

Chaining and nesting commands

Lecture #5 - COMP 364 January 15, 2010, updated 2012 Derek Ruths

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Snapping commands together

- Output & input redirection
- Pipes
- Executing multiple commands in sequence
 - Using the semicolon
 - Batch files

Output redirection

- Is -1 ~/Projects > projects.list
- egrep -o "^[[:space:]]*gene[[:space:]]+[[:digit:]]+\.\.[[:digit:]]+" > ~/Ecoli/genes.txt
- Exercise:
 - I have an address book file called *address.txt*. Each line has the format: *LName, FName, Street, City, Province, Zip*. How do I store all the names (and only the names) into a file called *names.txt*?

Input & output on the command line

- Standard out: almost everything that is printed as a result of executing a command
- Standard error: the error text that is printed when something bad happens (or you did something wrong). The redirection operator we just learned doesn't capture standard error.
- Standard in: an opportunity to input text by hand into a command.
 - Standard in is often expected if you don't specify a file for a command that expects one. Type *ctrl-D* to indicate that you're done entering text.
 - egrep -o "H."
 - How would I use *cat* to store a bunch of text into a file called *foo.txt*?

Complete output redirection

- Use "&>" to redirect **all** output to the file designated.
- ls -1 -a5 &> log.txt

Input redirection

- The "<" operator feeds the contents of a file to a command via standard input
- egrep ".*html" < files.txt this egrep command operates on the contents of files.txt

Pipeline exercises

- "|" makes the output from one command the input for another. (Standard out is "piped" into standard in)
- |s -1 | wc -|
- How would you count the number of characters in the first 13 lines of file data.txt?
- How would you store in *genes.txt* a list of all files in a directory that start with the word "gene", followed by a number between 200 and 300 (inclusive), and carries the extension ".fasta"?
- When would you use input redirection over pipes?

Semi-colons: executing multiple commands

- A semi-colon acts like a *return* at the end of a line.
- cp foo.txt bar.txt; cat bar.txt copies the file, then prints it out
- rm -rf backup/hsapiens; cp -r hsapiens backup

Batch files

- A file that executes a series of commands
- Can take arguments from the command line
- Good for:
 - Doing complex tasks
 - Capturing common tasks

#!/bin/sh egrep "^[[:space:]]*gene[[:space:]]+[[:digit:]]+\.\.[[:digit:]]+\$" \$1

Example batch files

#!/bin/sh

egrep "^[[:space:]]*gene[[:space:]]+[[:digit:]]+\.\.[[:digit:]]+\$" \$1 > \$2

#!/bin/sh
egrep "^ORGANISM[[:space:]]+" \$1
echo -n "File size: "
wc -c \$1
echo -n "Number of genes: "
egrep -c "^[[:space:]]*gene[[:space:]]+[[:digit:]]+\.\.[[:digit:]]+\$" \$1

1.Note: you need to make a script executable

2.Command to execute a script: ./<script name>