

## Command Line: Bash Scripting Workshop Handout

	1.cd data-shell/molecules/
	2. head -n 15 octane.pdb
	3. head -n 15 octane.pdb   tail -n 5
make	4.vi middle.sh
script	5.head -n 15 octane.pdb   tail -n 5
	6.bash middle.sh
argument	7.vi middle.sh
	8.head -n 15 \$1   tail -n 5
	9.bash middle.sh octane.pdb
	10.bash middle.sh "high octane.pdb"
quote your	11.vi middle.sh
variable	12.head -n 15 "\$1"   tail -n 5
	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 15 5
	19.bash middle.sh pentane.pdb 20 5
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

Expanding	27. cp *.dat original-*.dat
wildcard	28. vi copy_files.sh
Processing	29. for filename in *.dat
Files	30. do
	31.     echo "\$filename"
	32. done
	33. bash copy_files.sh
	34. vi copy_files.sh
	35. for filename in *.dat
	36. do
	37.     echo "cp \$filename original-\$filename"
	38. done
	39. bash copy_files.sh
Introduce \$@	40. vi copy_files.sh
	41. for filename in \$@
	42. do
	43.     echo cp "\$filename" original-"\$filename"
	44. done
	45. bash copy_files.sh *.dat
Permission	46. ls -l copy_files.sh
to execute	47. chmod +x copy_files.sh
and define	48. vi copy_files.sh
shebang	49. #!/usr/bin/env bash
	50. for filename in \$@
	51. do
	52.     echo cp "\$filename" original-"\$filename"
	53. done
	54. ../copy_files.sh *.dat