Data Centers Get Serious: Unlimited Demand Meets Practical Reality

(http://www.esp.org/briite/meetings)

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Abstract

By some estimates, more than half of all organizations will be facing a shortfall in data-center capacity in the next twelve months. Biomedical research organizations are no exception. Sequencers are now available than can produce 1.5 terabytes of data per run. Companies like Pacific Biosciences are developing single-molecule, real-time approaches to sequencing that hold out the promise of producing a billion bases of sequence every five minutes. That translates into a 15x coverage of the human genome in less than four hours the entire sequencing effort of the human genome project starting at breakfast and done before lunch. The storage, management, and analysis of such data flows will require prodigious computing power and staggering mass-storage capacity. Individual RO1 grants will easily require tens, or hundreds, of terabytes of disk space. It is now routine for institutions to offer dedicated 250node compute clusters to recruit individual computationally intensive faculty.

Information technology is critically important for the success of biomedical research institutions, but the demands on our data centers are rapidly outstripping our ability to deliver. What to do? Determining how best to meet the wave of data-center demand will be the topic of this meeting — Data Centers Get Serious.

Topics

- Driving Factors
 - Moore's Law / Ubiquitous Computing
 - Post-Genomic Science / New Technologies
- Possible Solutions.
 - Build More
 - Use Less (virtualization / green computing)
 - Use Someone Else's (COLO, Outsource, Cloud)

The Problem

- Demand for computing is increasing exponentially, while data center capacity is relatively static.
- We are outgrowing our ability to house and manage the hardware infrastructure for our information systems.
- This is a problem for everyone.
- But it is especially a problem for biomedical research: Moore's Law is driving advances in computing and advances in computing are driving advances in biomedical technology.

FHCRC Experience















Driving Factors

Moore's Law

The Law:

• The number of transistors that can be placed on a chip doubles approximately every 18 months.

Gordon Moore, 1965

The Results:

- The power of advanced computing continues to grow almost 60% per year.
- The price of constant computing continues to drop by almost 40% per year.



Declining prices create new opportunities for computer use.

These new opportunities push increasing demand beyond the ability of Moore's law to meet that demand.

Cost at constant performance decreases exponentially.

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The result is that growing demand for computational services is overwhelming our ability to meet that demand.

Cost at constant performance decreases exponentially.

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- Today, a single Powerpoint file is often larger than all of the hard disk capacity available on a typical personal computer in 1987.
- Storing a single music album in good quality MP3 files requires more space than available on a typical 1987 computer.

In 1987, a typical desktop computer was equipped with less than 40 mB of disk space. Today it is hard to buy a new desktop computer with less than 80 gB of disk and some can easily have a 1000 gB or more. This is a huge increase in just 20 years.

Even greater growth challenges are occurring in our data centers.

Cost at constant performance decreases exponentially.

Driving Factors

Post-genomic Science & New Technologies

Awash in Data

Public Data Explosion

Base Pairs in GenBank (1994)



Base Pairs in GenBank (1994)



Samples to Sequence



Samples to Sequence

A prediction from 1994...

This is no longer a joke.

A state-of-the-art modern sequencer can today produce 500,000 bases per minute. Only a minor increase in efficiency will be required to hit mega-base per minute speeds.

Next-generation systems will leave mega-base per minute systems in the dust.



Another prediction from 1994...



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The point is, sometimes even crazy predictions do come true.

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Is there a limit?

Sequencing Speed

How fast can we read sequences?			
ABI 377:	7,200	bases per hour	
ABI 3700:	20,000	bases per hour	
Illumina Solexa:	20,000,000	bases per hour	
454 GS FLX:	20,000,000	bases per hour	

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How fast can nature read sequences?

One E. coli cell:

4,600,000

bases per hour

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The rate at which one bacterial cell can replicate DNA is a good measure of how fast DNA can be manipulated at the molecular level.

All sequencing methods to date involve manipulating DNA at the molecular level, so this rate around 1,000 bases per second is probably a good estimate of the single-molecule speed limit for DNA processing.



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How fast can nature read sequences?

One E. coli cell: 4,600,000 bases per hour 10 E. coli cells: 46,000,000 bases per hour 100 E. coli cells: 460,000,000 bases per hour 1,000 E. coli cells: 4,600,000,000 bases per hour 10,000 E. coli cells: 46,000,000,000 bases per hour 100,000 E. coli cells: 460,000,000,000 bases per hour 1,000,000 E. coli cells: 4,600,000,000,000 bases per hour

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1,000 E. coli cells:

bases per hour

Working on 1,000 molecules in parallel would give about one copy of the human genome per hour. Molecules are small, why not do 1,000 at once?

4,600,000,000





Ready to leap...

A groundbreaking DNA sequencing technology is going to redefine the field. Single molecule real time.

Pacific Biosciences is a bold company developing a transformative DNA sequencing platform. Our breakthrough single molecule, real time (SMRT[™]) technology delivers the ultimate combination of long reads, low costs, and fast cycle times. A new paradigm for whole genome analysis is about to emerge.

NEWS >> Intel, Others Back New DNA Sequencer >> Genomes 'R' Us	EVENTS >> The Genomics of Common Diseases 2008	SMRT™ TECHNOLOGY View Our 4:05 minute Technology Demo
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Scale: 43.5 μ m wide x 32.8 μ m tall.

Each tiny PacBio SMRT chip contains thousands of zero mode waveguides.



TINY barely captures the size of the PacBio SMRT chip.



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Think of the letter O of IN GOD WE TRUST on a US quarter as a tiny bowl.



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You could pile more than 150 SMRT chips inside that bowl.



Each zero mode waveguide is a cylindrical hole tens of nanometers in diameter, perforating a thin metal film supported by a transparent glass layer.



Attenuated light from the excitation beam penetrates only the lower 20 to 30 nm of each waveguide, creating a detection volume of 20 zeptoliters (i.e., 10⁻²¹ liters).



A single DNA polymerase molecule is attached to the bottom of the ZMW using a proprietary-based immobilation process.



Phospholipid nucleotides are added into the ZMW at the high concentrations required for proper enzyme functioning.



Researchers at PacBio have demonstrated that this approach has the capability to produce reads that are thousands of nucleotides in length.



This design supports the continuous and simultaneous excitation and detection of the individual labeled molecules.





Sequence data are generated when the enzymatic incorporation of the labeled nucleotide creates a flash of light, which is converted into a base call using optimized algorithms.





single well

If we were to look at the bottom of a single well in the Pacific biosciences detection chip, we would see low intensity flickering of different colors of light as different nucleotides rapidly (microseconds) moved into and out of the detection chamber.

Periodically we would see a burst of a sustained (milliseconds) single color, corresponding to the incorporation of a single nucleotide into the growing DNA strand.

By recording the base name corresponding to the particular burst of color, the system can generate, in real time, a singlemolecule read of DNA sequence.

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single well

Although this process does run slower than the biological process of DNA synthesis, it is still capable of producing DNA sequence at a truly astounding rate.

In principle, you could start a run on a Pacific Biosciences sequencer before breakfast and by lunchtime have produced as much DNA sequence as was involved in the completion of the human genome project.

Pac BioSciences Sequencer



GenBank

Today









Problem

Other Challenges

Other Challenges

Many areas need computing horsepower:

- Epidemiological simulation
- Genome wide association studies
- Expression-array analysis
- Proteomics
- Clinical diagnostics
- Image analysis

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- Cheaper is also a problem, because people keep coming up with clever ways to use smaller, better, faster, cheaper computers at a rate faster than the computers are getting smaller, better, faster, and cheaper.
- As a result, our data centers are filling up.

Solutions

Summary

Build More Data-Center Space

- Sounds easy enough:
 - Dedicate or acquire space
 - Build a data center
- Challenges exist:
 - Current technology places great demands on data center design
 - Need lots of power
 - And lots of cooling
 - This can be very expensive

Data-Center problem



Data-Center problem













http://www.briite.org

















Decisions Are Tricky

- The options have different advantages and disadvantages.
- The options have different long- and short-term cost profiles.
- Some are primarily expense, others capital. Some are both.
- The options have different useful life expectancies.
- Comparing these is less like comparing apples and oranges and more like comparing apples and Buicks.

END

EXTRAS

Samples to Sequence



Moore's Law



Moore's Law

