



Grid Computing
at
St Jude Children's Research Hospital

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BOINC Workshop
18 Aug 2011



Outline

- Introduction
- Science Applications
- Queue System



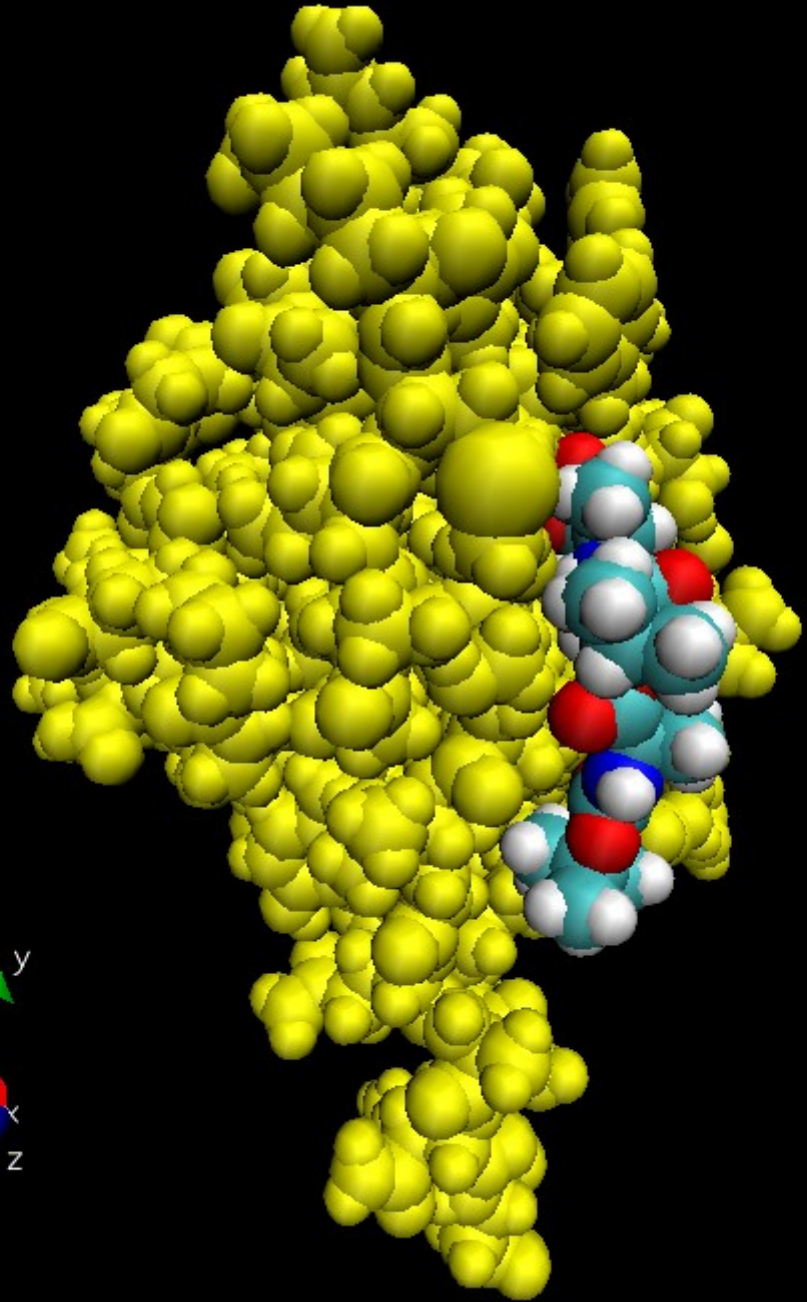
Introduction

- Grid Computing by Bashford Lab at St Jude
- Started 2010
- Goal
 - Computer Aided Drug Discovery using Molecular Dynamics based Free Energy calculation
- Utilize non-clinical St Jude computers
 - ≤ 2000 computers

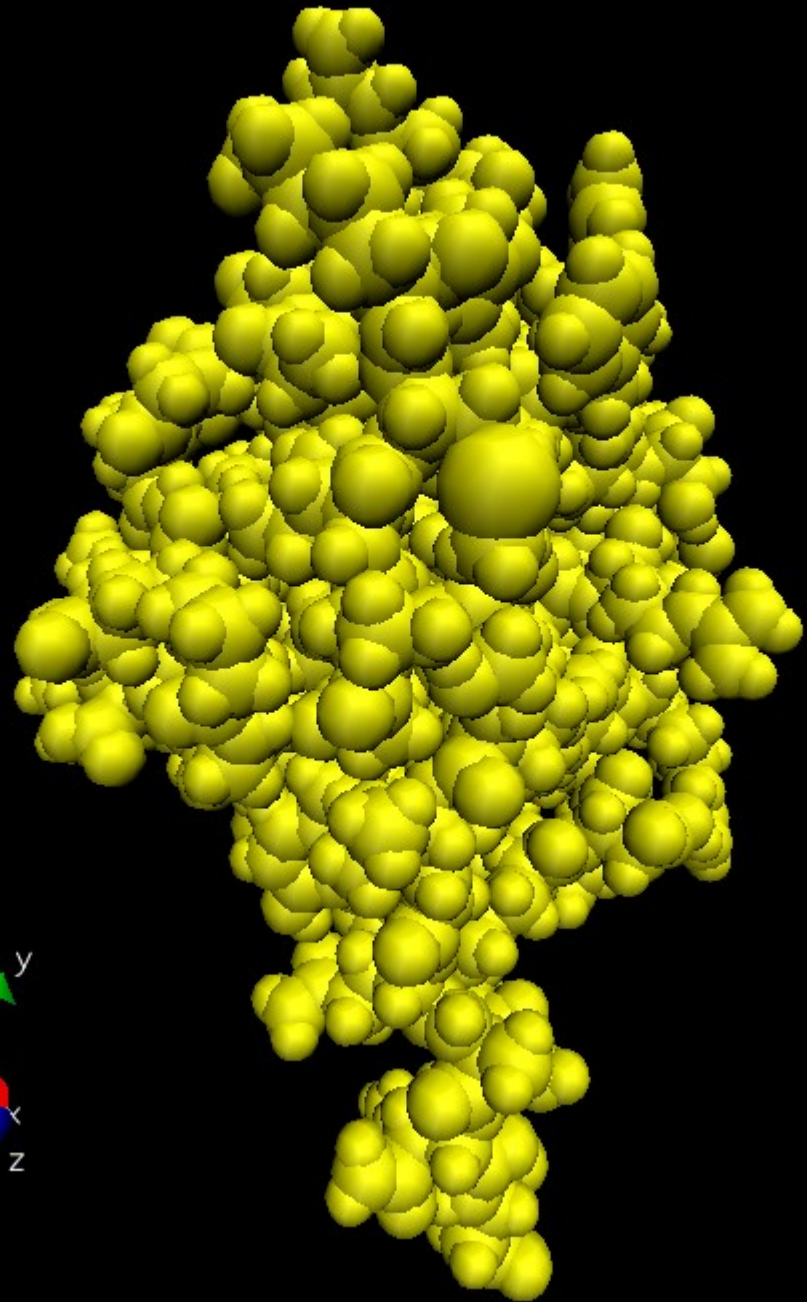


Science Applications

- Molecular Dynamics (MD)
 - *Sander* from *Amber 11*
- Free Energy Calculation
 - MMPBSA
 - In-house program, which...
 - performs Molecular Mechanics
 - Solves Poisson-Boltzmann equation using *libmead*
 - Calculates Surface Area
 - Able to use *Amber* and *Gromacs* input files

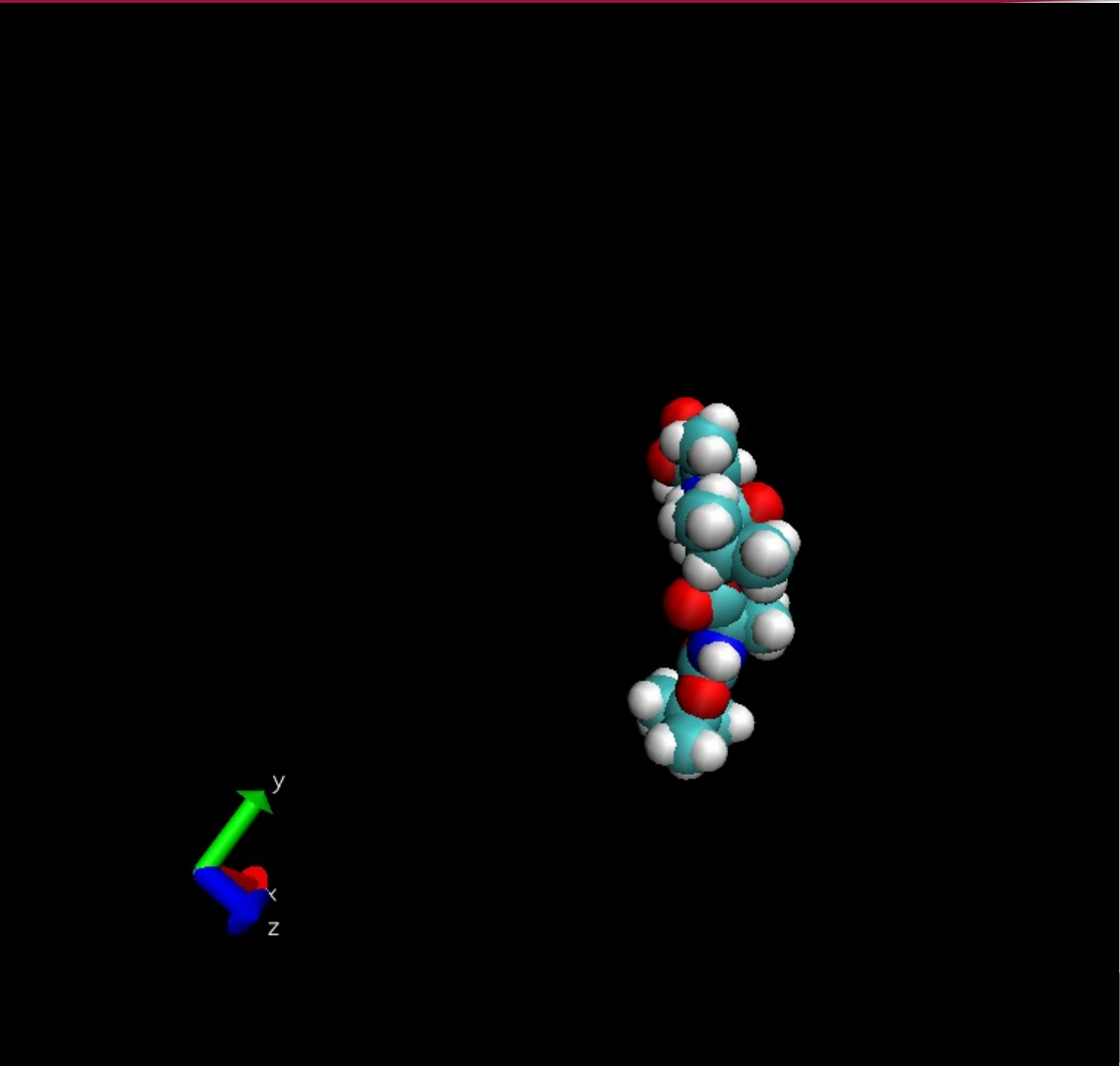


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6



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7



Parallelization

- MD calculations cannot be run in parallel on the grid
- MMPBSA segments can be run in parallel
- Solution:
 - Segment MD calculations
 - Follow MD segments will parallel MD calculations



Parallelization

Sander MD





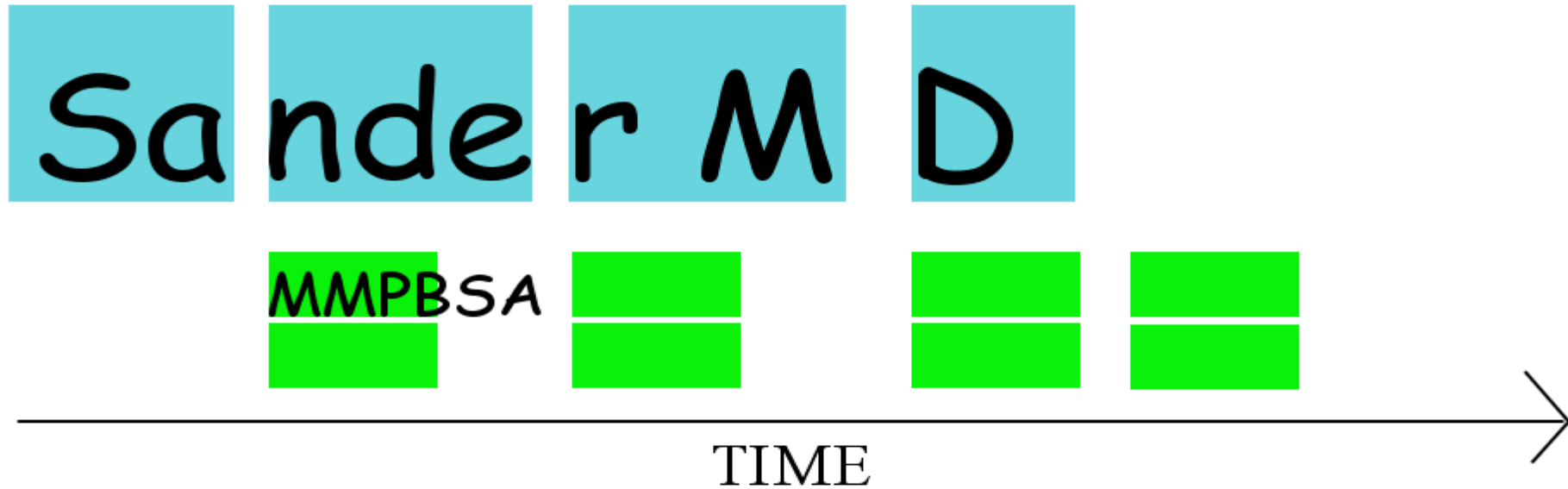
Parallelization

Sa n d e r M D





Parallelization



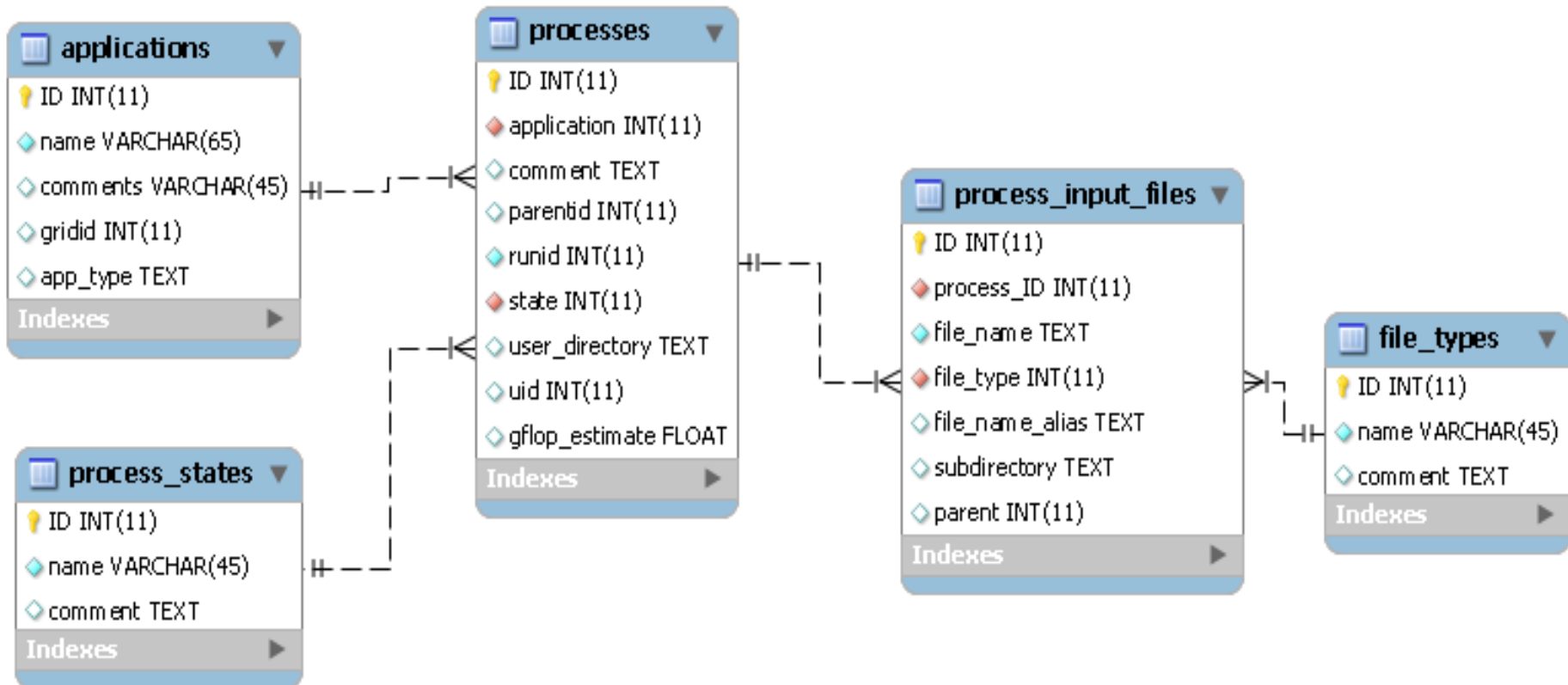


Job Submission

1. Commands written normally, similar to shell script
2. Commands are parsed and interdependency is resolved
3. Processes are segmented and stored in DB
4. Processes are assigned owner based on UID of person submitting work



Queue Database





Job Submission

[screen 7: stjudeathome dev] dcoss@stjudeathome2:/boinc/jobs/test_batches/302-1

File Edit View Terminal Tabs Help

```
[dcoss@stjudeathome2 302-1]$ cat amber.sub
#!/opt/grid_tools/bin/gsub
#sander -i watermin.in -o watermin.out -p com-sol.prmtop -c com-sol.inpcrd -r watermin.rst -ref com-sol.inpcrd
#sander -i drug.in -o drug.out -p com-sol.prmtop -c watermin.rst -r drug.rst -ref watermin.rst
#sander -i min.in -o min.out -p com-sol.prmtop -c drug.rst -r min.rst -ref drug.rst
#sander -i heat.in -o heat.out -p com-sol.prmtop -c min.rst -r heat.rst -x heat.mdcrd -ref min.rst
#sander -i density.in -o density.out -p com-sol.prmtop -c heat.rst -r density.rst -x density.mdcrd -ref heat.rst
#sander -i equil.in -o equil.out -p com-sol.prmtop -c density.rst -r equil.rst -x equil.mdcrd -ref density.rst
sander -i prod.in -o prod1.out -p com-sol.prmtop -c equil.rst -r prod.rst -x prod.mdcrd -ref equil.rst
mmpbsa -p com-sol.prmtop -c prod.mdcrd -o mmpbsa.xml -radii radii.siz
```



Job Submission

```
[dcoss@stjudeathome2 302-1]$ grid_master
grid_master -- Program for managing jobs on the grid.
Usage: grid_master [options] COMMAND PARAMETER

Commands:
close -- cancels the job.
process -- determines whether or not the job should run or continue to wait and acts accordingly.
recombine -- recombines files that belong specified recombination process ID.
start -- starts a job if it is waiting. If it depends on other process, those are started first, if they have not yet finished.
status -- prints the status of the process.
list -- prints the jobs in the queue system owned by the user. If a number is specified, all process in that job batch are listed.

Options:
-s, --simulate Simulates the database queries, without actually sending the job to the grid.
-v, --verbose=[INTEGER] Sets the verbosity of the program. Higher the level, the more verbose.
-h, --help This help dialog
    --usage Same as --help
[dcoss@stjudeathome2 302-1]$
```



Acknowledgments

- Work supported financially by
 - American Lebanese Syrian Associated Charities
 - National Institutes of Health grant ARRA R01GM086243