

## Command Line: Bash Scripting Workshop Handout

	1 cd data-shell/molecules/
	2 head -n 12 octane.pdb
	3 head -n 12 octane.pdb   tail -n 10
make	4 vi middle.sh
script	5       head -n 12 octane.pdb   tail -n 10
	6 bash middle.sh
argument	7 vi middle.sh
	8       head -n 12 \$1   tail -n 10
	9 bash middle.sh octane.pdb
	10 bash middle.sh "high octane.pdb"
quote your	11 vi middle.sh
variable	12       head -n 12 "\$1"   tail -n 10
	13 bash middle.sh "high octane.pdb"
multiple	14 vi middle.sh
arguments	15       # Select lines from the middle of a file.
	16       # Usage: bash middle.sh filename end_line num_lines
	17       head -n "\$2" "\$1"   tail -n "\$3"
	18 bash middle.sh pentane.pdb 12 10
	19 bash middle.sh pentane.pdb 19 17
loops	20 cd ../creatures
	21 vi list_creatures.sh
	22       for filename in basilisk.dat unicorn.dat
	23       do
	24           head -n 2 "\$filename"   tail -n 1
	25       done
	26 bash list_creatures.sh

**Note:** Line numbers are inserted for the ease of referring to each command. Indented are the lines that should be typed in the file.

Expanding	27 vi copy_files.sh
wildcard	28       for filename in *.dat

Processing	29	do
Files	30	echo "\$filename"
	31	done
	32	bash copy_files.sh
	33	vi copy_files.sh
	34	for filename in *.dat
	35	do
	36	echo 'cp "\$filename" original-"\$filename"'
	37	done
	38	bash copy_files.sh
	39	vi copy_files.sh
Introduce \$@	40	for filename in \$@
	41	do
	42	echo 'cp "\$filename" original-"\$filename"'
	43	cp "\$filename" original-"\$filename"
	44	done
	45	bash copy_files.sh *.dat
Permission	46	rm original*.dat
to execute	47	ls -l copy_files.sh
and define	48	chmod +x copy_files.sh
shebang	49	vi copy_files.sh
	50	#!/usr/bin/env bash
	51	for filename in \$@
	52	do
	53	echo 'cp "\$filename" original-"\$filename"'
	54	cp "\$filename" original-"\$filename"
	55	done
	56	./copy_files.sh *.dat

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