

ATLANTIC COMPUTATIONAL EXCELLENCE NETWORK

Shell Scripting

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Imagine ...

...you have a program you're tweaking, and 200 input files to run every time it changes

```
$ numol <methane.in >methane.out  
$ numol <ethane.in >ethane.out  
$ numol <propane.in >propane.out  
$ ...
```

How many kinds of wrong is this?

Get some files

```
$ mkdir Scripting
```

```
$ cd Scripting
```

```
$ pwd
```

```
~/Scripting
```

```
$ cp /home/rdickson/demo/Scripting/* .
```

```
$ ls
```

```
ethane.in      numol          propane.in
```

```
methane.in    numol-job     qstat
```

```
$
```

Submit jobs

```
$ cat numol_job
```

```
## -cwd
```

```
## -l h_rt=24:0:0
```

```
## -j yes
```

```
./numol < methane.in > methane.out
```

```
$ qsub numol_job
```

```
Your job 6254997 ("numol_job") has been  
submitted.
```

Only need one job script

```
$ cat numol_job  
## -cwd  
## -l h_rt=24:0:0  
## -j yes  
./numol < $1.in > $1.out  
$ bash numol_job methane  
$ qsub numol_job methane
```

\$1 is a **positional argument**,
a special case of a shell **variable**

Shell variables

```
$ pet=fido  
$ legs=4  
$ echo $pet, $legs  
fido, 4
```

Set **variables** with '='.

(Notice no spaces around '=')

Get value with '\$'.

'**echo**' is the analogue of 'print'.

Use script over and over...

```
$ for molecule in ethane methane propane  
> do  
>     qsub numol-job $molecule  
> done  
Your job...has been submitted...  
$
```

Keywords **for ... in ... do ... done.**
(**'>'** here is the *secondary prompt*,
not the redirection operator.)

Make a list of molecules

```
$ ls *.in >test-set  
$ vim test-set  
ethane.in  
methane.in  
propane.in  
~  
:1.$s/.in$//
```

There are advantages to learning a full-featured editor like vim or emacs. Global search-and-replace is one.

Use the list

```
$ for molecule in $(echo test-set)
> do
>     qsub numol-job $molecule
> done
Your job...has been submitted...
$
```

`$(command)` substitutes the output of the embedded *command* into that place in the outer command.

Seen so far

<code><input >output</code>	redirection
<code>\$1</code>	positional arguments
<code>var=value</code>	variables: setting
<code>echo \$var</code>	printing
<code>for var in list; do command</code>	looping
<code>done</code>	
<code>*</code>	wild card file matching
<code>\$(command)</code>	command substitution

Extracting results

```
$ ls *.out  
ethane.out      methane.out     ...  
$ grep 'energy' *.out  
ethane.out:The energy is -8.00  
methane.out:The energy is -5.00  
propane.out:The energy is -11.00
```

grep searches a file or files for the pattern given in the 1st argument

Another way to edit

```
propane.out:The energy is -11.00
$ grep 'energy' *.out >raw-energies
$ sed 's/.out:The energy is//' raw-ene..
ethane -8.00
methane -5.00
propane -11.00
```

sed stands for 'stream editor'. Does not change the file – sends results to stdout.

History

```
$ history 5
952  grep energy *.out
953  grep energy *.out >raw-energies
954  sed '/.out:The energy is//' raw-energies
955  sed 's/.out:The energy is//' raw-energies
956  history 20
```

Similar function to the up-arrow.

Joining things up

```
$ grep 'energy' *.out | sed \  
> 's/.out:The energy is//' >results  
$ cat results  
ethane -8.00  
methane -5.00  
propane -11.00
```

The pipe ' | ' redirects the stdout from one cmd to the stdin of the next.

Now seen:

grep	search files for strings
sed	edit a text stream
<i>s/regular expression/something else/</i>	substitution in <code>vim</code> or <code>sed</code>
history	prior commands
<i>cmd1 cmd2</i>	"pipe", output becomes input

More tools:

<code>ls -l</code>	show file permissions
<code>chmod +x</code>	change permissions
<code># comments</code>	
<code>#!/bin/bash</code>	"hash-bang"

Still more:

`cut` extract columns

`cmd | cmd | cmd | ...` "pipeline"

`^line$` beginning- and end-of-line
anchors in regexes