

Basic form:

command *modifier target* modifier(s) are usually optional and modify how the command works; target is what you want the command to work on, usually a file or directory

Getting help

- man *command* give manual page for command
- whatis *command* give short description of command

Directory commands

- pwd tells you the pathname of the current working directory
- cd set current working directory to home directory
- cd .. set current working directory one directory up from current
- cd *dirname* set current working directory to the directory named **dirname**
- cd *dir1/dir2* set current working directory to **dir2** which is inside **dir1**

File commands

- ls list all the files in the current directory
- ls -l returns detailed list of files in current directory
- ls *.ext list all files that end in .ext

Other useful commands

- passwd use this to change your password
- cat *filename* stream out entire contents of filename
- more *filename* display filename contents one page at a time; use "space" to go forward, "b" to go back, "q" to quit

Bioinformatics

- blastall -p *program* -d *database* -i *query* -o *output.file*
 - example with mandatory items:
blastall -p blastp -d swissprot -i mypep.tfa -o mypep.blastp
 - Other common settings (optional):
 - -T format output file as html (web page)
 - -e *number* set e cutoff value to *number*
 - -F turn filter on (T) or off (F)
 - -n use megablast (faster) algorithm
- RepeatMasker -species *species* *input.file*
 - -species -species can be one of mouse, rat, cow, pig, cat, dog, chicken, fugu, danio, cionasav, cionaint, drosophila, anopheles, elegans, diatom, arabidopsis, rice, wheat, and maize
- herne -s *sequence.file* -b *blast.output.file*
 - *sequence.file* sequence file used in blast search
 - *blast.output.file* output file with blast results, can be html or plain text
 - -m *rmsk.out* include repeat locations from RepeatMasker (optional)
 - -r use blue/red color scheme (optional)