
[...]$ condor_q 1234 -af ProcId ConcurrencyLimits "#Check current limit" 0 "jsmith:83" 1 "jsmith:83" ...
[...]$ condor_qedit 1234 ConcurrencyLimits "jsmith:50" Set attribute "ConcurrencyLimits".
[...]$ condor_q 1234 -af ProcId ConcurrencyLimits "#Check current limit" 0 "jsmith:50" 1 "jsmith:50" ...
```

Values may have to be specified using quotes; be careful if your value is a string since you will be need to combine simple and double quotes, like `"'...'"` (see example above).

**Note:** HTCondor may evaluate the attributes only when jobs begin to run, so new values may not affect the currently running jobs at the time of using `condor_qedit`, but they will be valid in jobs that begin to run after using the command.

## 4.9 How to ... do some complex operations in my submit file?

If you need to do some special operations in your submit file like evaluating expressions, manipulating strings or lists, etc. you can use the **predefined functions** and some **special macros** that are available in HTCondor. They are specially useful when defining conditions used in commands like `requirements`, `rank`, `on_exit_hold`, `noop_job`, etc. since they will allow you to modify the attributes received from the remote machines and adapt them to your needs. We have used some of these predefined functions in our examples, but there are many others that could be used:



- evaluate expressions: `eval()`, ...
- flow control: `ifThenElse()`, ...
- manipulate strings: `size()`, `strcat()`, `substr()`, `strcmp()`, ...
- manipulate lists: `stringListSize()`, `stringListSum()`, `stringListMember()`, ...
- manipulate numbers: `round()`, `floor()`, `ceiling()`, `pow()`, ...
- check and modify types: `isReal()`, `isError()`, `int()`, `real()`, ...
- work with times: `time()`, `formatTime()`, `interval()`, ...
- random: `random()`, `$RANDOM_CHOICE()`, `$RANDOM_INTEGER()`, ...
- etc.

Check the documentation to see the complete list of **predefined functions**, and also the **special macros**.

## 4.10 How to ... work with nested loops?

You can use `$(Process)` macro to simulate simple loops in the submit file and use the iterator to specify your arguments, input files, etc. However, sometimes simple loops are not enough and nested loops are needed. For example, assume you need to run your program with the arguments expressed in the next pseudocode:

```
MAX_I = 8 MAX_J = 5
```

```
for (i = 0; i < MAX_I; i++) for (j = 0; j < MAX_J; j++) ./myprogram -var1==i= -var2==j=
```

To simulate these 2 nested loops, you will need to use next macros in your HTCondor submit file:

```
MAX_I = 8 MAX_J = 5 N = MAX_I * MAX_J ... I = ($(Process) / (MAX_J)) J = ((Process) % $(MAX_J)) ...
```

```
executable = myprogram arguments = "-var1=$=INT=(I) -var2=$=INT=(J)" queue $(N)
```

Last code will produce a nested loop where macro `$(I)` will work like the external iterator with values from 0 to 7; and `$(J)` will be the internal iterator with values from 0 to 4.

If you need to simulate 3 nested loops like the next ones: `for (i = 0; i < MAX_I; i++) for (j = 0; j < MAX_J; j++) for (k = 0; k < MAX_K; k++) ...`

then you can use the following expressions: `N = $(MAX_I) * $(MAX_J) * $(MAX_K)`

```
I = ( (Process)/((MAX_K) * (MAX_J))) J = (((Process) / $(MAX_K)) % $(MAX_J)) K = ( $(Process) % $(MAX_K))
```

```
executable = myprogram arguments = "-var1 $=INT=(I) -var2 $=INT=(J) -var3 $=INT=(K)" ... queue $(N)
```

## 4.11 How to ... program my jobs to begin at a predefined time?

Sometimes you may want to submit your jobs, but those jobs should not begin at that moment (maybe because they depend on some input data that is automatically generated at any other time). You can use `deferral_time` command in your submit file to specify when your jobs should be executed. Time has to be specified in "Unix epoch time" (the number of seconds elapsed since 00:00:00 on January 1, 1970, Coordinated Universal Time), but, do not worry, there is a linux command to get this value:

```
date -date "MM/DD/YYYY HH:MM:SS" +%s
```

For instance, we want to run a job on April 23rd, 2016 at 19:25. Then, the first step is to get the epoch time:

```
[...]$ date -date "04/23/2016 19:25:00" +%s
```

Our value is 1461435900, so we only need to add next command to the submit file:

```
deferral_time = 1461435900
```

Bear in mind that HTCondor will run jobs at that time according to remote machines, not yours. If there are wrong dates or times in remote machines, then your jobs could begin at other dates and/or times.

Also you can add expressions, like the next one to run your jobs one hour after the submission:

```
deferral_time = (CurrentTime + 3600)
```

It may happen that your job could not begin exactly at that time (maybe it needs that some files are transferred and they are not ready yet), and in that case HTCondor may kill your job because the programmed time has expired and your job is not already running. To avoid that, you can specify a "time window" to begin the execution, a few minutes should be enough. For instance, add next command to tell HTCondor that your job could begin up to 3 minutes (180 seconds) after the programmed time:

```
deferral_window = 180
```

**Important:** When you submit your programmed jobs, HTCondor will check which machines are able to run them and once the match is done, those machines will wait for the programmed time and will not accept any other jobs (actually, it will show "Running" status while waiting for the programmed time). That means a considerable loss of resources that should be always avoided. Using `deferral_prep_time` command we can specify that HTCondor could use those matched machines till some time before really running your jobs.

Then, add next lines to begin your jobs on April 23rd, 2016 at 19:25, specifying that they can begin up to 3 minutes after that date and that HTCondor could run other jobs on the matched machines till one minute before the programmed time:

```
deferral_time = 1461435900 deferral_window = 180 deferral_prep_time = 60
```

HTCondor also allows you to use more powerful features, like specifying jobs that will be periodically executed at given times using the "CronTab Scheduling" functionality. Please, read the **Time Scheduling for a Job Execution** section in the official documentation to get more information.

## 4.12 How to ... run jobs that have dependencies among them?

If your jobs have dependencies related to inputs, outputs, execution order, etc., you can specify these dependencies using a "directed acyclic graph (DAG)". HTCondor has a manager (called [http://research.cs.wisc.edu/htcondor/manual/v8.6/2\\_10DAGMan\\_Applications.html](http://research.cs.wisc.edu/htcondor/manual/v8.6/2_10DAGMan_Applications.html) DAGMan) to deal with these jobs.

First, you have to create a DAG input file, where you specify the jobs (including the respective HTCondor submit file for each one) and the dependencies. Then, you submit this DAG input file using `condor_submit_dag <dag_file>`. Next code describes a basic example of DAG file where job A depends on B and C, that depend on D (diamond shape).

```
JOB A condorA.submit JOB B condorB.submit JOB C condorC.submit JOB D condorD.submit PARENT A CHILD B C
PARENT B C CHILD D
```

```
[...]*condor_submit_dag* diamond.dag
```

Examples about working with HTCondor DAGMan can be found in the [http://research.cs.wisc.edu/htcondor/manual/v8.6/2\\_10DAGMan\\_Applications.html#SECTION00310200000000000000](http://research.cs.wisc.edu/htcondor/manual/v8.6/2_10DAGMan_Applications.html#SECTION00310200000000000000) Official documentation mentioned above. You can also try the easy example located at the end of this page <http://research.iac.es/sieinvens/SINFIN/Condor/curso/course/node7.php> used in a course about HTCondor imparted by SIE some years ago (solution here <http://research.iac.es/sieinvens/SINFIN/Condor/curso/course/node9.php#SECTION00095000000000000000>).

## 4.13 How to ... know the attributes of the machines where our jobs are run?

There is a special macro to get the string attributes of target machines that we can use in our submit file. In this way, some of the parameters of each machine where HTCondor executes jobs can be accessed with `$(parameter)`. Also there are other special macros, like the one used to print the symbol `$` since it is reserved by HTCondor: `$(DOLLAR)`.

For example, we want to know the name of each slot and machine where our jobs were executed, adding `$.name.$` to the results of `stdout` and `stderr`. Then we should use next commands:

```
output = myprogram.$(ID).$(DOLLAR).
```

```
(Name).
```

```
(DOLLAR).out =error= = myprogram.(ID).(DOLLAR).
```

```
(Name).$(DOLLAR).err
```

Adding those commands in your submit file will create output and error files with names similar to `$.slot3@xilofon.ll.iac.es.$`.

## 5 FAQs

### 5.1 General Information

#### 5.1.1 What is Condor? How can Condor help me? Who can use it? Who could help me if I have any problems?

Condor is a software that may help you to get your computational results in much less time. The underlying idea is to use idle computers to run your programs when they are not being used by their owners. When running your programs with Condor, you only need to specify the name of your program and its location, where to find the inputs and where to place your outputs, and that is almost all in most cases; everything else will be done by Condor. IAC researchers with access to a linux desktop PC should be able to use Condor; the SIE will give you support if you have any issue with it. Please, visit our [introduction page](#) for more general information about Condor.

#### 5.1.2 How does Condor work? My machine is in "Owner/Unclaimed/Claimed" state, what does it mean?

Condor has to deal with complex situations, but here we will just give some outlines of its basic operation. Condor uses several daemons to essentially manage a queue of submitted jobs and a pool of "slots" where jobs can be executed (usually each "slot" is a core of the machines in the pool). Jobs have several requirements (requested memory, disk space, etc.) and slots have different specifications: what Condor does is to match jobs with suitable slots, and then execute those jobs on them.

You can try `*condor_status*` command to check the status of the pool of machines. The first column shows the name of the slots and machines, then some more info is shown, like the Operative System, Architecture, System load, Memory, etc. But we will focus on **State** and **Activity** columns, they can be used to understand how Condor works:

```
(:table border=1 cellpadding=5 cellspacing=0 width=95% align=center:)(:cell align=center valign=middle:) STATE
("Activity")(:cell align=center valign=middle width=120px:) Action(:cell align=center valign=middle:) Description
(:cellnr align=center valign=middle:) OWNER ("Idle")(:cell align=center valign=middle:) User is working on
his/her machine(:cell align=left valign=middle:)-If a user is working on his/her machine, Condor will detect mouse/key-
board activity, active remote connections, etc. In this case, all slots of this machine will get the Owner state and Condor
will not use it to run any job. The activity showed by Condor will be Idle since that slot is not doing any work for
Condor, but it does not mean the machine is idle, most likely it will be busy working for her owner. Owner state can be
assigned in other situations, like when the system load is high (Condor will not run any job to avoid interfering with user's
programs), there are some time restrictions, etc. When user finishes working with the machine, Condor will still wait
a prudential period of time (by default, 15 min.) since last activity was detected before using it.-](:cellnr align=center
valign=middle:) UNCLAIMED ("Idle")(:cell align=center valign=middle:) Slot is idle(:cell align=left valign=middle
```

:) [-If the machine has not being used by his/her owner for a while, then Condor will run some benchmarks to update its info about performance and all slots will get the **Unclaimed** state and **Idle** activity. That means Condor is allowed to run jobs on the idle slots and the jobs queue will be checked to match any suitable job.-] (:cellnr align=center valign=middle :) **CALIMED** ("Busy") (:cell align=center valign=middle :) Slot is running Condor jobs (:cell align=left valign=middle :) [-If there is a positive match, Condor will begin to run the matched job on the slot. Condor will copy the executable and input files to the remote machine and run the program there. The slot(s) running Condor jobs will get the **Claimed** state and **Busy** activity, and the jobs will get the **Running** state.-] (:cellnr align=center valign=middle :) **CLAIMED** ("Suspended") (:cell align=center valign=middle :) User begins to work on a machine that is running Condor jobs (:cell align=left valign=middle :) [-When Condor is running jobs in a machine and any user's activity is detected, Condor will immediately suspend all running jobs in all the slots. Some seconds (or few minutes) may be needed in this operation, depending on the job(s), the number of involved files, etc. The machine may get unresponsive at that time, but after a short while the machine should be ready again for the user. At this time the machine has the **Claimed** state and the **Suspended** activity, and it will keep this state for a period of time (by default, 15 minutes). This is done to prevent killing jobs when there is no real activity (for instance, the cleaning service accidentally moved the mouse, etc.). If it was an isolated activity, the machine gets idle again and then Condor will "wake up" the jobs and continue running them from the last point, recovering the **Claimed** state and the **Busy** activity.-] (:cellnr align=center valign=middle :) **OWNER** ("Idle") (:cell align=center valign=middle :) User is working on his/her machine (:cell align=left valign=middle :) [-If there were suspended jobs in a machine and user is working again on it for a period of time (it is not an isolated activity), Condor will kill all suspended jobs and then the machine will get the **Owner** state. All killed jobs will go again to the queue with the **Idle** state to be executed when possible.-] (:tableend:)

States mentioned above are the most common and representative, but there are **other possible states** [http://research.cs.wisc.edu/htcondor/manual/v8.6/3\\_7Policy\\_Configuration.html#fig:machine-states](http://research.cs.wisc.edu/htcondor/manual/v8.6/3_7Policy_Configuration.html#fig:machine-states), like **Matched** (only shown for a few seconds when there is a successful match), **Preempting** (job is being killed or vacating from that slot), **Backfill** (slot is idle and queue is empty, so it can run some low priority jobs assigned by the administrators), etc. Visit the **Useful commands page** to get more information about commands in Condor.

### 5.1.3 Sometimes Condor runs jobs on my computer when I am working on it, can I avoid that?

Condor should run jobs ~~only~~ on idle computers that are not being used by their owners. Idle computers are those where there has not been keyboard/mouse activity for more than 15 minutes, system load is low enough (to avoid interfering with owner's programs), there are no active remote ssh connections, there are no time restrictions, it has enough free space, etc.

If Condor is running job(s) on your computer when you begin to use it, Condor will detect your activity and it will immediately suspend all running jobs. That process is usually quite fast, most users do not even notice it, but some jobs are heavy and complex and it could take a while to suspend them (it could take from several seconds to a few minutes). If that happens, your machine could get unresponsive for a few that moments, but you just need to wait a bit and it will be ready soon (this is a normal process, sorry for the inconvenience).

Anyway, performance problems could be caused by a wide range of different situations, like an exceeded home or disk quota, heavy load (check that your browser is not consuming a lot of CPU time if you have a large number of open tabs), configuration problems, etc. Please, use **df -h** and **quota -s** commands to get information about your available space and **htop** command to find out what processes are using your CPU and memory, that may help a lot to solve a low performance problem.

If you want to check whether Condor has been executing jobs on your machine at any time, you can use the Stats Web we have developed: [http://carlota:81/condor\\_stats/](http://carlota:81/condor_stats/). There you can get some stats about which machines have been used by Condor, when and for how long, etc. Anyway, if you still think that you are experiencing any kind of problems related to Condor, just contact us and we will find a solution.

### 5.1.4 I am using Condor, should I add an acknowledgement text in my publications?

Yes, you should mention it in the acknowledgments of your papers or any other publications where you have used HTCondor. Although there is no standard format, we suggest the following:

""This paper made use of the IAC Supercomputing facility HTCondor (<http://research.cs.wisc.edu/htcondor/>)"".

If you have used any other IAC Supercomputing facilities (LaPalma, TeideHPC, etc.), please, add also them in the acknowledgments:

**LaPalma:** ""The author thankfully acknowledges the technical expertise and assistance provided by the Spanish Supercomputing Network (Red Española de Supercomputación), as well as the computer resources used: the LaPalma Supercomputer, located at the Instituto de Astrofísica de Canarias.""

**TeideHPC:** ""The author(s) wish to acknowledge the contribution of Teide High-Performance Computing facilities to the results of this research. TeideHPC facilities are provided by the Instituto Tecnológico y de Energías Renovables (ITER, SA). URL: <http://teidehpc.iter.es/>""

## 5.2 Preparing and submitting your jobs

### 5.2.1 I have developed a program, do I need to make any modification to run it with Condor?

For a basic execution in Condor, you do not need to compile your program with any special library or add calls to external functions to be executed by Condor, the program runs as is. According to our experience, in most cases you will not need to change anything in your program, or only a few minor modifications may be required:

- Your program should accept arguments, since changing arguments is the way used to specify different jobs with the same executable. For instance, if your program reads a file to make the same computations with the values of each line, you can modify it to accept the number of the line as an argument, and then Condor will launch a different job for each line. Arguments can be also different data, paths to files or whatever your application use as input.
- Paths to your input/output files may change when executing with Condor, so you should be able to change them in your application if needed.

### 5.2.2 How do I run my application with Condor? (submitting jobs to queue)

All the information needed by Condor to run your program should be written in a **Condor submit file**. You must include in that file one (and only one) **executable** command to specify what your program is (the path can be either absolute or relative to the directory where the submission is done). Additionally, if your executable is not accessible from other machines, use **should\_transfer\_files = YES** command and Condor will copy it to the remote machines. With the **arguments** command you can specify your parameters (they can be either fixed values or depend on a counter) and then use **queue <N>** command to launch N jobs. You can repeat **arguments** and **queue** commands as many times as needed. A very basic submit file could be the following one, that assumes your application is located in the same directory where you will use the **condor\_submit** command. "Please, visit **Condor submit file page** for more info and examples."

```
"# Condor submit file" "# Running myprogram with arguments "-v 235" and "-kf 'cgs' -v 6543"" universe = vanilla
should_transfer_files = YES
executable = myprogram
arguments = "-v 235" queue
arguments = "-kf 'cgs' -v 6543" queue
\$\
```

Once the submit file is ready, you can submit your jobs to the Condor queue using next command in your shell console: **\*condor\_submit\*** submit<sub>file</sub>

To check your jobs, use next command: **\*condor\_q\***

Visit the **Useful commands page** to get more information about commands in Condor.

**Caution!:** Before submitting your real jobs, always sdo ome simple tests in order to make sure that both your submit file and program work in a proper way: if you are going to submit hundreds of jobs and each job takes several hours to finish, before doing that try with just a few jobs and change the input data in order to let them finish in minutes. Then check the results to see if everything went fine before submitting the actual jobs. Bear in mind that submitting untested files and/or jobs may cause a waste of time and resources if they fail, and also your priority will be worse in following submissions.

### 5.2.3 How do I check the Condor queue and my submitted jobs?

You can check the general status of the queue using **\*condor\_status\***, then you will see how many slots are used by their owners (state will be **Owner**), how many are free to be used by Condor (**Unclaimed** state) and how many are already executing Condor jobs (**Claimed** state); these states are explained in this **FAQ states** . If you use **condor\_status -submitters**, you will get a summary of who has jobs in the queue and their status; there are many other **useful commands and options**, please, check them. To see some graphs and stats about Condor, you can visit **nectarino** -> <http://nectarino/> (there you can also find information about Condor queue and machines states) and also [http://carlota:81/condor\\_stats/](http://carlota:81/condor_stats/).

If you want to check only your submitted jobs, then use **\*condor\_q\***. It will show the info related to your jobs, like the cluster and process ID, owner, submission date, time they have been running, state, priority, Size, Command, etc. For instance, following lines show a possible output of this command:

```
[... ]$ *condor_q*
ID OWNER SUBMITTED RUNTIME ST PRI SIZE CMD 418.0 jsmith 3/13 17:00 0+00:37:32 I 0 317.4 myprogram
-c 7 418.*1* jsmith 3/13 17:00 0+00:30:25 < 0 488.3 myprogram -c 14 418.*2* jsmith 3/13 17:00 0+01:12:10 R 0 231.4
myprogram -c 21 418.*3* jsmith 3/13 17:00 0+02:15:52 S 0 423.5 myprogram -c 62 418.*4* jsmith 3/13 17:00 0+06:31:34
> 0 623.1 myprogram -c 28 418.*5* jsmith 3/13 17:00 0+03:41:52 H 0 432.6 myprogram -c 35
```

The first value is the **Job ID**, it is composed by two numbers, the first one is the "Cluster ID" that identifies the submission, all jobs submitted with the same submit file will share this Cluster ID (in this example Cluster ID is 418). The second number is the "Process ID" and it is a consecutive number, from 0 for the first job to N-1 for last job when N jobs are submitted. To understand what is happening to your jobs, check "State" column (**ST**), the common values are:

- **=\*I=\*** "idle" job, waiting for a slot to be executed on (it can take a while before your jobs are executed, but if they are always in this state, check **this FAQ** -> **#idle**)
- **=\*<=\*** your job is about to be executed, executable and input files are being transferred to the remote machine
- **=\*R=\*** "running", your job is being executed at this moment
- **=\*S=\*** "suspended", the machine that was running this job is being used, jobs are suspended while waiting for the machine gets idle again
- **=\*>=\*** execution is finished, output files are being transferred
- **=\*H=\*** "on hold", there are problems with your job that have to be solved (check **this FAQ** -> **#hel**)

- `*<q*` or `=*>q=*` if you see those symbols, your transfers are waiting for the completion of other active transfers. This is done to avoid an excessive use of the available bandwidth.

Once your jobs are finished, they will leave the queue so they will be not listed when using `condor_q` (use `condor_history` command instead). There are other states that normally do not appear in basic executions, like `C` (completed) or `X` (removed). If you have a special need and want that your jobs stay in the queue after completion with these or other states, you can force that by using some commands in your submit files (check [this FAQ](#) -> `#lesstime` or [this one](#) -> `#badinputs`).

#### 5.2.4 Where should I put my input files so that Condor will be able to find them?

If you are using `stdin` as input (i.e. you directly specify your input data using the keyboard, or you run your program using `./myprogram < /path/to/input_file.txt`), then you should use the `input` command to specify the file that contains the input data (you can use either an absolute path or a relative one to the submitting directory):

```
input = /path/to/input_file.txt
```

If your program needs to read some input files, they have to be transferred to all remotes machines on which your application will be executed, so your program will be able to find them. You do not need to deal with copying files, Condor will do all the work, the only thing you need to do is to use `transfer_input_files` to specify the name and location of your files. For instance, suppose that your executable `myprogram` needs two input files as arguments: `data1.in` (it is now located in `/home/myuser/mydata`) and `data2.in` (it is located in the same directory where you will do the submission). Then, use next commands:

```
... should_transfer_files = YES ... transfer_input_files = /home/myuser/mydata/data1.in, data2.in
executable = myprogram arguments = "data1.in data2.in" ...
```

Although those input files are in different locations on your machine, Condor will copy them to the same directory where the executable will be placed on the remote machine, that is why we have used no paths when specifying files in the `arguments` command. You can also use `transfer_input_files` to copy directories (if you add a `/` at the end of the directory, then Condor will copy the content of the directory, but it will not create the directory itself). There are many possibilities when working with input and output files. Please, visit [Condor submit file page](#) -> [CondorSubmitFile#example\\_simplefiles](#) where there is an example that explains how to work with files, step by step.

If you have a huge amount of input files and/or they are very big (GB or so), there is another solution to avoid the copy process that could last a long while. In these situations, you can place your files in a shared location (like `/net/yourmachine/scratch`) so all machines could directly have access to the files without copying them. But that is not recommended at all since an intensive use of the shared network system could produce blocking accesses and possibly a significant slowdown in your and others' machine performance. Files should be always copied to remote machines to let them work locally. Only when you are dealing with really huge files, it might be better to use shared locations, but then you should **limit the number of concurrent running jobs** -> [CondorHowTo#howto\\_limit](#) to avoid stressing the network. Please, before submitting your jobs, contact us if you have doubts about this.

#### 5.2.5 If Condor runs my program on different machines, how I can get my output files?

Condor will copy your output files back to your machine after the execution is finished, you only need to use some commands to specify those files and Condor will do everything else.

If your output is written in `stdout` (printed on the screen), then you have to use `output` command in your submit file to specify a file where Condor will write the output of each job. Obviously, filenames have to be different or all jobs will write in the same file and it will not be valid. To avoid that, you can use the ID of each job to write in distinct files. This ID is composed by two numbers (X.Y), where the first one is the cluster ID (it changes every time you do a submission) and the process ID (it goes from 0 to N-1 where N is the number of queued jobs). Also you should indicate a file where Condor will write the **errors** (those in `stderr`) and a **log** file. Therefore, all your submit files should include next commands (note that `ID` and `FNAME` are not commands, but some macros we have defined to make it clearer):

```
ID = $(Cluster).$(Process) FNAME = filename
```

```
output = $(FNAME).$(ID).out error = $(FNAME).$(ID).err log = $(FNAME).$(Cluster).log
```

If your program also generates **output files**, most times you do not need to use any command since after the execution Condor will copy to your machine all files created or modified by your job that are located in the same directory where your application was executed. You only need to check your submit file to make sure that the file transfer mechanism is active with next commands:

```
should_transfer_files = YES when_to_transfer_output = ONEXIT
```

But sometimes we want to specify that Condor must transfer only some specific files (and avoid transferring useless files, like temporary ones), or we want to also transfer whole directories or specific files placed inside some sub-directories. In those situations you should use `transfer_output_files` command to specify which files or directories(\*) you want that Condor copies back to your machine (paths should be relative to the executable):

```
transfer_output_files = data(Process).out, dir(Process)_out, dir_outputs/
```

**():-if your directory ends with an slash \*/=, Condor will copy the content of the directory, but it will not create the directory itself]**

Of course, output files should have distinct names (if you use the same name, files will be overwritten when copying them to your machine). If your application uses always the same name for output files, you can use `transfer_output_remaps` command to change their names in destination (it will only work with files, not with directories). For instance, suppose that your application creates an output file named `data.out` and you want to use distinct names to avoid overwriting those files, then you could use the `$(Process)` macro to include the process ID of the job to generate different names (`data0.out, data1.out, data2.out, ...`):

```
transfer_output_files = data.out transfer_output_remaps = "data.out=data=$(Process).out"
```

If you only want to get the output file from the screen (using `output` command) but **not** any other generated or modified file, you can use `should_transfer_files = NO` command. But this command will also affect your input files. If you want to copy input files, but NOT the output files, you should use:

```
should_transfer_files = YES +TransferOutput = ""
```

Bear in mind that `transfer_output_files` command is **not** used to specify where you would like that Condor places output files in your machine (you can use `initialdir` command for that, check [this FAQ -> #initialdir](#)), but where the output files will be located in the remote machine so Condor can find them (paths to your output files must be relative to the directory where your program will be run).

There are many possibilities when working with input and output files. Please, visit [Condor submit file page -> CondorSubmitFile#example<sub>simplefiles</sub>](#) where there is an example that explains how to work with files, step by step.

**Read this when dealing with huge input/output files:** If your program generates a huge amount of output files and/or they are very big (GB or so), there is another solution to avoid the copy process that could last a long while. In these situations, you can prepare your program to write the output files directly in a shared location (like `/net/yourmachine/scratch`). But that is not recommended at all since an intensive use of the shared network system could produce blocking accesses and possibly a significant slowdown in your and others' machine performance. Files should be always copied from remote machines to let them work locally. Only when you are dealing with really huge files, it might be better to use shared locations, but then you should **limit the number of concurrent running jobs** -> [CondorHowTo#howto<sub>limit</sub>](#) to avoid stressing the network. Please, before submitting your jobs, contact us if you have doubts about this.

### 5.2.6 Can I tell Condor to use a different directory for input/output files?

Sometimes you are submitting your jobs from the directory where your executable is located, but your input/output files are placed in a different location. You could add the path to that location every time you have to specify a file, but it is much easier to use the `initialdir` command. For instance, if your input data is located in `/home/myuser/mydata` and you want that your output data will also be placed there, you can add this statement in your submit file:

```
initialdir = /home/myuser/mydata
```

Bear in mind that it will affect both your input and output files, but it has no effect over the executable file.

### 5.2.7 I would like to use a loop to send my jobs with different arguments... can I do that?

Yes, a loop is the most natural way of submitting different jobs in Condor. Many users have created shell scripts to generate different submit files, one per each set of arguments, but this is unnecessary in most cases and it is not recommended: the shell script can be quite complex; managing dozens, hundreds or even thousands of submit files is bothersome, as it will also be managing all those independent jobs; and, even worse, efficiency will be reduced (every time you submit, Condor creates a "cluster" for that execution, which involves an overhead. So we should try to create only one cluster with N jobs rather than N clusters with only one job each, which makes also easier managing all generated jobs).

The easiest way to work with loops is to use the predefined `$(Process)` macro in your submit file. Condor will assign the id of each job to this macro, so if you are submitting N jobs, `$(Process)` will be 0 in the first job, 1 in the second one, till N-1 in the last job. This is the loop we need. For instance, next easy submit file will use perl to calculate the cube of the first N numbers creating one job per number (in this example we will use N = 50, beginning with 0):

```
N = 50
```

```
should_transfer_files = YES when_to_transfer_output = ON_EXIT
```

```
output = cube.$(Cluster).$(Process).out error = cube.$(Cluster).$(Process).err log = cube.$(Cluster).log
```

```
executable = /bin/perl transfer_executable = False arguments = "-e 'print $(Process)**3'"
```

```
queue $(N)
```

As you can see, it is very easy to simulate a loop, we only need to use the predefined macro `$(Process)` to get the iteration value. We can use it in our arguments, inputs, outputs, name of files, etc... Since we have only submitted once, just one cluster will be created. Please, visit [Condor submit file page -> CondorSubmitFile](#) to see more detailed examples. If you need a more complex loop including some arithmetic operations using the iteration value, then you can define your own macros using Condor syntax, see [this example -> CondorSubmitFile#example<sub>complexmacros</sub>](#). Condor also has \*more predefined macros -> [http://research.cs.wisc.edu/htcondor/manual/v8.6/3\\_5Configuration\\_Macros.html#SECTION00451800000000000000](http://research.cs.wisc.edu/htcondor/manual/v8.6/3_5Configuration_Macros.html#SECTION00451800000000000000) to generate random numbers, randomly choose one value among several of them, etc.

### 5.2.8 Do I need to rename my input/output files to work with Condor?

Using filenames with a known pattern makes it much easier to specify files to transfer in your Condor submit file. When possible, we recommend you use a common text and then an index to refer to your files, for instance: `data0.in`, `data1.in`, `data2.in`, `data3.in`, ..., `data154.in`. Then it will be very easy to specify each input file: you only need to add a command similar to next one: `transfer_input_file = data$(Process).in`. This is the easiest situation, but this approach is also valid in more complex scenarios, like when the index depends on an expression and/or has some leading zeros, like 0001, 0002, 0003, ... (see [this example -> CondorHowTo#howto<sub>numberfmt</sub>](#)). Also remember that you can run scripts (or other programs) before and after executing your main application (see [this FAQ -> #prepostsripts](#)), so you could use this feature to change the name of your files as needed (for instance, using shell commands or scripts).

But sometimes you can use a known pattern in your files, or you have a variable number of files to transfer, or maybe your program does not generate any output file under certain conditions... In those situations, it is much better to transfer directories rather than deal with individual files. Then, you only need to place your input and/or output files in directories, and then specify that Condor has to transfer these directories and their content.

Remember that you can use `transfer_input_file` and `transfer_output_file` to specify which files and directories to transfer. Paths in the local machine can be absolute or relative to the directory where the submission is performed (or the one set using `initialdir` command). Paths in remote machines should be relative to the directory where your program is placed and executed (be careful if you use absolute paths, they have to exist in every machine).

### 5.2.9 Should I delete temporary files?

No, that is not needed if you are only using local directories (those that belong to Condor). Condor will run your program on remote machines, and once the execution is finished and the output files are transferred, Condor will delete files and directories related to that execution, so you do not need to delete any file. If you are using other locations like those in external or shared systems (`/scratch`, `/home`, `/net/nas3`, etc.), then you need to delete all unnecessary files since Condor will not check those directories.

Condor also has periodic checks on every machine and it will analyze all directories belonging to Condor in order to remove extraneous files and directories which may be left over from Condor processes that terminated abnormally due to either internal errors or a system crash.

### 5.2.10 What are the technical specifications of machines running Condor? Can I restrict and/or prioritize those specifications in my jobs?

To see an overview of the hardware and software available when running with Condor, please visit the **introduction page** -> **Condor#condor\_machines**. You can also use next commands to get information about slots:

```
condor_status -server "#List attributes of slots, like memory, disk, load, flops, etc." condor_status -sort Memory
"#Sort slots by Memory, you can try also with other attributes"
```

If you have an application that has hardware/software limitations, you can add restrictions or directly specify which machines you want to run your application on. Typical limitations are the OS version (due to dependencies on libraries), RAM, disk space, etc., but there are many more parameters. To apply your restrictions use the `requirements` command and the conditions (you can use several **operators**, **predefined functions**, etc. -> [http://research.cs.wisc.edu/htcondor/manual/v8.6/4\\_1HTCondor\\_s\\_ClassAd.html#SECTION00512300000000000000](http://research.cs.wisc.edu/htcondor/manual/v8.6/4_1HTCondor_s_ClassAd.html#SECTION00512300000000000000)) in your submit file.

To see the complete list of parameters, try command `condor_status -l <your_machine>` and the values for each slot of your machine will be displayed. Most of the parameters showed in that list can be used to add requirements. Also you can use other commands in your submit file like `request_memory`, `request_disk`, etc.

If you want to specify preferences in one or several parameters, use the `rank` command in your submit file (Condor will always give more preference to higher values of the specified parameters). For instance, add next lines to your submit file if you want to run your jobs only in slots with Fedora19 and more than 1GB of RAM, prioritizing those slots with the highest amount of RAM:

```
rank = Memory request_memory = 1024 requirements = (OpSysAndVer == "Fedora19")
```

Rank is evaluated as float point expression, so you can weight several parameters in different ways. For instance, we want to choose slots with higher RAM, but those with at least 15GB of disk are also important for us, so will give them 100 extra "points":

```
rank = Memory + (100 * (Disk >= 15120000))
```

**Caution!:** Be careful when choosing your restrictions, using them will reduce the number of available slots for your jobs so it will be more difficult to execute them. Also check that you are asking for restrictions that can be satisfied by our current machines, or your jobs will stay always in Idle status. Before adding a requirement, always check if there are enough slots that satisfy it. For instance, to see which slots have more than 1GB of RAM, try next command in your shell (you can filter and see only the available ones adding flag `-avail`):

```
[...]$ condor_status -constraint '((Memory > 1024) && (OpSysAndVer == "Fedora19"))'
```

"Please, visit **Condor submit file page** -> **CondorHowTo#howto\_requirements** for more info and examples."

### 5.2.11 How can I get/set environment variables when running with Condor (python and other programs may need them)?

If you are running a python program it is likely it will need to access the environment variables when importing some modules. Other programs and scripts also need to get or set environment variables to properly work. If you use `getenv = True` command in your submit file, Condor will copy your current shell environment variables and they will be available when running your job (copy will be performed at the time of submitting). If you need to declare or change the value of any variable, you can use the `environment` command in the submit file, like the following example:

```
environment = "var1=val1 var2=\"val2\" var3=val3"
```

If you use both commands, variables specified with `environment` command will override those copied by `getenv` if they have the same name. Using `$ENV(variable)` allow the access to environment variables in the submit file (for example, `$ENV(HOME)`).

Please, see also **this FAQ about python** -> <http://research.iac.es/sieinvens/siepedia/pmwiki.php?n=HOWTOs.CondorFAQs#python-fedora> for more details about how to define environment variables with python, and visit also **Condor submit file page** -> **CondorHowTo#howto\_env** for more info and examples.

### 5.2.12 Can I change my jobs attributes after submitting them?

Yes, most of the jobs attributes can be changed after the submission (but not all of them, for example, you cannot change the owner, clusterId, procId, jobStatus, etc.). Of course, you can only change your own jobs.

To change attributes, use command `*condor_qedit*` and specify the name of the attribute and its new value (new attributes can be defined, too). See next examples (attributes to be changed are underlined and new values are set just after them):

```
[...]$ condor_qedit 1234 {+NiceUser+} TRUE "# Enable NiceUser in all jobs belonging to cluster 1234" [...]
$ condor_qedit 1234.6 {+Requirements+} '(UtsnameNodename ! "arco")'="# Job 1234.6 will not be executed on machine "arco"
[...]$ condor_qedit -constraint 'JobStatus = 1' {Environment} '""'="# Clean environment variables in all idle jobs"
```

#### Notes:

- [-Remember to quote strings. For instance, to specify that attribute `A` has a value `"foo"` you should use:  
`condor_qedit ... A "'foo"'`.-]
- [-Use `condor_q` with option `-long` to get the full list of attributes of each job and their current values. Depending on which attributes you have changed/added, new values may be valid only after those attributes are re-evaluated, usually when jobs restart (so changing attributes of running jobs may not work till those jobs are stopped and executed again).-]
- [-Be careful when changing attributes like `Requirements`, `Environment`, etc., since new values will replace the old ones (they will ~~not~~ be appended to the previous values, so you may need to get them before and add them to your expression).-]
- [-As you can see in the examples above, you can select which jobs you want to edit specifying their clusterId, clusterId.procId and/or with a constraint (use your username to select all your jobs), with the same syntax that you use in `condor_q` (and other commands like `condor_release`, `condor_hold`, `condor_rm`, etc.). We recommend that you use `condor_q` to check the selection of jobs before editing, to avoid making unwanted changes to other jobs.-]

## 5.3 Having some troubles with your jobs

### 5.3.1 I cannot submit jobs, what is wrong?

If you use `condor_submit <submit_file>` and your jobs do not appear in the list when using `condor_q`, there might be errors in your submit file. If so, Condor should print those errors and some related information when doing the submission (use `-debug` flag if you do not see that info). Most problems are easy to fix since they are related to wrong paths, lack of permissions, missing required commands, etc., but if you do not have an idea about how to fix any error, please contact us.

### 5.3.2 How can I check that my program is running fine? Can I access to the input/output files in the remote machine?

There are several ways to check in real-time what is happening on the remote machine while it executes your jobs, so you can see how results are being generated and whether they are fine or not. All these methods only work ~~{when processes are running}~~, remember that you can get the `job_id` using command `condor_q`, be sure that the job you choose is running with state `"R"` (you can select them using `condor_q -run`).

A) You can check what your program is printing on the `"screen"` (`stdout` and `stderr`) and/or in output files on the remote machine while it executes your program. To display outputs, use `*condor_tail* <job_id>` command and it will show the latest lines of the specified output like the linux command `tail` does (you can also add `-f` option to keep showing new content). For instance, if you want to check the running job `123.45`, just use next commands:

```
[...]$ condor_tail 123.45 "# Show stdout (normal output on screen)" [...]
$ condor_tail -f 123.45 "# Show stdout, it keeps showing new content" [...]
$ condor_tail -no-stdout -stderr 123.45 "# Show stderr (errors on screen)" [...]
$ condor_tail -no-stdout 123.45 file.out "# Show output file file.out (*)"
```

[- (\*) The output file must be listed in the `transfer_output_files` command in the submit file.-]

B) You can also establish SSH connections to the remote machines where your jobs are being executed, using the command `*condor_ssh_to_job* <job_id>` (again, make sure that the job is running). Once the SSH connection is established, you will be placed in the directory where your program is being run, so you can check input and output files to see whether the program is running properly (you should NOT make any modifications in any file to avoid errors). To open an ssh connection you only need to specify the jobId, see example for job `123.45`:

```
[...]$ condor_ssh_to_job 123.45
```

If you need to upload or download files, you can open an `sftp` connection using flag `-ssh sftp` or you can also use `rsync`, see following examples:

```
[...]$ condor_ssh_to_job -ssh sftp 123.45 [...]
$ rsync -v -e condor_ssh_to_job 123.45:<remote filename> <local directory>
```

**Important:** ~~{close ssh connection when you are not using it}~~. Jobs with open connections cannot leave the queue, so they will appear as `"running"` even if they are already done, waiting till you close the connection.

C) There is a third method, but it is not recommended: the directory where Condor executes jobs is usually located in the scratch, so in most cases it will be directly accessible, you only need to know the name of the machines running your jobs. Use `condor_q -run` to get these names and then access to the working directory located



in `/net/<remote_machine>/scratch/condor/execute/dir_XXXXX` (where "XXXXX" changes in every execution, but it should be easy to recognize due to owner's name). Note that this is the default configuration, but some machines have other configurations and/or you may have no permit to access to those directories.

### 5.3.3 My submitted jobs are always in Idle status, why do they never run (and what about users' priority)?

If your jobs are always in Idle status, it may be caused by several reasons, like restrictions that you have specified in the submit file, a low user's priority, etc. With `condor_q` command you can find out what the reason is, just choose one of your idle jobs and use next commands:

```
condor_q -analyze <job_id> condor_q -better-analyze <job_id>
```

Condor will display then some detailed information about machines that rejected your job (because of your job's requirements or because they are not idle but being used by their owners), machines that could run your job but are busy executing other users' jobs, available machines to run your job if any, etc. It will also display the reason why that job is idle and some suggestions if you have non-suitable requirements.

Check that information and be sure that your requirements can be satisfied by some of the current machines (pay attention to the suggestions, they may help a lot!). For instance, if you ask for slots with more than 6GB of RAM, there are just few of them and they need to be idle to run Condor jobs, so you may need to wait for a long while before running there (also check that there are no impossible values, like asking for machines with 16GB per slot, we have none of them). Before adding a requirement, always check if there are enough slots that satisfy it (for example, to see which slots have more than 6GB of RAM, try next command in your shell: `condor_status -constraint 'Memory > 6144'`. "Please, visit **Condor submit file page** -> **CondorSubmitFile** for more info and examples."

You can also get messages like **Reason for last match failure: insufficient priority**. Bear in mind that Condor executes jobs according to users' priority, so that message means that Condor is right now executing jobs submitted by users with a better priority than yours, so you will still have to wait a bit. You can check yours and other users' priority running `condor_userprio -all -allusers`: all users begin with a priority value of 0.5, the best one possible, and once you begin to run jobs with Condor, it will increase your priority value (that means worse priority) according to the number of machines you are using and the consumed time (the more you use Condor's resources, the faster your priority value will be increased). On the other hand, your priority will be gradually decreased when you are not using Condor.

If your Condor priority is important for you and you want to run some not urgent jobs, you can submit them using `nice_user = True` command in your submit file: those jobs will be run by another user called `nice_user.<your_user>` and they will not affect your real user's priority. But this new user has an extremely low priority, so its jobs can stay in the queue for a long while before being executed (but they can be run very fast if the Condor queue is almost empty).

Besides user's priority, all jobs have also their own priority, and you can change it to specify whether some jobs are more important than others so they should be executed first (please, **check this FAQ** -> **#priority**).

### 5.3.4 Condor have problems with input and/or output files... are my paths wrong?

If Condor is not able to find your input files, probably your jobs will get the "on hold" status (see **this FAQ** -> **#held**). It is not needed to place your input files in any special location, but you need to specify the path to each file (it could be absolute or relative to the directory where you will do the submission) and make sure that the path is correct and you have access permits. Check **this FAQ** -> **#inputs** to see which commands you can use to specify the input files.

On the other hand, you also have to specify the output files that will be generated by your program so Condor can copy them from the remote machines to your computer. Check **this FAQ** -> **#outputs** to see which commands you can use for this purpose.

### 5.3.5 My jobs are 'on hold' status and never finish, what does it mean?

When there is an error, jobs change their state to "on hold". It means that Condor is expecting an action from the user to continue with those jobs. Most times the reason to hold jobs are related to permissions or missing files. A common problem is to specify files that cannot be accessed from other machines, like those in your home or desktop directories (use Condor commands to copy files instead), or the destination directory for output files does not exist or is not reachable, etc. You can check all your held jobs and the reason for that running next command in your shell: `condor_q -hold`. Once you have fixed the problems, run command `condor_release -all` and Condor will check all held jobs again and change their status accordingly.

### 5.3.6 Condor is copying unwanted files to my machine, how can I avoid that?

By default, Condor will copy all files generated or modified by your application that are located in the same directory where your program was executed on the remote machine, what could include some unwanted content like temporary files, etc. If you want to avoid that, then you can use the `transfer_output_files` command (see **this FAQ** -> **#outputs**) to specify which files and/or directories you want that Condor copies from the remote machine to your machine once your application has finished (then Condor will copy **only** those files and ignore all remaining ones).

If you only want to get the output file from the screen (using `output` command), but not any other generated or modified file, you can use `should_transfer_files = NO` command. That command will deactivate the Condor transfer

mechanism, affecting both your input and output files, so it can be only used when you have none of them. If you want to copy input files, but NOT the output files, then you should use next commands:

```
should_transfer_files = YES +TransferOutput = ""
```

### 5.3.7 Some of my jobs are failing due to wrong inputs, can I fix that problem and then run again only those jobs that failed?

First of all, we strongly recommend you always perform some simple tests before submitting your actual jobs in order to make sure that both your submit file and program work in a proper way: if you are going to submit hundreds of jobs and each job takes several hours to finish, before doing that try with just a few jobs and change the input data in order to let them finish in minutes. Then check the results to see if everything went fine, and if so, then submit your real jobs. Bear in mind that submitting untested files and/or jobs may cause a waste of time and resources if they fail, and also your priority will be worse in following submissions.

Sometimes we discover too late that there were some problems, most times related to the executable and/or the input files. If some of the jobs have run correctly while others have failed, we will try to fix the problems and execute again only those that have failed, to avoid wasting time and resources executing again jobs that worked fine. For the same reason, we should stop as soon as possible all those running (or idle jobs) that will fail. Every submission is different, and it is not possible to give general advice, but next steps should help you (and you can always contact us to study your particular situation):

- **Identify those jobs that failed:** if your queue only contains failing jobs since all correct ones have already finished, then it will be very easy to manage them. But most times you will have different jobs in your queue: correct ones that are running, incorrect ones also running, some of them that are held, others that are idle so we do not know whether they are correct or not, etc. The first thing we have to do is to find an expression to identify all failing jobs. Usually when jobs fail there is a way to recognize them, for example, they have been executing for a very long time (many hours when they only need a few minutes to finish), or very short, or the exit code is not the expected one, etc. Use `condor_q` command to list them with `-constraint` option and an expression, we will give you some tips to find those jobs:

- All held jobs (`JobStatus = 5=`) from Cluster with ID 453 (`ClusterID = 453=`) are not correct. To list them we simply use next command:

```
condor_q -constraint '((JobStatus = 5) && (ClusterID = 453))'
```

- Our jobs need less than 10 minutes to finish, those that are running (`JobStatus = 2=`) for more than 30 minutes (`((CurrentTime - JobStartDate) > 1800)`) are not correct. Then we can list them using next command:

```
condor_q -constraint '((JobStatus == 2) && ((CurrentTime - JobStartDate) > 1800))'
```

- All those idle jobs (`JobStatus = 1=`) that have been running for more than 2 hours (`CumulativeSlotTime > 7200`) are wrong:

```
condor_q -constraint '((JobStatus == 1) && (CumulativeSlotTime > 7200))'
```

Note the difference between "cumulative time" (the sum of the time consumed in different executions if the job have been evicted) and the "consumed time" of the present execution. To see the consumed time of all running jobs you can use `condor_q -run -currentrun` (or use `-cputime` to see the real CPU time consumed without being suspended), and you can also use `condor_ssh_to_job` to connect and see what is happening (check [this FAQ](#) -> `#ssh`).

- Jobs have many other attributes that can be used in the constraints, just choose a incorrect job (for example job with ID XXX.YYY) and run `condor_q -long XXX.YYY` to get all attributes of that job. Then try to find which attributes can be used to identify all wrong jobs. All valid `JobStatus` could be displayed using shell command: `condor_q -help status`

- **Stop all failing jobs and run them again with correct data:** Once you have all your failing jobs listed and the problem with input is fixed, we will try to stop those wrong jobs and re-execute them with the right data. There are two situations, depending on how you solved the problem:

- "Situation A: to solve the problem you only need to correct the executable and/or the input files, but the submit files was NOT changed." This is the easiest situation, you have to be sure that the new input files are in the same location that they were previously and exactly with the same names. Then you only need to hold all those wrong jobs and release them again, so the new executable and input files will be copied. To do it, use the same expression you had before to list the jobs, but change command to `condor_hold`:

```
condor_q -constraint '(XXX)' "List all failing jobs, XXX is the expression to identify them"
condor_hold -constraint '(XXX)' "Hold all failing jobs"
condor_release -all "Execute again all held jobs (we assume that all held jobs are those failing," "if not, just find and use a -constraint expression)"
```

And that should be all, now all released jobs will have the correct input files, so executions should go fine.

- "Situation B: to solve the problem you need to change the submit file". Sometimes we cannot avoid changing the submit file because we have to modify the commands to add or remove input files, change the arguments, etc. In those situations, holding and releasing failing jobs will not work because the submit file is only processed at the submission time. Then we need to use `*condor_qedit*` (see [this FAQ](#) -> `#chsubmit`) to change the values of the attributes specified in the submit file; or you can also remove the wrong jobs and

submit them again. For the last option, simply follow next steps (we are assuming here that all jobs belong to the same Cluster, if you have done several submission, then you will have to repeat these steps several times):

- \* Get the list of Process ID of all failing jobs (use the same expression (XXX) that you get in the first step):  
`condor_q -constraint '(XXX)' -format "%d," ProcID`  
 For example, assume that the output of the last command is 0,4,67,89,245,
- \* Remove all those failing jobs: `condor_rm -constraint '(XXX)'`
- \* Change your submit file as needed and add next command to only execute the failing jobs  
`noop_job = !=*stringListMember=("$ (Process)", "0,4,67,89,245")`  
 Important!! When re-submitting, output, log, and error files of ALL jobs (even those correct ones) may be overwritten, so save the old ones if they are important.
- \* Submit again.  
`condor_submit your_submit_file`
- \* Jobs that are not in the `noop_job` list will not be executed, but they may stay in the queue with **Complete** status, use next command to remove them from the queue (read **this FAQ** -> **#repeat** for more info)  
`condor_rm -constraint 'JobStatus == 4'`

As you can see, the steps to follow strongly depend on each particular problem, so it might be easier if you just come to our office.

### 5.3.8 Some of my jobs randomly fail (or I know they will fail in some specific machines)... how can I prevent that?

If you see that some of your jobs fail with apparently no reasons, but they properly run when resubmitted, the problem might not be in your program, but on the machine(s) where they were executed (for example, an application or library that is used by your program is not installed on those machines, or its version is too old/new, or it is misconfigured, etc.). To detect this, simply check the machine where the failing job was executed, which is written in your condor log file, though it is easier to check it using the `condor_history` command. For instance, to check where job XXX.YYY was run, launch next command in the {~~same machine~~} where you did the submission:

```
[...]$ condor_history XXX.YYY -af LastRemoteHost
```

Maybe some of your jobs finished with no problems, but others finished abnormally soon. You can use `condor_history` to get a list of those jobs. For instance, suppose that you have submitted some jobs with `clusterId=XXX` and each job needs at least 30 minutes to properly finish, so you are sure that those that lasted less than 10 minutes (600 seconds) failed. Then you can use next commands to get those jobs (first command will give you a list of the jobs that failed and the second one will show two lines for each of them, the first line is where the jobs was executed on and the second line is the `procId` of the job):

```
[...]$ condor_history -constraint '((ClusterId==XXX) && ((CompletionDate-JobStartDate) < 600))' [...]$ condor_history -constraint '((ClusterId==XXX) && ((CompletionDate-JobStartDate) < 600))' -af ProcId LastRemoteHost
```

Most times these problems are simply solved by forcing these failing jobs to go again into the queue after an unsuccessful execution to be re-executed (see last paragraph). If you see that all jobs that failed were executed on the same machine(s) or you already know that your application is not able to run on some machines, then you can force Condor to avoid sending your jobs to those machines. For instance, suppose that your jobs have problems in machines with names "agora", "lapiz" and "madera" and you want to avoid them. Then, add either of the next lines (both are equivalent) to your Condor submit file (if you had some previous requirements, append the new ones to them):

```
requirements = ((UtsnameNodename ! "agora") && (UtsnameNodename ! "lapiz") && (UtsnameNodename ! "madera")) requirements = !=*stringListMember=(UtsnameNodename, "agora,lapiz,madera")
```

You can also block all machines that satisfy a pattern. For instance, to avoid executing your jobs in those machines with names beginning with "a", "l" and "m", add next lines (you can specify more complex patterns using the \*predefined functions and macros -> [http://research.cs.wisc.edu/htcondor/manual/v8.6/4\\_1HTCondor\\_s\\_ClassAd.html#SECTION00512400000000000000](http://research.cs.wisc.edu/htcondor/manual/v8.6/4_1HTCondor_s_ClassAd.html#SECTION00512400000000000000)):

```
letter = substr=(toLower(Target.Machine),0,1) =requirements = !=*stringListMember=($(letter), "a,l,m")
```

On the opposite situation, if your application can ONLY run on those machines, then you only need to negate the previous expressions (or remove the negation):

```
requirements = ((UtsnameNodename = "agora") || (UtsnameNodename = "lapiz") || (UtsnameNodename = "madera")) =requirements = =stringListMember=(UtsnameNodename, "agora,lapiz,madera")... letter = substr=(toLower(Target.Machine),0,1) =requirements = =stringListMember=($(letter), "a,l,m")
```

Then you should execute again only {~~those jobs that failed~~} (check **this FAQ** -> **#repeat** to see how). Please, do not execute again all your jobs to avoid wasting time and resources. If your program could fail and never end (for example, for some sets of data it never converges), you can use utilities like linux command `timeout` to limit the time it can be running. Failing machines can cause a problem called **black hole** that could produce that most of your jobs fail. Please, visit **Condor submit file section** -> **CondorHowTo#howto~~failing~~** for more info and examples to avoid that. In this section we also describe some Condor commands that you can add in your submit file to deal with failing machines, like `on_exit_hold` and `on_exit_remove`. For instance, using these commands you can specify that any job that finishes with a non valid exit code and/or before X minutes, has to be held or sent to the queue again to be re-executed, respectively. Some examples (before using these commands, make sure that the problem is on remote machines and not on your code in order to avoid re-executing failing jobs):

[`-#` Held jobs if they finished in less than 10 minutes. Later we can check what was wrong with those jobs and re-execute again them-] [`-#` using `condor_release` (we can also use `periodic_release` to automatically release held jobs every X minutes)-] `on_exit_hold = ((CurrentTime - JobStartDate) < (10 * 60))`

[`-#` Remove from the queue only those jobs that finished after 10 or more minutes. If a job finished before that period of time,-] [`-#` it will be sent again to the queue with 'Idle' status to be re-executed (most probably on a different machine)-] `on_exit_remove = ((CurrentTime - JobStartDate) > (10 * 60))`

### 5.3.9 I want to repeat (resubmit) ONLY some of my jobs, is that possible?

If you submit a large number of jobs and for any reason some of them fail and leave the queue, you should not waste time and resources running again all of them, just try with those that failed (after solving the problems they had). Unfortunately there is **not** a `condor_resubmit` command to easily resubmit jobs that have already left the queue. You could try to obtain the "ClassAd" of those jobs using `condor_history -l <job.id>`, but Condor will not accept it as input when using `condor_submit`.

If there are just a few jobs to resubmit, you could try to add pairs of `arguments` and `queue` commands to execute only those jobs, but there is an easier way to do it using `noop_job` command. For instance, suppose you want to repeat jobs with Process ID 0, 4, 9, 14 and those from 24 to 32. Then, add next line to your submit file and submit it again:

```
noop_job = *(( stringListMember="$(Process)", "0,4,9,14") || (($(Process) > 24) && $(Process) <= 32)) )
```

Condor will **not** run jobs where that expression is `True`, so only jobs in the list will be executed. Note that we have added an exclamation mark symbol (`!!`) before your expression to change its value: `noop_job = *((...)`. When using `noop_job`, Condor will still create output and error files for all jobs, but they will be empty for those jobs that will not be executed (be careful to avoid that new executions overwrite output files of previous ones).

Jobs that are not executed may stay in the queue with `Complete` status (when using `condor_q` you will see that `ST` column is `C`). To remove all `C` jobs from the queue, try next command in your shell (use the second one to only remove `Complete` jobs that belongs to cluster `XXX`):

```
condor_rm -constraint 'JobStatus = 4' =condor_rm -constraint 'JobStatus = 4 && clusterID = XXX'
```

### 5.3.10 I see that my jobs complete after being running for N+X minutes/hours, when they only need N to finish. Is that normal?

Yes, it is normal. Bear in mind that executing a Condor job in a machine is only possible when it is not used by its owner. If Condor detects any user's activity in a machine when executing jobs, they will be suspended or moved to another machines, increasing the consumed time (and that may happens several times, so the extra time could be quite long).

Condor has several ways to show the time that jobs have been running. If you use `condor_q`, the time showed is the cumulative one by default (the result of adding the time consumed in all executions), so it could be really high if the job has been killed and restarted several times. If you use `-currentrun` option, then Condor will only display the time consumed in the current execution, which is a more realistic time (although if the job has been suspended, that time is also included). You can also use `-cputime` option to get only the CPU time (but if the job is currently running, time accumulated during the current run is not shown).

If your jobs finish in a reasonable amount of time, everything is fine. If they never finish or need an excessive amount of time to complete, you will have to modify the application to create checkpoints.

### 5.3.11 I have submitted jobs that need some hours to finish. They have been running for days and just few have finished... what is happening?

First of all, check that your program is properly running. Maybe there are some problems with the data, input files, etc. You can open a shell and check the running job using the `condor_ssh_to_job` command (see [this FAQ -> ##ssh](#)). If you discover that there are some problems with your job and it will not produce valid results, you should stop it as soon as possible to avoid wasting more time and resources, see [this FAQ -> ##badinputs](#) for more details. If your job is working fine, maybe your job has been killed and restarted several times. Condor shows the "cumulative running time" by default, you can see the consumed time of the present execution using `condor_q -run -currentrun` command.

The reason why Condor kill and restart jobs is that it has several runtime environments called "universes". By default, all your jobs will go to the most basic (also the simplest) one called `vanilla` universe. In that universe, when Condor detects that a machine is not idle anymore, it will suspend all running jobs for a while, waiting the machine to get idle again. If that does not happen in a given (short) time interval, then Condor will kill all jobs and send them again to the queue with "Idle" status, so those jobs will start from the beginning. If your jobs need some hours to finish, probably some of them will be killed before their completion and restarted in other machines, that could happen even several times.

However, most times we can solve this problem simply changing the arguments of our jobs. For instance, suppose you have to process 10,000 inputs and each input needs about 2 minutes to be done. You can create 100 jobs to process 100 inputs each, but they will need more than 3 hours to finish and it is likely they will be killed several times. It is better to choose faster jobs that can be finished in about 15-30 minutes so they will have more possibilities to be processed on the same machine without being killed and restarted on other machines. If you choose that each job works with 10 inputs, then you will have 1000 jobs and they will need about 20 minutes to finish, that could be a good approach.

### 5.3.12 Some of my python programs work fine, but other fail...

If you are executing python programs with HTCondor and some jobs work fine and other fail, most probably you are experiencing problems related to the version of Fedora. Most of the old Linux Desktop PCs have installed Fedora21, but newer machines have a more recent version, mostly Fedora26 (although we also have a few with Fedora25). Paths to python libraries are different on the old and new machines, therefore your programs will only work properly on those machines that have the same Fedora version as the machine where you have submitted the jobs.

To fix this issue, you can force HTCondor to only execute jobs on machines with your same version of Fedora, then your environment variables and paths will work. For instance, if you are working on a machine with Fedora21, add the next requirement to force that all your jobs will be executed on machines running Fedora21:

```
*requirements* = (*OpSysMajorVer* = 21)=
```

But adding that requirement will limit the number of available machines to execute your program: if you only run on machines with Fedora21, you will be missing all new and faster machines, and if you only run on machines with Fedora26, then you will be losing a big amount of slots since still most of the machines run Fedora21. We recommend you change a bit your submit script to be able to run your python programs on all machines, independently of their O.S (we will only avoid the few machines beginning with 'f', since they have a special purpose and python installation there is not the usual one):

```
... transfer_input_files = your_program.py
getenv = True environment = "PYTHONPATH=/usr/pkg/python/python2.7/lib/python2.7/site-packages" requirements
= (*!=stringListMember=(substr=(ToLower=(Target.Machine),0,1), "f"))
transfer_executable = False executable = /usr/bin/env arguments = python your_program.py
queue ...
```

Example above is just a basic one, you might need to adapt it adding some other commands to transfer your input/output files, add requirements, etc., and, of course, all common commands (see **common template** -> **HOWTOs.CondorSubmitFile**). Contact us if you have any doubts.

### 5.3.13 I receive an error when running HTCondor jobs that use python and matplotlib...

If you are running some python jobs that use matplotlib (for example, to make some plots and save them to png images) and receive errors like:

- no display name and no \$DISPLAY environment variable
- : cannot connect to X server :0

it might be caused because matplotlib (and/or some other packages) needs a DISPLAY environment variable, which means you have to execute it in a X server, and that is not available when running on HTCondor. In this case, simply use another background that does not need a X server, like Agg. For instance, you can adapt next python code when using matplotlib:

```
import matplotlib as mpl mpl.use('Agg') import matplotlib.pyplot as plt
"# Now use plt as usual" "... "fig = plt.figure()" "... "fig.savefig('image.png')"
```

You can find more info about this issue **here** -> <http://stackoverflow.com/questions/4931376/generating-matplotlib-graphs>

### 5.3.14 I would like to get more information about the execution, is there an easy way to see the logs created by Condor?

Yes, there are several possibilities for that. The first step is to create the "condor log file" adding the next command to your submit file:

```
log = file.log "#(we recommend you use your_executable_name.$(Cluster).log as name for your log file)"
```

Once you have your condor log file, you can display the information using the following options:

- Directly check the content of the condor log file with any text editor (not recommended)
- Use `condor_userlog <file.log>` to get a summary of the execution.
- Run `condor_history -userlog <file.log>` command in your shell to list basic information contained in the log file.
- Use `condor_logview <file.log>` to open the "Condor log viewer" and see more detailed information in graphical mode, showing the timeline of your jobs and allowing you to perform zooms, filter jobs, etc.
- There is also an online tool to analyze your log files and get more information: "Condor Log Analyzer" (<http://condorlog.cse.nd.edu/>).

If you just want some general information about Condor queue, the pool of machines, where jobs have been executed on, etc., you can also try our online stats about Condor: [http://carlota:81/condor\\_stats/](http://carlota:81/condor_stats/) and **nectarino** -> <http://nectarino/>.

## 5.4 Special needs

### 5.4.1 I am running many jobs, but some are more important than others, how can I prioritize them?

You can prioritize your jobs (and only your jobs, not other users' jobs) using `priority = <value>` command in your submit files (the higher value, the better priority). Once you have submitted your jobs, you can check or modify their priority by running `condor_prio` in a console. Please, check **Condor submit file page** -> **CondorHowTo#howto<sub>priority</sub>** to see more examples, and also **this FAQ** -> **#idle** for more info about users' priorities.

### 5.4.2 I am receiving hundreds of emails from Condor, can I stop that?

Yes, by default Condor send an email notifying any event related to each job (termination, errors, etc.). If you launch 1000 jobs, that could be really annoying. To avoid that, use next command in your submit file: `notification = Never` (use `Complete` if you only want to know when they finish, `Error` when they fail or `Always` to receive all notifications; we recommend you use `Error`). Also you can change the email address using `notify_user = <email>`.

"Please, visit **Condor submit file page** -> **CondorSubmitFile** for more info and examples."

### 5.4.3 What happens with my IDL or Matlab jobs that require licences to run?

There is a limited number of IDL licences, so if you try to run a large number of IDL jobs they could fail since there may not be enough licences. But using IDL Virtual Machine does not consume any licence, so there will not be limit in the number of simultaneous IDL running jobs, just the number of available slots. See **detailed information here** -> **CondorAndIDLVirtualMachine**.

There is a similar limitation with Matlab licences, that could be saved if it is possible for you to create Matlab executables using the **Matlab Compiler** -> <http://www.mathworks.es/products/compiler/>. You have more info about this topic **here** -> <https://htcondor-wiki.cs.wisc.edu/index.cgi/wiki?p=HowToRunMatlab>.

### 5.4.4 I need to run some commands or scripts before/after my executable, is that possible?

Yes, it is possible adding the `+PreCmd` and `+PostCmd` commands to your submit file, respectively. Running scripts before/after jobs could be useful if you need to do some operations in your input or output files, like changing their names, moving or copying them to other locations, etc. Also you can use these commands for debugging purposes, like using the shell command `tree` to check where your input/output are placed:

```
+PreCmd = "preScript.sh" +PreArguments = "-iv" +PostCmd = "tree" +PostArguments = "-o tree.out"
should_transfer_files = YES transfer_input_files = preScript.sh, /usr/bin/tree
```

Generally, you also have to add or update the `transfer_input_files` command to include your scripts in the list of files to be copied to the remote machines (make sure that command `should_transfer_files = YES` is present, too). These commands are intended to be used with user's scripts. If you want to run shell commands (like `tree` in the example), you have to transfer that command (use `which <cmd>` to know its location).

### 5.4.5 Is it possible to limit the maximum number of concurrent running jobs?

There are some situations where it could be interesting to limit the number of jobs that can concurrently run. For instance, when your application needs licences to run and few of them are available, or when your jobs access a shared resource (like directly reading/writing files located at `/scratch`, too many concurrent access could produce locks and a considerable slowdown in your and others' computer performance). Please, visit **Condor submit file page** -> **CondorHowTo#howto<sub>limit</sub>** to see details and example about how you can add these limits.

### 5.4.6 I need to do some complex operations in my submit file, is that possible?

Yes, Condor has some **predefined functions** and some **special macros** that you can use in your submit file:

- evaluate expressions: `eval()`, ...
- flow control: `= ifThenElse()`, ...
- manipulate strings : `size()`, `strcat()`, `substr()`, `strcmp()`, ...
- manipulate lists: `stringListSize()`, `stringListSum()`, `stringListMember()`, ...
- manipulate numbers: `round()`, `floor()`, `ceiling()`, `pow()`, ...
- check and modify types: `isReal()`, `isError()`, `int()`, `real()`...
- work with times: `time()`, `formatTime()`, `interval()`, ...
- random: `random()`, `$RANDOM_CHOICE()`, `$RANDOM_INTEGER()`, ...
- etc.

Check documentation to see the complete list of **predefined functions** -> [http://research.cs.wisc.edu/htcondor/manual/v8.6/4\\_1HTCondor\\_s\\_ClassAd.html#SECTION00512400000000000000](http://research.cs.wisc.edu/htcondor/manual/v8.6/4_1HTCondor_s_ClassAd.html#SECTION00512400000000000000), and also the **function and pre-defined macros** -> [http://research.cs.wisc.edu/htcondor/manual/v8.6/3\\_5Configuration\\_Macros.html#SECTION00451800000000000000](http://research.cs.wisc.edu/htcondor/manual/v8.6/3_5Configuration_Macros.html#SECTION00451800000000000000)

#### 5.4.7 I would like to submit my jobs now, but they should run at a programmed time, can I do that?

Sometimes it might be interesting to run your jobs at a specific time, maybe your application depends on some data that are automatically generated at a given time and you want to run your jobs after that moment. Or you want to submit your jobs now, but for any reason they have to run in X hours from the submission time, or you want to regularly run the some jobs several times every day, or every week. . . Condor has several commands to deal with these situations, please, visit **Condor submit file page -> CondorHowTo#howto<sub>runtime</sub>** to see details and examples about how you can specify that jobs begin at a programmed time, and also how to program periodical programmed executions.

#### 5.4.8 Jobs leave the queue after finishing. If something went wrong... could they be held or automatically re-executed instead?

By default all your jobs will leave the queue after completion. But it could happen that some of your jobs get "complete" status because they failed (for instance, they could fail due to bad inputs, or there is a missing software package in an specific machine, etc., see also **#blackholes | this FAQ**). If that happens and you are able to detect it, you can force that they stay in the queue with 'on hold' status or get the 'Idle' status so they will be executed again. You can control which jobs you want to change the status according to their execution time (if it is abnormally short or long), their exit code, etc. Use **on\_exit\_hold** command to change its state to "'on hold'"; or **on\_exit\_remove** command to re-execute the job (it will get the "Idle" status again), adding a reason and/or subcode if you want to do that. Please, visit **Condor submit file section -> CondorHowTo#howto<sub>failing</sub>** to get detailed info and examples about this feature.

#### 5.4.9 I have a fault tolerant application, can I save the state and restore it when executing with Condor?

Yes, Condor allows you to use your fault tolerant programs. You only need to use next command to specify that Condor has to save files when your program fails or Condor needs to evict it:

```
when_to_transfer_output = ONEXITOREVICT
```

You have more information in the Condor manual: "The **ON\_EXIT\_OR\_EVICT** option is intended for fault tolerant jobs which periodically save their own state and can restart where they left off. In this case, files are spooled to the submit machine any time the job leaves a remote site, either because it exited on its own, or was evicted by the HTCondor system for any reason prior to job completion. The files spooled back are placed in a directory defined by the value of the **SPOOL** configuration variable. Any output files transferred back to the submit machine are automatically sent back out again as input files if the job restarts."

#### 5.4.10 My jobs have some dependencies, is it possible to specify that?

Yes, if you have some dependencies in your inputs, outputs or execution order, you can specify it using a "directed acyclic graph (DAG)". Condor has a manager (called [http://research.cs.wisc.edu/htcondor/manual/v8.6/2\\_10DAGMan\\_Applications.html](http://research.cs.wisc.edu/htcondor/manual/v8.6/2_10DAGMan_Applications.html) | **DAGMan**) to deal with these jobs, but you must use special commands, like submitting your jobs with **condor\_submit\_dag**. Please, visit **Condor submit file page -> CondorHowTo#howto<sub>dagman</sub>** for more info and examples.

### 5.5 More info

#### 5.5.1 My question is not in this list or I need further information, where can I find it?

There are more **FAQs and How-to recipes** -> <https://htcondor-wiki.cs.wisc.edu/index.cgi/wiki?p=HowToAdminRecipes> available at Condor site and the **official Users' Manual** -> [http://research.cs.wisc.edu/htcondor/manual/v8.6/2\\_Users\\_Manual.html](http://research.cs.wisc.edu/htcondor/manual/v8.6/2_Users_Manual.html) is useful, too. Also you can visit other sections of Condor at the SIEpedia, like **useful commands** -> **CondorUsefulCommands** or **Submit files** -> **CondorSubmitFile**. If you need further information, please, contact us (you can find **here** -> **Condor#contact** our contact data).

## 6 HTCondor and IDL

A recurring question to us has been whether IDL jobs can be run with HTCondor. The **use of IDL with HTCondor is limited by the number of available licenses** at any given time (which meant that perhaps you could run 20-30 jobs simultaneously). However, we strongly recommend you use the **IDL Virtual Machine (IDL VM)** when possible since it lets you run an IDL "executable" file (SAVE file) **without the need for licenses**, so there will be no limits on the number of jobs you can concurrently run. Most of you probably know the necessary steps to create a **SAVE** file, but if in doubt see \* [http://www.exelisvis.com/docs/Creating\\_SAVE\\_Files\\_of\\_P.html](http://www.exelisvis.com/docs/Creating_SAVE_Files_of_P.html) | here\* for an example on how to create such a file.

The problem is that the IDL Virtual Machine is meant to be run interactively in a server with X running and HTCondor is not particularly well suited for this. But you can manage it with a little ingenuity. Ángel de Vicente developed a little program some years ago to take care of all the details and overall it works without any problems, and now we can submit hundreds of IDL jobs simultaneously to our HTCondor pool! Read on for all the details. . .

**Note:** If for any reason you are **not able** to generate a **SAVE** file, please, **contact us** -> **Condor#contact** and we will help you to find other ways of executing IDL with HTCondor. Remember that running jobs in IDL with no Virtual

Machine consumes licences and you must **limit the number of concurrent jobs** -> `CondorSubmitFile#howto` limit using a command like `concurrency_limits = idl:40`

## 6.1 Submitting a job to HTCondor using the IDL Virtual Machine (for the impatient)

All you will need to do in order to run your IDL jobs with the Virtual Machine is:

- Modify your IDL program so that it will take an argument (from 0 to the number of jobs you want to submit with HTCondor) and act according to that argument. A sample IDL program to illustrate this could be the following one (we will name it `subs.pro`):

```
PRO SUBS
args = command_line_args()
print, 'Original argument ', args(0) print, 'Modified ', args(0)*2
print, 'Wasting ', args(0), ' seconds' wait, args(0)
print, 'I (IDL) have finished...' END
```

- Create a `SAVE` file from it. Usually you just need to compile your program and generate the `SAVE` file with your compiled routines. The name of the `SAVE` file has to be the same as the routine you want to execute. If you have any issue creating this file, please, check \* [http://www.exelisvis.com/docs/Creating\\_SAVE\\_Files\\_of\\_P.html](http://www.exelisvis.com/docs/Creating_SAVE_Files_of_P.html) | more information and examples\*):

```
[...]$ idl IDL> .FULL_RESET_SESSION IDL> .COMPILE subs.pro IDL> RESOLVE_ALL IDL> SAVE, /ROUTINES,
FILENAME='subs.sav' IDL> exit [...]$
```

- Verify that this works with the IDL Virtual Machine without HTCondor (the IDL Virtual Machine will show you a Splash screen, where you will have to press the button "Click to Continue", and which then will proceed with the execution of the program).

```
[...]$ idl -vm=subs.sav -args 10 IDL Version 8.3 (linux x86_64 m64). (c) 2013, Exelis Visual Information Solutions, Inc.
```

```
Original argument 10 Modified 20 Wasting 10 seconds I (IDL) have finished... [...]$
```

- Write the HTCondor submit file. If you are new to HTCondor, you might need to look our \* documentation about submit files -> <http://research.iac.es/sieinvens/siepedia/pmwiki.php?n=HOWTOs.CondorSubmitFile>\* (check also other sections like **Introduction** -> <http://research.iac.es/sieinvens/siepedia/pmwiki.php?n=HOWTOs.Condor>, \*Useful commands -> <http://research.iac.es/sieinvens/siepedia/pmwiki.php?n=HOWTOs.CondorUsefulCommands>\* or **FAQs** -> <http://research.iac.es/sieinvens/siepedia/pmwiki.php?n=HOWTOs.CondorFAQs>). In the following example you will need to modify:

- The arguments line, which has 4 items: the first one is the path to the `SAVE` file; the second one is the argument to pass to it; the third one is 1 if you use a left-handed mouse, and 0 otherwise; and the fourth one is 1 if you want verbose messages for debugging, or 0 otherwise)
- NOTE: leave the line `"next_job_start_delay = 1"`  
`N = 20 ID = $(Cluster).$(Process) FNAME = idlvm Universe = vanilla Notification = error should_transfer_files = YES when_to_transfer_output = ON_EXIT`  
`output = $(FNAME).$(ID).out error = $(FNAME).$(ID).err Log = $(FNAME).$(Cluster).log`  
`transfer_input_files = subs.sav "#Use next command when specific output files has to be copied back to your machine:" "#=transferoutput_files = " Executable = /home/condor/SIE/idlvmwithcondor.sh arguments = subs.sav $(Process) 0 1`  
`next_job_start_delay = 1 queue $(N)`

- Submit it to HTCondor and go for a cup of coffee while the programs are executed...

**[-Note: Why some of my jobs get the "on hold" status?]**

[-When executing jobs with the IDL VM, it could happen that some jobs get the "on hold" status. That means some problems occurred with your jobs and HTCondor is waiting that you solve them before continuing with the execution. You can use `condor_q -hold` command to get more info about the reason why they were held. If there is no apparent cause and you are sure that your jobs are correct, the problem might be related to the initialization of the IDL Virtual Machine: sometimes this process takes longer than usual on some specific machines, and if in the meanwhile more jobs try to initialize other IDL VM on the same machine, some of them could fail and your jobs will get the "on hold" status. This could randomly happen and there is not an easy way to avoid that.-]

[-If you are 100% sure that your program runs fine and the problem is caused by IDL, then you can use `condor_release -all` command and all your held jobs will get the idle status again so they will hopefully run with no problems on other machines. If some of your jobs fail again, you may need to repeat the `condor_release` command several times till all the jobs are done. If that happens too many times, you can use some commands to perform recurring releases: for instance, you can add a `periodic_release` command in your submit file (see this **example** -> [CondorSubmitFile#howto](#)<sub>failing</sub>) and HTCondor will periodically release your held jobs, or you can use a combination of `condor_release` and some shell commands like `crontab`, `watch`, etc.-]

[-On the other hand, if after releasing jobs they get the "on hold" state again, then the problem might not be related to IDL and you should check your application to find the error (remember that you can get more information about held jobs using `condor_q -hold`)-]



## 6.2 How is it all done?

All the real work to avoid having to press the "Click to continue" button in all the virtual machines is done by the alpha-version `idlvwithcondor.sh` script. This script makes use of: <http://en.wikipedia.org/wiki/Xvfb> | **Xvfb** to create a virtual X11 server where the IDL splash screen will be created (but without showing anything in the screen); and <http://hoopajoo.net/projects/xautomation.html> | **xautomation** to automatically press the button for you. The script has to take care of two important things: how to create several virtual X servers on multicore machines without conflicting with each other; and how to cleanly kill all processes when HTCondor wants to reclaim the machine for its "owner" before the IDL code has finished. The script is still work in progress (since some things could be performed probably more efficiently), but in its present form seems to work pretty well (let me know if you have any trouble with it). The script is:

```
[@ #!/bin/bash
##### Script to run an IDL executable file (a SAVE file) in the IDL Virtual Machine ##### with HTCondor.
##### Written by Angel de Vicente - 2009/10/26
##### Usage: ##### /home/condor/SIE/idlvwithcondor.sh idlprog argument zurdo verbose #####
Example: ##### /home/condor/SIE/idlvwithcondor.sh /home/angelv/test.sav 10 0 1 ##### will press button
as a right-handed person, and will print messages ##### of its progress, and will also print debugging messages.
XVFBBIN="/home/condor/SIE/Xvfb" XTEBIN="/home/condor/SIE/xte"
## This allows for job control inside the script set -o monitor
## if [ $3 -eq 1 ]; then mousebutton=3 else mousebutton=1 fi
if [ $4 -eq 1 ]; then echo "Running on machine 'uname -a'" fi
## When we do a condorrm or when the job is evicted, a SIGTERM to the executable file ## (i.e., this script is
issued, so we make sure we catch that signal, and then kill the ## virtual X and the IDL Virtual Machine trap cleanup
SIGINT SIGTERM SIGTSTP
function cleanup () { kill %2 if [ $4 -eq 1 ]; then echo "IDL Terminated" fi
sleep 1
kill %1 if [ $4 -eq 1 ]; then echo "Xvfb killed" fi
exit }
## Find free server number
## A cheap way of avoiding two HTCondor processes in the same (multicore) machine to have a race condition
## and ending up with the same server number is to sleep a random number of seconds before trying to find ##
which server number is free ## NOT ROBUST ENOUGH AND A BIT WASTEFUL. SHOULD FIND A BETTER
WAY OF DOING THIS ## ## We comment this out, assuming the submit HTCondor file has nextjobstartdelay = 1
#RANGE=10 #number=$RANDOM #let "number %= $RANGE" #if [ $4 -eq 1 ]; then #echo "Sleeping $number
seconds" #fi #sleep $number
## Find the free number i=1 while [ -f tmp.Xi - lock ]; do i=$((i + 1))
if [ $i -eq 10 ]; then i=1 if [ $4 -eq 1 ]; then echo "No servers available under 10. Waiting 5 minutes..." sleep 300 fi
fi done
$XVFBBIN :$i -screen 0 487x299x16 & sleep 5 export DISPLAY=":$i.0" if [ $4 -eq 1 ]; then echo "Virtual X Server
$i created" fi
idl -vm=$1 -args $2 & sleep 10 if [ $4 -eq 1 ]; then echo "IDL Virtual Machine started" fi
$XTEBIN 'mousemove 394 235' $XTEBIN "mouseclick $mousebutton" if [ $4 -eq 1 ]; then echo "Click to continue
pressed" fi
if [ $4 -eq 1 ]; then echo "Waiting for IDL" fi wait %2
if [ $4 -eq 1 ]; then echo "IDL Finished" fi
sleep 2
kill %1 if [ $4 -eq 1 ]; then echo "Xvfb killed" fi @]
```