Using Julia on the Submit cluster

Workshop on Basic Computing Services in the Physics Department

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Research problems requiring extensive computing:

- (1) Exploring exponentially large space of geometries for string theory vacua, by, e.g., (1a) Systematic exploration in complexity parameter, (1b) Monte Carlo approaches
- (2) Dynamics of complex ecological systems related to (2a) discrete stochastic lattice models (complicated non-deterministic CAs), (2b) generalized LV ODE systems with complex structure of equilibria (~ matrix models in glassy regime)

Computational approach:

- Run thousands of CPU-days on Submit condor cluster
- Use Julia as computing language

Note: Have been using the Tier-2/submit system sporadically over the last couple of years. With some help from Zhangqier and Christoph, everything has gone very smoothly!

Julia?

Julia is a relatively new high-performance language for scientific computing, developed in part by folks at MIT (Edelman, etc.)

- High level language, easy to program like python
- Uses "just-in-time" compilation for higher speed, high performance
- Dynamically typed, good interactive interface
- Various libraries coded at low level, compatible with parallel systems
- First use on Tier-2/Submit!

Workflow

0. Files and account based on submit.mit.edu and relatives (submit01, etc.).

```
% ssh -l wati submit.mit.edu
% pwd
/home/submit/wati
% cd example-project
```

- 1. Can use a script to generate submission file $submit_file$ for N separate jobs
- 2. Submission file submitted to condor, each of *N* jobs runs with different inputs, generates different output files
- 3. Move output files to your usual machine, work with data.

A simple example: 1. Julia code

Some Julia code takes various inputs and produces an output file (output)

Simplest option: put all code in a single file

```
dynamics.jl:
# solves dynamics of LV with multiple stable equilibria
# version 3: only a single variance in off-diagonal.
import Pkg
Pkg.add("DifferentialEquations")
using DifferentialEquations
using Random
using LinearAlgebra
# pick a random matrix, with given size, mean for diagonal, off, sigma
# for example, usage: randommatrix(5, 1, 2, 0.1)
function randommatrix(size, dm, om, sd)
a = Matrix(Float64)(undef, size, size)
y = fill!(a, om) + sd*randn((size, size)) + (dm-om)*I
return y
end
```

Single instance of code is invoked by

```
% julia dynamics.jl <parameters>
```

Submission file: Can generate from simple script or (suggested by Qier) have parameters as (integer) functions of process number

submit-dynamics:

```
# Submit description file for dynamics-random-g.jl program
Executable = run-dynamics

Requirements = (BOSCOCluster =!= "t3serv008.mit.edu" && BOSCOCluster =!= "ce03.cmsaf.mit.edu" && BOSCOCluster =!= "ce03.cmsaf.mit.edu
+DESIRED_Sites = "mit_tier3"
Universe
                                                                            = vanilla
                                                                                = True
#Get Env
transfer input files = dynamics-random-q.jl
should transfer files = YES
RequestMemory = 2000
when to transfer output = ON EXIT
Log = dynamics-random-g.log
Arguments = dynamics-random-g.jl 20 0.2 1000 0
transfer output files = dynamics 0.result
                                                                              = dynamics 0.out
Output
Error
                                                                               = dynamics 0.err
Onene
                                                                                   = dynamics-random-q.jl 20 0.4 1000 1
Arguments
transfer output files = dynamics 1.result
                                                                              = dynamics 1.out
Output
Error
                                                                                 = dynamics l.err
Queue
```

Can also use process number in arguments (tip from Qier):

```
Arguments = "dynamics-random-g.jl 20 0.2 1000 $(Process)"
transfer_output_files = dynamics_$(Process).result
...
Oueue 10
```

run-dynamics:

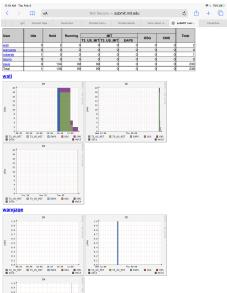
```
#!/bin/bash
# Script to run julia. Likely you have some organizational work to do before you get to the true
# julia command. Here is the place to do it.
# fix problem with loading new packages, as suggested by Qier
export JULIA DEPOT PATH="$PWD/.julia"
# show my running environment
echo ""; echo " ## Environment"
env
# show the directory
echo "": echo " ## Directory"
pwd
echo ""
1.s
# show the arguments
echo ""; echo " ## Arguments"
echo $@
# now let's do what we came for ($@ is just the full set of arguments provided to the run script)
echo ""; echo " ## Julia: julia $@"
julia $@
# let's make sure we name our output correctly
JOBID="${@: -1}" # last value in the command line arguments
echo ""; echo " ## Julia: mv output dynamics ${JOBID}.result"
mv output dynamics ${JOBID}.result
```

Simple example: 3. Running the submission file

Now that we have everything together it's off to the races!

```
% condor submit submit-single-5
Submitting job(s).....
20 job(s) submitted to cluster 378098.
% condor q
-- Schedd: SUBMIT.MIT.EDU : <18.4.134.251:9615?... @ 02/04/21 10:41:47
OWNER
        BATCH NAME
                      SUBMITTED
                                  DONE
                                         RIIN
                                                IDLE TOTAL JOB IDS
wati
        ID: 378098
                     2/4 10:41
                                                         20 378098.0-19
Total for query: 20 jobs; 0 completed, 0 removed, 20 idle, 0 running, 0 held, 0 suspended
Total for wati: 20 jobs; 0 completed, 0 removed, 20 idle, 0 running, 0 held, 0 suspended
Total for all users: 254 jobs: 0 completed, 0 removed, 21 idle, 113 running, 120 held, 0 suspended
% condor a
-- Schedd: SUBMIT.MIT.EDU : <18.4.134.251:9615?... @ 02/04/21 11:01:11
OWNER
        BATCH_NAME
                      SUBMITTED
                                   DONE
                                          RUN
                                                IDLE
                                                       HOLD TOTAL JOB IDS
wati
        ID: 378098 2/4 10:41
                                           18
                                                          2
                                                                20 378098.0-19
Total for query: 20 jobs: 0 completed, 0 removed, 0 idle, 18 running, 2 held, 0 suspended
Total for wati: 20 jobs: 0 completed, 0 removed, 0 idle, 18 running, 2 held, 0 suspended
Total for all users: 254 jobs; 0 completed, 0 removed, 1 idle, 125 running, 128 held, 0 suspended
%!!
condor a
-- Schedd: SUBMIT.MIT.EDU : <18.4.134.251:9615?... @ 02/04/21 13:09:03
OWNER
         BATCH NAME
                      SUBMITTED
                                  DONE
                                                IDLE
                                                       HOLD TOTAL JOB IDS
wati
        ID: 378098 2/4 10:41
                                    18
                                                                20 378098.2-13
Total for query: 2 jobs; 0 completed, 0 removed, 0 idle, 0 running, 2 held, 0 suspended
Total for wati: 2 jobs; 0 completed, 0 removed, 0 idle, 0 running, 2 held, 0 suspended
Total for all users: 98 jobs; 0 completed, 0 removed, 1 idle, 79 running, 18 held, 0 suspended
e,
```

Nice graphical interface to track your jobs: condormon

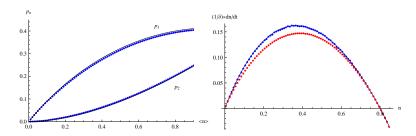


After jobs finish, have separate results/shell output/error files

```
% 1s
base-single
                  single 409.result single 501.out
                                                       single 513.err
generate sub-single
                      single_410.err
                                      single 501.result single 513.out
generate sub-single-1 single 410.out
                                      single 502.err
                                                         single 513.result
generate sub-single-2 single 410.result single 502.out
                                                           single 514.err
generate sub-single-3 single 411.err single 502.result single 514.out
generate sub-single-4 single 411.out
                                      single 503.err
                                                         single 514.result
generate sub-single-5 single 411.result single 503.out
                                                           single 515.err
output-test
                 single 412.err single 503.result single 515.out
run-single
                 single 412.out single 504.err
                                                    single 515.result
single 401.err
                     single 412.result single 504.out
                                                          single 516.err
```

Just move output files to your usual machine, and analyze data!

Results: lots of data \rightarrow good match between "experiment" and theory!



Summary:

- Fairly easy to get up and running, run large jobs
- Works with Julia, familiar linux tools, can remotely mount file system, sshfs submit05.MIT.edu:/home/submit/wati /var/tmp/wati
- Issues encountered (and fixed): Julia/packages only on some systems, selecting memory