Expanding Serial Analysis with Slurm Arrays

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Serial job limitations

- Serial jobs are limited to one core as they are not multi-threaded
- How to take advantage of a huge system then without threading, or MPI?



Expanding Serial job analysis

Solution:

- If the job's and their data are independent then we can
- Submit a bunch of similar serial jobs each with their own job script
- Create a for loop which aids in the above:

for i in `seq 1 1000`; do sbatch jobscript_\$i.sh;done

• Demo!



Expanding Serial job analysis

• That's all I have folks, any questions? ... wait no theres a better way!



Expanding Serial job analysis

- The previous example works, but we have to maintain a jobscript file for each job. What a pain!
- Slurm arrays can help!
- Create many jobs from one job script! Even 100's of thousands!
- Can be used in many different scenarios:
 - One analysis program, many data inputs
 - One analysis program, one data input, many constraints
 - One input, many programs
 - Many commands



Slurm Arrays!



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Slurm Arrays

3. Job is launched with eight instances running in parallel



Useful environment variables

SLURM_ARRAY_JOB_ID:the job array's ID (parent)SLURM_ARRAY_TASK_ID:the id of the job array member n (child)%A%a



Example Slurm Arrays

Demos!





Summary

- Job arrays are an easy way to achieve some parallelism from single core jobs
- According to the man page, Slurm supports job arrays of size 4M
 - slurm.conf config value: MaxArraySize
- I've tested job arrays of 40K, some sites support 100K



Questions?



Thank you!

Demo files:

• goo.gl/XNiiev

7bb15a56486c84a87f16039e4ec352c1 (md5sum) - slurm_arrays.tar

Slides:

• goo.gl/H5wTJx

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Whoa, lets slow it down a bit!

- If after creating the huge job arrays you've decided that you, or your admin would prefer you to run only "n" at a time, instead of all at once (if you were permitted).
- In your array declaration use "%n" to limit how many can be run at a time

Example: --array=1-24%4 # only allow 4 jobs at a time to run from your array

