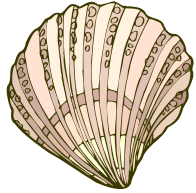
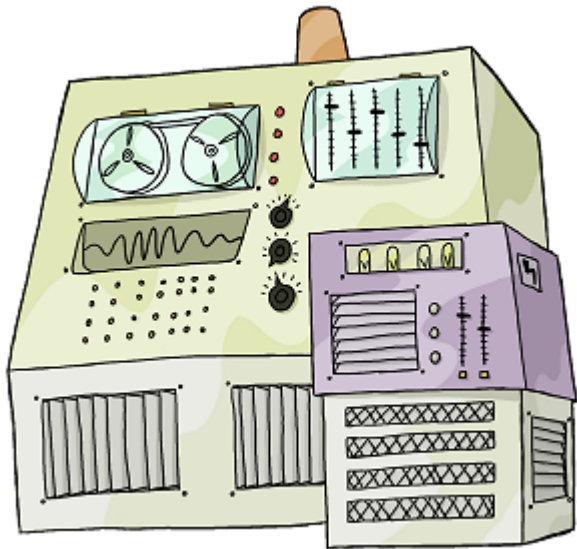


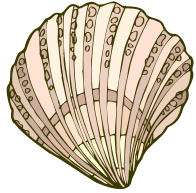
# The Unix Shell

## Pipes and Filters

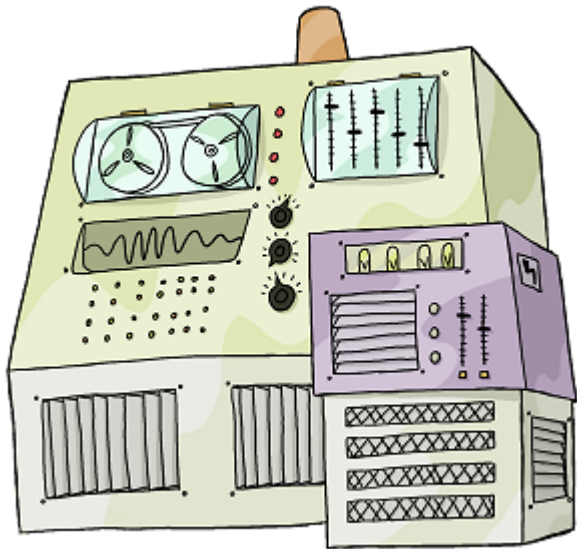


shell



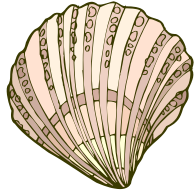


shell

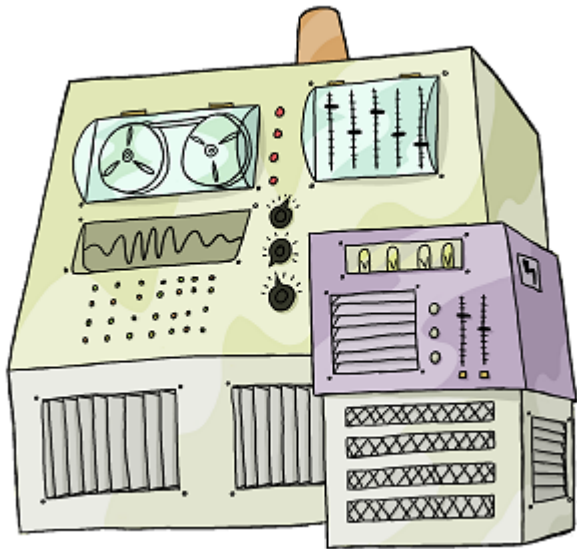


<code>pwd</code>	<code>mkdir</code>
<code>cd</code>	<code>nano</code>
<code>ls</code>	<code>rm</code>
<code>.</code>	<code>rmdir</code>
<code>..</code>	<code>mv</code>
	<code>cp</code>





# shell



pwd	mkdir
cd	nano
ls	rm
.	rmdir
..	mv
	cp

*More powerful  
when combined*

```
$ ls molecules
```

```
cubane.pdb
```

```
ethane.pdb
```

```
methane.pdb
```

```
octane.pdb
```

```
pentane.pdb
```

```
propane.pdb
```

```
$
```

```
$ ls molecules
```

```
cubane.pdb      ethane.pdb      methane.pdb
```

```
octane.pdb      pentane.pdb     propane.pdb
```

```
$ cd molecules
```

```
$
```

```
$ ls molecules
```

```
cubane.pdb      ethane.pdb      methane.pdb
```

```
octane.pdb      pentane.pdb     propane.pdb
```

```
$ cd molecules
```

```
$ wc *.pdb
```

```
$ ls molecules
```

*cubane.pdb*      *ethane.pdb*      *methane.pdb*

*octane.pdb*      *pentane.pdb*      *propane.pdb*

\$ cd molecules

\$ wc \*.pdb ← \* is a *wild card*



```
$ ls molecules
```

```
cubane.pdb      ethane.pdb      methane.pdb
```

```
octane.pdb      pentane.pdb     propane.pdb
```

```
$ cd molecules
```

```
$ wc *.pdb
```



*\* is a wild card*

matches zero or more characters

```
$ ls molecules
```

```
cubane.pdb      ethane.pdb      methane.pdb
```

```
octane.pdb      pentane.pdb     propane.pdb
```

```
$ cd molecules
```

```
$ wc *.pdb
```

← *\* is a wild card*

matches zero or more characters  
so \*.pdb matches all filenames  
ending in .pdb

```
$ ls molecules
```

```
cubane.pdb      ethane.pdb      methane.pdb
```

```
octane.pdb      pentane.pdb     propane.pdb
```

```
$ cd molecules
```

```
$ wc *.pdb
```

```
wc cubane.pdb ethane.pdb methane.pdb octane.pdb pentane.pdb propane.pdb
```

```
$ ls molecules
```

```
cubane.pdb      ethane.pdb      methane.pdb
```

```
octane.pdb      pentane.pdb     propane.pdb
```

```
$ cd molecules
```

```
$ wc *.pdb
```

← word count

```
$ ls molecules
```

*cubane.pdb*      *ethane.pdb*      *methane.pdb*

*octane.pdb*      *pentane.pdb*      *propane.pdb*

\$ cd molecules

\$ wc \*.pdb ← word\_count

## counts lines, words, and characters in files

```
$ ls molecules
```

```
cubane.pdb      ethane.pdb      methane.pdb  
octane.pdb      pentane.pdb     propane.pdb
```

```
$ cd molecules
```

```
$ wc *.pdb
```

```
20  156 1158 cubane.pdb  
12   84  622 ethane.pdb  
 9   57  422 methane.pdb  
30  246 1828 octane.pdb  
21  165 1226 pentane.pdb  
15  111  825 propane.pdb  
107 819 6081 total
```

```
$
```

\$ wc **-l** \*.pdb ← report only lines

20	<i>cubane.pdb</i>
12	<i>ethane.pdb</i>
9	<i>methane.pdb</i>
30	<i>octane.pdb</i>
21	<i>pentane.pdb</i>
15	<i>propane.pdb</i>
107	<i>total</i>

\$

```
$ wc -l *.pdb ← report only lines
20  cubane.pdb
12  ethane.pdb
9   methane.pdb
30  octane.pdb
21  pentane.pdb
15  propane.pdb
107 total
$
```



20 *cubane.pdb*  
12 *ethane.pdb*  
9 *methane.pdb*  
30 *octane.pdb*  
21 *pentane.pdb*  
15 *propane.pdb*  
107 *total*

Which file is shortest?

```
20  cubane.pdb
12  ethane.pdb
 9  methane.pdb
30  octane.pdb
21  pentane.pdb
15  propane.pdb
107 total
```

Which file is shortest?

Easy to see when there are six...

```
20  cubane.pdb
12  ethane.pdb
 9  methane.pdb
30  octane.pdb
21  pentane.pdb
15  propane.pdb
107 total
```

Which file is shortest?

Easy to see when there are six...

...but what if there were 6000?

```
$ wc -l *.pdb > lengths
```

```
$
```

```
$ wc -l *.pdb > lengths
```

```
$
```

*redirect output to a file*

```
$ wc -l *.pdb > lengths
```

```
$
```

*redirect* output to a file  
create file if it doesn't exist

```
$ wc -l *.pdb > lengths
```

```
$
```

*redirect* output to a file  
create file if it doesn't exist  
overwrite it if it does

```
$ wc -l *.pdb > lengths
```

```
$
```

no screen output



```
$ wc -l *.pdb > lengths
```

```
$ ls lengths
```

*lengths*

```
$
```

```
$ wc -l *.pdb > lengths
```

```
$ ls lengths
```

*lengths*

```
$ cat lengths
```

```
20  cubane.pdb
```

```
12  ethane.pdb
```

```
9   methane.pdb
```

```
30  octane.pdb
```

```
21  pentane.pdb
```

```
15  propane.pdb
```

```
107 total
```

```
$
```

```
$ wc -l *.pdb > lengths
```

```
$ ls lengths
```

```
lengths
```

```
$ cat lengths
```

← *concatenate files*

```
20 cubane.pdb
```

```
12 ethane.pdb
```

```
9 methane.pdb
```

```
30 octane.pdb
```

```
21 pentane.pdb
```

```
15 propane.pdb
```

```
107 total
```

```
$
```

```
$ wc -l *.pdb > lengths
```

```
$ ls lengths
```

```
lengths
```

```
$ cat lengths
```



*concatenate* files

in this case, only one

so file contents printed to screen

```
20 cubane.pdb
```

```
12 ethane.pdb
```

```
9 methane.pdb
```

```
30 octane.pdb
```

```
21 pentane.pdb
```

```
15 propane.pdb
```

```
107 total
```

```
$
```

```
$ sort -n lengths
```

```
9 methane.pdb
```

```
12 ethane.pdb
```

```
15 propane.pdb
```

```
20 cubane.pdb
```

```
21 pentane.pdb
```

```
30 octane.pdb
```

```
107 total
```

```
$
```

```
$ sort -n lengths > sorted-lengths
```

```
$
```

```
$ sort -n lengths > sorted-lengths
```

```
$ head -1 sorted-lengths
```

```
9  methane.pdb
```

```
$
```

```
$ sort -n lengths > sorted-lengths
```

```
$ head -1 sorted-lengths
```

```
9 methane.pdb
```

get the first line of the file

```
$
```



```
$ sort -n lengths > sorted-lengths
```

```
$ head -1 sorted-lengths
```

```
9 methane.pdb
```

```
$
```

get the first line of the file  
this must be the PDB file  
with the fewest lines,  
since sorted-lengths holds  
files and line counts in  
order from least to greatest

```
$ sort -n lengths > sorted-lengths
```

```
$ head -1 sorted-lengths
```

```
9 methane.pdb
```

```
$
```

not particularly obvious

get the first line of the file  
this must be the PDB file  
with the fewest lines,  
since sorted-lengths holds  
files and line counts in  
order from least to greatest

```
$ sort -n lengths | head -1  
9 methane.pdb  
$
```

```
$ sort -n lengths | head -1  
9 methane.pdb  
$
```

*a pipe*

```
$ sort -n lengths | head -1
```

```
9 methane.pdb
```

```
$
```

*a pipe*

use output of left side

```
$ sort -n lengths | head -1  
9 methane.pdb  
$
```

*a pipe*  
use output of left side  
as input to right side

```
$ sort -n lengths | head -1
```

9 *methane.pdb*

\$

*a pipe*

use output of left side

as input to right side

*without creating temporary file*

```
$ wc -l *.pdb | sort -n | head -1
```

```
9  methane.pdb
```

```
$
```

don't need to create lengths file



```
$ wc -l *.pdb | sort -n | head -1  
9  methane.pdb  
$
```

This simple idea is why Unix has been so successful

```
$ wc -l *.pdb | sort -n | head -1
9  methane.pdb
$
```

This simple idea is why Unix has been so successful

Create simple tools that:

```
$ wc -l *.pdb | sort -n | head -1  
9 methane.pdb  
$
```

This simple idea is why Unix has been so successful

Create simple tools that:

- do one job well

```
$ wc -l *.pdb | sort -n | head -1
9  methane.pdb
$
```

This simple idea is why Unix has been so successful

Create simple tools that:

- do one job well
- work well with each other

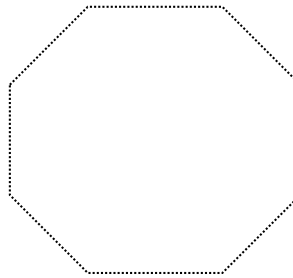
```
$ wc -l *.pdb | sort -n | head -1  
9 methane.pdb  
$
```

This simple idea is why Unix has been so successful

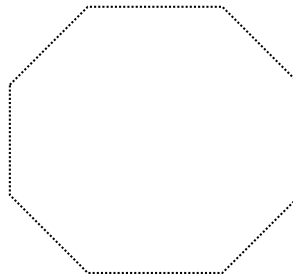
Create simple tools that:

- do one job well
- work well with each other

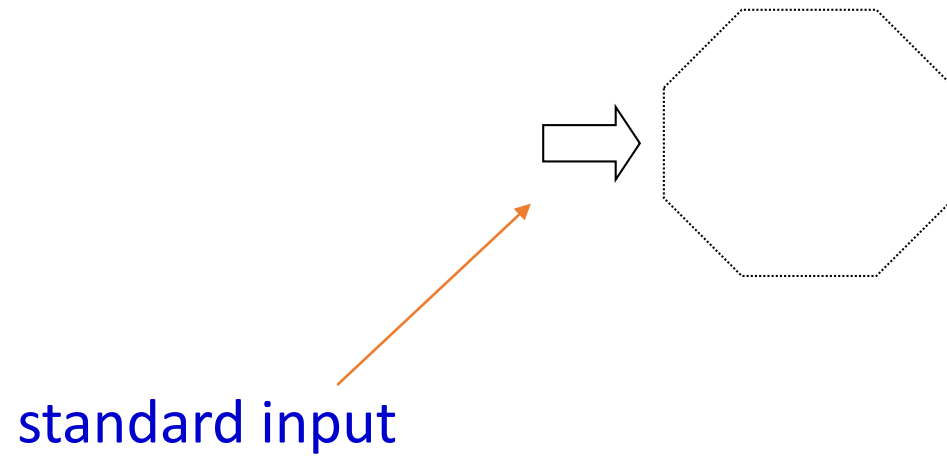
10 tools can be combined in 100 ways



running program

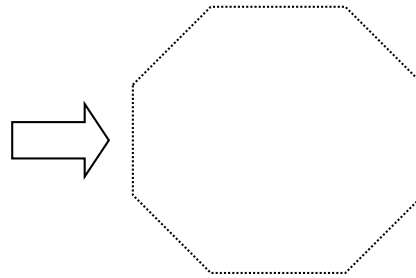


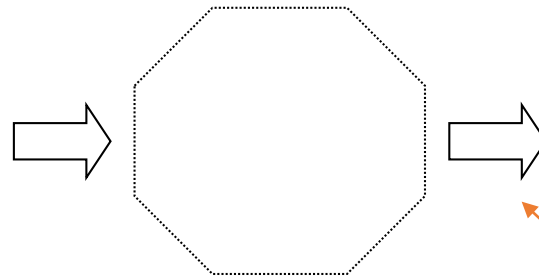
running program  
*process*





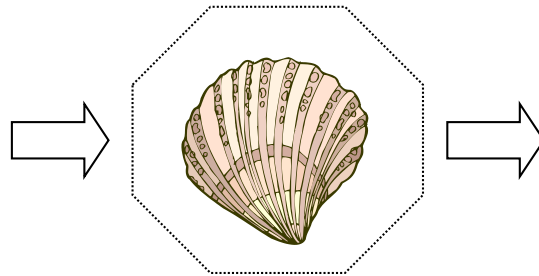
standard input  
stdin



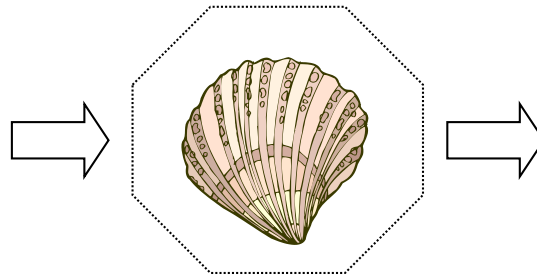


standard output  
stdout

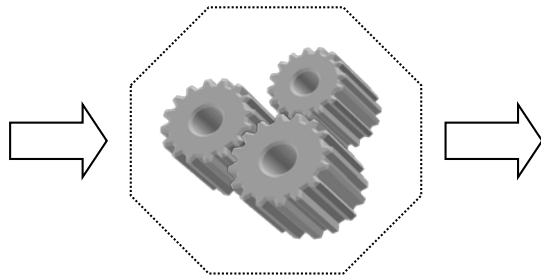




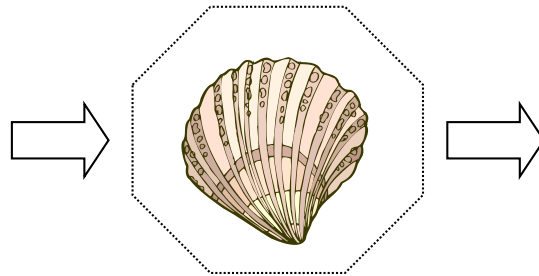
```
$ wc -l *.pdb > lengths
```



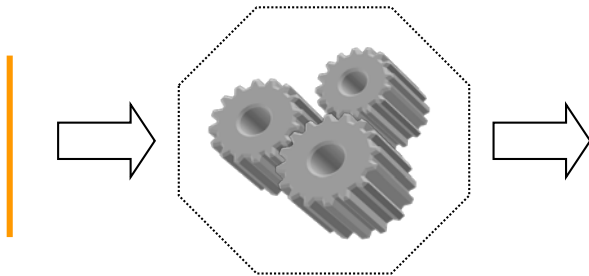
WC



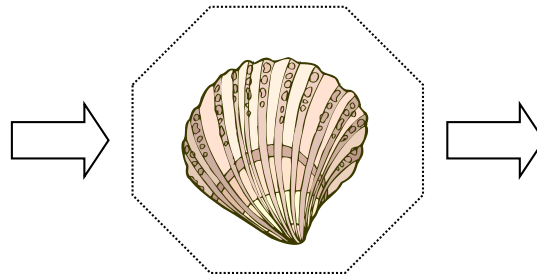
```
$ wc -l *.pdb > lengths
```



WC



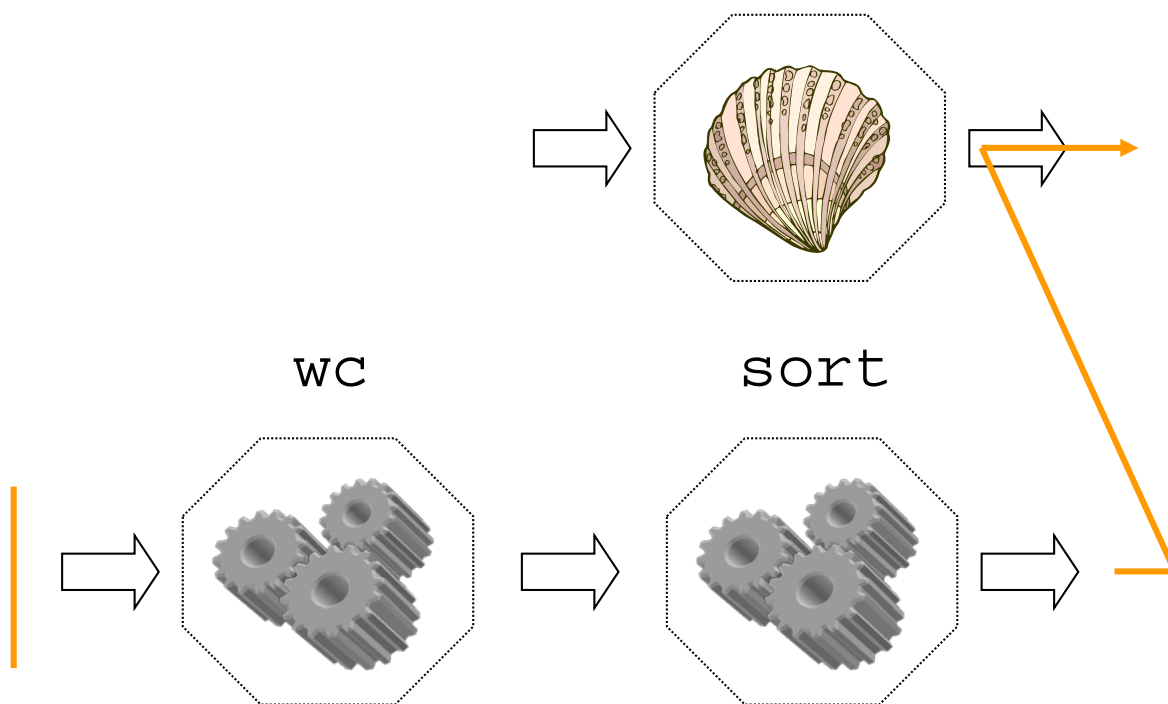
```
$ wc -l *.pdb > lengths
```



WC

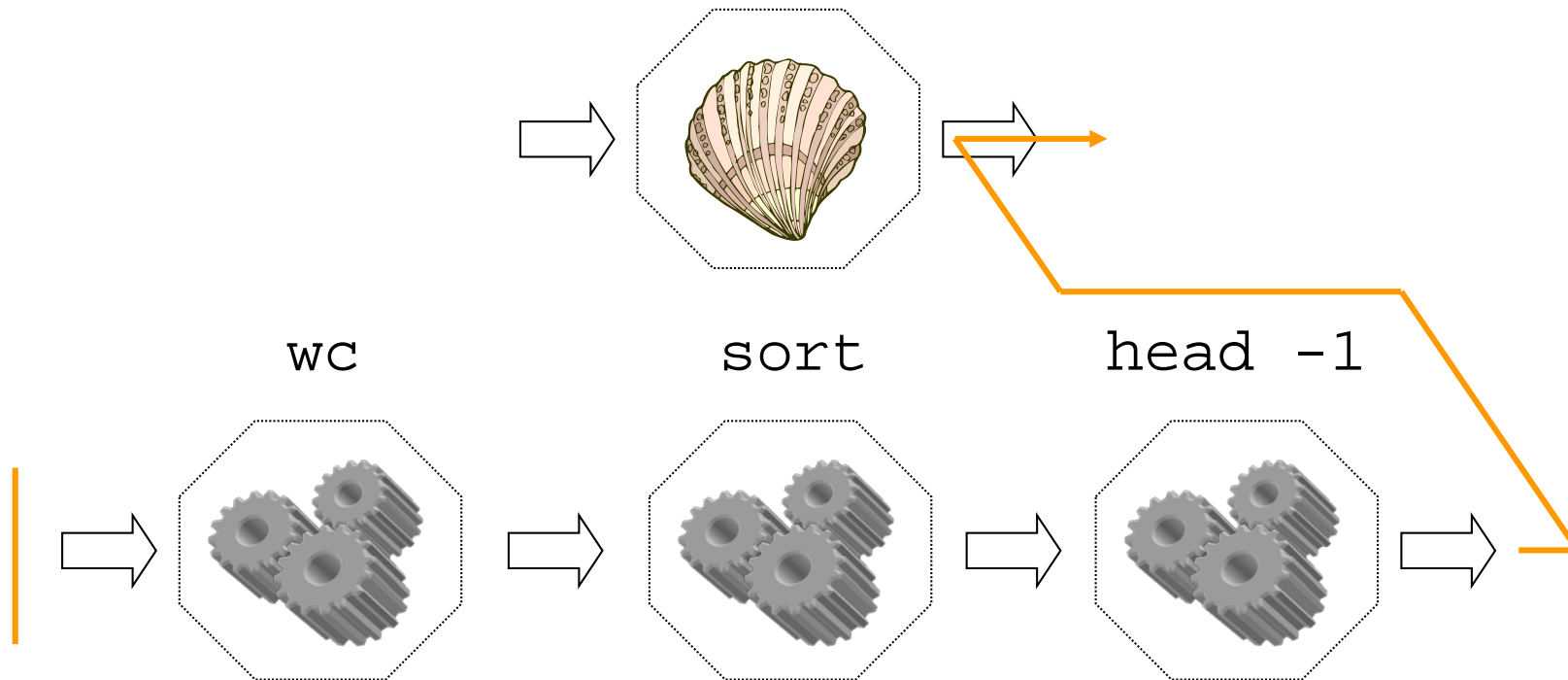


```
$ wc -l *.pdb > lengths
```



```
$ wc -l *.pdb | sort
```





```
$ wc -l *.pdb | sort | head -1
```

This programming model called *pipes and filters*

This programming model called *pipes and filters*

A *filter* transforms a stream of input into a stream of output

This programming model called *pipes and filters*

A *filter* transforms a stream of input into a stream of output

A *pipe* connects two filters

This programming model called *pipes and filters*

A *filter* transforms a stream of input into a stream of output

A *pipe* connects two filters

Any program that reads lines of text from standard input, and writes lines of text to standard output, can work with every other

# You can (and should) write such programs

<code>pwd</code>	<code>mkdir</code>
<code>cd</code>	<code>nano</code>
<code>ls</code>	<code>rm</code>
<code>.</code>	<code>rmdir</code>
<code>..</code>	<code>mv</code>
	<code>cp</code>

<code>pwd</code>	<code>mkdir</code>	<code>wc</code>
<code>cd</code>	<code>nano</code>	<code>sort</code>
<code>ls</code>	<code>rm</code>	<code>head</code>
<code>.</code>	<code>rmdir</code>	
<code>..</code>	<code>mv</code>	
	<code>cp</code>	



pwd	mkdir	wc
cd	nano	sort
ls	rm	head
.	rmdir	<i>tail</i>
..	mv	<i>split</i>
	cp	<i>cut</i>
		<i>uniq</i>

pwd	mkdir	wc	*
cd	nano	sort	>
ls	rm	head	
.	rmdir	<i>tail</i>	
..	mv	<i>split</i>	
	cp	<i>cut</i>	
		<i>uniq</i>	

pwd	mkdir	wc	*
cd	nano	sort	>
ls	rm	head	
.	rmdir	<i>tail</i>	<
..	mv	<i>split</i>	?
	cp	<i>cut</i>	
		<i>uniq</i>	



created by

Greg Wilson

August 2010



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