launcher_creator.py

Create SGE or SLURM launchers for Stampede and Lonestar

launcher_creator.py is a convenience utility that automates creating a launcher for TACC clusters based on parameters (and commands) you give it. It outputs a either a SLURM or SGE file that can be submitted to Stampede or Lonestar using `sbatch` or `qsub`. (It detects which machine it is being executed on, so the same code should work on either cluster.) It can run both Bash commands on a single node and/or a parametric list of commands to be dispatched to multiple nodes.

How To Use It

At the command line:

```
$ launcher_creator.py <options listed below>
```

<table>
<thead>
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<th>Option</th>
<th>Description</th>
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<td>-n</td>
<td>name</td>
</tr>
<tr>
<td>-a, -A</td>
<td>allocation</td>
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<tr>
<td>-q</td>
<td>queue</td>
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<tr>
<td>-w</td>
<td>wayness</td>
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<tr>
<td>-N</td>
<td>number of nodes</td>
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<td>-t</td>
<td>time</td>
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<td>-e</td>
<td>email</td>
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<td>-l</td>
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<td>-m</td>
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<td>-b</td>
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<td>-j</td>
<td>Command list</td>
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<td>-s</td>
<td>stdout</td>
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</table>

Note that while the "-b" and "-j" options are both optional, using neither would pass no work to Lonestar, so you want to use at least one of them!

Manage Modules

Use the `-m` option to load and swap modules for the script. Use the exact same syntax to load or swap module as you would at the command line.

*Example:* `-m "module load luatools"

To run several module commands in the launcher, just separate the commands with a semicolon, as you would in the shell.

*Example:* `-m "module swap intel gcc; module load bedtools"

Or you can use the shortcut `ml` command to perform several module actions in one command.

*Example:* `-m "ml -intel gcc bedtools"
Run multi-line shell commands

The `-b` option lets you insert shell commands into the launcher script. For a short number of commands, separating them with a semicolon may be convenient. For longer commands you may want to write the commands on several lines. To insert a multi-line bash script into a `launcher_creator.py` command, you can use a heredoc like so:

```bash
jelly_bash=$(cat <<-JELLY
ulimit -s unlimited
Trinity.pl --seqType $seqtype --JM 900G $input_data --output $trinity_dir
--CPU $cpu_per_node --no_run_chrysalis
JELLY
)

launcher_creator.py -n jelly -t 6:00:00 -b "$jelly_bash"
```

Create and submit a launcher in one line using `-s`

The `-s` option outputs the name of the launcher to STDOUT. With command substitution you can immediately submit the new launcher file.

```bash
sbatch $(launcher_creator.py -n variant_calling -t 3:00:00 -q normal -b "freebayes -f mapping/bwa_TAIR10/TAIR10_all.fasta alignments.sorted.bam > alignments.vcf" -w 1 -s)
```

Examples

Distributing Shrimp to four nodes

- Make a list of the Shrimp commands to run. You can do this in a text editor, algorithmically with a Bash loop, whatever. Let's pretend this text is saved as `mapping_commands.list`

```
List of Shrimp commands

<table>
<thead>
<tr>
<th>Command</th>
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<tr>
<td>gmapper-1s -N 6 --qv-offset 33 -p opp-in --fastq -1 Sample_R1-00.fq -2 Sample_R2-00.fq reference.fasta &gt; Sample_mapped-00.sam</td>
</tr>
<tr>
<td>gmapper-1s -N 6 --qv-offset 33 -p opp-in --fastq -1 Sample_R1-01.fq -2 Sample_R2-01.fq reference.fasta &gt; Sample_mapped-01.sam</td>
</tr>
<tr>
<td>gmapper-1s -N 6 --qv-offset 33 -p opp-in --fastq -1 Sample_R1-02.fq -2 Sample_R2-02.fq reference.fasta &gt; Sample_mapped-02.sam</td>
</tr>
<tr>
<td>gmapper-1s -N 6 --qv-offset 33 -p opp-in --fastq -1 Sample_R1-03.fq -2 Sample_R2-03.fq reference.fasta &gt; Sample_mapped-03.sam</td>
</tr>
</tbody>
</table>
```
• Generate a launcher using `launcher_creator.py`.

```bash
Using launcher_creator.py
launcher_creator.py -q normal -a MyAllocation -n MapSample -j mapping_commands.list -w 2 -t 6:00:00 -l map_sample.sge -m "module load shrimp"
```

• Submit the newly-created launcher.

```bash
qsub the new launcher on Lonestar
qsub map_sample.sge
```

```bash
sbatch the new launcher on Stampede
sbatch map_sample.slurm
```