

# **Linux command line basics**

## **II: downloading data and controlling files**

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Fall 2015

# Things you should know about programming

**Learning programming has to go through the hands-on practice, a lot of practice**

Hearing what I describe about a command or a program helps, but you will not be able to do it unless you type in the codes and run it to see what happens

Reading others' codes helps but often is harder than writing it by yourself from scratch

**Although painful and frustrating, trouble-shooting is normal and part of the learning experience (ask experienced people or google)**

**To avoid errors, you have to follow rules; most errors occurred in programming are because of not knowing rules or forgetting rules**

Use comments in case you forget what you've written means

write-> run -> errors -> edit-> errors -> ..... -> run -> success

**Good news: finished scripts could be reused or edited for later use**

# Homework #7

Create a folder under your home called hw7

Change directory to hw7

Go to NCBI ftp site, find the genome, bacteria, ecoli MG1655 folder, and download the ptt file and the faa file in there

Create a copy of the ppt file, if the original file is called A.ppt, name the copied file A.ppt.bak

Do the same thing for the faa file

For the ppt file, use vi to replace .. in the location column with a tab space

For the faa file, use vi to delete anything after a space in the description line

Write a report (in **word or ppt**) to include all the operations/commands and screen shots.

**Due on Nov 10** (send by email)

Office hour:

**Tue, Thu and Fri 2-4pm, MO325A**

**Or email: [yyin@niu.edu](mailto:yyin@niu.edu)**

## What we learned last class:

file system,  
relative/absolute paths,  
working folder, home folder

ssh, pwd, ls  
cd, mkdir, rmdir, rm, man  
cp, mv

If things go wrong, try:

Ctrl+c (sometimes multiple times)

q to exit from man page

The absolute basics	File control	Viewing, creating, or editing files	Misc. useful commands	Power commands	Process-related commands
ls	mv	less	man	uniq	top
cd	cp	head	chmod	sort	ps
pwd	mkdir	tail	source	cut	kill
	rmdir	touch	wc	tr	
	rm	nano		grep	
	(pipe)			sed	
	> (write to file)				
	< (read from file)				

View files: more, less, head, tail

## How you use Tab key to autocomplete

less /home/ then hit tab twice, you will see all files/folders under /home/

less /home/yyin/ then hit tab twice, you will see ...

less /home/yyin/U then hit tab once, Unix\_and\_Perl\_course will be autocompleted

less /home/yyin/Unix\_and\_Perl\_course/ keep doing this until you get

less /home/yyin/Unix\_and\_Perl\_course/Data/Arabidopsis/At\_proteins.fasta

q: quit viewing                   ↑ or ↓: move up or down a line

space: next page                 />>: search for text '>'

B or PgUp: back a page           F or PgDn: forward a page

n: find next occurrence of 'abc'

G: go to the end     ?: find previous occurrence of 'abc'

See next page for screen shots

## How you use Tab key to autocomplete

```
yyin@ser:~$ less /home/
elfitzek/ yyin/
yyin@ser:~$ less /home/yyin/
.bash_history          .gconf/                .mission-control/
.bash_logout          .gksu.lock            .mozilla/
.bashrc               .gnome/               .pki/
.cache/              .gnome2/              .profile
.compiz-1/           .goutputstream-11LJX .pulse/
.config/             .gstreamer-0.10/     .pulse-cookie
current.zip          .gtk-bookmarks        .ssh/
.dbus/               .gvfs/                Unix_and_Perl_course/
.dmrc                 .ICEauthority         .Xauthority
Documents/           .lftp/                .xsession-errors
Downloads/           .local/                .xsession-errors.old
.fontconfig/         __MACOSX/
yyin@ser:~$ less /home/yyin/Unix_and_Perl_course/
Applications/  Data/          .DS_Store
Code/          Documentation/ .profile
yyin@ser:~$ less /home/yyin/Unix_and_Perl_course/Data/
Arabidopsis/  GenBank/      Unix_test_files/
.DS_Store     Misc/
yyin@ser:~$ less /home/yyin/Unix_and_Perl_course/Data/
Arabidopsis/  GenBank/      Unix_test_files/
.DS_Store     Misc/
yyin@ser:~$ less /home/yyin/Unix_and_Perl_course/Data/GenBank/
E.coli.genbank  Y.pestis.genbank
yyin@ser:~$ less /home/yyin/Unix_and_Perl_course/Data/GenBank/E.coli.genbank
```

more is similar to less, but can do less than less

```
more /home/yyin/Unix_and_Perl_course/Data/Arabidopsis/At_genes.gff
```

head to dump the top few lines to the screen

```
head /home/yyin/Unix_and_Perl_course/Data/Arabidopsis/chr1.fasta
```

```
head -20 /home/yyin/Unix_and_Perl_course/Data/Arabidopsis/chr1.fasta
```

tail to dump the last few lines to the screen

```
tail /home/yyin/Unix_and_Perl_course/Data/Arabidopsis/intron_IME_data.fasta
```

```
tail -20 /home/yyin/Unix_and_Perl_course/Data/Arabidopsis/intron_IME_data.fasta
```

more, less, head, tail do not load all file content to the memory  
You can edit the file content either, they are just viewers



# Create or edit files

Text editors:

nano

pico

vi

Suppose you are at your home:

Write the top part of the `intAt_genes.gff` file to a new file

```
head -20 /home/yyin/Unix_and_Perl_course/Data/Arabidopsis/At_genes.gff > head
```



Try nano (Intuitive user interface)

```
nano head
```

Try vi (command-driven interface, but much more power)

```
vi head
```

Create a file from scratch using vi.

- 1) you type *vi filename* and hit *enter*
- 2) after you are in *vi*, type *i* to get into edit mode and copy & paste content in *vi*
- 3) hit *Esc* to exit edit mode and then *:x* to save the file and exit *vi*.

# Input and output redirection: **the greater-than sign**

Unix has a special way to direct input and output from commands or programs.

By default, the input is from keyboard (called standard input, *stdin*): you type in a command and Shell takes the command and executes it.

The standard output by default is to the terminal screen (*stdout*);

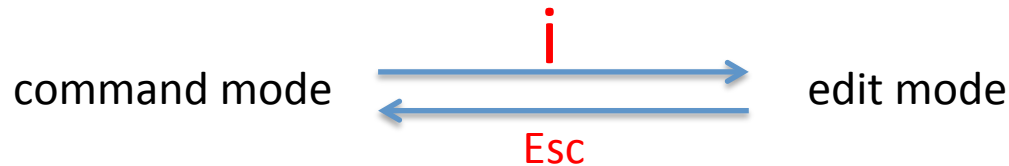
if the command or program failed, you will also have standard errors dumped to the terminal screen (*stderr*).

However, if you do not want the output dumped to the screen, you can use “>” to redirect/write the output into a file. For example, try

```
ls /home/yyin  
ls /home/yyin > list  
ls /home/yyim  
ls /home/yyim 2> err
```

“2>” to dump the error message  
No space here!

# vi basics



The following commands **operate in command mode (hit Esc before using them)**

<b>x</b>	delete one character at cursor position
<b>u</b>	undo
<b>dd</b>	delete the current line
<b>G</b>	go to end of file
<b>1G</b>	go to beginning of file
<b>10G</b>	go to line 10
<b>\$</b>	go to end of line
<b>1</b>	go to beginning of line
<b>:q!</b>	exit without saving
<b>:w</b>	save (but not exit)
<b>:wq or :x</b>	save and exit
<b>Arrow keys:</b>	move cursor around (in both modes)

<http://cbsu.tc.cornell.edu/ww/1/Default.aspx?wid=36>

# Search and substitution in vi

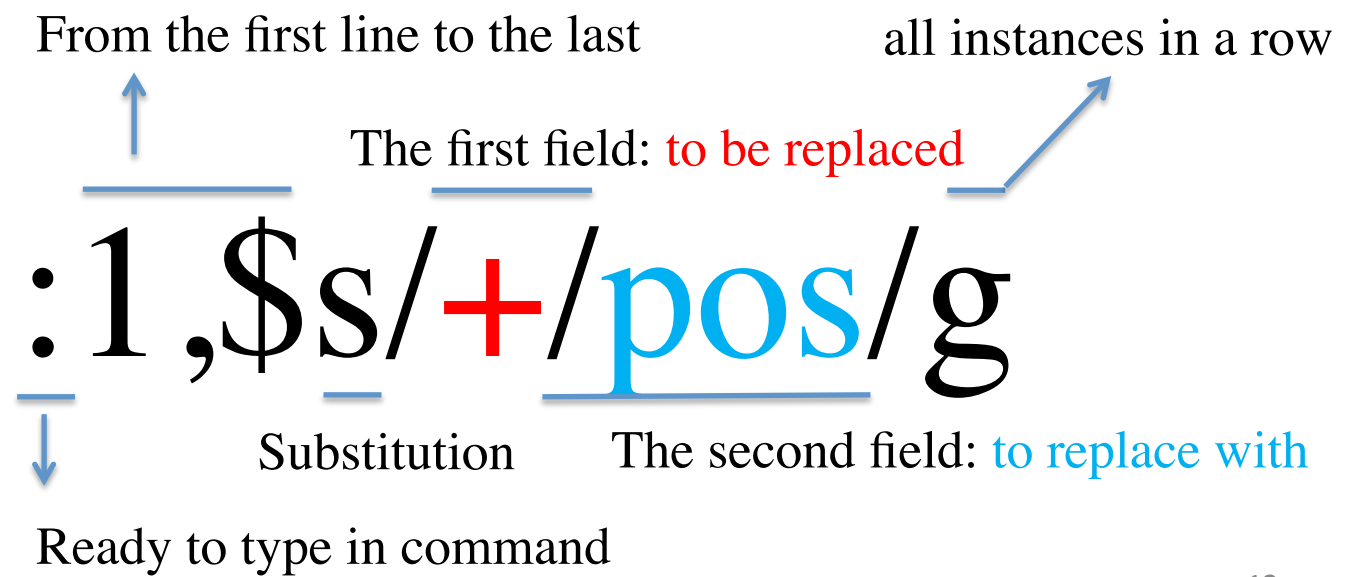
In command mode, you can do a number of fancy things. The most useful are:

- **Search**: hit slash ("/") to get the cursor to the left-bottom corner; you can type any word or letter to search it; type *n* to go to the next instance

- **Replace**: hit *Esc* (at any time, hitting *Esc* to get back to the default status is the safest thing to do) and type `:1,$s/+/pos/g` and then enter will replace all "+" to "pos".

Try this in  
`vi head`

- 1) hit *Esc* to exit edit mode and then `:q!` to NOT save the file and exit *vi*.



## Wild cards and regular expression

Regular expression (regex or regexp) is a very powerful tool for text processing and widely used in text editors (e.g. vi) and programming languages (e.g. Shell commands: sed, awk, grep and perl, python, PHP) to automatically edit (match and replace strings) texts.

Finding and replacing exact words or characters are simple, e.g. the vi example shown above

However, if you want to match multiple words or characters, you will need wildcards or patterns.

# a list of commonly used wildcards and patterns:

- \* any numbers of letters, numbers and characters except for spaces and special characters, e.g. `()[]+\V/$@#%;;,?`
- .
- ^ start of a line **caret**
- \$ end of a line
- ^\$ an empty line, i.e. nothing between ^ and \$
- [] create your own pattern, e.g. `[ATGC]` matches one of the four letters only, `[ATGC]{2}` matches two such letters; `[0-9]`: any numbers
- \w any letter (a-z and A-Z)
- \d any number (0-9)
- + previous items at least one times, e.g. `\w+` matches words of any sizes
- {n} previous items n times, e.g. `\w{5}` matches words with exactly five letters
- \s space **Curly brackets**
- \t tabular space
- \n new line

## Use regex inside vi

This overwrite the head file:

```
head -20 /home/yyin/Unix_and_Perl_course/Data/Arabidopsis/At_proteins.fasta > head
```

```
vi head
```

Inside vi, try

```
:1,$s/ *///g
```

Hit u to undo

What about

```
:1,$s/ .*//g
```

- 1) hit **Esc** to exit edit mode and then **:x** to save the file and exit *vi*.

# Get data from remote ftp/http website

ftp  
lftp  
sftp  
ncftp

<b>lftp</b> addr	command to connect to a remote ftp server
<b>cd</b> dir	change to the directory
cd ..	change to the upper folder (..)
<b>ls</b>	list files and folders in the current directory at once
<b>ls</b> dir	list files and folders in dir at once
<b>ls</b>   less	list page by page (good if the list is too long)
<b>get</b> file	get a file
<b>mirror</b> dir	get a folder
<b>zless</b> file	view the file content
<b>by</b> or <b>bye</b>	exit lftp



NCBI ftp site :

Connect to NCBI ftp site:

```
lftp ftp.ncbi.nih.gov
```

The prompt will change to:

```
lftp ftp.ncbi.nih.gov: />
```

After '>' you can type in command and hit enter:

```
lftp ftp.ncbi.nih.gov: />ls
```

The ftp site can also be accessed through a web browser



```

lftp ftp.ncbi.nih.gov: /> ls
dr-xr-xr-x  3 ftp      anonymous      4096 May 27  2011 1000genomes
-r--r--r--  1 ftp      anonymous     10738466816 Dec  6 14:25 10GB
-r--r--r--  1 ftp      anonymous     1074790400 Dec  6 14:25 1GB
-r--r--r--  1 ftp      anonymous      1868 Dec  5 21:45 README.ftp
lr--r--r--  1 ftp      anonymous      29 Dec  5 22:08 asn1-converters -> toolbox/ncbi_tools/converters
dr-xr-xr-x 12 ftp      anonymous     184320 Dec 14 23:00 bigwig
dr-xr-xr-x  4 ftp      anonymous      4096 Jan 28 16:10 bioproject
dr-xr-xr-x  2 ftp      anonymous      4096 Jan 28 09:53 biosample
dr-xr-xr-x 10 ftp      anonymous      4096 May 24  2012 blast
dr-xr-xr-x  3 ftp      anonymous      4096 Sep 13  2004 cgap
dr-xr-xr-x  4 ftp      anonymous      4096 May 25  2011 cn3d
dr-xr-xr-x 30 ftp      anonymous      4096 Jan 14 20:20 dbgap
dr-xr-xr-x 11 ftp      anonymous      4096 Jun  4  2006 entrez
dr-xr-xr-x  7 ftp      anonymous      4096 Oct 13  2011 epigenomics
dr-xr-xr-x  6 ftp      anonymous      4096 Aug  4  2006 fa2htgs
-r--r--r--  1 ftp      anonymous     3262 Dec  5 21:45 favicon.ico
dr-xr-xr-x 12 ftp      anonymous     65536 Dec 21 18:02 genbank
dr-xr-xr-x  6 ftp      anonymous      4096 Dec 13 19:24 gene
dr-xr-xr-x 97 ftp      anonymous      4096 Jan  9 22:54 genomes
dr-xr-xr-x 1073741824 ftp      anonymous      0 Jan 28 20:06 geo
dr-xr-xr-x 25 ftp      anonymous      4096 Sep 20  2011 hapmap
dr-xr-xr-x 13 ftp      anonymous      4096 Jan 27  2012 mmdb
dr-xr-xr-x  6 ftp      anonymous     49152 Dec 21 17:05 ncbi-asn1
dr-xr-xr-x 164 ftp      anonymous     8192 Dec  2 17:49 pub
dr-xr-xr-x 11 ftp      anonymous      4096 Nov 29 13:17 pubchem
dr-xr-xr-x  2 ftp      anonymous      4096 Jan 28 09:03 pubmed
dr-xr-xr-x 15 ftp      anonymous      4096 Jan 14 18:59 refseq
dr-xr-xr-x 57 ftp      anonymous      4096 Aug 20  2008 repository
-r--r--r--  1 ftp      anonymous      26 Dec  5 21:45 robots.txt
dr-xr-xr-x  5 ftp      anonymous      4096 Nov 14 14:07 sequin
dr-xr-xr-x  9 ftp      anonymous      4096 May 24  2010 sky-cgh
dr-xr-xr-x 17 ftp      anonymous      4096 Jan 18 18:23 snp
dr-xr-xr-x 13 ftp      anonymous      4096 May 16  2012 sra
dr-xr-xr-x  2 ftp      anonymous      4096 Sep 29  2004 tech-reports
dr-xr-xr-x 12 ftp      anonymous      4096 Jun 29  2011 toolbox
dr-xr-xr-x  5 ftp      anonymous      4096 Apr 24  2009 tpa
dr-xr-xr-x  4 ftp      anonymous      4096 Sep 13 15:46 variation
lftp ftp.ncbi.nih.gov: /> █

```

ls command:

list files and folders

Where bacterial genomes are in the ftp site?

```
lftp ftp.ncbi.nih.gov: /> cd genomes/  
lftp ftp.ncbi.nih.gov: /genomes> cd Bacteria  
lftp ftp.ncbi.nih.gov: /genomes/Bacteria> █
```

---

## The end of the page after `ls`

```
dr-xr-xr-x  2 ftp      anonymous      4096 Dec  6  2010 \_Nostoc\_azollae\_\_0708\_uid49725
-r--r--r--  1 ftp      anonymous 455294518 Jan 28 08:08 all.GeneMark.tar.gz
-r--r--r--  1 ftp      anonymous 102841288 Jan 28 08:14 all.Glimmer3.tar.gz
-r--r--r--  1 ftp      anonymous 227990948 Jan 28 12:02 all.Prodigal.tar.gz
-r--r--r--  1 ftp      anonymous 4532882964 Jan 28 08:42 all.asn.tar.gz
-r--r--r--  1 ftp      anonymous 1515030808 Jan 28 09:03 all.faa.tar.gz
-r--r--r--  1 ftp      anonymous 2190975020 Jan 28 09:20 all.ffn.tar.gz
-r--r--r--  1 ftp      anonymous 2416170041 Jan 28 09:55 all.fna.tar.gz
-r--r--r--  1 ftp      anonymous 9095708 Jan 28 10:29 all.frn.tar.gz
-r--r--r--  1 ftp      anonymous 6720488727 Jan 28 10:45 all.gbk.tar.gz
-r--r--r--  1 ftp      anonymous 548255240 Jan 28 11:37 all.gff.tar.gz
-r--r--r--  1 ftp      anonymous 182962489 Jan 28 11:41 all.ptt.tar.gz
-r--r--r--  1 ftp      anonymous 2600313 Jan 28 11:43 all.rnt.tar.gz
-r--r--r--  1 ftp      anonymous 357580 Jan 28 11:44 all.rpt.tar.gz
-r--r--r--  1 ftp      anonymous 4107354627 Jan 28 11:53 all.val.tar.gz
dr-xr-xr-x  2 ftp      anonymous      4096 Sep 25 04:11 alpha\_proteobacterium\_HIMB59\_uid175778
dr-xr-xr-x  2 ftp      anonymous      4096 Sep 25 04:12 alpha\_proteobacterium\_HIMB5\_uid175779
dr-xr-xr-x  2 ftp      anonymous      4096 Dec 20 05:32 bacterium\_BT\_1\_uid184079
dr-xr-xr-x  2 ftp      anonymous      4096 Dec  6  2010 cyanobacterium\_UCYN\_A\_uid43697
dr-xr-xr-x  2 ftp      anonymous      4096 Dec  6  2010 gamma\_proteobacterium\_HdN1\_uid51635
dr-xr-xr-x  2 ftp      anonymous      4096 Sep  1  2011 halophilic\_archaeon\_DL31\_uid72619
dr-xr-xr-x  2 ftp      anonymous      4096 Aug 20 04:10 secondary\_endosymbiont\_of\_Ctenarytaina\_eucalypti\_uid172737
dr-xr-xr-x  2 ftp      anonymous      4096 Nov  2 16:10 secondary\_endosymbiont\_of\_Heteropsylla\_cubana\_Thao2000\_uid172738
dr-xr-xr-x  2 ftp      anonymous      4096 Jan 28  2011 uncultured\_Termite\_group\_1\_bacterium\_phylotype\_Rs\_D17\_uid59059
lftp ftp.ncbi.nih.gov:/genomes/Bacteria> █
```

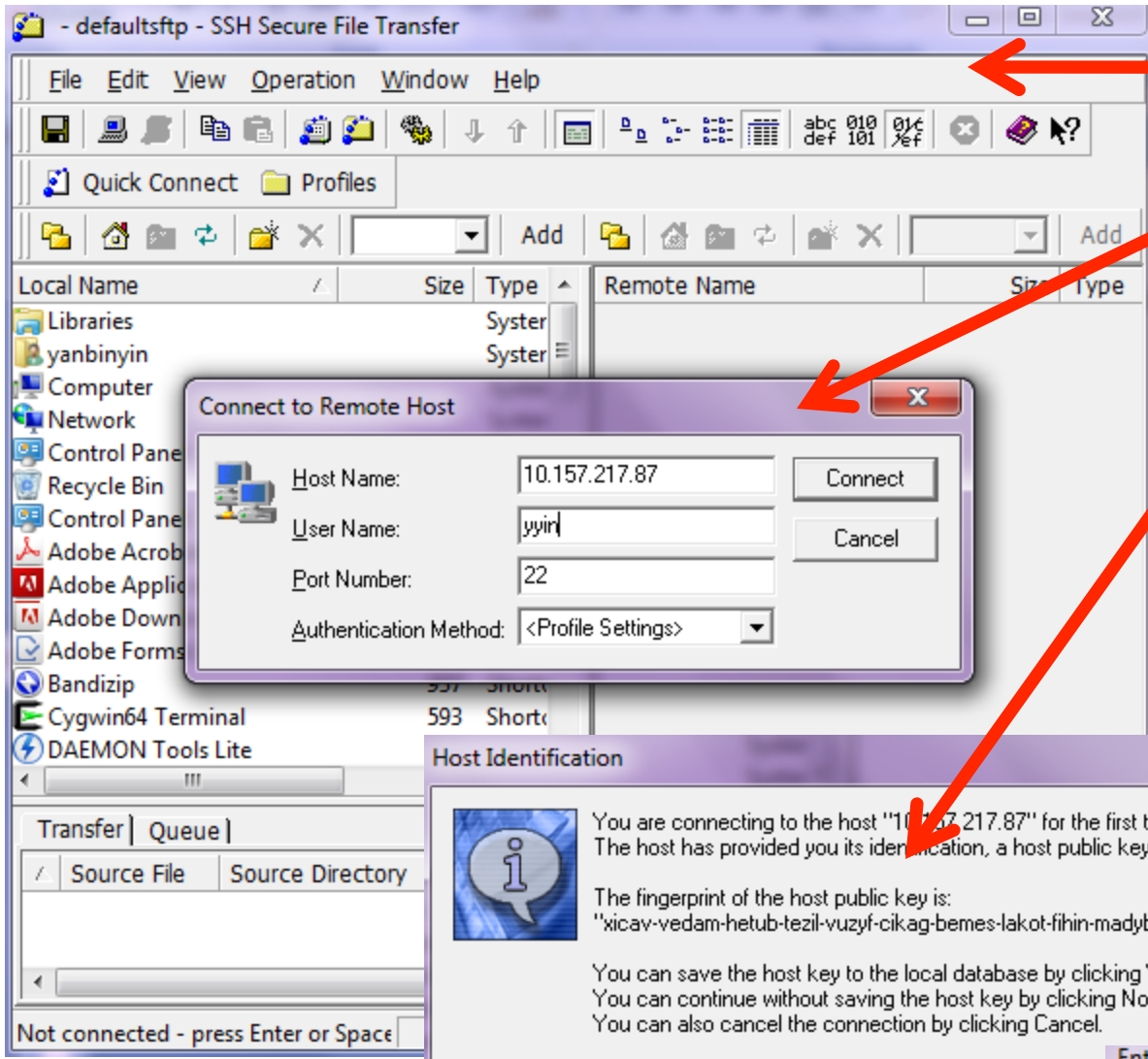
cd ne

Then press **tab key** to auto-complete or list

```
lftp ftp.ncbi.nih.gov:/genomes/Bacteria> cd Ne
Neisseria_gonorrhoeae_FA_1090_uid57611/
Neisseria_gonorrhoeae_NCCP11945_uid59191/
Neisseria_gonorrhoeae_TCDC_NG08107_uid161097/
Neisseria_lactamica_020_06_uid60851/
Neisseria_meningitidis_053442_uid58587/
Neisseria_meningitidis_8013_uid161967/
Neisseria_meningitidis_FAM18_uid57825/
Neisseria_meningitidis_G2136_uid162085/
Neisseria_meningitidis_H44_76_uid162083/
Neisseria_meningitidis_M01_240149_uid162079/
Neisseria_meningitidis_M01_240355_uid162075/
Neisseria_meningitidis_M04_240196_uid162081/
Neisseria_meningitidis_MC58_uid57817/
Neisseria_meningitidis_NZ_05_33_uid162077/
Neisseria_meningitidis_WUE_2594_uid162093/
Neisseria_meningitidis_Z2491_uid57819/
Neisseria_meningitidis_alpha14_uid61649/
Neisseria_meningitidis_alpha710_uid161971/
Neorickettsia_riisticii_Illinois_uid58889/
Neorickettsia_sennetsu_Miyayama_uid57965/
lftp ftp.ncbi.nih.gov:/genomes/Bacteria> cd Ne
```

# How to transfer file between a linux and a windows machine?

## Use SSH secure file transfer client



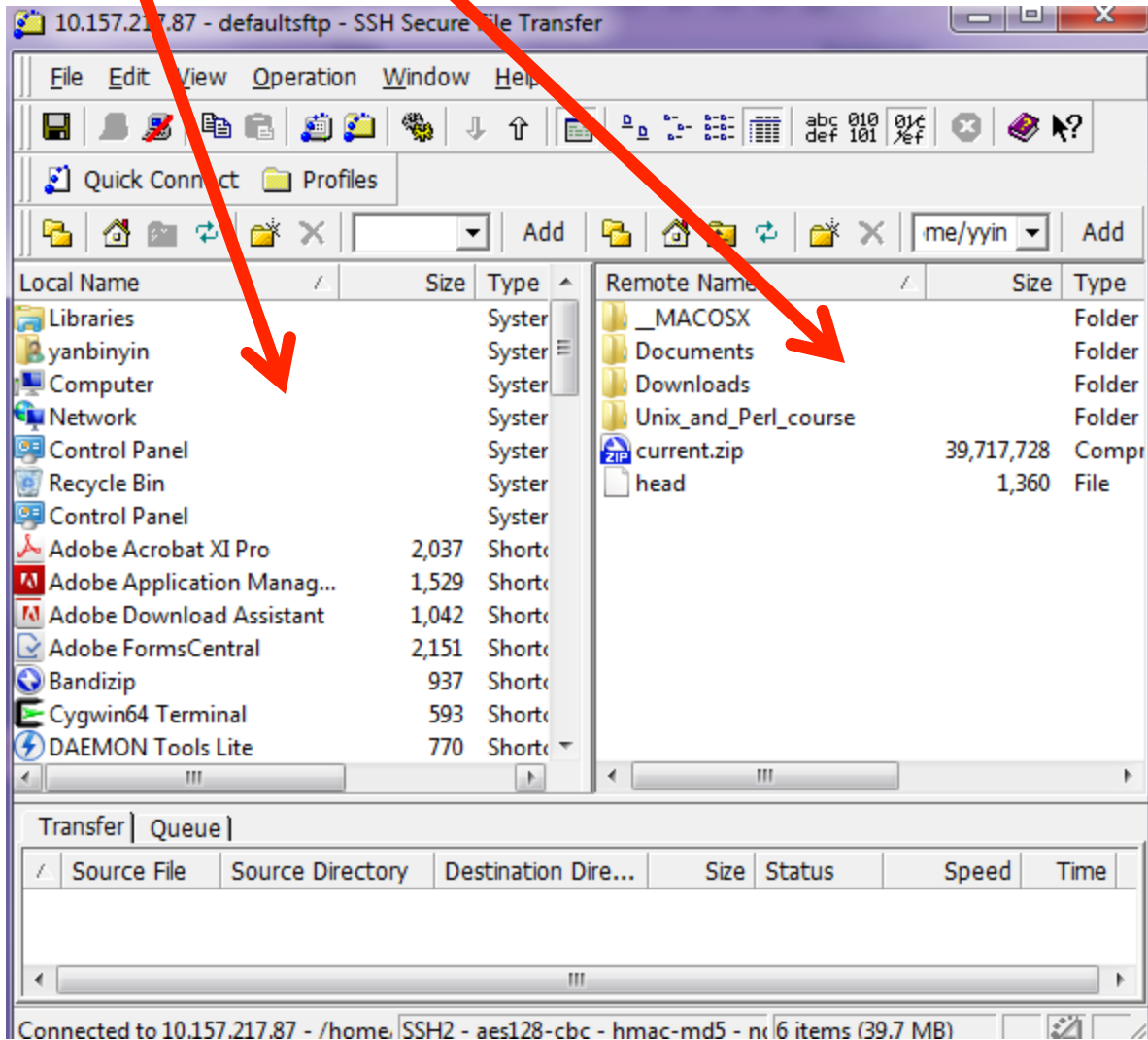
Open the software  
Hit enter

Put IP address  
Put user name  
Hit connect

Choose yes

Put password  
Hit ok

If transfer from local to remote: locate your file and drag to the right  
If transfer from remote to local: locate your file and drag to the left



# Transfer files between two Linux machines (or mac and linux)

**scp**: secure copy files/folders between hosts on a network

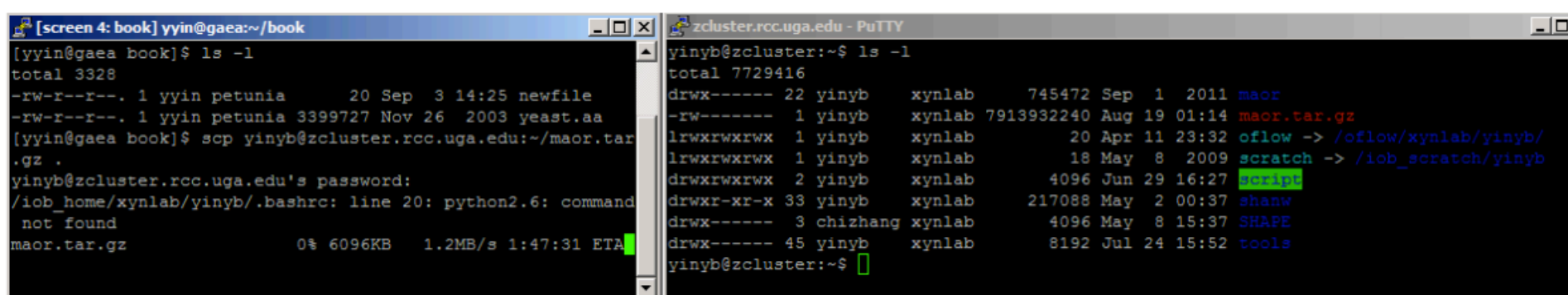
You are at a Linux or Mac machine, e.g. your laptop with Ubuntu installed and you want to copy some file from ser

Open a terminal in your machine

```
scp yyin@10.157.217.87:/home/yyin/Unix_and_Perl_course/Data/Arabidopsis/At_genes.gff .
```

```
scp username@IP:/path .
```

You will be asked for password on ser



The image shows two terminal windows side-by-side. The left window is titled '[screen 4: book] yyin@gaea:~/book' and shows the execution of the scp command. The right window is titled 'zcluster.rcc.uga.edu - PuTTY' and shows the remote host's directory listing.

```
[yyin@gaea book]$ ls -l
total 3328
-rw-r--r--. 1 yyin petunia    20 Sep  3 14:25 newfile
-rw-r--r--. 1 yyin petunia 3399727 Nov 26  2003 yeast.aa
[yyin@gaea book]$ scp yinyb@zcluster.rcc.uga.edu:~/maor.tar
.gz .
yinyb@zcluster.rcc.uga.edu's password:
/lob_home/xynlab/yinyb/.bashrc: line 20: python2.6: command
not found
maor.tar.gz          0% 6096KB  1.2MB/s 1:47:31 ETA
```

```
yinyb@zcluster:~$ ls -l
total 7729416
drwx----- 22 yinyb    xynlab    745472 Sep  1  2011 maor
-rw-----  1 yinyb    xynlab 7913932240 Aug 19  01:14 maor.tar.gz
lrwxrwxrwx  1 yinyb    xynlab    20 Apr 11 23:32 oflow -> /oflow/xynlab/yinyb/
lrwxrwxrwx  1 yinyb    xynlab    18 May  8  2009 scratch -> /lob_scratch/yinyb
drwxrwxrwx  2 yinyb    xynlab    4096 Jun 29 16:27 script
drwxr-xr-x 33 yinyb    xynlab 217088 May  2  00:37 shanw
drwx-----  3 chizhang xynlab    4096 May  8 15:37 SHAPE
drwx----- 45 yinyb    xynlab    8192 Jul 24 15:52 tools
yinyb@zcluster:~$
```



# wget

wget is a program useful for downloading files from both FTP and HTTP sites.

**wget is non-interactive:** you simply enter the necessary options and arguments on the command line and the file is downloaded for you.

**You must identify the links first:** browse a http webpage or a ftp site and locate the remote files/folders you want to download and then go to the terminal and type

```
wget http://cys.bios.niu.edu/yyin/teach/PBB/cesa-pr.fa
```

```
wget -q ftp.ncbi.nih.gov/blast/db/FASTA/yeast.aa.gz
```

```
wget -r -q
```

```
ftp://ftp.ncbi.nih.gov/genomes/Bacteria/  
Escherichia\_coli\_K\_12\_substr\_\_MG1655\_uid57779
```

```
wget -q
```

```
ftp.ncbi.nih.gov/blast/executables/LATEST/ncbi-blast-2.2.27+-  
x64-linux.tar.gz
```

```
wget ftp://emboss.open-bio.org/pub/EMBOSS/emboss-latest.tar.gz
```

It take time to download

**Put & at the end of command line to put the job to the background**

-q quiet

-r recursive (for folders)

# Archive and compress files/folders

To save disk space, we can compress large files if we do not intend to use them for a while. A lot of files downloaded from the web are compressed and need to be uncompressed before any processing can take place.

Common compressed formats:

**zless to view zipped files**

- **gzip** (gz)

**gzip my\_file** (*compresses file my\_file, producing its compressed version, my\_file.gz*)

**gzip -d my\_file.gz** (*decompress my\_file.gz, producing its original version my\_file*)

- **bzip2**

**bzip2 my\_file** (*compresses file my\_file, producing its compressed version, my\_file.bz2*)

**bunzip2 my\_file.bz2** (*decompress my\_file.bz2, producing its original version my\_file*)

Common compressed formats (continued):

- **zip**

**zip my\_file.zip my\_file1 my\_file2 my\_file3** *(create a compressed archive called my\_files.zip, containing three files: my\_file1, my\_file2, my\_file3)*

**zip -r my\_file.zip my\_file1 my\_dir** *(if my\_dir is a directory, create an archive my\_file.zip containing the file my\_file1 and the directory my\_dir with all its content)*

**zip -l my\_file.zip** *(list contents of the zip archive my\_file.zip)*

**unzip my\_files.zip** *(decompress the archive into the constituent files and directories)*

- **tar**

**tar -cvf my\_file.tar my\_file1 my\_file2 my\_dir** *(create a compressed archive called my\_files.tar, containing files my\_file1, my\_file2 and the directory my\_dir with all its content)*

**tar -tvf my\_file.tar** *(list contents of the tar archive my\_file.tar)*

**tar -xvf my\_files.tar** *(decompress the archive into the constituent files and directories)*

Use man tar to learn more

Common compressed formats (continued):

- **tgz** (also, **tar.gz** – essentially a combo of “tar” and “gzip”)

**tar -czvf my\_file.tgz my\_file1 my\_file2 my\_dir** *(create a compressed archive called my\_files.tgz, containing files my\_file1, my\_file2 and the directory my\_dir with all its content)*

**tar -tzvf my\_file.tgz** *(list contents of the tar archive my\_file.tar)*

**tar -xzvf my\_files.tgz** *(decompress the archive into the constituent files and directories)*

Wget the book materials of **Unix and Perl Primer for Biologists**

[http://korflab.ucdavis.edu/Unix\\_and\\_Perl/](http://korflab.ucdavis.edu/Unix_and_Perl/)

```
mkdir book
```

```
cd book
```

```
wget http://korflab.ucdavis.edu/Unix\_and\_Perl/current.zip
```

```
unzip current.zip
```

Unpackage the emboss package

```
cd
```

```
mkdir tools
```

```
cd tools
```

```
mv ../emboss-latest.tar.gz tools
```

```
tar -zxf emboss-latest.tar.gz &
```

# Check disk usage

Disk space is a limited resource, and you want to frequently monitor how much disk space you have used. To check the disk space usage for a folder, use the *du* (disk usage) command

```
yyin@ser:~$ du -hs .
```

```
318M      .
```

```
yyin@ser:~$ du -hs Unix_and_Perl_course/
```

```
131M      Unix_and_Perl_course/
```

To check how much space left on the entire storage file system, use the *df* command

```
yyin@ser:~$ df -h
Filesystem      Size  Used Avail Use% Mounted on
/dev/sdb1       412G   8.1G  383G   3% /
udev            24G    4.0K   24G   1% /dev
tmpfs           4.8G   900K   4.8G   1% /run
none            5.0M     0   5.0M   0% /run/lock
none            24G    156K   24G   1% /run/shm
/dev/sde        2.7T   202M   2.6T   1% /disk4
/dev/sda        2.7T   202M   2.6T   1% /disk1
/dev/sdc        2.7T   202M   2.6T   1% /disk2
/dev/sdd        2.7T   202M   2.6T   1% /disk3
none            24G    144M   24G   1% /tmp/guest-4ynGWF
```

- Save history of your commands:

```
history > hist1
```

```
less hist1
```

- Send message to other online users

```
write username (ctrl+c to exit)
```

- Change your password

```
passwd
```

**Ctrl+c** to tell Shell to stop current process

**Ctrl+z** to suspend

**bg** to send to background

**Ctrl+d** to exit the terminal (logout)