

## The Unix Shell

### **Advanced Shell Tricks**



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"How should I do this?"

Some technical problem...



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With smartphones, you'll often hear people say something like

"There's an app for that... check this out!"





"How should I do this?"

# With smartphones, you'll often hear people say something like

"There's an app for that... check this out!"





Whereas Unix shell programmers will say

"There's a shell trick for that... check this out!"

- 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 -l \*.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

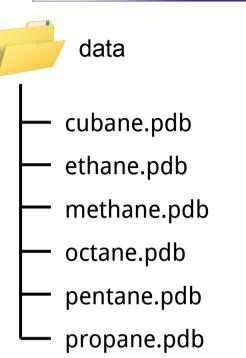


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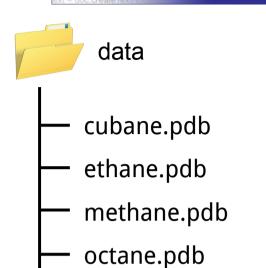
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But there are other useful things we can do with these – let's take a look...





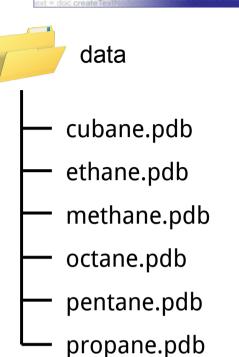
software carpentry



pentane.pdbpropane.pdb

The 'redirection' operator

#### software carpentry



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?

\$ ls \*.ent > more-files



- cubane.pdb
- ethane.pdb
  - methane.pdb
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- pentane.pdb
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- decane.ent

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

\$ cat files more-files > all-files—files into a

Instead, we can do...

\$ ls \*.ent >> files



append

file

single new

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

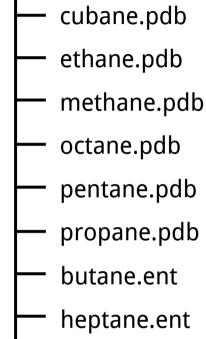
data

#### First, let's revisit redirection...

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

Instead, we can do...

Note the double >'s - the append' operator



hexane.ent

nonane.ent

decane.ent

append

file

single new



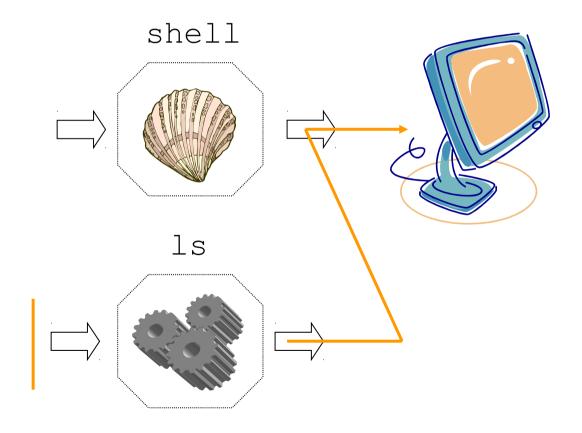
We know that...

Normally, standard output is directed to a display:



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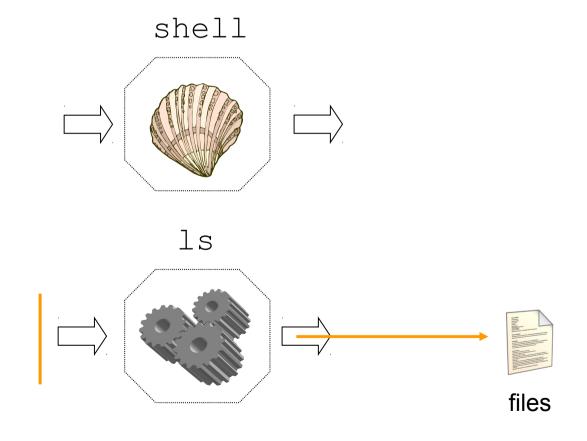




We know that...

Normally, standard output is directed to a display:

But we have redirected it to a file instead:





**Unix Shell** 



For example...

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

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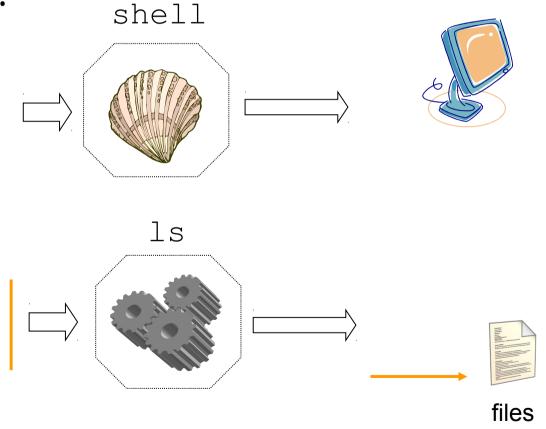
But why isn't the error message in files?





So what was happening with the previous

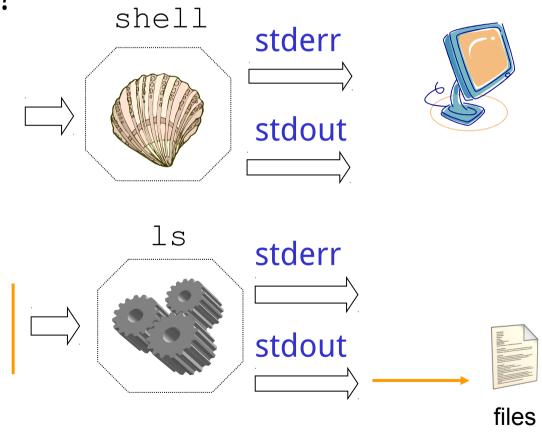
example?





So what was happening with the previous

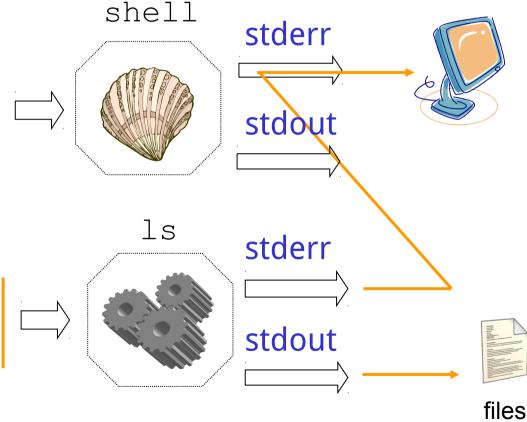
example?





So what was happening with the previous

example?





Unix Shell Advanced Shell Tricks

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

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

Redirect as before, but with a slightly different operator

**Unix Shell** 

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

Now we have any error messages stored in *error-log* 

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

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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.



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

**Unix Shell** 

Both stdout and stderr can be referenced by numbers:

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

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Refers to Refers stdout to stderr

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\$ 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

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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



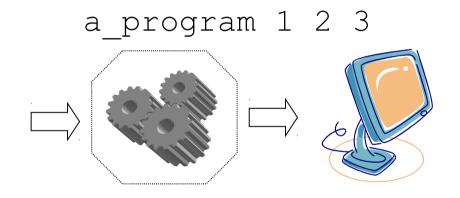
- > 1> Redirect stdout to a file
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- > 1> Redirect stdout to a file
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- >> 1>> Redirect and append stdout to a file
  - 2>> Redirect and append stderr to a file
  - &>> Redirect and append both stdout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





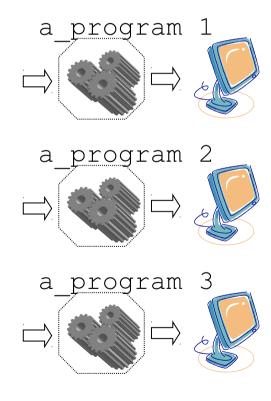




But what about running the same program separately, for each input?

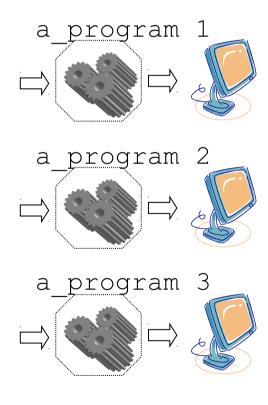


But what about running the same program separately, for each input?





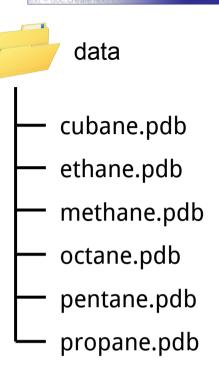
But what about running the same program separately, for each input?



We can use *loops* for this...



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





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

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

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%) ← from the zip

The zip file

we wish to

create
```

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%) ← from the zip

The zip file The file(s) command

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

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
cotane.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
```





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 ==> cubane.pdb <== (it's not in the file) COMPND CUBANE ==> ethane.pdb <== COMPND FTHANF ==> methane.pdb <== COMPND MFTHANF



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



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

Perhaps we only want the actual first lines...





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

Unix Shell Advanced Shell Tricks



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

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



```
$ 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 ls \*.pdb; do head -1 \$file; done) | sort -r

Unix Shell Advanced Shell Tricks



Simple!

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

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



## Simple!

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

COMPND PROPANE

COMPND PENTANE

COMPND OCTANE

COMPND METHANE

COMPND ETHANE

COMPND CUBANE

zip

for ...; do ... done;

Create a compressed zip file

with other files in it

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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