

# Linux on the HPC Cluster

Harry Mangalam

[harry.mangalam@uci.edu](mailto:harry.mangalam@uci.edu)

# Before We Begin

- You know Linux (..?)
- You're bright: can Google, and read further by yourself.
- If I speak too fast; **let me know**
- Questions, **ASK THEM**, but I may not answer them immediately. – “*You don't know what you don't know*”

# Computing Philosophy

- Unlike your Science...
- Be lazy.
- Copy others.
- Don't invent anything you don't have to.
- Re-USE, re-CYCLE, DON'T re-invent.
- Don't be afraid to ask others.
- Resort to new code **only when absolutely necessary.**
- Add comments to your code - **ALWAYS**

# Philosophy – Take Away

- You're not CS, not programmers
- Don't try to be them
- **But! Try to think like them**, at least a bit
- Google is your friend

# Getting Help

- Fix IT Yourself with Google  
<[goo.gl/05MnTi](http://goo.gl/05MnTi)>
- Listservs, forums, IRCs are VERY useful for more involved questions
- The HPC HOWTO <[goo.gl/kz1q1](http://goo.gl/kz1q1)>
- Us – Jenny, Adam, Harry, Garr, Joseph.
- BUT!! Unless you **ask questions intelligently**, you will get nothing but grief.

# How to Ask Questions

- **Reverse the situation**: if you were answering the question, what information would you need?
- Not Science, but it is **Logic**.
- **Include enough info to recreate the problem**.
- Exclude what's not helpful or ginormous (use <pastie.org> or <tny.cz>)
- Use text, not screenshots if possible.

# Bad Question

Why doesn't "X" work?

# Good Question

I tried running the new podunk/2.8.3 module this morning and it looks like I can't get it to launch on the Free64 queue. My output files aren't helping me figure out what is wrong.

I am working out of /bio/joeuser/RNA\_Seq\_Data/ and the qsub script is 'job12.sh'. The output should be in /bio/joeuser/RNA\_Seq\_Data/output

When I submit the job, it appears to go thru the scheduler but then dies immediately when it hits the execution node.

I can't find any output to tell me what's wrong, but the Error messages suggest that there's a problem finding libgorp.so.3



# HELP US HELP YOU

We Need:

- the directory in which you're working (*pwd*),
- the machine you're working on (*hostname*)
- modules loaded (*module list*)
- computer / OS you're connecting from
- the command you used and the error it caused (in /text/, not screenshot)
- much of this info is shown by your prompt

see <<http://goo.gl/6eZORd>>

# On to HPC

What is the H<sub>igh</sub> P<sub>erformance</sub> C<sub>omputing</sub>  
Cluster?

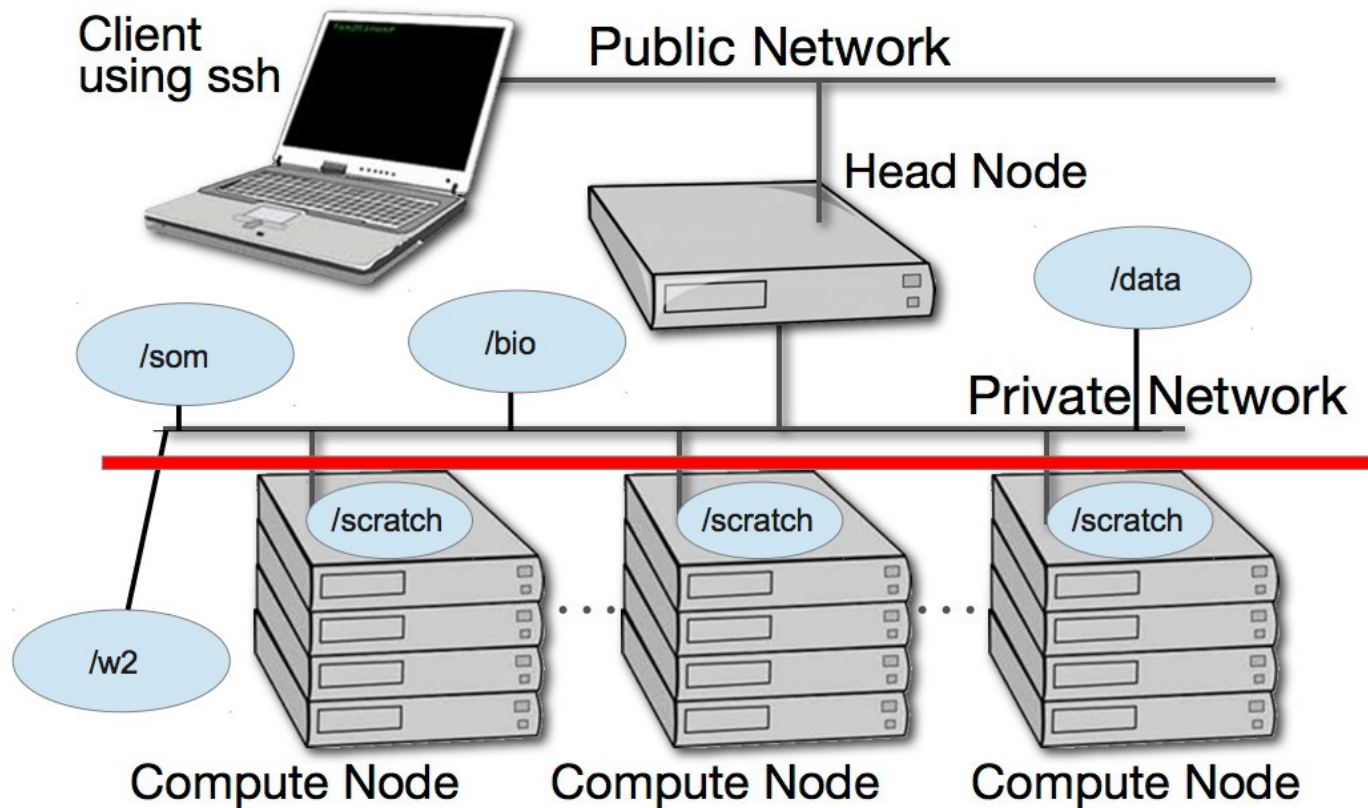
and...

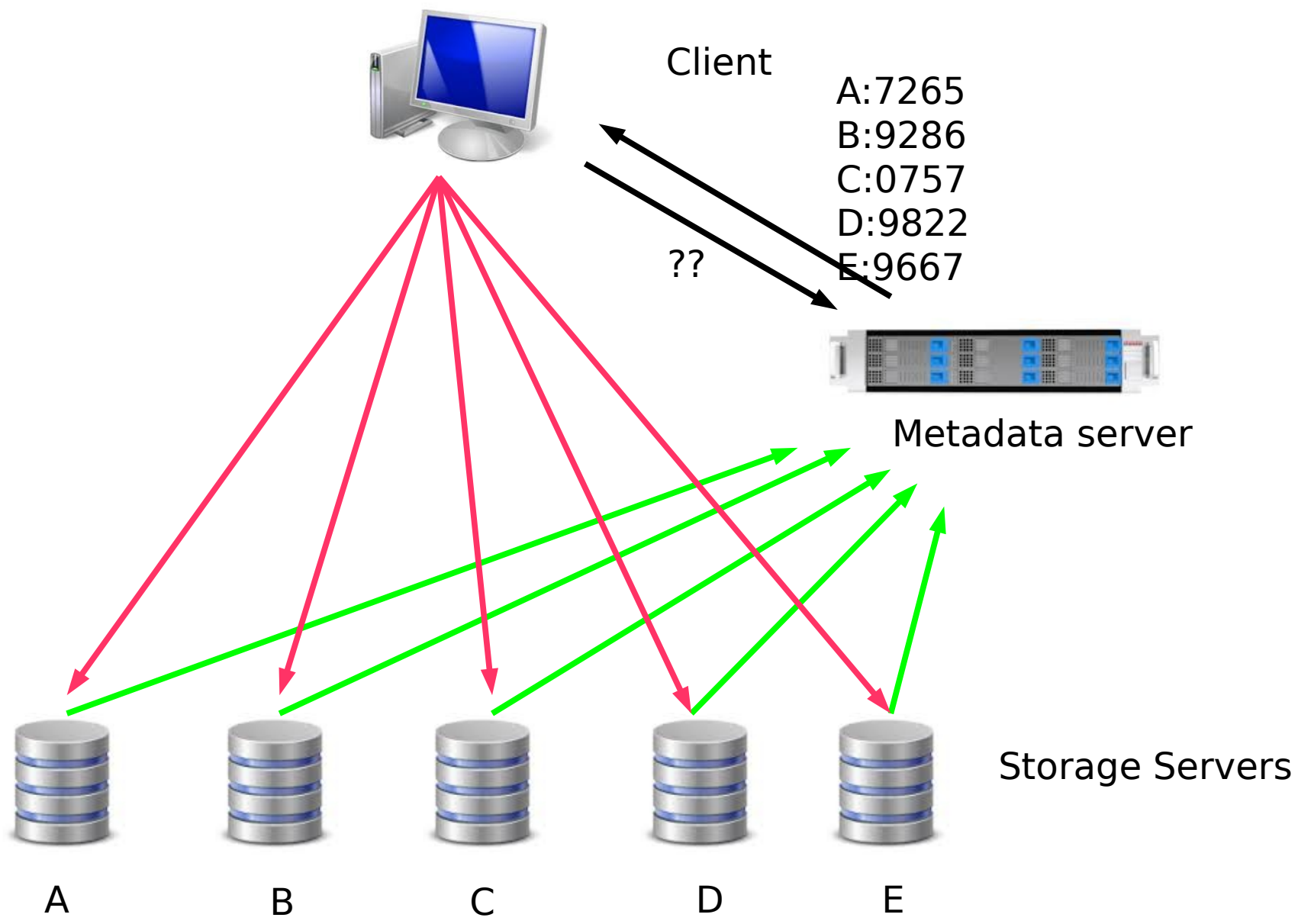
Why do I need HPC?

# What is a Cluster?

- bunch of big general purpose computers
- running the Linux Operating System
- linked by some form of networking
- have access to networked storage
- that can work in concert to address large problems
- by scheduling jobs very efficiently

# Overview





# HPC @ UCI in Detail

- ~5800 64b Cores – Mostly AMD, few Intel
- ~14TB aggregate RAM
- ~1PB of storage (1000x slower than RAM)
- Connected by 1Gb ethernet (100MB/s)
- Connected by QDR IB (800MB/s)
- Grid Engine Scheduler to handle Queues
- > 650 users, 100+ are online at anytime

# What HPC is NOT

- **NOT:** your personal machine – shared resource
- NO DATA IS BACKED UP – WHAT SO EVER
- Well secured from mischief and disasters – **not an invitation**

# DATA IS NOT BACKED UP

- **NO DATA IS BACKED UP – WHAT SO EVER** – Agitate to your PIs to get us more \$ if you want this.
- Most data is stored on **RAID6**
- **BUT!** Any of that can disappear at any moment
- **IF ITS VALUABLE**, back it up elsewhere --- or the code that generated it.



# HPC FileSystem Layout

Orange – Cluster Wide

Black – Node Specific

/			
— data/	NFS Mount		
— apps	All Programs are installed here		
— users	Users home directory		– 50 GB LIMIT PER USER
— w1/	Public NFS Server	→ Going away	– 14TB Space
— w2/	Public NFS Server	→ Going away	– 40TB Space
---- pub/	Replacement for /w1, /w2		
— bio/	Space for BIO group	→ /dfs1	
— som/	Space for SOM group	→ /dfs1	
— cbcl/	Space for CBCL group	→ /dfs2	
— dfs1/	Fraunhofer FileSystem – new, Distributed File System		~380TB Space
— scratch	Node-specific temporary storage per job (faster than all above)		~1TB – 14TB of Space
— fast-scratch	High Speed Fraunhofer FileSystem for temporary storage		- 13TB
---- ssd-scratch	Very High IOPS for DB, other jobs.		
— /tmp	Same as scratch		

# Disk Space / Quotes / Policies

- You can only have so much space
- 50GB for /data/ (home directory)
- 6months or older **without** use – please remove from cluster
- More for Condo owners or Groups who have bought extra disk space.
- Regardless, **NO DATA IS BACKED UP**

# Data Sizes

- Your data will be BIG – “BigData”
- BigData is somewhat 'dangerous' due to its **bigness**.
- Think before you start. You can't predict everything, but you can predict a lot of things – more on this later

# How to: Login with SSH

- SSH is an encrypted protocol so that info over the connection can't be deciphered by others.
- You **MUST** use SSH to connect to HPC – think command line
- Underlies 'scp' (secure copy), sftp
- Also 'sshfs' which allows you to attach your filesystem to HPC (or vice versa).

# Command Line Cons

- The tyranny of the blank page
- No visual clues
- Type vs click
- Have to know what to type
- **HOW DO YOU KNOW WHAT TO TYPE???**

# Command Line Pros

- It doesn't get much worse than this
- When you do learn it, you'll know it and it probably won't change for the rest of your life
- It's a very efficient way of interacting with the computer (which is why it's survived for 50+yrs).
- You can use it to create simple, but very effective pipelines and workflows.

# Keeping SSH Session Alive

- If you need to maintain a live connection for some reason, use 'byobu or screen'.
- It allows you to multiplex and maintain connections in a single terminal window.
- Somewhat unintuitive interface but very powerful.
- You know about cheatsheets (Google!!)

# Graphics Apps on HPC

- Linux uses X11 for graphics
- X11 is very chatty, high bandwidth, sensitive to network hops/latency.
- If you need graphics programs on HPC, use **x2go** vs native X11.
- **x2go** is described in the Tutorial & HOWTO, also GOOGLE



# How to: SSH & The Shell

- Once logged in to HPC via SSH you are now using the *Shell*, which is..
- A program that intercepts and translates what you type, to tell the computer what to do.
- What you will be interacting with mostly.
- HPC shell is '**bash**', altho there are others.

# Know the shell, Embrace the Shell

- If you don't get along with the shell, life will be hard.
- Before you submit anything to the cluster via qsub, get it going in your login shell.
- You're welcome to start jobs in on the IO node, type: `qrsh`
- “*DO NOT RUN JOBS ON THE LOGIN NODE*”

# How to know if I am on Login Node?

- Look at your shell prompt!
- Mon Apr 28 07:08:59 hmangala@hpc-s:~  
678 \$
- [aebrenne@hpc ~]\$ ← 'HPC' is the login node
- [aebrenne@compute-6-1 ~]\$ ← On compute 6-1
- May also use the command `hostname`

# STDIN, STDOUT, STDERR

- STD = Standard
- STDIN is usually the keyboard, but...
- STDOUT is usually the screen, but...
- STDERR is *also* usually the screen, but...
- All can be **redirected** all over the place
- to files, to pipes, combined, split (by 'tee'), etc
- recombined to make simple **filters** or **workflows**

# File & Directories

- Files & folders much like on Mac & Win
- Except...
- Names are case-sensitive, 256 char long
- 'Folders' → 'Directories' , separated by '/'
- No spaces in names\*
- . means 'in this dir'
- .. means parent dir
- ~ means 'home dir'
- A leading '/' means 'from the root dir'

# Foreground & Background Jobs

- Foreground (fg) jobs are connected to the terminal. You kill a fg job with `^C`.
- Background (bg) jobs have been disconnected from the terminal.
- Send a job to the bg by appending `&`
- Recall a job to the fg with `fg`.
- Send a fg job to the bg with `^z` (suspend), then `'bg'`.

# Pipe |

- Works with STDIN/OUT/ERR to create 'pipelines'
- Very similar to plumbing; can add 'tee's to introduce splits
- STDOUT of one program goes to the STDIN of another command whose STDOUT goes to the STDIN of another program ad infinitum.
- Sooooo.....

# Pipe Example

```
w | cut -f1 -d ' ' | egrep -v " (^$|USER)" | sort | uniq -c | wc
```

**w** spits out who is on the system right now

**cut -f1 -d ' '** chops out the 1st field (the user), based on the space token

**egrep -v " (^\$|USER)"** filters out both blank lines and lines with 'USER'

**sort** sorts the usernames alphabetically

**uniq -c** counts the unique lines

**wc -l** word-counts that output.

**Example: Now on HPC!**



# Help on Commands

- `cmd -h`
- `cmd -help`
- `man cmd`
- `info cmd` (but you hope not)
- **And ..... Google...**

# Some Useful Commands

- `ls [many options]` = list fil<tab><tab>
- `cd [up or down]` = change directory
- `find [from] -name [name]` = find files
- `locate [name]` = where is this file?
- `tree [options]` = show the dir tree
- `file [name(s)]` = what is this?
- `du` = disk usage
- `df` = disk free
- `less [names]` = view files
- `cols [file]` = view file in columns

# Creative / Destructive Commands

- `mkdir [name]` – make a dir
- `rmdir [name]` – remove a dir
- `mv [from] [to]` = move or rename
- `cp [from] [to]` = copy file(s)
- `rm [file]` = delete file(s)
- `wget [URL]` = get a file from the Internet
- `curl -O [URL]` = ditto, but on steroids

# More Useful Commands

- `mc` = Midnight Commander
- `[ah]top` = top CPU-using processes
- `time [command]` = how long does it take?
- `[aef]grep [regex] [files]` = find regex in files
- `cat [files]` = print the files to STDOUT
- `head/tail [files]` = dump the top / bottom of files

# Regular Expressions

- Among the most powerful concepts in pattern matching
- Simple in concept, NASTY in implementation
- Among the ugliest / most confusing things to **learn well**
- But pretty easy to learn the simple parts.
- You will **NEED** to learn it – it's central to computers and **especially biology**

# Regexes

- Simplest form is called globbing: **a\***
- Barely more complicated : **a\*.txt**
- A bit more: **a\*th.txt**
- Can be MUCH more complex:
- **[aeiou]** = any of 'aeiou'
- **F{3,5}** = 3-5 'F's
- **H+** = 1 or more 'H's
- **.** = any character
- Also classes of characters (**#s**, alphabetic, words)

# Archiving / Compression

- tar = std archive format for Linux
- zip = common archive format, from Windows
- gzip/unzip = common compressed format
- bzip2/bunzip2 = another compressed format
- pigz = parallel gzip (for large files)
- pbzip – parallel bzip2 (ditto)

# Customize Your Environment

- Change your prompt to something useful to you (and to us):
- `PS1="\n\t \u@\h:\w\n!\ \ $"`
- Set aliases (`alias nu="ls -lt |head -22"`)
- Set Environment Variables (`export EDITOR=vim`)
- Make these permanent via `.bash_profile` & `.bashrc` files in your *home directory*



# Editing Files: simple & complex

- Text-based:
  - nano, joe, vi/vim, emacs
  
- GUI-based:
  - gedit, nedit, kate, jedit, emacs

(choose one and learn it, *well*)

# Move Data to / from HPC

- Covered in detail in HPC USER HOWTO, which references: [goo.gl/XKFEp](http://goo.gl/XKFEp)
- scp, bbcp, netcat/tar on Mac, Linux.
- WinSCP, Filezilla, CyberDuck, FDT on Win
- Everyone should know how to use rsync. Not the easiest to learn, **but very powerful & scriptable.**
- rsync GUIs for Linux, Windows, MacOSX

# Using Software on HPC

- 3 main sets of programs
- Your personal set (typically in ~/bin)
- The default system utilities  
cut, grep, ls, mv, cp, rm, cd, etc...
- The **module system** programs

# The Module System

- `module avail` shows all installed software
- `module load R/3.01` loads program R version 3.01 (but doesn't start it)
- `module unload` unloads the specified program
- `module purge` removes all loaded programs
- `module list` lists all the currently loaded ones

# How to Find Software

- `locate` <partial search term>
- `apropos` <search term>
- `na<tab><tab>` → name
- `yum search <search term>` # CentOS
- `module avail` (will dump all modules)
- Google
- Ask us.

# The Scheduler (GE)

- Just another program that juggles requests for resources
- Make sure a program is working on a small set of test data on an interactive shell.
- Need a short bash script (aka ***qsub script***) to tell the GE what your program needs to run.
- Can improve the performance of your program in a variety of ways (staging data, running in parallel, using array jobs, etc)

# The Scheduler: qsub vs qrsh

- *qrsh* will log you into an Interactive Node (IO Node) where you can test out your scripts
- IO Nodes are useful for GUI programs (X11 & x2go needed) or testing / running SMALL and FAST data sets
- A *qsub* script is just a series of bash commands that sets up your resource requirements, PATHs, executes your jobs, and does the post-processing. – **NO USER INVOLVEMENT** during the process

# GE Useful Commands

- qstat - Queue Status
- queue / q – What queues you have access to
- qdel – Delete/Stop your job
- qhost – Show all nodes and their status
  
- Use `man cmd` to find out more information on above
- <http://hpc.oit.uci.edu/PHPQstat>
  
- Ref:
- <http://hpc.oit.uci.edu/running-jobs>



# Sample QSUB Script

- Visit:
- <http://hpc.oit.uci.edu/guides/qsub-biolinux.html>
- Ref:
- <http://goo.gl/hrcXBg>

# GE – Request Node Resources

- Use Case: **You know** your program requires **at least**
- 24GB Memory
- 16 CPU Cores
- You need to tell the scheduler
- `#$ -pe openmp 16`
- `#$ -l mem_free=24G`
- **This does not make your program run faster or use all cores – you simply reserve this amount**

# GE – Queues

- As you noticed, the scheduler uses queues to handle your job.
- Some queues have higher priority than others.
- Type `queue` or `q` to see what you have access to
- `#$ -q som, free*`

# GE – Free and All Queue

- The free\* queue allows anyone to use CPU cycles when they are not in use on any queue/node cluster wide
- When owners want to use their nodes, free\* jobs are suspended
- Similar to the free\* queue, the 'all' queue is group-specific: abio, asom, etc.

# Big Data

- Volume
- Scary sizes, and getting bigger
- Velocity
- Special approaches to speed analysis
- Variety
- Domain-specific standards (HDF5/netCDF, bam/sam, FITS), but often aggregations of unstructured data
- **BigData Hints for Newbies**  
<<http://goo.gl/aPj4az>>

# Big Data – How Big is Big?

# Bytes	Byte name / Abbrev'n	Approximation
1/8	bit (b)	0 or 1: the smallest amount of information.
1	Byte (B)	8 bits, the smallest chunk normally represented in a programming language.
$2^{10}$	1,024 B (1 KB)	a short email is a few KBs
$2^{20}$	1,048,576 B (1 MB)	a PhD Thesis ; Human Chr 1 is ~250 MB
$2^{30}$	1,073,741,824 B (1 GB)	the Human Genome is 3,095,693,981 B (optimized, ~780 Mb @ 2b/base) ; a BluRay DVD holds 25GB per layer (most movie BluRays are dual-layer = 50GB); a Genomic bam file is ~150GB
$2^{32}$	4,294,967,296 (4GB)	<b>fuzzy border between SmallData (32b) and BigData (64b)</b>
$2^{40}$	1,099,511,627,776 B (1 TB)	1/10th Library of Congress (LoC); the primary data fr. an Illumina HiSeq2K is ~5 TB
$2^{50}$	1,125,899,906,842,624 B (1 PB)	100X LoC; ~HPC's aggregate storage; ~100 PB is the yearly storage requirements of YouTube.
$2^{60}$	1,152,921,504,606,846,976 B (1 EB)	the est. capacity of the NSA's data facility is ~12 EB

# Integer Byte Sizes

word size	#bits	range of variable
byte or char	8	256
int	16	65,536
long int	32	4,294,967,296
long long int	64	1.84467440737e+19

# Inodes and ZOT Files

- Inodes contain the metadata for files and dirs
- Inodes are **pointers** to the data
- Regardless of size, a file needs at least one inode to locate it.
- A file of 1 byte takes up the same minimum inode count as a file of 1TB
- **DO NOT USE ZOTFILES!!** – Zillions of Tiny Files



# Streaming Reads & Writes

Let me demonstrate with a card trick.

# Pointless Data Replication

- How informative is this?
- How informative is this?
- How informative is this?
- How informative is this?
- How informative is this?
- vs
- How informative is this? [5x]
- LINE

# Editing Big Data

- Use format-specific utilities to view such files and hash values to check if they're identical to what they should be.
- Try not to be the person who tries to open a **200GB** compressed data file with nano/vim/joe/emacs, etc.

# [De]Compression

- If your applications can deal with compressed data, **KEEP IT COMPRESSED**.
- If they can't, try to use pipes (|) to decompress in memory and feed the decompressed stream to the app. Many popular apps now allow this.
- Use native utilities to examine the compressed data (zcat/unzip/gunzip, grep, archivemount, Vitables, ncview, etc).

# Moving BigData

- 1st: Don't.
- Otherwise, plan where your data will live for the life of the analysis, have it land there, and don't move it across filesystems.
- Don't DUPLICATE DUPLICATE DUPLICATE BigData
- See: <http://goo.gl/2iaHqD>
- **rsync** for modified data
- **bbcp** for new transfers of large single files, regardless of network
- **tar/netcat** for deep/large dir structures over LANs
- **tar/gzip/bbcp** to copy deep/large dir structures over WANs

# Checksums

- They work. Choose one and use it.
- **md5sum / jackson**
- Use MANIFEST files & copy them along with the data files.
- See Checksum example
- <http://goo.gl/uvB5Fy>

# Processing BigData

- Files (HDF5, bam/sam) and specialized utilities (nco/ncview, [Py/Vi]tables, R, Matlab)
- Relational Dbs (SQLite, Postgres, MySQL)
- NoSQLs (MongoDB, CouchDB)
- Binary Dumps (Perl's Data::Dumper, Python's pickle)
- Non-Storage (pipes, named pipes/FIFOs, sockets)
- Keep it RAM-resident.

# BigData, not foreverData

- HPC is not backed-up.
- Cannot tolerate old, unused BigData.
- Quotas on Size & # of files
- Please help us by doing your own data triage.
- Ask your PIs to bug our boss to provide more resources so we can provide more resources.



# Follow Along

- Take a few moments to login to cluster and follow along if you want.
- After logging in, follow me on screen
- Ref:
- [http://moo.nac.uci.edu/~hjm/biolinux/Linux\\_Tutorial\\_12.html](http://moo.nac.uci.edu/~hjm/biolinux/Linux_Tutorial_12.html)