

## Tutorial 03 - Pipelines and Loops

for loop challenge

**Challenge:** Use the files in `molecules/` to print each # of atoms:

## for loop challenge - solution 1

```
for file in *.pdb
do
    cat $file | wc -l
done
```

What could we improve?

## for loop challenge - solution 2

```
for file in *.pdb
do
    echo $file
    cat $file | wc -l
done
```

What could we improve?

## for loop challenge - solution 3

```
for file in *.pdb
do
    echo $file
    a=$(cat $file | wc -l)
    b=$((a - 4))
    echo $b
done
```

What could we improve?

## for loop challenge - solution 4

```
for file in *.pdb
do
    echo $file | sed 's/\.pdb//'
    echo $((`cat $file | wc -l` - 4))
done
```

What could we improve?

## echo vs. cat

When to use echo and when to use cat?

- ▶ echo returns text, including evaluating shell variables to stdout
- ▶ cat access contents of a file and returns it to stdout

## echo vs. cat

Very different behaviors that are each useful in their own way.

echo file.txt vs. cat file.txt

echo also useful for “testing” a for loop before actually using it

```
for file in NENE*[AB].txt
do
    echo "bash goostats $file stats-$file"
done
```

```
## bash goostats NENE*[AB].txt stats-NENE*[AB].txt
```



## pipes vs. for loops

pipes help you work within files

and

for loops help you work outside of files and within directories

“I am struggling to remember all the functions and flags”

DON'T TRY TO MEMORIZE ALL OF THIS!

- ▶ Use google and man to look up a function or flag when needed; your TAs and instructor do this all the time. . .
- ▶ Make a cheatsheet!

## “How can I get more practice”

- ▶ make sure you are working through and typing out the SWC tutorials
- ▶ work through the embedded SWC challenges on your own computer before looking at the answers
- ▶ work on the challenges in and out of class
- ▶ the weekly graded exercises are an important place to practice too

## challenges

1. Compile the maximum value from each of Nene's good (A or B, but not Z) data files in `data-shell/north-pacific-gyre/2012-07-3/` into a single file called `NENE_max.txt`.
2. Compile the median value from each of Nene's good (A or B, but not Z) data files in `data-shell/north-pacific-gyre/2012-07-3/` into a single file called `NENE_median.txt`.

## solution 1

```
for file in NENE*[AB].txt
do
    cat $file | sort -n | tail -n 1 >> NENE_max.txt
done
```

## solution 2

```
for file in NENE*[AB].txt
do
    cat $file | sort -n | head -n 151 | tail -n 1 >> NENE_r
done
```

## solution 2

```
for file in NENE*[AB].txt
do
    nlines=$(cat $file | wc -l)
    halflines=$((($nlines / 2 + 1))
    cat $file | sort -n | head -n $halflines | tail -n 1 >>
done
```

## function review

for

\$

history

\$()

\$(( ))

*up arrow*

*Ctrl-c*

*Ctrl-a*

*Ctrl-e*