An overview of batch processing

01-Jun-2023
One-on-one

Your computer

Your program
One way to speed things up within ROOT: multi-threaded code (RDataFrame, PROOF)
Outside of ROOT, you can have multiple programs on a single computer (UNIX command “at”)

You have to remember not to submit too many jobs or you’ll overload the computer
A batch system managing multiple programs on a single computer (UNIX command “batch”)
A batch system managing multiple programs on multiple computers

Your computer

Batch manager

Batch node

Batch node

Batch node

Batch node

Your program

Your program

Your program

Your program

Your program

Your program

on hold

Your program

Your program

Your program

Your program

Your program

Your program
The standard software for managing batch systems in scientific computing is HTCondor (or just Condor)

Main web page

http://research.cs.wisc.edu/htcondor/

Quick start


Full manual

https://htcondor.readthedocs.io/en/latest/

• Stick to the “vanilla” universe; the “standard” universe won’t work for ROOT or any other particle-physics software (so you don’t need condor_compile).
Condor will halt a queue in favor of an interactive program.
Condor managing multiple programs on multiple computers with multiple configurations
Condor uses “ClassAds” to match your requirements with what each node offers.

Your program

on hold

Your program

Your program

Your program

Your program

Your program

Your program

Submit machine

Condor master

Condor pool

Batch node

Batch node

Batch node

Batch node

Your requirements (job ClassAd)

What a node offers (machine ClassAd)
Resource Planning

- Condor can’t do everything for you.
- Think about input files (including programs) and output files and how they’ll be accessed.
- Think about disk space. “df -h” and “du -shx *” can help.
- Fun fact: The particle-physics Condor pools can’t see your home directory!
- Moral: Let condor transfer your files... when possible.

**Execution environment**

- **input = <input_file>**
  (an input file)
- **should_transfer_files = YES**
  (any other files needed)
- **transfer_input_files = <file1>,...**
  (any other files needed)
- **executable = <my_program>**
  (your program)
- **initial_dir = <directory>**
  (where to look for input files)
  (where output files will be sent)
- **output = <file>.out**
- **error = <file>.err**
- **log = <file>.log**
- **transfer_output_files = <file1>,...**
  (files copied back to initial_dir)
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When you can’t let condor transfer your files, here are disk-sharing methods outside of condor:

• NFS – used at Nevis
• CVMFS – Fermilab and CERN
• Grid, BlueArc – only used at Fermilab
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What we *don’t* do
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Bringing the job to the data

- Some wrapper script
- Submit machine
  - requirements = (machine = node04.nevis.columbia.edu)
- Condor master
  - node01: bigfile1.root
  - node02: bigfile2.root
  - node03: bigfile3.root
  - node04: bigfile4.root
  - node05: bigfile5.root
  - node06: bigfile6.root
Final tips

• Split up your task so each condor job takes 20-60 minutes

• If your job must be preempted, it will have to run from the beginning on the same machine that cancelled the job

• Test your job with one process before submitting it for 10,000 processes!
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Nevis particle-physics condor guide
https://twiki.nevis.columbia.edu/twiki/bin/view/Nevis/Condor

Basic Condor@Nevis tutorial