Linux Cheat Sheet : Cygwin on Windows

Commands in Course Order

Command	Usage	Comment
pwd	pwd	Print your current directory (folder) location
ls	ls	List the files in the current folder
mkdir	mkdir Blast	Make a new folder. Example Blast
cd	cd /Blast	Change to another folder like Blast
cd	cd c:/	Change to C drive
cd	cd /	Change to the root directory. Cygwin files are here
man	man pwd	Show the manual pages for all command
cat >	cat > file1	Create file1 and write data to it
cat >>	cat >> file1	Add new lines to the bottom of file1
cat	cat file1	Show/display contents of file1 to the screen
cat	cat file1 file2	Show/display contents of file1 and file2 to the screen
sort	sort file1	Sort the contents of file1
sort	sort file1 file2	Sort the contents of file1 and file2 together
alias	alias dog = “cat”	Assign the work dog to the cat command
alias	alias path = “/BioDownload/bin/”	Type path instead of /BioDownload/bin/
|	cat file1 file2 | sort	Called Pipe. Places output of cat into sort
head	head TA496Seq1	View the first few lines of a file, especially a large file
tail	tail TA496Seq1	View the first few lines of a file, especially a large file
less	less TA496Seq1	View a large file and control the output
cp	cp file1 file2_copy	Make a copy of file1 and call it file2_copy
cp	cp file1 /Bioinfo	Make a copy of file1 and place it in the folder Bioinfo
cp	cp file1 /Bioinfo/cp_test	Copy file1 into the folder Bioinfo and call it cp_test
mv	mv file1 /Bioinfo	Move file1 into the folder Bioinfo
rm	rm file1	Permanently delete file1
rm	rm /Bioinfo/file2	Delete file2 which is located in the Bioinfo folder
rmdir	rmdir /Bioinfo	Remove the folder called Bioinfo
grep	grep “ATG” file1	Search for ATG in file1
grep	grep “ATG” file1 file2	Search for ATG in file1 and file2
grep	grep -i “ATG” file1	Search for ATG in file1 regardless of case: Atg, atg, ATg, and so on
grep	grep -ic “ATG” file1	Search but return only a count of occurrences of all ATG
grep	An excellent reference	www.cyberciti.biz/faq/howto-use-grep-command-in-linux-unix/

Commands in Alphabetical Order

Command	Usage	Comment
|	cat file1 file2 | sort	Called Pipe. Places output of cat into sort
alias	alias dog = “cat”	Assign the work dog to the cat command
alias	[1]alias pathx = “/BioDownload/bin/”	Type pathx instead of /BioDownload/bin/
cat	cat file1	Show/display contents of file1 to the screen
cat	cat file1 file2	Show/display contents of file1 and file2 to the screen
cat >	cat > file1	Create file1 and write data to it
cat >>	cat >> file1	Add new lines to the bottom of file1
cd	cd /Blast	Change to another folder like Blast
cd	cd c:/	Change to C drive
cd	cd /	Change to the root directory. Cygwin files are here
cp	cp file1 file2_copy	Make a copy of file1 and call it file2_copy
cp	cp file1 /Bioinfo	Make a copy of file1 and place it in the folder Bioinfo
cp	cp file1 /Bioinfo/cp_test	Copy file1 into the folder Bioinfo and call it cp_test
grep	grep “ATG” file1	Search for ATG in file1
grep	grep “ATG” file1 file2	Search for ATG in file1 and file2
grep	grep -i “ATG” file1	Search for ATG in file1 regardless of case: Atg, atg, ATg, and so on
grep	grep -ic “ATG” file1	Search but return only a count of occurrences of all ATG
grep	An excellent reference	www.cyberciti.biz/faq/howto-use-grep-command-in-linux-unix/
head	head TA496Seq1	View the first few lines of a file, especially a large file
less	less TA496Seq1	View a large file and control the output
ls	ls	List the files in the current folder
man	man pwd	Show the manual pages for all command
mkdir	mkdir Blast	Make a new folder. Example Blast
mv	mv file1 /Bioinfo	Move file1 into the folder Bioinfo
pwd	pwd	Print your current directory (folder) location
rm	rm file1	Permanently delete file1
rm	rm /Bioinfo/file2	Delete file2 which is located in the Bioinfo folder
rmdir	rmdir /Bioinfo	Remove the folder called Bioinfo
sort	sort file1	Sort the contents of file1
sort	sort file1 file2	Sort the contents of file1 and file2 together
tail	tail TA496Seq1	View the first few lines of a file, especially a large file

[1] Note: there are certain words that are reserved as “commands”. For example we could not use “path” as an alias, but we could use “pathx”.