

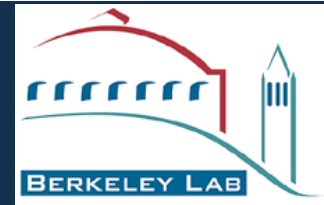
# Progress on bringing High Performance Computing to MAP D&S

Robert Ryne

*LBL*

*Nov 2, 2012*

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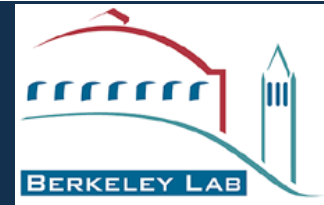


# Bringing High Performance Computing (HPC) to MAP D&S



- Incorporating HPC is an integral part of our D&S plans.
- Enables:
  - inclusion of more realistic physics models
  - running jobs with higher resolution
  - running jobs with higher statistics
  - running medium-scale jobs faster
  - scanning problem parameters (e.g. lattice parameters)
  - faster turn-around for human-driven optimization
  - computer-driven design optimization

Brute force computer power is not a replacement for being innovative. Goal is to use powerful computational tools AND be innovative in order to explore concepts and ultimately develop the best designs for MAP.



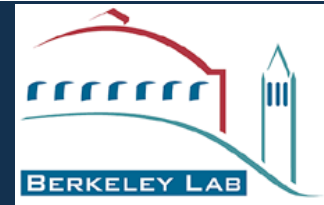
# National Energy Research Scientific Computing Center (NERSC)



- About NERSC\*:
  - the primary computing facility for the DOE Office of Science
  - provides HPC/information/data/communications services for research sponsored by DOE Office of Science
  - Largest system is Hopper, a Cray XE6 with 153,000 compute cores
- A new repository (called “map”) has been set up at NERSC
- A new project directory (/project/projectdirs/map/) enables sharing of data and codes, and a place to work in addition to \$HOME and /scratch/
- We are now using Hopper (hopper.nersc.gov) to perform MAP simulations



\*<http://www.nersc.gov/>



# Obtaining a NERSC account for MAP modeling



First, email me:

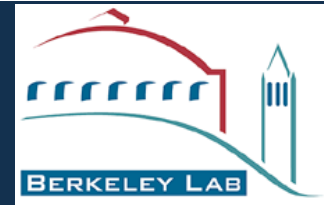
- your name, institution, phone, preferred userid, citizenship

Next, go to

- <http://www.nersc.gov/users/accounts/user-accounts/nersc-computer-use-policies-form/>

Read and sign the form, then upload (preferred) or email or fax the form to NERSC

Accounts are usually set up within 24 hrs



# NERSC “getting-started” notes



## web pages, getting help:

NERSC has excellent web pages: <http://www.nersc.gov>

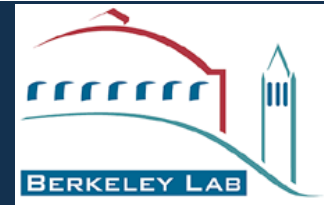
If you need to speak to a consultant, dial 1-800-66NERSC

## To login:

```
ssh -Y hopper.nersc.gov -l youruserid  
<enter your password>
```

**To move files from a remote computer** (such as your laptop or personal computer) using a Terminal window:

```
scp filename your_user_id@hopper.nersc.gov:.  
<enter your password>
```



# NERSC “getting-started” notes



## **To compile:**

The fortran compiler is invoked via "ftn" and the C compiler is invoked using "cc"

See "Compiling Code" at [www.nersc.gov/users/getting-started/](http://www.nersc.gov/users/getting-started/)  
The default fortran compiler is PGI

## **Modules:**

For detailed info see "Modules" in the middle of the page at <http://www.nersc.gov/users/getting-started/>

Here are the basics:

To see what is loaded, type  
module list

To see what is available, type  
module avail



# NERSC “getting-started” notes



## Submitting batch jobs:

```
qsub your_batch_script_file_name
```

Following the qsub command, you will see the jobid that is assigned to it

## Monitoring jobs:

```
qs -u your_user_id
```

## To kill an already submitted job:

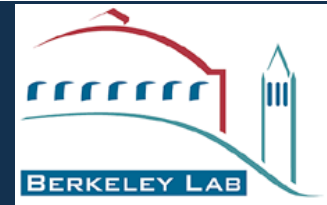
```
qdel your_job_id
```

## Sample batch script:

```
#PBS -q debug
#PBS -A map
#PBS -l mppwidth=512
#PBS -l
walltime=00:30:00
cd $PBS_O_WORKDIR
aprun -n 512 ./icool.x
```

## Interactive jobs:

[www.nersc.gov/users/computational-systems/hopper/running-jobs/interactive-jobs/](http://www.nersc.gov/users/computational-systems/hopper/running-jobs/interactive-jobs/)

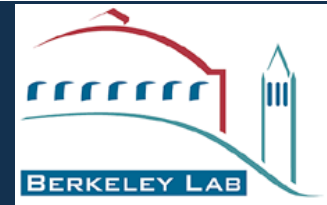


# MAP project directory



- /project/projectdirs/map/
- map/
  - Archives/
  - Baseline/
  - Benchmarks/
  - Codes/
  - Geant4Data
  - Users/
- Baseline/
  - ProtonDriver/
  - FrontEnd/
  - Cooling/
  - AccStorage/
  - Collider/
- Codes/
  - icool330/
  - icool331a
  - icool\_warp/
  - ScanParams/
  - Warp\_input/
  - ...
- Users/
  - diktys/
  - hsayed/
  - ryne/
  - tjrob/
  - ...



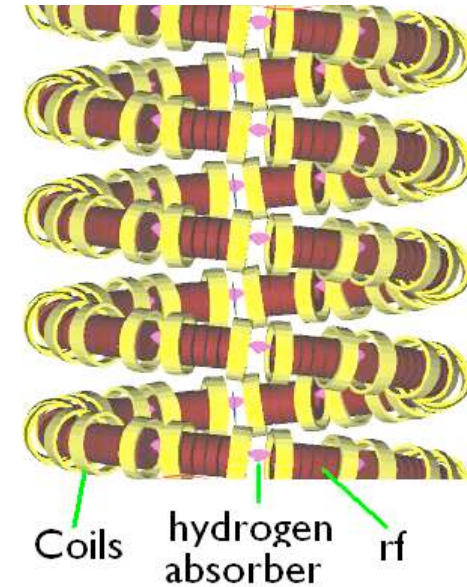
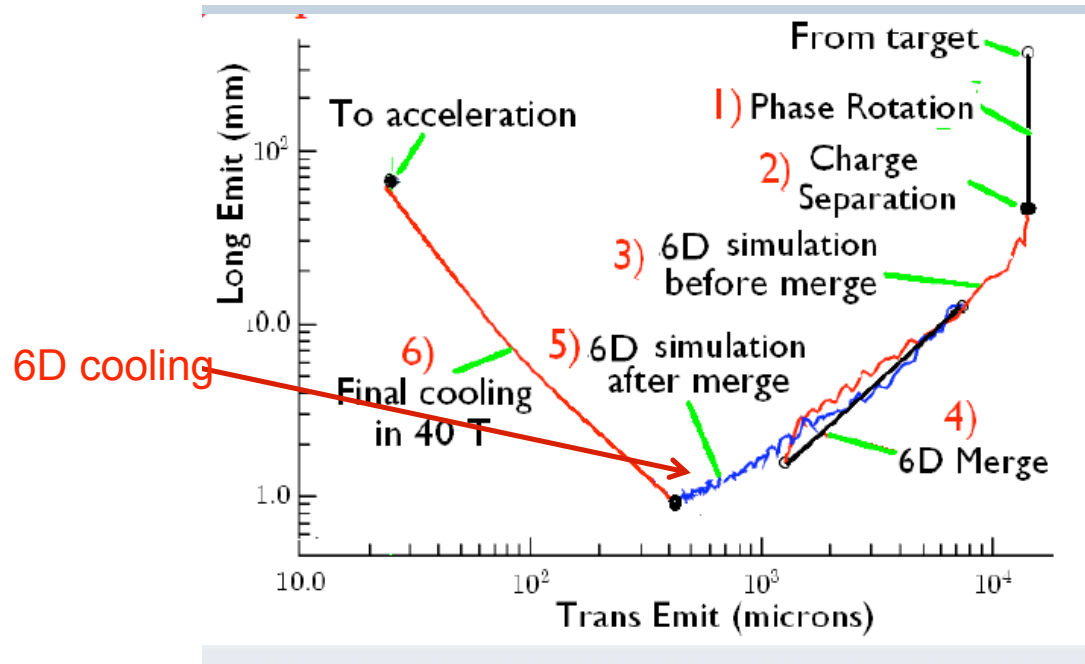


# Accomplishments

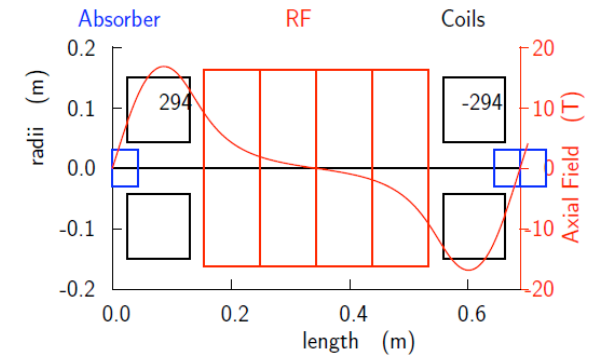
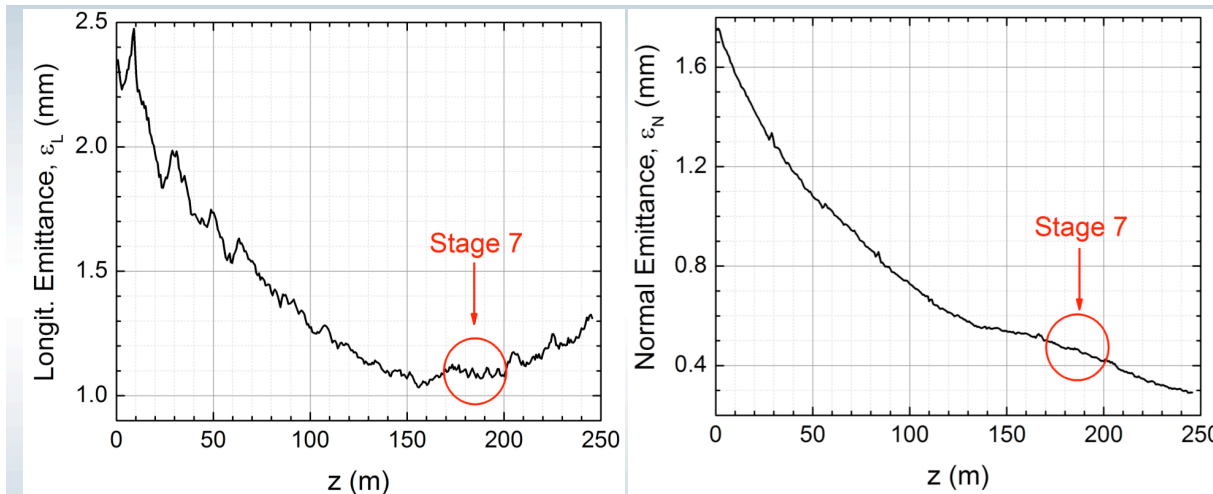


- Serial version of ICOOL 3.31 installed
- Parallel version of G4BL installed
  - major performance improvements achieved (see Tom Roberts talk)
- Developed scripts to perform parallel parameter scans
- Archived previous NF and MC designs
- Extracted ICOOL beam-material interaction (BMI) routines
- Incorporated BMI routines in Warp
- ICOOL Front-End simulations underway
- Warp cooling simulations w/ space charge underway

# Simulation of 6D cooling with space charge (D. Stratakis, D. Grote)

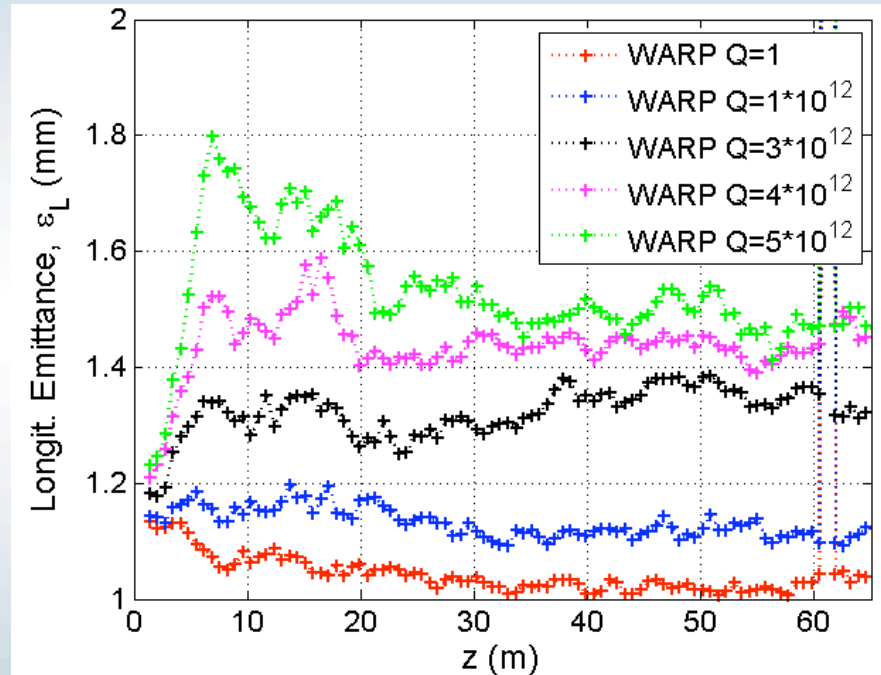
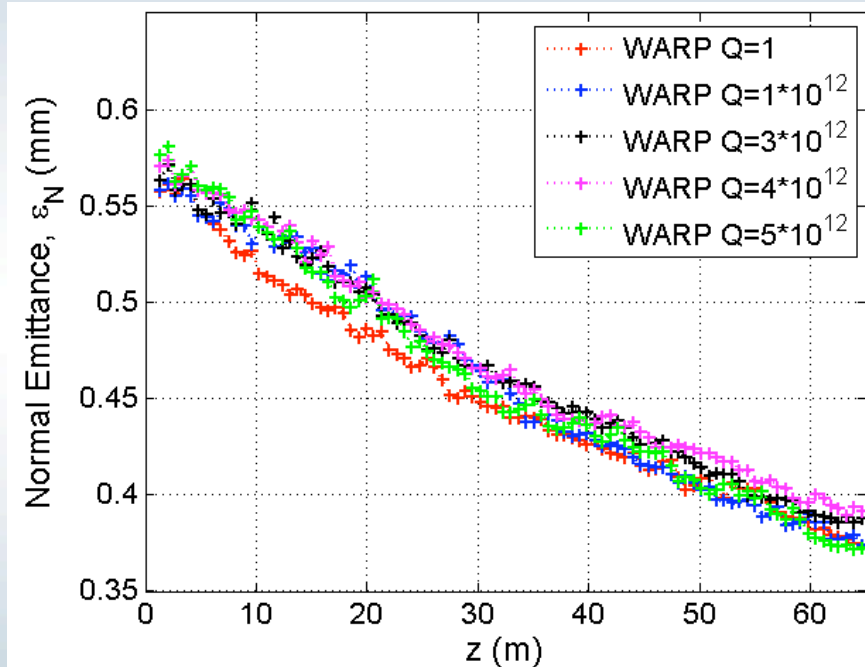


ICOOL sim of 8 stages of cooling w/ a field-flip lattice. Each stage contains ~50 cells

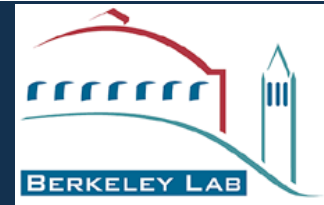


Initial studies look at Stage 7, use Warp to examine effects of space charge

# Muon Cooling with Space-Charge (1)



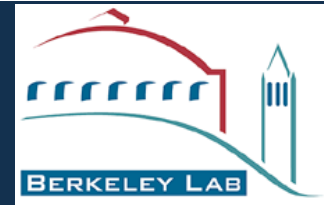
D. Stratakis, D. Grote



# Tutorial on running parallel parameter scans



- Very little extra work beyond what you would do anyway to run a single job
  - 1. prepare your input files as usual
  - 2. prepare 1 new (small) input file describing what parameters are to be varied
  - 3a. make minor edits to a batch script (example provided) to run multiple serial jobsor
  - 3b. make minor edits to a unix script (example provided) to run multiple parallel jobs



# Parameter scans with a serial executable

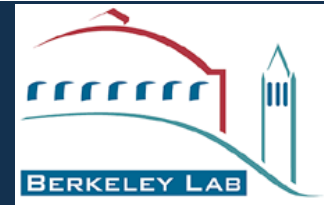


1. Login to Hopper
2. Prepare your input files as usual
3. Create a new file called "scanparams.in" describing parameters to be scanned, plus names of any other input files
4. Create a PBS batch script. Here it is called `scanscript`
  - `edit scanscript` to set walltime, queue, exec code
5. Submit `scanscript`

Results will appear in separate subdirectories. A list of the parameters used for each case will be found in a file called "scanparams.out"

Note: To copy a sample version of `scanscript` :

```
cp /project/projectdirs/map/Codes/Scanparams/scanscript .
```



# Parameter scans with a parallel executable



1. Login to Hopper
2. Prepare your input files as usual
3. Create a new file called "scanparams.in" describing parameters to be scanned, plus names of any other input files
4. Create a unix script. Here it is called `pscanparams`
  - edit `pscanparams` to set `walltime`, `queue`, `exec code`, `cores/exec`
5. Run `pscanparams`
  - this will create a batch script and submit it for you

Only difference compared to the serial case is that you  
(1) edit a unix script instead of a PBS batch script, and  
(2) also specify the # of cores per parallel executable

Results will appear in separate subdirectories. A list of the parameters used for each case will be found in a file called "scanparams.out"

Note: To copy a sample version of `pscanparams` :

```
cp /project/projectdirs/map/Codes/Scanparams/pscanparams .
```



# Example with a serial executable: scanning two quantities in an ICOOL run



- Login to Hopper: `ssh -Y hopper.nersc.gov -l your_user_name`
- Prepare your input files as usual
- Create a new file called "scanparams.in" describing parameters to be scanned, plus names of any other input files\*

```
for001.dat float 0.30 0.40 24 's/0.365 1 .001/##### 1 .001/'
for001.dat float 0.01 0.03 20 's/0.02 1 .001/##### 1 .001/'
```

\*note: to specify a file for which no parameters are varied, just list the name followed by /  
`ptcls.in /`

- Edit PBS batch script, called `scanscript`, to set execution time, queue, and location of serial executable

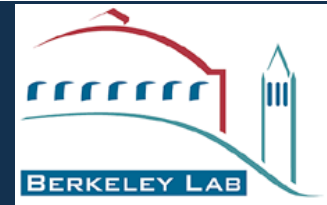
```
#PBS -q debug
#PBS -A map
#PBS -l mppwidth=480
#PBS -l walltime=00:03:00
cd $PBS_O_WORKDIR
aprun -n 480 /project/projectdirs/map/Codes/Scanparams/scanparams.x /project/projectdirs/map/Codes/icool330/icool
```

you edit this

you edit this to point to your serial executable

edit to match above

- Submit batch script: `qsub scanscript`



## Example with a serial executable: scanning the seed in an ICOOL run

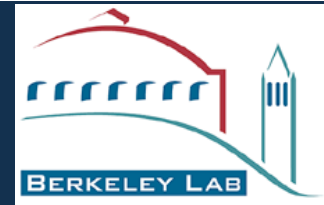


- File "scanparams.in" could look like this:

```
for001.dat integer -1 -10000 480 's/rnseed=-1/rnseed=#####/'
```

- Note: In general, besides scanning using `real` and `integer` you can also specify `octal`





# Example with a parallel executable: scanning two quantities in an MLI run



- Same as for the serial case, you create a file "scanparams.in"

```
mli.in float 0.30d0 0.40d0 4 's/dr365: drift, l=0.365  slices=36/dr365: drift, l=#####  slices=36/'  
mli.in float 0.01d0 0.03d0 5 's/dr02: drift, l=0.02  slices=20/dr02: drift, l=#####  slices=20/'
```

- Instead of editing the PBS script called scanscript, you edit the beginning and end of a unix script called pscanparams

```
#!/bin/bash -l  
  
nprocs_per_job=24  
walltime='00:04:00'  
queue='premium'  
...  
...  
...  
...  
echo "aprun -n $nprocs_per_job ~/MLIjuly2012/mli.x >& std$m &" >> qscript  
...
```

you edit this

you edit this to point to your parallel executable

- Launch the job (i.e. run the unix script) by typing: `./pscanparams`