

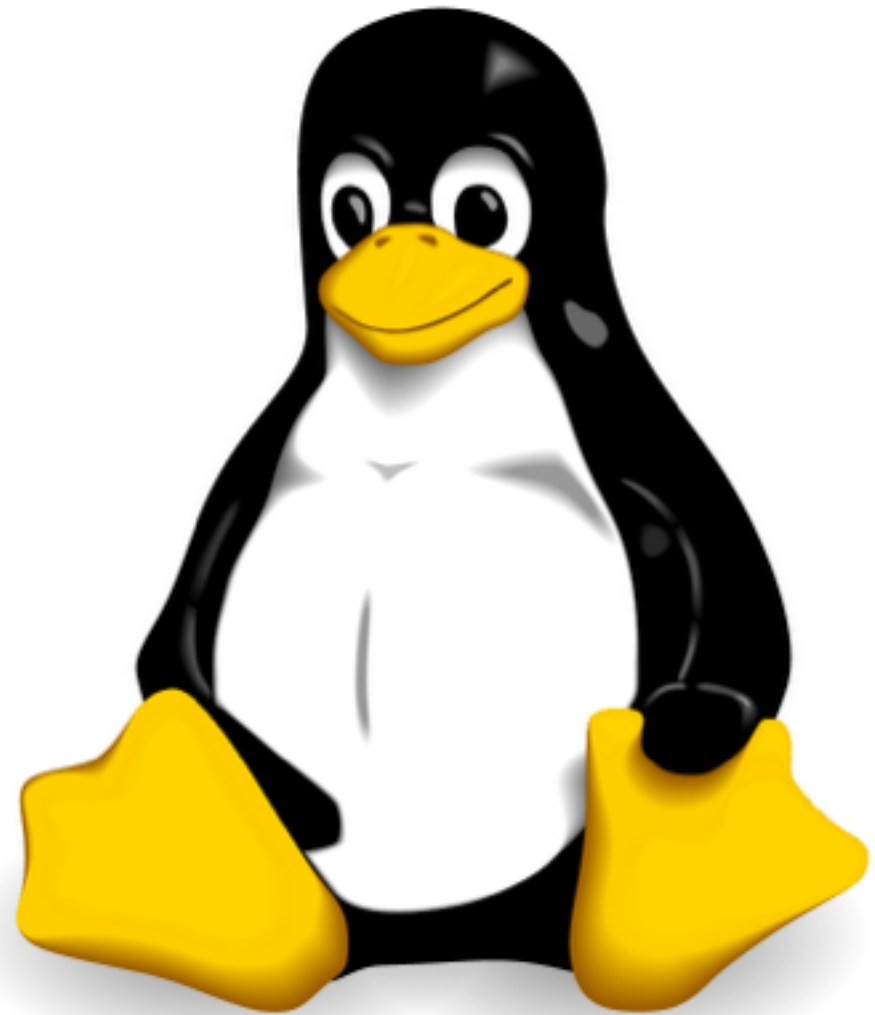
# Linux command line

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# Course practicalities

- Break after 1h40 minutes (13.40-14.00)
- Mixed theoretical and hands-on parts
- Feel free to leave the room when needed
- Provide feedback before going home
- All materials available at [bit.ly/lcl15052015slides](http://bit.ly/lcl15052015slides)
- Online discussion at [bit.ly/discussion15052015](http://bit.ly/discussion15052015)

# Reasons to use Linux



# You will learn the following:

- How to work with files
- How to work with file content
- How to control jobs
- And few advanced tricks

# Most important command

- man

```
man(1) man(1)
```

**NAME**

man - format and display the on-line manual pages

**SYNOPSIS**

**man** [-acdfFhkKtW] [--path] [-m system] [-p string] [-C config\_file]  
[-M pathlist] [-P pager] [-B browser] [-H htmlpager] [-S section\_list]  
[section] name ...

**DESCRIPTION**

**man** formats and displays the on-line manual pages. If you specify section, **man** only looks in that section of the manual. name is normally the name of the manual page, which is typically the name of a command, function, or file. However, if name contains a slash (/) then **man** interprets it as a file specification, so that you can do **man ./foo.5** or even **man /cd/foo/bar.1.gz**.

See below for a description of where **man** looks for the manual page files.

# Getting out of things

- type 'q', if that does not work
- 'ctrl-c', if that does not work
- log in with new session, read **man** about the program you are stuck in.
- **kill** the process from another session.

# Our server for the course

`elixir.cs.ut.ee`

`user and password given to You`

`command line ssh or putty to log in`

# Working with files and directories



# Knowing where you are

- **pwd** - gives working directory

```
6un:~ peterson$ pwd
/Users/peterson
```

- **cd** - move to desired directory

```
6un:~ peterson$ cd ~/linux/
6un:linux peterson$
```

```
6un:linux peterson$ cd ../
6un:~ peterson$
```

Relative paths



```
6un:~ peterson$ cd /Users/peterson/linux/
6un:linux peterson$
```

Absolute path

# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -l** - lists directory contents with more info

```
6un:linux peterson$ ls -l
-rw-r--r--@ 1 peterson  staff  61632026 14 mai   12:17 HG-U133_Plus2.full.flat
-rw-r--r--@ 1 peterson  staff  16850959 14 mai   12:17 biogrid_tab.txt
```

# File listing

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-rw-r--r--@ 1 peterson  staff  16850959 14 mai   12:17 biogrid_tab.txt
```

## Access rights

# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -l** - lists directory contents with more info

```
6un:linux peterson$ ls -l
-rw-r--r--@ 1 peterson staff 61632026 14 mai 12:17 HG-U133_Plus2.full.flat
-rw-r--r--@ 1 peterson staff 16850959 14 mai 12:17 biogrid_tab.txt
```

Owner

# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -l** - lists directory contents with more info

```
6un:linux peterson$ ls -l
-rw-r--r--@ 1 peterson staff 61632026 14 mai 12:17 HG-U133_Plus2.full.flat
-rw-r--r--@ 1 peterson staff 16850959 14 mai 12:17 biogrid_tab.txt
```

Group

# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -l** - lists directory contents with more info

```
6un:linux peterson$ ls -l
-rw-r--r--@ 1 peterson  staff  61632026 14 mai   12:17 HG-U133_Plus2.full.flat
-rw-r--r--@ 1 peterson  staff  16850959 14 mai   12:17 biogrid_tab.txt
```

File size in bytes

# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -l** - lists directory contents with more info

```
6un:linux peterson$ ls -l
-rw-r--r--@ 1 peterson  staff  61632026 14 mai   12:17 HG-U133_Plus2.full.flat
-rw-r--r--@ 1 peterson  staff  16850959 14 mai   12:17 biogrid_tab.txt
```

File modification time

# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -l** - lists directory contents with more info

```
6un:linux peterson$ ls -l
-rw-r--r--@ 1 peterson  staff  61632026 14 mai   12:17 HG-U133_Plus2.full.flat
-rw-r--r--@ 1 peterson  staff  16850959 14 mai   12:17 biogrid_tab.txt
```

File name



# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -lh** - lists directory contents with more info

```
6un:linux peterson$ ls -lh
-rw-r--r--@ 1 peterson  staff  59M 14 mai   12:17 HG-U133_Plus2.full.flat
-rw-r--r--@ 1 peterson  staff  16M 14 mai   12:17 biogrid_tab.txt
```

File size for humans

# File listing

- **ls** - lists directory contents

```
6un:linux peterson$ ls
HG-U133_Plus2.full.flat biogrid_tab.txt
```

- **ls -a** - show all files in the directory

```
.      .readme      biogrid_tab.txt
..     HG-U133_Plus2.full.flat
```

# Moving files around

- `cp` - keeps the original file
- `mv` - moves the original file

# Creating directories

- `mkdir` - create a directory

```
6un:linux peterson$ mkdir firstdir
```

```
6un:linux peterson$ ls
```

```
HG-U133_Plus2.full.flat biogrid_tab.txt
```

```
firstdir
```

# Access rights

- **chmod** - change user rights for files or folders

```
-bash-4.2$ ls -l packedfile.tar.gz
-rw-r--r--. 1 student1 student1 16860560 11. mai    19:02 packedfile.tar.gz
-bash-4.2$ chmod 755 packedfile.tar.gz
-bash-4.2$ ls -l packedfile.tar.gz
-rwxr-xr-x. 1 student1 student1 16860560 11. mai    19:02 packedfile.tar.gz
```

# Creating and removing

- **rm** - remove / no UNDO in unix

```
6un:firstdir peterson$ ls
```

```
biogrid_1000.tab
```

```
6un:firstdir peterson$ rm biogrid_1000.tab
```

```
6un:firstdir peterson$ ls
```

```
6un:firstdir peterson$
```

# Disk usage

- **du -h**

```
6un:linux peterson$ du -h
 0B    ./firstdir
75M    .
```

- **df -h**

```
-bash-4.2$ df -h
```

Failisüsteem	Maht	Kasut	Vaba	Kas%	Haagitud
/dev/mapper/centos-root	47G	2,8G	44G	6%	/
devtmpfs	7,6G	0	7,6G	0%	/dev
tmpfs	7,6G	0	7,6G	0%	/dev/shm
tmpfs	7,6G	8,5M	7,6G	1%	/run
tmpfs	7,6G	0	7,6G	0%	/sys/fs/cgroup
/dev/vda1	497M	227M	271M	46%	/boot

# Conserving space packing

```
6un:linux peterson$ du -h
```

```
0B    ./firstdir  
75M    .
```

```
6un:linux peterson$ ls -lh HG-U133_Plus2.full.flat
```

```
-rw-r--r--@ 1 peterson  staff      59M 14 mai   12:17 HG-  
U133_Plus2.full.flat
```

```
6un:linux peterson$ tar -zcvf packedfile.tar.gz  HG-  
U133_Plus2.full.flat  
a HG-U133_Plus2.full.flat
```

```
6un:linux peterson$ ls -lh packedfile.tar.gz
```

```
-rw-r--r--  1 peterson  staff      16M 14 mai   18:03  
packedfile.tar.gz
```



# Conserving space unpacking

```
6un:linux peterson$ tar -zxvf packedfile.tar.gz
x ./._HG-U133_Plus2.full.flat
x HG-U133_Plus2.full.flat
```

Working with file content

# Creating content

- -bash-4.2\$ **emacs** test.txt

Save file - CTRL+x, CTRL+x

Quit file - CTRL+x, CTRL+x

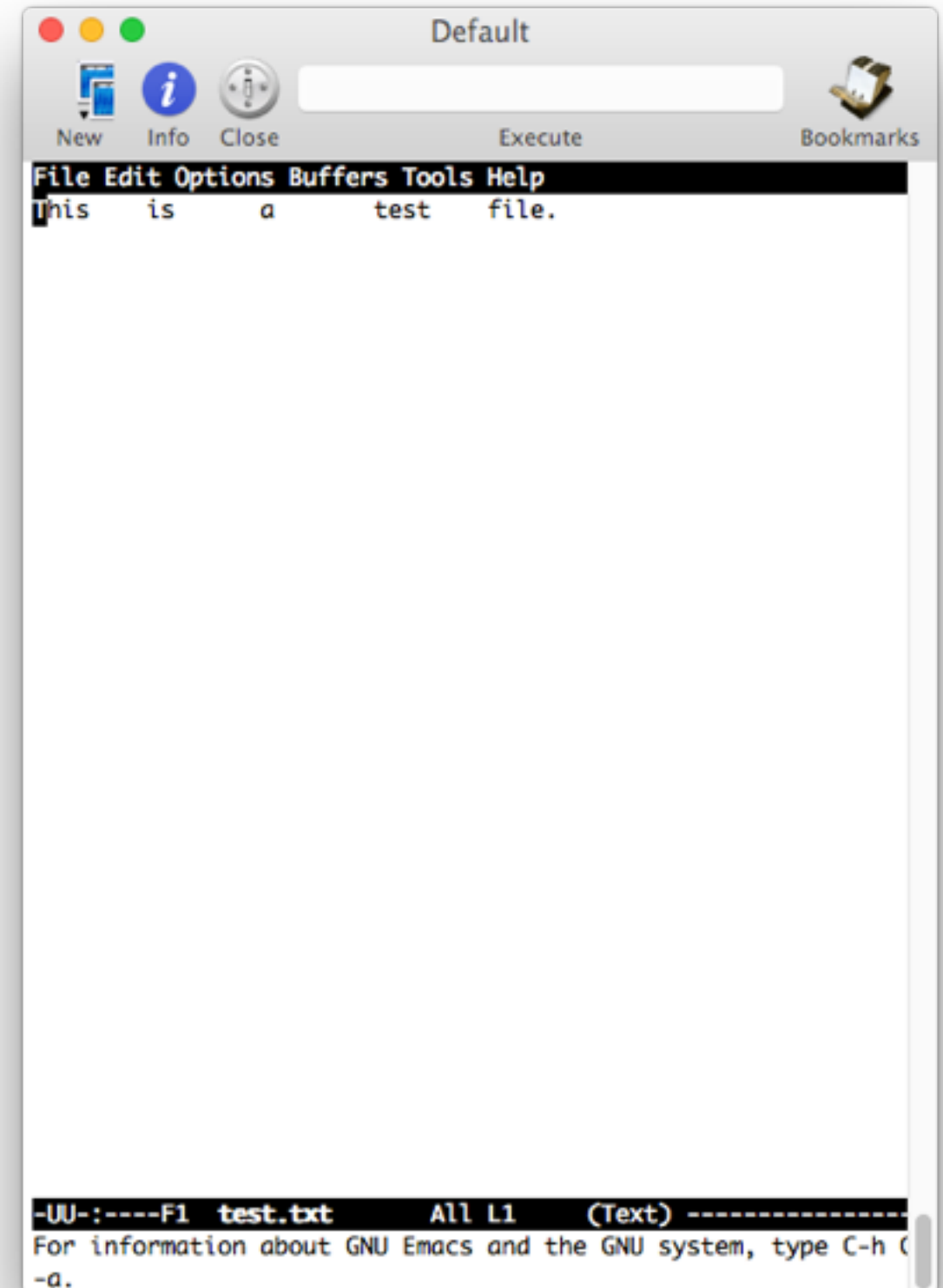
Write file - CTRL+x, CTRL+w

Get to line end - CTRL+e

Get to line start - CTRL+a

Remove full line - CTRL+k

Remove one character - CTRL+d



# Creating content

- -bash-4.2\$ **vim** test2.txt

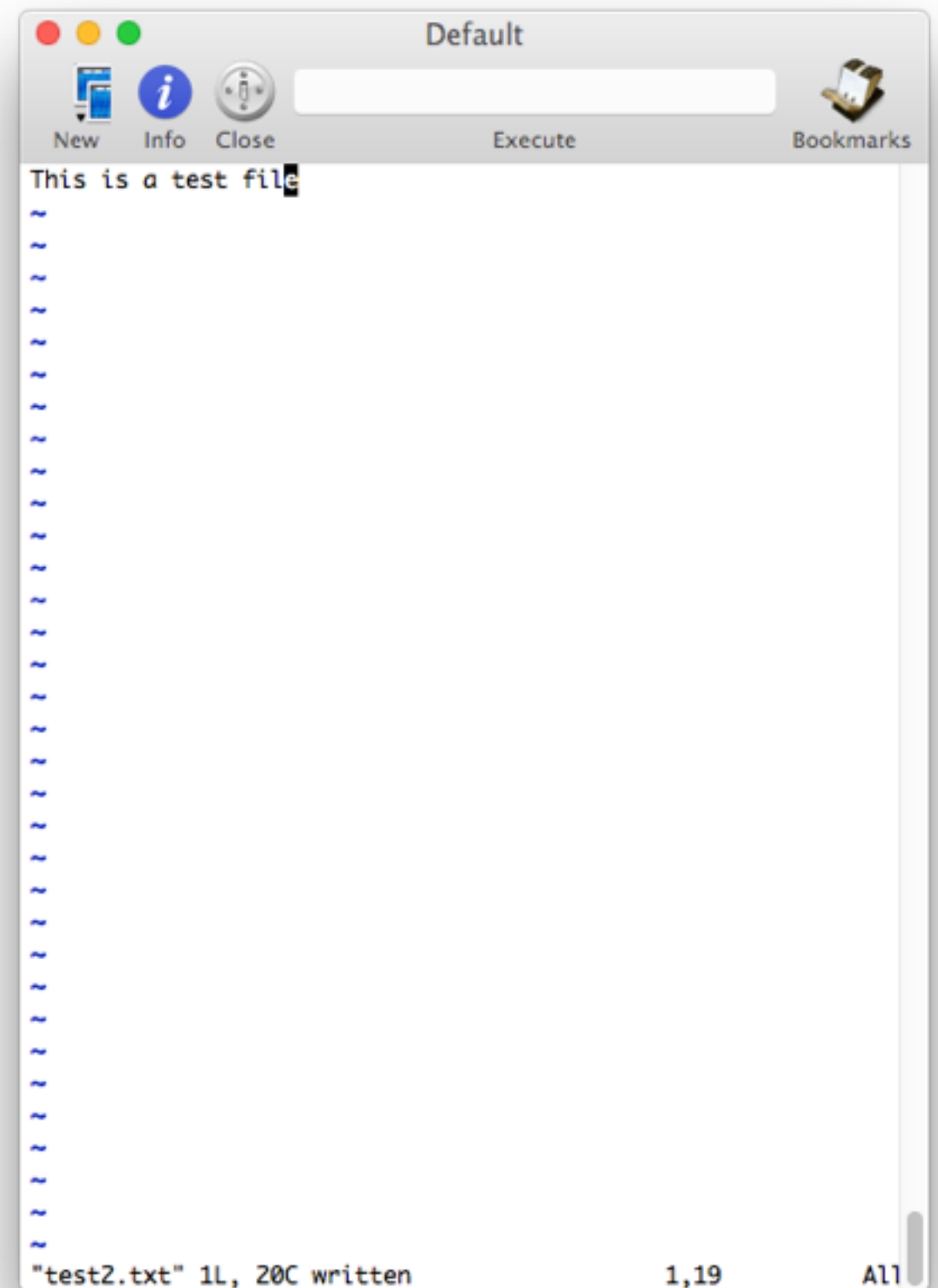
Edit file - :e

Save file - :w

Quit file - :q

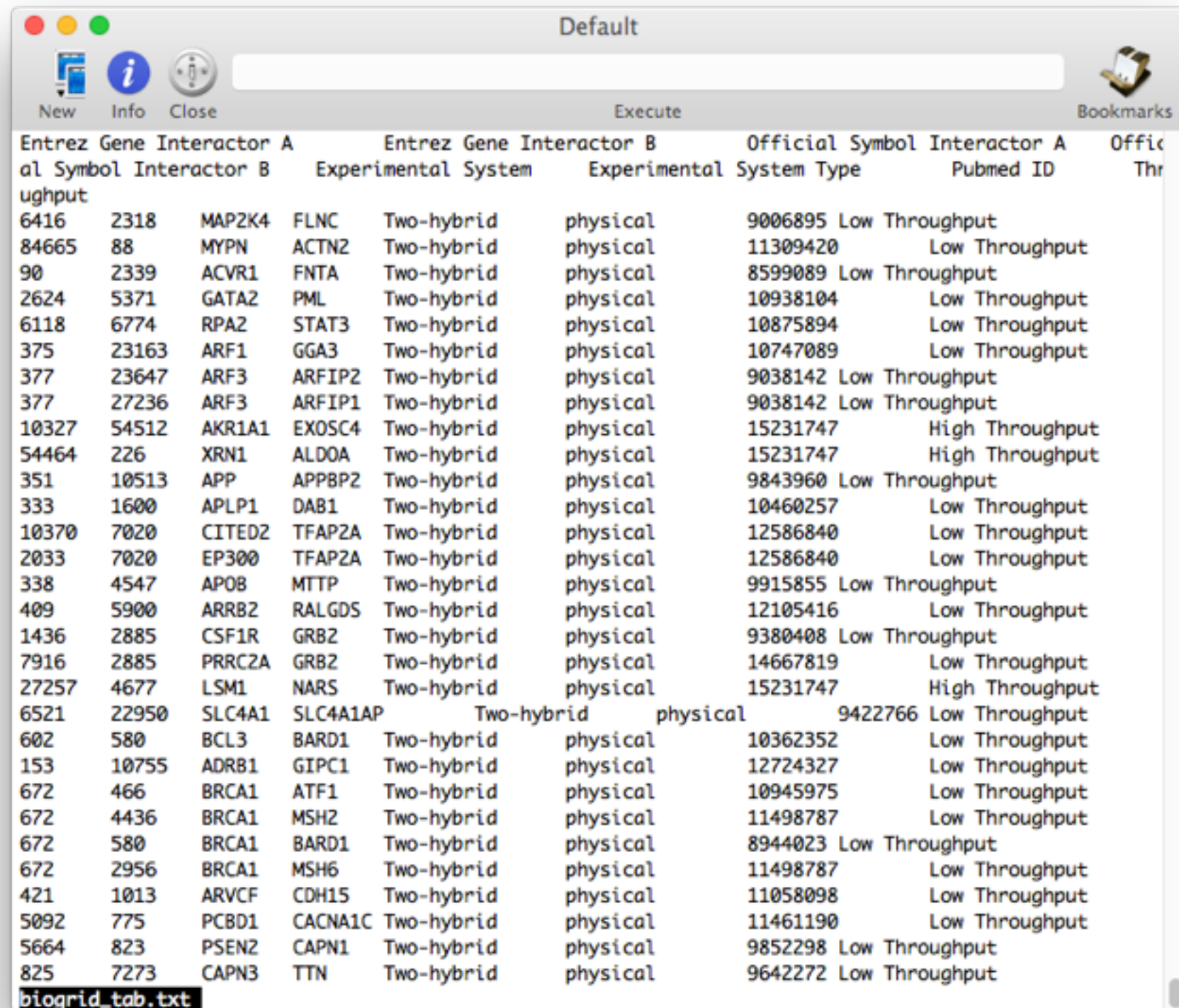
Save and quit file - :x

Write file - :w newfile



# Getting what you want from files

- `less` - look into file



Entrez Gene	Gene	Interactor A	Interactor B	Experimental System	Interaction Type	Official Symbol	Interactor A	Official
al Symbol		Interactor B				System Type	Pubmed ID	Thr
6416	2318	MAP2K4	FLNC	Two-hybrid	physical	9006895	Low Throughput	
84665	88	MYPN	ACTN2	Two-hybrid	physical	11309420	Low Throughput	
90	2339	ACVR1	FNTA	Two-hybrid	physical	8599089	Low Throughput	
2624	5371	GATA2	PML	Two-hybrid	physical	10938104	Low Throughput	
6118	6774	RPA2	STAT3	Two-hybrid	physical	10875894	Low Throughput	
375	23163	ARF1	GGA3	Two-hybrid	physical	10747089	Low Throughput	
377	23647	ARF3	ARFIP2	Two-hybrid	physical	9038142	Low Throughput	
377	27236	ARF3	ARFIP1	Two-hybrid	physical	9038142	Low Throughput	
10327	54512	AKR1A1	EXOSC4	Two-hybrid	physical	15231747	High Throughput	
54464	226	XRN1	ALDOA	Two-hybrid	physical	15231747	High Throughput	
351	10513	APP	APPBP2	Two-hybrid	physical	9843960	Low Throughput	
333	1600	APLP1	DAB1	Two-hybrid	physical	10460257	Low Throughput	
10370	7020	CITED2	TFAP2A	Two-hybrid	physical	12586840	Low Throughput	
2033	7020	EP300	TFAP2A	Two-hybrid	physical	12586840	Low Throughput	
338	4547	APOB	MTTP	Two-hybrid	physical	9915855	Low Throughput	
409	5900	ARRB2	RALGDS	Two-hybrid	physical	12105416	Low Throughput	
1436	2885	CSF1R	GRB2	Two-hybrid	physical	9380408	Low Throughput	
7916	2885	PRRC2A	GRB2	Two-hybrid	physical	14667819	Low Throughput	
27257	4677	LSM1	NARS	Two-hybrid	physical	15231747	High Throughput	
6521	22950	SLC4A1	SLC4A1AP	Two-hybrid	physical	9422766	Low Throughput	
602	580	BCL3	BARD1	Two-hybrid	physical	10362352	Low Throughput	
153	10755	ADRB1	GIPC1	Two-hybrid	physical	12724327	Low Throughput	
672	466	BRCA1	ATF1	Two-hybrid	physical	10945975	Low Throughput	
672	4436	BRCA1	MSH2	Two-hybrid	physical	11498787	Low Throughput	
672	580	BRCA1	BARD1	Two-hybrid	physical	8944023	Low Throughput	
672	2956	BRCA1	MSH6	Two-hybrid	physical	11498787	Low Throughput	
421	1013	ARVCF	CDH15	Two-hybrid	physical	11058098	Low Throughput	
5092	775	PCBD1	CACNA1C	Two-hybrid	physical	11461190	Low Throughput	
5664	823	PSEN2	CAPN1	Two-hybrid	physical	9852298	Low Throughput	
825	7273	CAPN3	TTN	Two-hybrid	physical	9642272	Low Throughput	

# Getting what you want

## from files

- **WC** - count characters and lines for a file

```
-bash-4.2$ wc biogrid_tab.txt  
220019  2150719 16850959 biogrid_tab.txt
```

# Getting what you want

## from files

- **head** - get top rows from file
- **tail** - get last rows from file

```
-bash-4.2$ head -n 3 biogrid_tab.txt
```

Entrez Gene	Interactor A	Entrez Gene	Interactor B	Official Symbol	Interactor A	Official Symbol	Inter
ctor B	Experimental System	Experimental System	Type	Pubmed ID	Throughput		
6416	2318	MAP2K4	FLNC	Two-hybrid	physical	9006895	Low Throughput
84665	88	MYPN	ACTN2	Two-hybrid	physical	11309420	Low Throughput

```
-bash-4.2$ tail -n 3 biogrid_tab.txt
```

10537	728689	UBD	EIF3CL	Affinity Capture-MS	physical	23862649	High Throughput
10537	645899	UBD	RPS28P4	Affinity Capture-MS	physical	23862649	High Throughput
10537	646195	UBD	RPS28P7	Affinity Capture-MS	physical	23862649	High Throughput

```
-bash-4.2$
```

# Getting what you want

from files

- `cat` - concatenate files together

```
-bash-4.2$ cat test.txt test2.txt  
This is a test file.  
This is a test file number two
```



# Getting what you want

## from files

- **cut** - extract sections of lines

```
-bash-4.2$ cut -f3,4,6,8 biogrid_tab.txt | tail -n+2 > pairs.tab
```

```
-bash-4.2$ head pairs.tab
```

MAP2K4	FLNC	physical	Low	Throughput
MYPN	ACTN2	physical	Low	Throughput
ACVR1	FNTA	physical	Low	Throughput
GATA2	PML	physical	Low	Throughput
RPA2	STAT3	physical	Low	Throughput
ARF1	GGA3	physical	Low	Throughput
ARF3	ARFIP2	physical	Low	Throughput
ARF3	ARFIP1	physical	Low	Throughput
AKR1A1	EXOSC4	physical	High	Throughput
XRN1	ALDOA	physical	High	Throughput

# Getting what you want

from files

- **uniq** - find uniq and repeating lines in file

```
-bash-4.2$ wc pairs.tab  
220019 1100554 8192802 pairs.tab
```

```
-bash-4.2$ uniq pairs.tab |wc  
214381 1072364 7986583
```

```
-bash-4.2$ uniq -cd pairs.tab |head -n5  
2 NR5A1 NRIP1 physical Low Throughput  
2 TNFRSF1A PSMD2 physical Low Throughput  
2 VHL FLNA physical Low Throughput  
2 HTR2C MPDZ physical Low Throughput  
2 AR RNF4 physical Low Throughput
```

# Getting what you want

from files

- **sort** - sort lines of text files

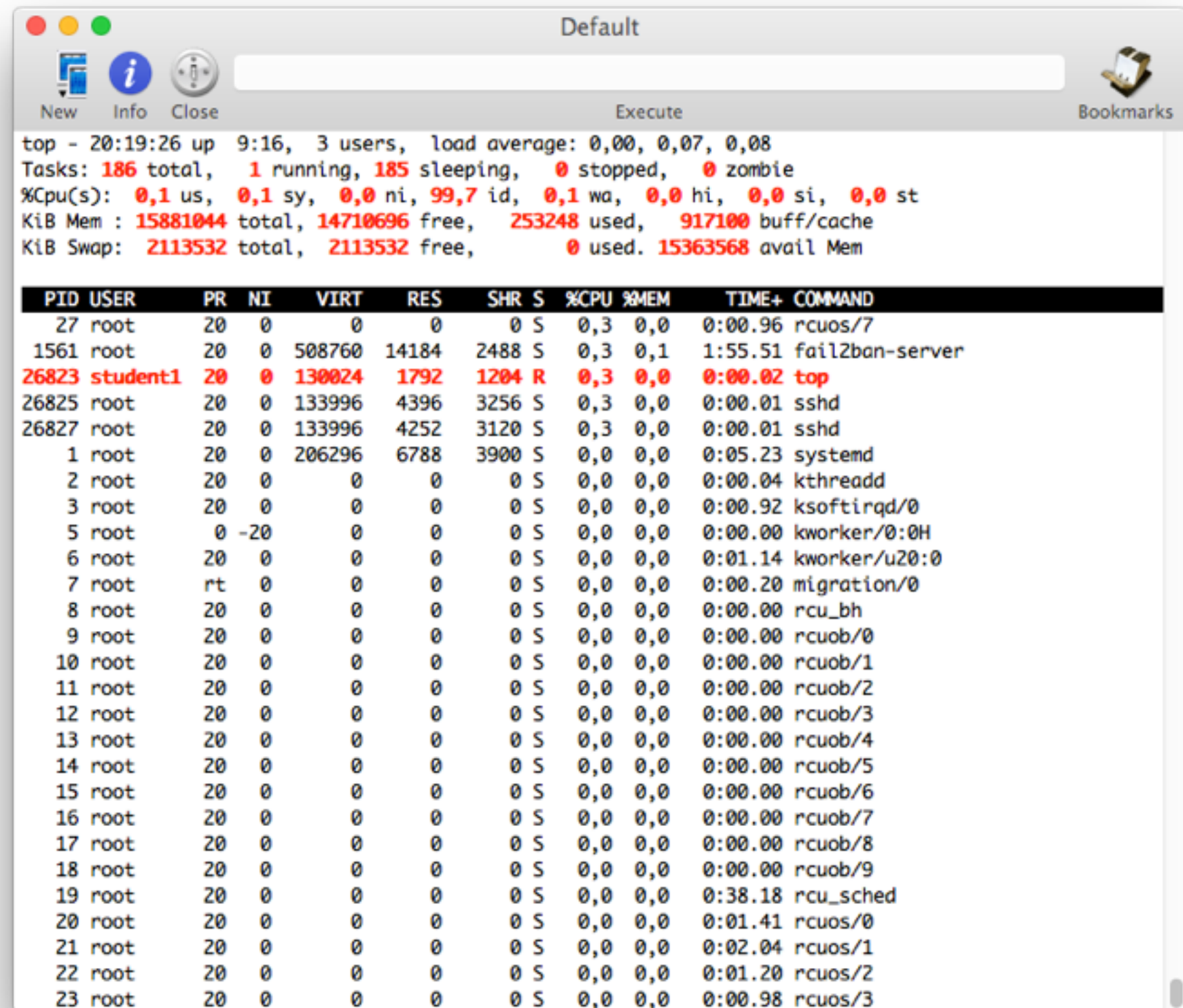
```
-bash-4.2$ cut -f1,2 pairs.tab | sort | uniq -c | sort -k1g | tail
```

48	VHL	HIF1A
54	IKBKG	UBC
58	MAPK8	JUN
60	EGFR	CBL
61	TRAF6	UBC
73	UBC	TP53
85	EGFR	UBC
131	TP53	UBC
152	TP53	MDM2
192	MDM2	TP53

Controlling jobs

# Process information

- **top** - check how much computer resources are used

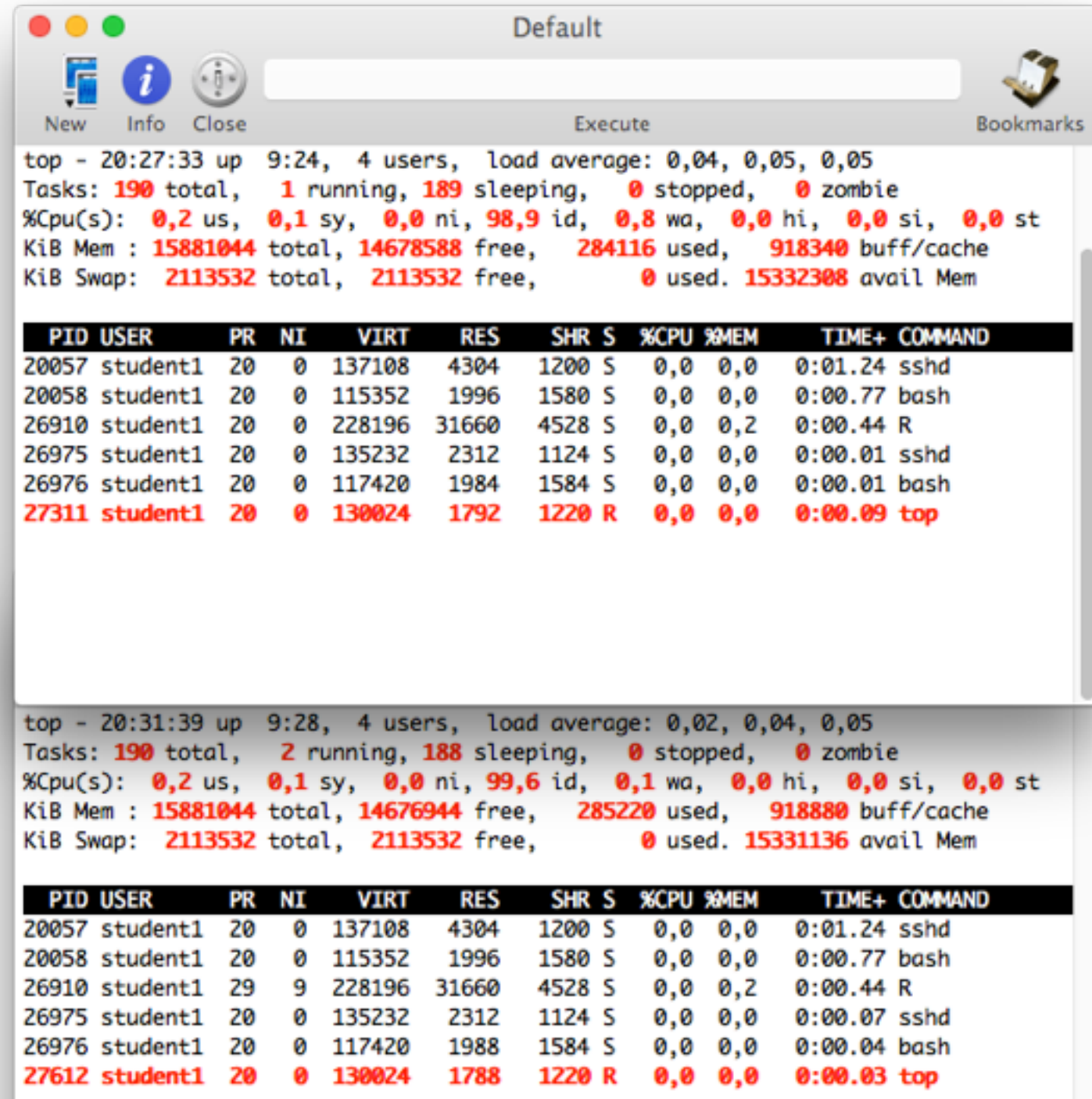


top - 20:19:26 up 9:16, 3 users, load average: 0,00, 0,07, 0,08  
Tasks: 186 total, 1 running, 185 sleeping, 0 stopped, 0 zombie  
%Cpu(s): 0,1 us, 0,1 sy, 0,0 ni, 99,7 id, 0,1 wa, 0,0 hi, 0,0 si, 0,0 st  
KiB Mem : 15881044 total, 14710696 free, 253248 used, 917100 buff/cache  
KiB Swap: 2113532 total, 2113532 free, 0 used. 15363568 avail Mem

PID	USER	PR	NI	VIRT	RES	SHR	S	%CPU	%MEM	TIME+	COMMAND
27	root	20	0	0	0	0	S	0,3	0,0	0:00.96	rcuos/7
1561	root	20	0	508760	14184	2488	S	0,3	0,1	1:55.51	fail2ban-server
26823	student1	20	0	130024	1792	1204	R	0,3	0,0	0:00.02	top
26825	root	20	0	133996	4396	3256	S	0,3	0,0	0:00.01	sshd
26827	root	20	0	133996	4252	3120	S	0,3	0,0	0:00.01	sshd
1	root	20	0	206296	6788	3900	S	0,0	0,0	0:05.23	systemd
2	root	20	0	0	0	0	S	0,0	0,0	0:00.04	kthreadd
3	root	20	0	0	0	0	S	0,0	0,0	0:00.92	ksoftirqd/0
5	root	0	-20	0	0	0	S	0,0	0,0	0:00.00	kworker/0:0H
6	root	20	0	0	0	0	S	0,0	0,0	0:01.14	kworker/u20:0
7	root	rt	0	0	0	0	S	0,0	0,0	0:00.20	migration/0
8	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcu_bh
9	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/0
10	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/1
11	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/2
12	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/3
13	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/4
14	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/5
15	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/6
16	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/7
17	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/8
18	root	20	0	0	0	0	S	0,0	0,0	0:00.00	rcuob/9
19	root	20	0	0	0	0	S	0,0	0,0	0:38.18	rcu_sched
20	root	20	0	0	0	0	S	0,0	0,0	0:01.41	rcuos/0
21	root	20	0	0	0	0	S	0,0	0,0	0:02.04	rcuos/1
22	root	20	0	0	0	0	S	0,0	0,0	0:01.20	rcuos/2
23	root	20	0	0	0	0	S	0,0	0,0	0:00.98	rcuos/3

# Process information

- **renice** - change priority of existing process



The screenshot shows a terminal window with the 'top' command output. The window title is 'Default'. The top bar contains icons for 'New', 'Info', 'Close', 'Execute', and 'Bookmarks'. The output is divided into two sections by a horizontal line. The first section shows the system state at 20:27:33, with 4 users and a load average of 0.04, 0.05, 0.05. The second section shows the system state at 20:31:39, with 4 users and a load average of 0.02, 0.04, 0.05. Both sections show a table of processes with columns: PID, USER, PR, NI, VIRT, RES, SHR, S, %CPU, %MEM, TIME+, and COMMAND. In the first section, process 26910 (student1) has priority 20. In the second section, process 26910 (student1) has priority 29. The process 27311 (student1) has priority 20 in the first section and 20 in the second section. The process 27612 (student1) has priority 20 in the second section.

```
top - 20:27:33 up 9:24, 4 users, load average: 0,04, 0,05, 0,05
Tasks: 190 total, 1 running, 189 sleeping, 0 stopped, 0 zombie
%Cpu(s): 0,2 us, 0,1 sy, 0,0 ni, 98,9 id, 0,8 wa, 0,0 hi, 0,0 si, 0,0 st
KiB Mem : 15881044 total, 14678588 free, 284116 used, 918340 buff/cache
KiB Swap: 2113532 total, 2113532 free, 0 used. 15332308 avail Mem
```

PID	USER	PR	NI	VIRT	RES	SHR	S	%CPU	%MEM	TIME+	COMMAND
20057	student1	20	0	137108	4304	1200	S	0,0	0,0	0:01.24	sshd
20058	student1	20	0	115352	1996	1580	S	0,0	0,0	0:00.77	bash
26910	student1	20	0	228196	31660	4528	S	0,0	0,2	0:00.44	R
26975	student1	20	0	135232	2312	1124	S	0,0	0,0	0:00.01	sshd
26976	student1	20	0	117420	1984	1584	S	0,0	0,0	0:00.01	bash
27311	student1	20	0	130024	1792	1220	R	0,0	0,0	0:00.09	top

```
top - 20:31:39 up 9:28, 4 users, load average: 0,02, 0,04, 0,05
Tasks: 190 total, 2 running, 188 sleeping, 0 stopped, 0 zombie
%Cpu(s): 0,2 us, 0,1 sy, 0,0 ni, 99,6 id, 0,1 wa, 0,0 hi, 0,0 si, 0,0 st
KiB Mem : 15881044 total, 14676944 free, 285220 used, 918880 buff/cache
KiB Swap: 2113532 total, 2113532 free, 0 used. 15331136 avail Mem
```

PID	USER	PR	NI	VIRT	RES	SHR	S	%CPU	%MEM	TIME+	COMMAND
20057	student1	20	0	137108	4304	1200	S	0,0	0,0	0:01.24	sshd
20058	student1	20	0	115352	1996	1580	S	0,0	0,0	0:00.77	bash
26910	student1	29	9	228196	31660	4528	S	0,0	0,2	0:00.44	R
26975	student1	20	0	135232	2312	1124	S	0,0	0,0	0:00.07	sshd
26976	student1	20	0	117420	1988	1584	S	0,0	0,0	0:00.04	bash
27612	student1	20	0	130024	1788	1220	R	0,0	0,0	0:00.03	top

-bash-4.2\$ **renice** -n 9 26910

26910 (process ID) old priority 0, new priority 9

# Process information

- `ps` - current processes

```
-bash-4.2$ ps -U student1 -h
20057 ?          S          0:01 sshd: student1@pts/2
20058 pts/2      Ss         0:00 -bash
26910 pts/2      S+         0:00 /usr/lib64/R/bin/exec/R
26975 ?          S          0:00 sshd: student1@pts/1
26976 pts/1      Ss         0:00 -bash
27019 pts/1      R+         0:00 ps -U student1 -h
```



# Process information

- `kill` - quit a process

```
-bash-4.2$ kill 26910
```



# Advanced tricks

# Getting along with the server

- **screen** - virtual terminal; helps to keep programs running while you need to disconnect the computer
- **uptime** - check for how long server has been continuously running

# Awk when cut does not cut!

```
-bash-4.2$ cut -f1,3 sorted_pairs.tab | head -n 5
```

```
1 1810055G02Rik  
1 1810055G02Rik  
1 1810055G02Rik  
1 2810046L04Rik  
1 2810046L04Rik
```

```
-bash-4.2$ awk '{print $1,$3}' sorted_pairs.tab | head -n 5
```

```
1 MPRIP  
1 RAI14  
1 TPM1  
1 ARF1  
1 ARF3
```

# Searching

- grep - grep for patterns in files

```
-bash-4.2$ grep BRCA1 sorted_pairs.tab |tail -n5
14 BRCA1    UBE2D3
19 BRCA1    BRIP1
21 BRCA1    RBBP8
24 BARD1    BRCA1
48 BRCA1    BARD1
```

# Exercise #1

In Your home catalog make directory called **data**.  
Also choose a text editor and start a new file, where  
You can write the commands You used to solve  
exercises as well answers to questions.

# Exercise #2

File : `/home/student1/data/mart_export_14_05_15.txt.tar.bz2`

- copy to Your own **data/** catalog, extract the file to plain text.
- make Yourselfs familiar with the file, explore, look inside, open in text editor.
- how many lines does the file have?
- unique lines, can You find repeated lines? Remove them.

# Exercise #3

From the edited file:

- Make new file, where You only have lines matching chromosomes 1 - 22, X and Y.
- What gene has the highest / lowest %GC?
- How many genes have %GC above 70, how many below 30?
- Can You find the longest / shortest gene?

# Exercise #4

File: /home/student1/data/  
mart\_export\_variation\_14\_05\_15.tar.gz

- copy to Your own **data/** catalog, extract the file to plain text.
  - express the size difference in percentages
- Make table of “Consequence Type” frequencies
- Make table of “Variant Alleles” frequencies (top 25)



# Exercise #5

File: `/home/student1/data/variation.tar.gz`

- copy to Your own **data/** catalog, extract the archive. Essentially the same as last file, split into chromosomes.
- make the same tables as in last exercise for chromosomes 20 - 22 combined
- Given all the files available to You, think of exercise relevant to You, ask help if needed to solve it!

**R basics course**  
next Thursday  
room 202

# Provide us feedback

- [bit.ly/linux15feedback](https://bit.ly/linux15feedback)