



# Informatics Challenges

## Next-generation sequencing

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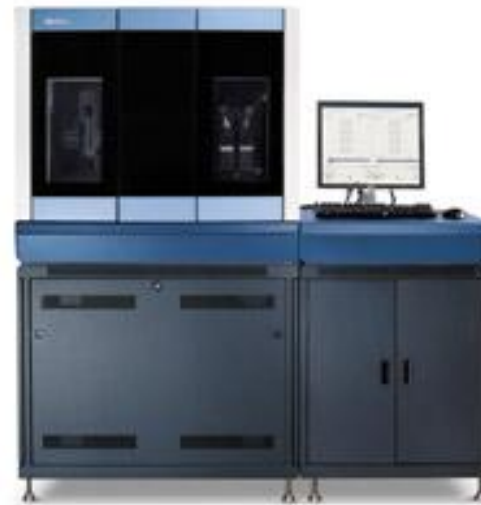
**<http://bioinformatics.unc.edu>**



THE UNIVERSITY  
of NORTH CAROLINA  
at CHAPEL HILL

# Now-Generation Sequencing

2010



- $> 1,000,000,000$  bases (1 GB) per hour





# Challenges ....

## 1. Data volume



# Challenge for the end-user...

- 3.6G Apr 27 20:13 s\_2\_sequence.txt
- 6.0G Apr 27 20:20 s\_3\_sequence.txt
- 6.1G Apr 27 20:21 s\_1\_sequence.txt
- 5.0G Apr 27 20:21 s\_5\_sequence.txt
- 6.0G Apr 27 20:25 s\_4\_sequence.txt
- 4.9G Apr 27 20:30 s\_6\_sequence.txt
- 5.5G Apr 27 20:42 s\_8\_sequence.txt
- 5.6G Apr 27 20:42 s\_7\_sequence.txt



# Would you like fries with that ...

- 5.0G Apr 27 20:21 s\_5\_sequence.txt
- 4.2G Apr 27 20:40 s\_5\_eland\_extended.txt
- 3.6G Apr 27 22:19 s\_5\_sorted.txt
- 13 GB of data **for one sample**



# HiSeq 2000

Changes loom in the data landscape .. yet again\*

- Image Data – 32 TB (not kept)
- Intensity Data – 2 TB (may want to keep)
- Base Call/Quality data – 250 GB
- Alignment Output – 6 TB (1.2 TB if intermediates removed)

\* Numbers from Illumina



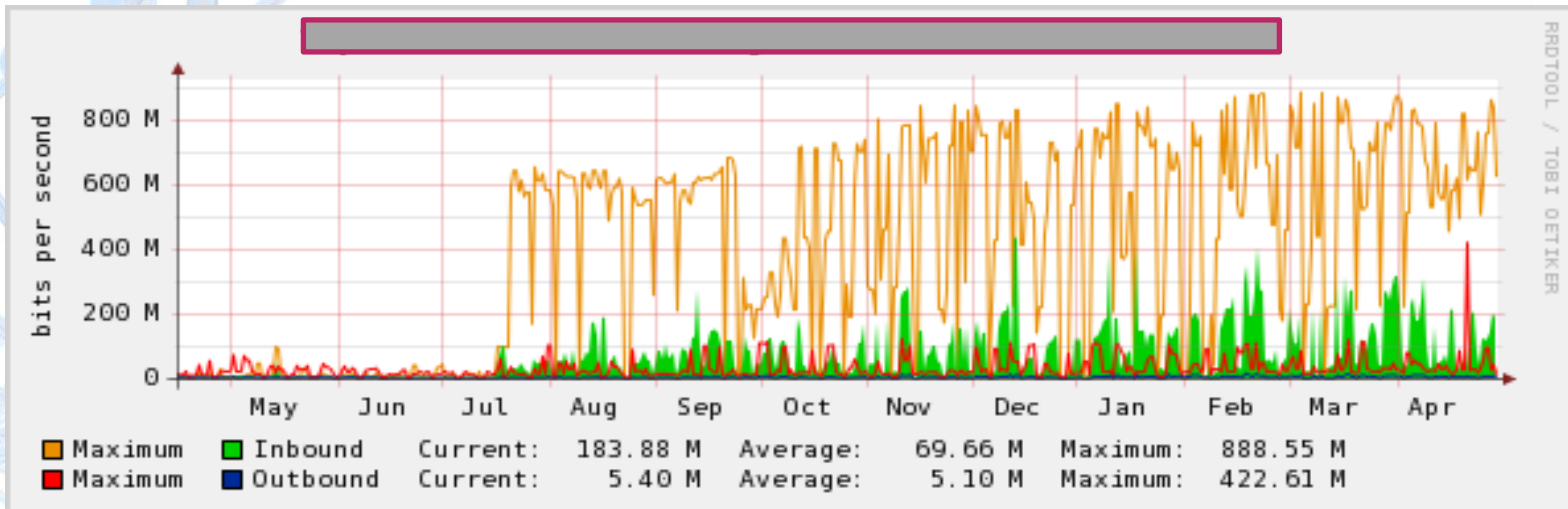
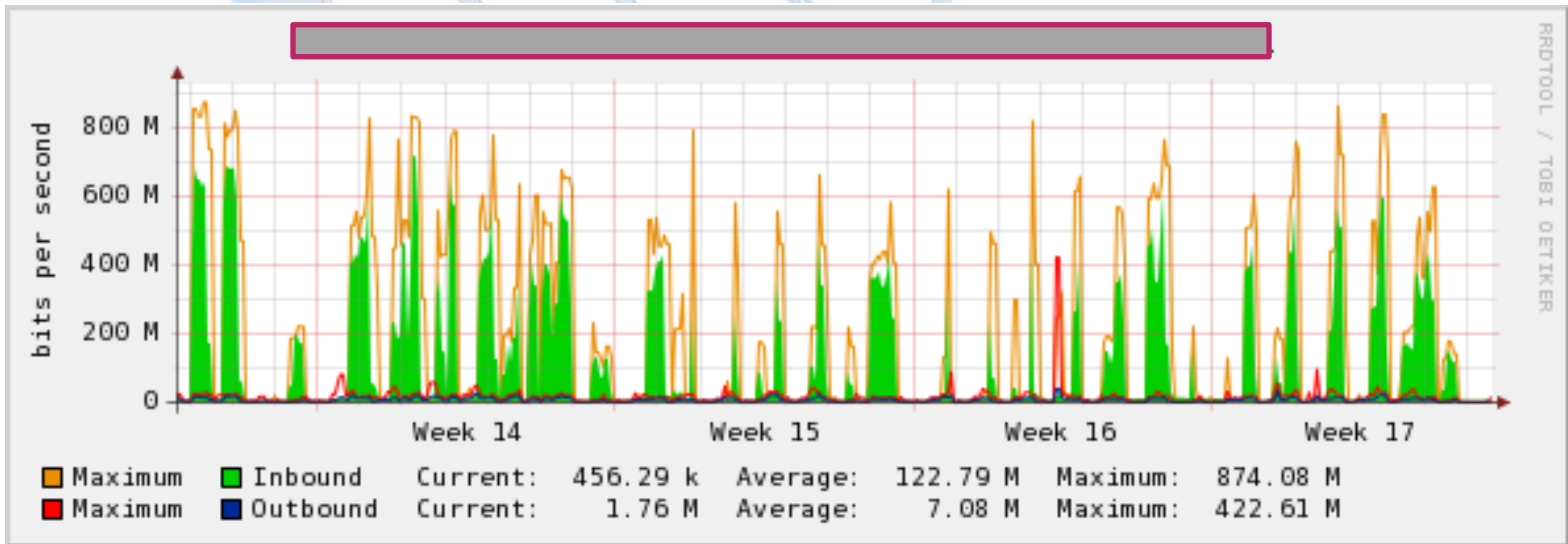


# Challenges ....

1. Data volume
2. Network bandwidth



# Network under siege





# Challenges ....

1. Data volume
2. Network bandwidth → cross-mounting partitions across WAN/VLANs may not be a viable option
3. Time



# Time

- Time to download/copy/delete/process
- Copying data takes significant amount of time (1-2 GB/min)
- Time to align/assemble 20-30 million reads (e.g. few hours to human genome)
- Hard to do truly parallel software
- I/O bottlenecks



# Challenges ....

1. Data volume
2. Network bandwidth
3. Time
4. Hardware



# Hardware

Client side :

- Storage may not be a big issue
- Do remember to have a plan for data backup
- 64-bit OS (Windows, Mac OS X, Linux)
- A dedicated workstation .. if possible

Facility end :

- Storage is a big issue – how much/how long/long term
- Data backup strategy (tape, archival disk storage, ILM)
- LIMS
- Data release mechanism



# Challenges ....

1. Data volume
2. Network bandwidth
3. Time
4. Hardware
5. Sharing/Publishing



# Sharing data

- NCBI GEO accepts HT sequence data
- NLM – SRA (sequence read archive)
- SRF file format developed at Sanger  
<http://sequenceread.sf.net>
- Web .. Bandwidth
- Cloud computing .. Specific storage formats



# Challenges ....

1. Data volume
2. Network bandwidth
3. Time
4. Hardware
5. Sharing/Publishing
6. Personnel

