Colorado School of PUBLIC HEALTH



University of Colorado Anschutz Medical Campus Statistical Methods Research: Running Simulations with R in a High Performance Computing Environment

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My Project

- Working towards a Ph.D. in Biostatistics
- Explain the interaction between day-of-cycle, age, and time-to-menopause observed in the changes to reproductive hormone profiles expressed during the menopausal transition.
- Aim 1: Parsimonious B-Spline Regression Model via Control Polygon Reduction (CPR)
- I've developed a novel method selection approach for enumeration and placement of knots for B-splines.

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Why I Needed A HPC

- Simulations to show how CPR compares to
 - A standard likelihood-based forward-step model selection approach,
 - A standard likelihood-based backward-step model selection approach,
 - P-splines
- Start with L internal knots:
 - \circ CPR requires L+1 regression fits,
 - \circ Forward-step requires L+1 regression fits,
 - o Backward-step requires L(L+1)/2+1 regression fits,
 - P-splines requires L+1 regression fits.
- For L = 80 a total of 3,484 regression models to fit.

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Why I Needed A HPC

- Simulations:
 - Four functions.
 - Modeling under ordinary least squares and under mixed effect models.
 - Differing sample sizes, model, and subject specific errors.
- 144 sets of initial conditions.
- 501, 696, 000 total regression models to fit.
- As a beta user I used:
 - 176,742 core hours
 - \circ \$0.116 per core hour = \$20,502.07

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My HPC Pipeline

Hardware, Software, RAM, and Disk Usage

- Hardware
 - A lot of computation cores
- Software
 - SLURM
 - R
 - tar
- RAM
 - Low enough that the 4GB per core was default sufficient.
- Disk Space
 - Less than 2 GB, tarballs total 633 MB.
 - A lot of small files where generated.
 - Originally only had 50,000 inode limit on \$HOME and \$SCRATCH, extended to 100,000 inode limit.

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Difficulties

- Number of Files.
 - Solution: generate a controlled number of files and place into a tarball for each set of initial conditions.
- Getting a Job to run to completion.
 - Option 1: Request lots of nodes and cores.
 - Use GNU parallel to manage the run.
 - Did not work well for me.
 - Queue time for resources was high.
 - Getting a good estimate for the time required to run the sim was difficult. (More on this later.)
 - Option 2: Use SLURM Arrays to request a few resources many times.
 - This worked well for me.
 - Less queue time.
 - Leaves more resource open for others.

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Estimating Time Need For An Iteration

Differences between my desktop and Rosalind

	Rosalind	My Desktop
OS	Red Hat Enterprise 7.2	Debian 8.7 (jessie)
CPU	Intel(R) Xeon(R) E5-2680 v3	Intel(R) Core(TM) i7-3770
Speed	2.50 GHz	3.40 GHz

- I have configured my desktop to use OpenBLAS for linear algebra.
- QR Decompositions is the biggest time consuming part of my work.
- Benchmarking on desktop was not helpful.
- My one wish for Rosalind: A Testing QOS.

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My Workflow

- Three types of files
 - 1. R scripts for generating one data set and running the sim.
 - 2. bash script for submitting a job
 - 3. bash script for submitting all jobs.
- Examples follow.

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Example R Script

```
# file: doppler-lmer-sim.R
#
# Five input args
# s obs_per_subject sigma_alpha sigma_epsilon outdir
inparams <- commandArgs(trailingOnly = TRUE)
# Build a data set
# ....
# Run the sim
# ....
# Save results
# ....
```

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Example Job Submission File

```
#!/bin/bash
# file: doppler-lmer-sruns.sh
#SBATCH --nodes 1
#SBATCH --ntasks-per-node=20
#SBATCH --cpus-per-task=1
if [ $# -ne 5 ]; then
  echo "expected five arguments"
  exit 1
fi
module load R
mkdir -p $5
mkdir -p $5/results
mkdir -p $5/timers
mkdir -p $5/logs
Rscript --vanilla doppler-lme4-sim.R $1 $2 $3 $4 $5 > \
  $5/logs/log.${SLURM_ARRAY_JOB_ID}_${SLURM_ARRAY_TASK_ID} &
# ... omitted lines ...
Rscript --vanilla doppler-lme4-sim.R $1 $2 $3 $4 $5 > \
  $5/logs/log.${SLURM_ARRAY_JOB_ID}_${SLURM_ARRAY_TASK_ID} &
wait.
```

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Example Submit all Jobs

```
#!/bin/bash
# submitjobs.sh
sbatch --array=1-50 --time=01:00:00 --job-name=d2a \
  doppler-lme4-sruns.sh 2 100 0.1 0.1 dop2-sa01-se01-n0100
sbatch --array=1-50 --time=02:00:00 --job-name=d2b \
  doppler-lme4-sruns.sh 2 500 0.1 0.1 dop2-sa01-se01-n0500
sbatch --array=1-50 --time=04:00:00 --job-name=d2c \setminus
  doppler-lme4-sruns.sh 2 1000 0.1 0.1 dop2-sa01-se01-n1000
# ... omitted lots of rows ...
# ... omitted lots of rows ...
```

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Interesting Results

- Control Polygon Reduction vs. other model selection tools:
 - Faster,
 - Regression models with as good, or better fits, on a degree-of-freedom for degree-of-freedom comparison.
- Want to know more:
 - Dissertation defense April 10.
 - Control Polygon Reduction,
 - Control Net Reduction,
 - Software, and
 - Clinical inference.

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Wish List

- A Testing QOS
 - At least two Nodes.
 - Low wall time.
 - High priority use.
- Add to the "Getting Started" document
 - Limits on storage, size and quantity.
 - Details on queueing priority.
- Community site to hosting examples, Q&A.
- Configuration and Testing to minimize cost.
 - o 20 parallel jobs, one core each, or
 - o 10 parallel jobs, two cores each, or
 - o 5 parallel jobs, four cores each?

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