





The Unix Shell

Advanced Shell Tricks



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"How should I do this?"

Some technical problem...



Combine existing programs using pipes & filters

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



- Combine existing programs using pipes & filters
- Redirect output from programs to files

wc -1 *.pdb > lengths

- Combine existing programs using pipes & filters
- Redirect output from programs to files
- Use variables to control program operation
- \$ SECRET_IDENTITY=Dracula \$ echo \$SECRET_IDENTITY

Dracula

- Combine existing programs using pipes & filters
- Redirect output from programs to files
- Use variables to control program operation

Very powerful when used together

員

In previous episodes, we've seen how to:

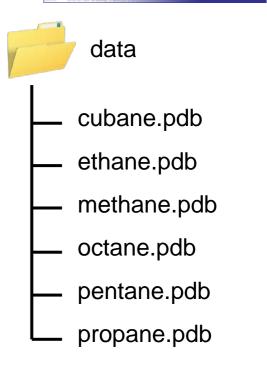
- Combine existing programs using pipes & filters
- Redirect output from programs to files
- Use variables to control program operation

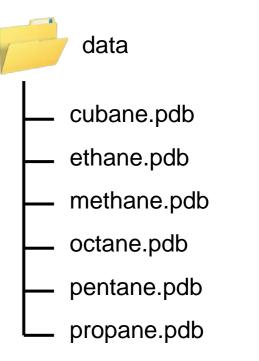
Very powerful when used together

But there are other useful things we can do with these – let's take a look...

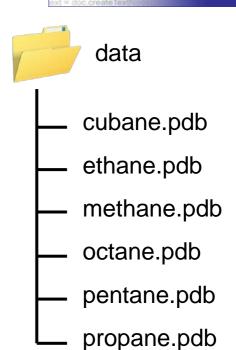
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First, let's revisit redirection...





The 'redirection' operator



But what about adding this together with other results generated later?



- cubane.pdb
- ethane.pdb
- methane.pdb
- octane.pdb
- pentane.pdb
- propane.pdb
 - butane.ent
- heptane.ent
 - hexane.ent
 - nonane.ent
 - decane.ent

But what about adding this together with other results generated later?

\$ Is *.ent > more-files



- cubane.pdb
- ethane.pdb
- methane.pdb
- octane.pdb
- pentane.pdb
- propane.pdb
 - butane.ent
 - heptane.ent
 - hexane.ent
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But what about adding this together with other results generated later?



data

cubane.pdb

ethane.pdb

methane.pdb

octane.pdb

pentane.pdb

propane.pdb

- butane.ent

heptane.ent

hexane.ent

nonane.ent

decane.ent

But what about adding this together with other results generated later?

Instead, we can do...



- cubane.pdb
- ethane.pdb
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 - hexane.ent
 - nonane.ent
- decane.ent

But what about adding this together with other results generated later?

Instead, we can do...

Note the double >'s - the append' operator



data

cubane.pdb

ethane.pdb

methane.pdb

octane.pdb

pentane.pdb

propane.pdb

butane.ent

heptane.ent

hexane.ent

nonane.ent

decane.ent



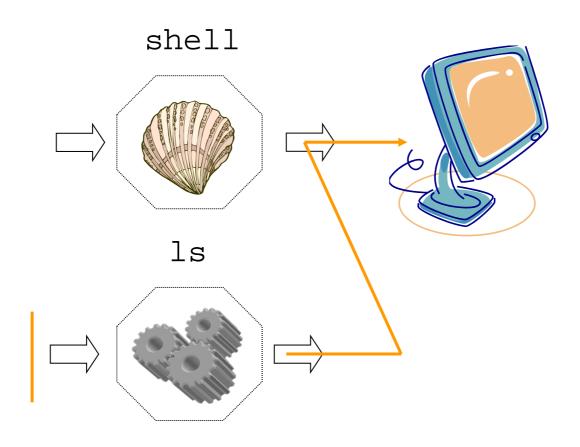
We know that...

Normally, standard output is directed to a display:



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Normally, standard output is directed to a display:



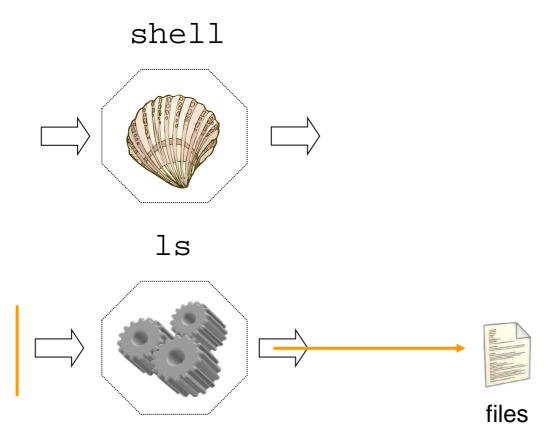
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We know that...

Normally, standard output is directed to a display:

But we have redirected it to a file instead:



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But what happens with error messages?



But what happens with error messages?

For example...

\$ Is /some/nonexistent/path > files

Is: /some/nonexistent/path: No such file or directory



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Is: /some/nonexistent/path: No such file or directory

No files are listed in *files*, as you might expect.



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\$ Is /some/nonexistent/path > files
Is: /some/nonexistent/path: No such file or directory

No files are listed in *files*, as you might expect.

But why isn't the error message in files?



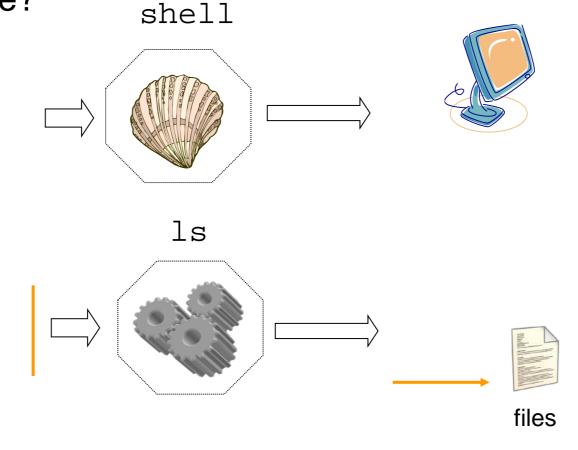
This is because error messages are sent to the standard error (stderr), separate to stdout





This is because error messages are sent to the *standard error* (stderr), separate to stdout

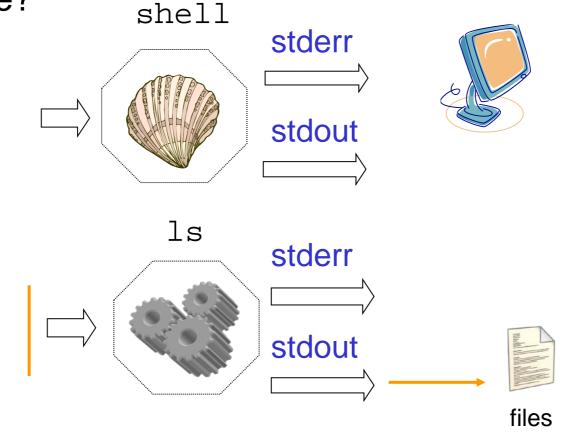
So what was happening with the previous example?





This is because error messages are sent to the *standard error* (stderr), separate to stdout

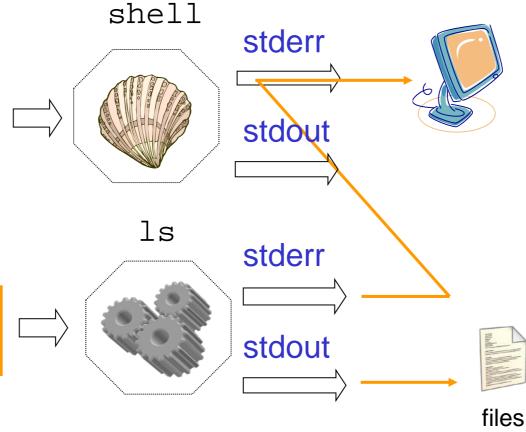
So what was happening with the previous example?



This is because error messages are sent to the *standard error* (stderr), separate to stdout

So what was happening with the previous

example?







To redirect the standard error to a file, we can do:

\$ Is /some/nonexistent/path 2> error-log

Redirect as before, but with a slightly different operator



To redirect the standard error to a file, we can do:

\$ Is /some/nonexistent/path 2> error-log

Now we have any error messages stored in error-log



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To redirect both stdout and stderr, we can then do:

\$ Is /usr /some/nonexistent/path > files 2> error-log



To redirect the standard error to a file, we can do:

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Now we have any error messages stored in error-log

To redirect both stdout and stderr, we can then do:

\$ Is /usr /some/nonexistent/path > fles 2 > error-log

We can use both stdout and stderr redirection – at the same time



To redirect the standard error to a file, we can do:

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Now we have any error messages stored in error-log

To redirect both stdout and stderr, we can then do:

\$ Is /usr /some/nonexistent/path > files 2> error-log

Which would give us contents of */usr* in *files* as well.

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So why a '2' before the '>'?



So why a '2' before the '>'?

Both stdout and stderr can be referenced by numbers:

\$ Is /usr /some/nonexistent/path 1> files 2> error-log



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\$ Is /usr /some/nonexistent/path 1> files 2> error-log

Refers to Refers

stdout to stderr



So why a '2' before the '>'?

Both stdout and stderr can be referenced by numbers:

\$ Is /usr /some/nonexistent/path 1> files 2> error-log

To just redirect both to the same file we can also do:

\$ Is /usr /some/nonexistent/path &> everything

With '&' denoting both stdout and stderr



So why a '2' before the '>'?

Both stdout and stderr can be referenced by numbers:

\$ Is /usr /some/nonexistent/path 1> files 2> error-log

To just redirect both to the same file we can also do:

\$ Is /usr /some/nonexistent/path &> everything

With '&' denoting both stdout and stderr

We can also use append for each of these too:

\$ Is /usr /some/nonexistent/path 1>> files 2>> error-log

Unix Shell



>	1>	Redirect stdout to a file
	2>	Redirect stderr to a file
	&>	Redirect both stdout and stderr to the same file



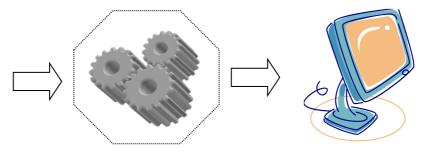
>	1>	Redirect stdout to a file
	2>	Redirect stderr to a file
	&>	Redirect both stdout and stderr to the same file
>>	1>>	Redirect and append stdout to a file
	2>>	Redirect and append stderr to a file
	&>>	Redirect and append both stdout and stderr to a file

We've seen how pipes and filters work with using a single program on some input data...







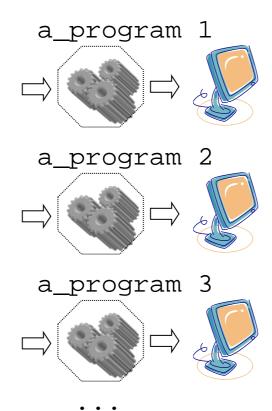




But what about running the same program separately, for each input?

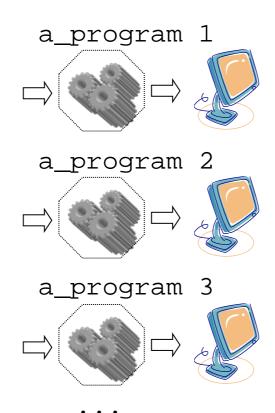


But what about running the same program separately, for each input?





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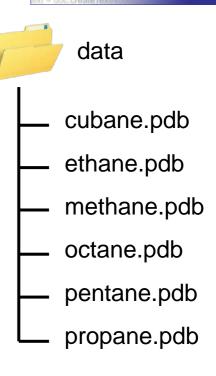


We can use *loops* for this...

So what can we do with loops?

So what can we do with loops?

Let's go back to our first set of pdb files, and assume we want to compress each of them



So what can we do with loops?

Let's go back to our first set of pdb files, and assume we want to compress each of them

We could do the following for each:

\$ zip cubane.pdb.zip cubane.pdb adding: cubane.pdb (deflated 73%)

data

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

So what can we do with loops?

Let's go back to our first set of pdb files, and assume we want to compress each of them

We could do the following for each:

\$ zip cubane.pdb.zip cubane.pdb typical output adding: cubane.pdb (deflated 73%) — from the zip

data

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

command

So what can we do with loops?

Let's go back to our first set of pdb files, and assume we want to compress each of them

We could do the following for each:

data

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

```
$ zip cubane.pdb cubane.pdb typical output adding: cubane.pdb (deflated 73%) from the zip command we wish to create
```

So what can we do with loops?

Let's go back to our first set of pdb files, and assume we want to compress each of them

We could do the following for each:

data

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

```
$ zip cubane.pdb.zip cubane.pdb adding: cubane.pdb (deflated 73%) typical output from the zip

The zip file The file(s) command

we wish to we wish to add to the zip file
```

Unix Shell

So what can we do with loops?

Let's go back to our first set of pdb files, and assume we want to compress each of them

We could do the following for each:

\$ zip cubane.pdb.zip cubane.pdb adding: cubane.pdb (deflated 73%)

Not efficient for many files

data

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



\$ for file in *.pdb; do zip \$file.zip \$file; done



```
$ for file in *.pdb; do zip $file.zip $file; done
```

For each pdb file in this directory...



\$ for file in *.pdb; do zip \$file.zip \$file; done

Run this command

\$ for file in *.pdb; do zip \$file.zip \$file; done

This is the end of the loop



\$ for file in *.pdb; do zip \$file.zip \$file; done

The semicolons separate each part of the loop construct



\$ for file in *.pdb; do zip \$file.zip \$file; done

This expands to a list of every pdb file



\$ for file n *.pdb; do zip \$file.zip \$file; done

This variable holds the next pdb file in the list



\$ for file in *.pdb; do zip \$file.zip \$file; done

We reference the 'file' variable, and use '.' to add the zip extension to the filename



\$ for file in *.pdb; do zip \$file.zip \$file; done

We reference the 'file' variable again





```
$ for file in *.pdb; do zip $file.zip $file; done adding: cubane.pdb (deflated 73%) adding: ethane.pdb (deflated 70%) adding: methane.pdb (deflated 66%) adding: octane.pdb (deflated 75%) adding: pentane.pdb (deflated 74%) adding: propane.pdb (deflated 71%)
```



```
$ for file in *.pdb; do zip $file.zip $file; done adding: cubane.pdb (deflated 73%) adding: ethane.pdb (deflated 70%) ...
```

In one line, we've ended up with all files zipped



```
$ for file in *.pdb; do zip $file.zip $file; done adding: cubane.pdb (deflated 73%) adding: ethane.pdb (deflated 70%) ...
```

In one line, we've ended up with all files zipped

```
$ ls *.zip
cubane.pdb.zip methane.pdb.zip pentane.pdb.zip
ethane.pdb.zip octane.pdb.zip propane.pdb.zip
```

Now instead, what if we wanted to output the first line of each pdb file?

We could use head -1 *.pdb for that, but it would produce:

```
==> cubane.pdb <==
COMPND CUBANE
```

```
==> ethane.pdb <==
COMPND ETHANE
```

```
==> methane.pdb <==
COMPND METHANE
```

. . .



```
We could use head -1 *.pdb for that, but it would
produce:
                     head produces this
                     (it's not in the file)
==> cubane.pdb <== *
COMPND
          CUBANE
==> ethane.pdb <==
COMPND
           FTHANF
==> methane.pdb <==
COMPND METHANE
```



We could use head -1 *.pdb for that, but it would produce: head produces this (it's not in the file) ==> cubane.pdb <== this is actually the first COMPND *CUBANE***←** line in this file! ==> ethane.pdb <== COMPND FTHANF ==> methane.pdb <== COMPND METHANE



```
We could use head -1 *.pdb for that, but it would
produce:
                     head produces this
                     (it's not in the file)
==> cubane.pdb <== 	
           CUBANE this is actually the first
COMPND
                       line in this file!
==> ethane.pdb <==
COMPND
           FTHANF
==> methane.pdb <==
COMPND METHANE
```

Perhaps we only want the actual first lines...

However, using a loop:



However, using a loop:

\$ for file in *.pdb; do head -1 \$file; done



However, using a loop:

\$ for file in *.pdb; do head -1 \$file; done

We use \$file as we did before, but this time with the head command



However, using a loop:

```
$ for file in *.pdb; do head -1 $file; done
```

COMPND CUBANE

COMPND ETHANE

COMPND METHANE

COMPND OCTANE

COMPND PENTANE

COMPND PROPANE





Simple!

\$ (for file in Is *.pdb; do head -1 \$file; done) | sort -r



Simple!

\$ (for file in Is *.pdb; do head -1 \$file; done) sort -r

Using a pipe, we can just add this on the end



Simple!

```
$ (for file in Is *.pdb; do head -1 $file; done) | sort -r
```

COMPND PROPANE

COMPND PENTANE

COMPND OCTANE

COMPND METHANE

COMPND ETHANE

COMPND CUBANE



zip	Create a compressed zip file with other files in it
for; do done;	Loop over a list of data and run a command once for each element in the list





created by

Steve Crouch

July 2011



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All this typing is giving me RSI

Didn't we use a file to store the commands in earlier examples?

All this typing is giving me RSI

Didn't we use a file to store the commands in earlier examples?

 Yes we did. Let's have a look at how that works...



If you put commands in a file and chmod the file to be executable then you can run the file as a command.

```
SSTDMSJP01:test sjp23$ cat > y.sh

for i in *

do

echo == $i ==

head -1 $i

tail -1 $i

Done

SSTDMSJP01:test sjp23$ chmod 700 y.sh
```

```
SSTDMSJP01:test sjp23$ ./y.sh
== a.txt ==
Hi there
XXX
== b.txt ==
File B
File B
== y.sh ==
for i in *
done
SSTDMSJP01:test sjp23$
```

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What happens when I try to run a file that is not a script?

```
$ more a.txt
Hi there
this
is
file a
Xxx$
```

Unintended consequences

```
$ chmod 700 a.txt
$ ./a.txt
./a.txt: line 1: Hi: command not found
./a.txt: line 2: this: command not found
./a.txt: line 3: is: command not found
a: cannot open `a' (No such file or directory)
./a.txt: line 5: xxx: command not found
$
```

```
Hi there
this
is
file a
Xxx
```

Unix Shell

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How to make sure your script is a script

- 1) Only use the execute (x) permission if you are going to execute it.
- 2) Use an interpreter header as the first line of the file. (You can use the which bash to find your bash programs location.)

```
#!/bin/bash
for j in *
```

What about other control structures

```
If test —e myfile; then ...; fi
Case ...; Esac
While ...
```

I'm not going to tell you because

- 1)you can find this out on your own (man bash)
- 2)if you find yourself using if and case then you should probably switch to a programming language like python. It's safer.

Unix Shell