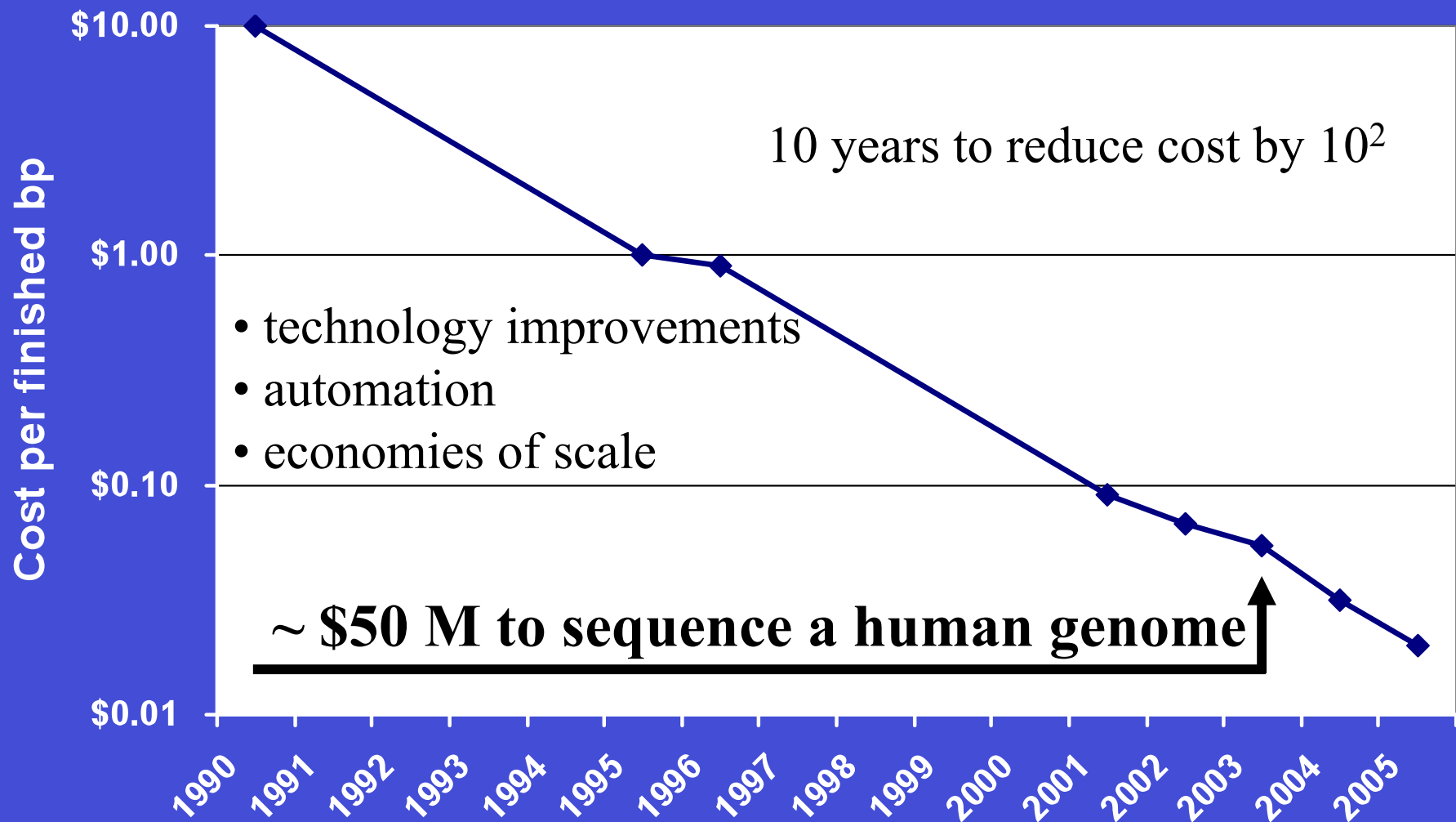
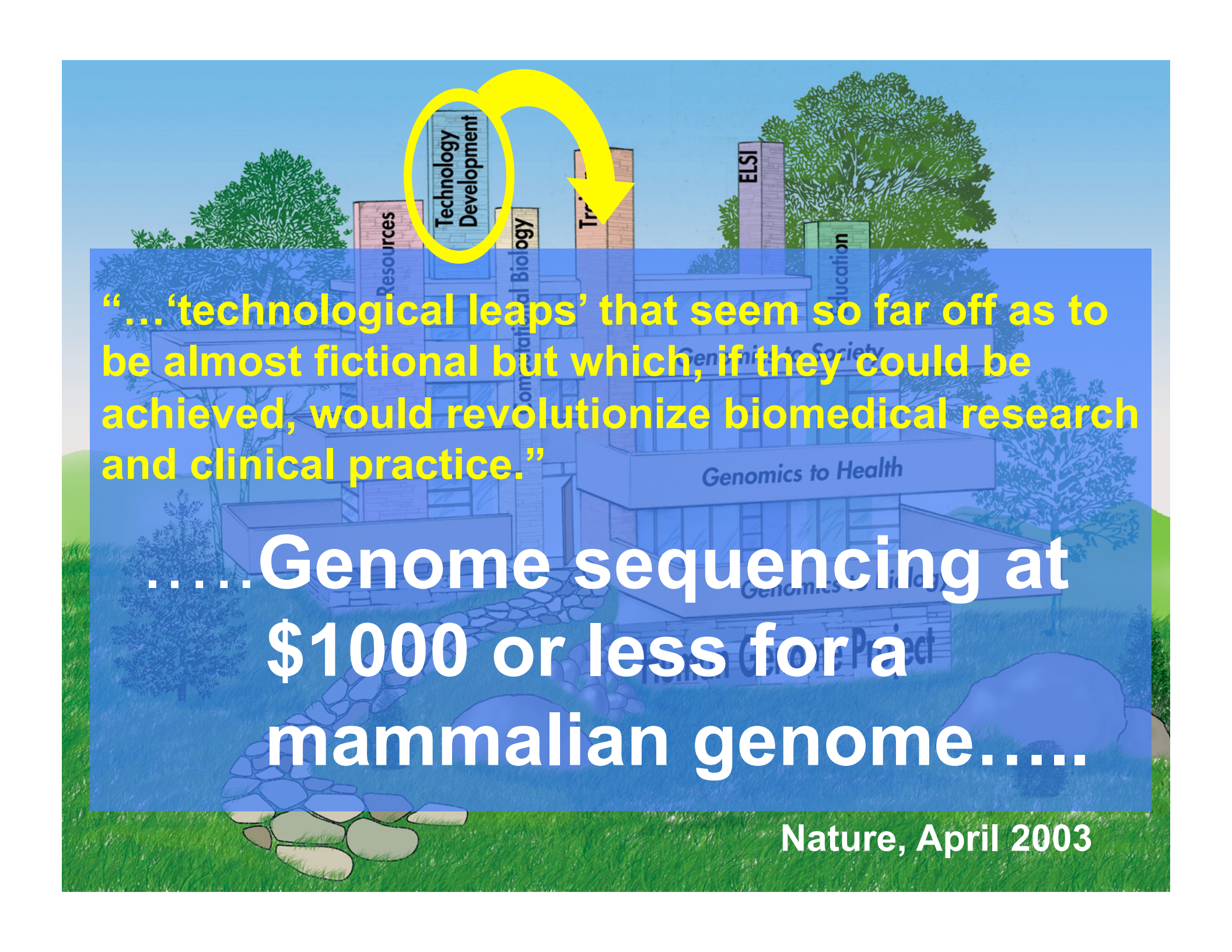




# Decrease in the Cost of Finished DNA Sequencing







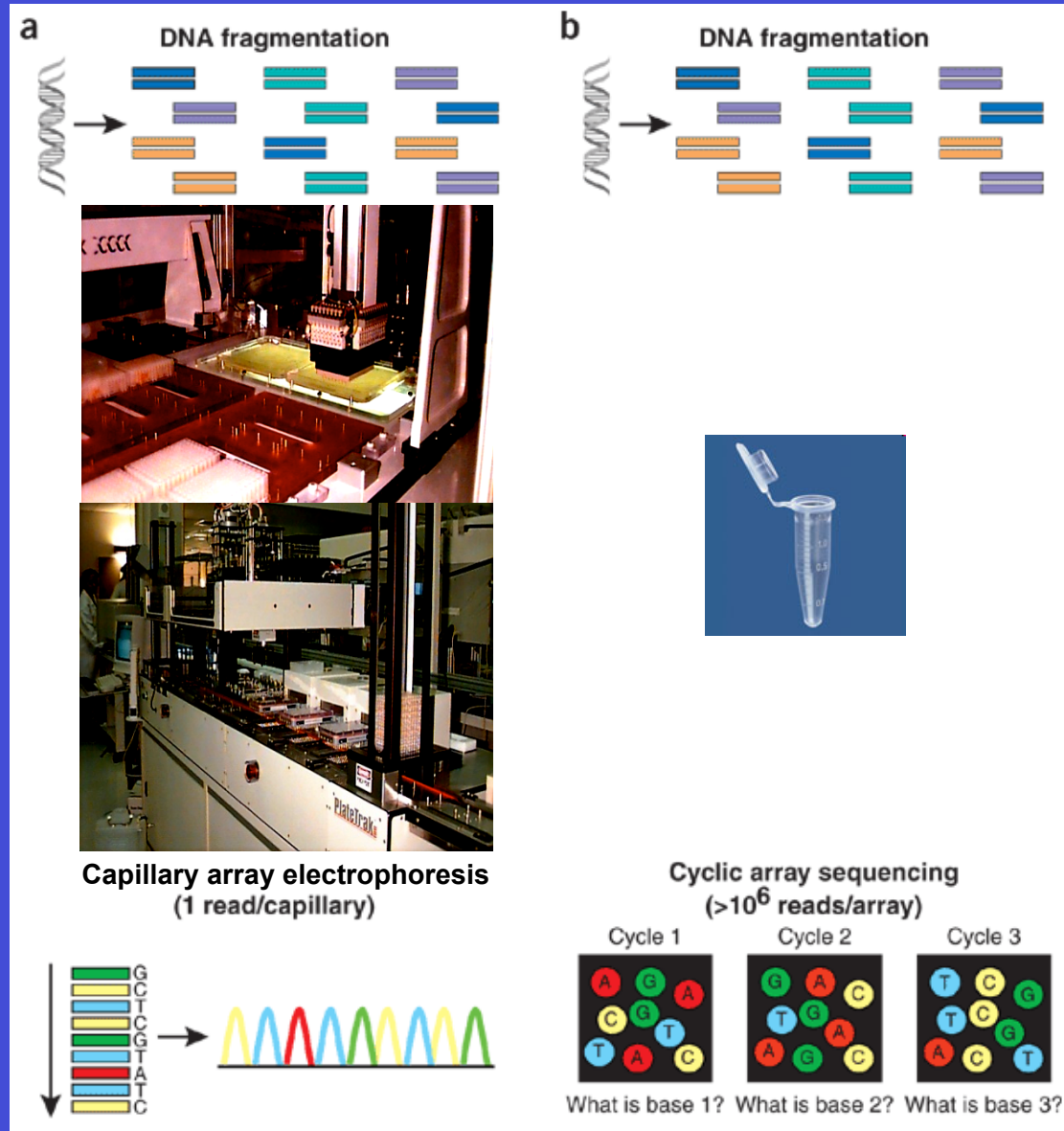
Technology  
Development

“...‘technological leaps’ that seem so far off as to be almost fictional but which, if they could be achieved, would revolutionize biomedical research and clinical practice.”

..... Genome sequencing at  
\$1000 or less for a  
mammalian genome.....

Nature, April 2003

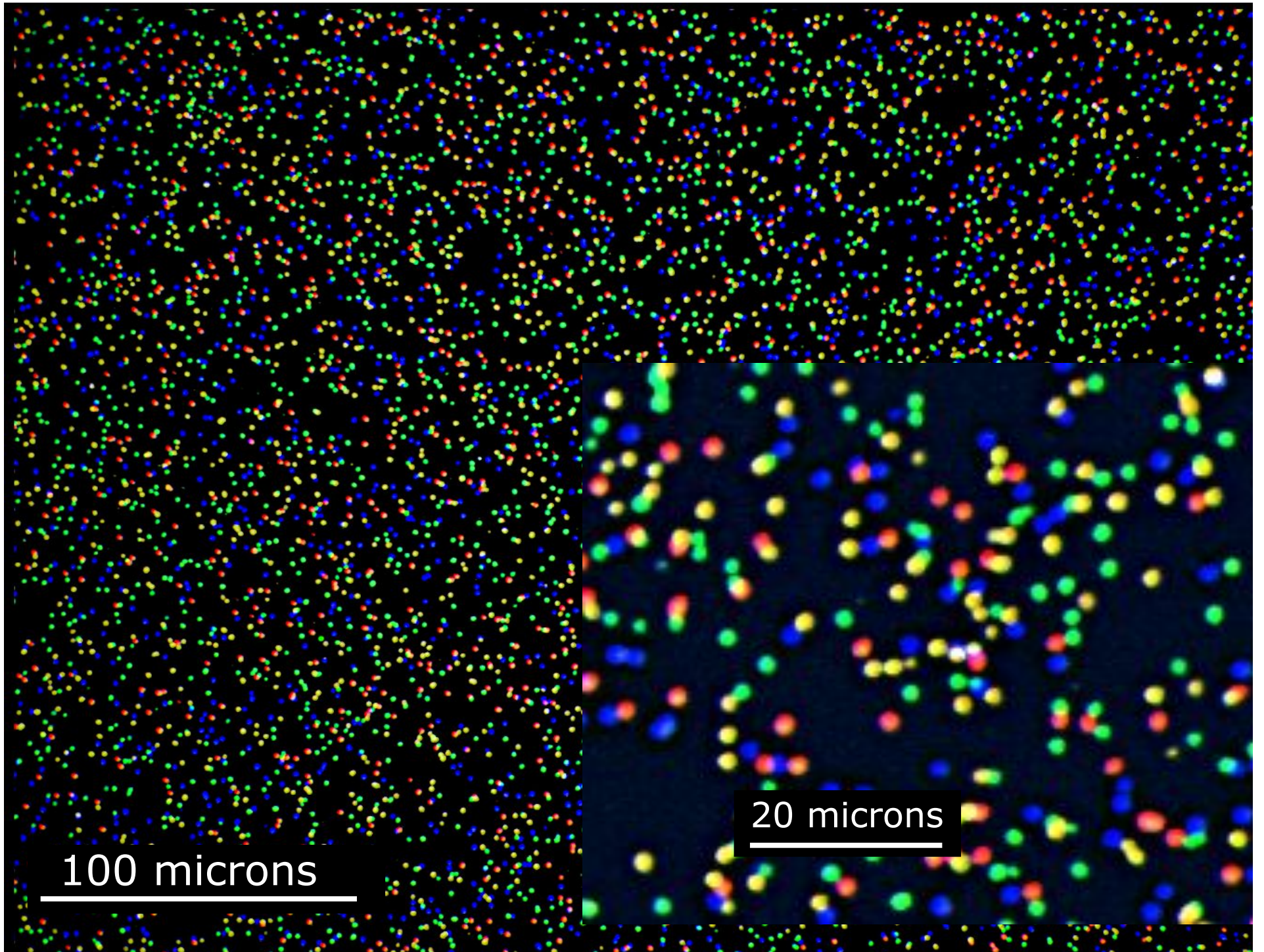
# Workflow: Sequencing in 2003 vs. Sequencing today



100  
per run

>100  
million  
per run





100 microns

20 microns





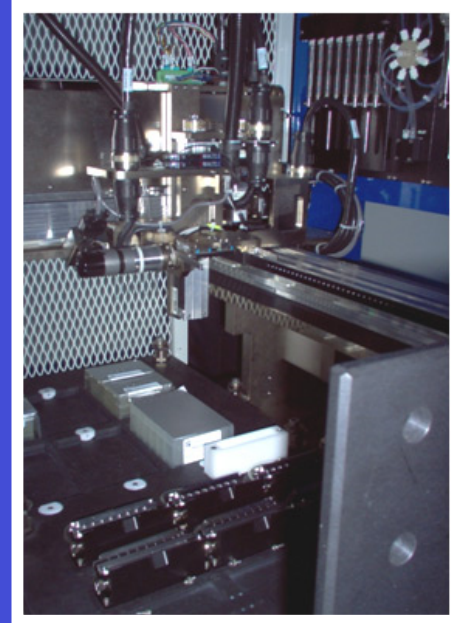
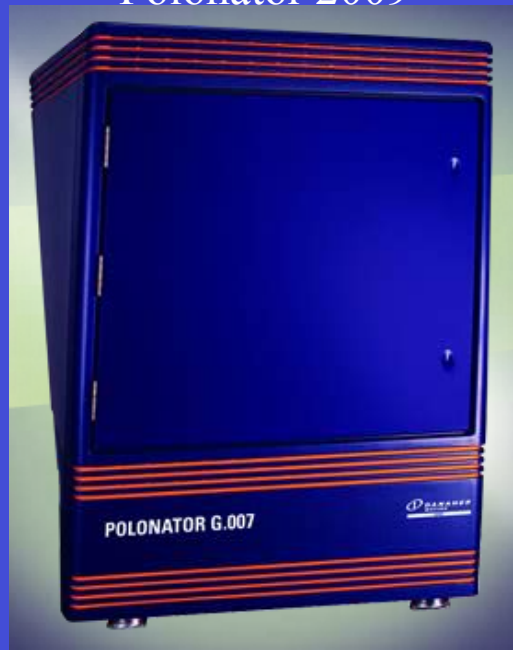
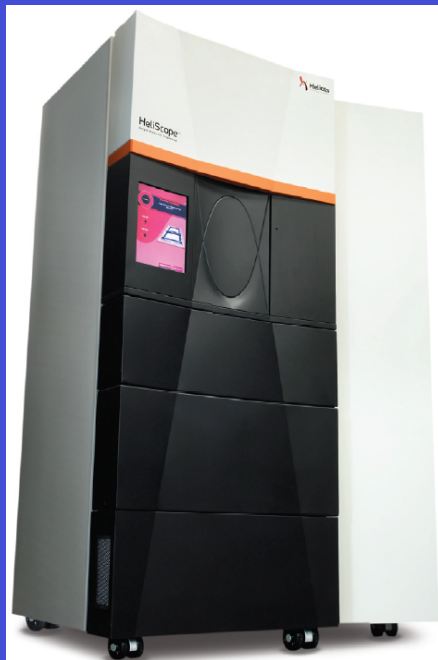
Roche/454 2005  
Helicos 2008



Illumina / Solexa 2006  
Polonator 2009



Applied Biosystems/Agencourt 2007  
Complete Genomics 2010





# Latest commercial systems 2010...



Roche / 454 FLX  
Helicos HeliScope



Illumina HiSeq 2000



Applied Biosystems SOLiD 4



Pacific Biosciences RS



Ion Torrent PGM



...to scale

# Throughput overview (estimated, snapshot)

<u>Vendor</u> <u>(~cost/run)</u>	<u>method</u>	<u>read length</u>	<u>reads /run (B)</u>	<u>Gb /run</u>	<u>Gb /day</u>	<u>run time</u>
Roche/454 (\$ 7,000)	pyro-sequencing	400	0.001	0.5	1	10 hrs
Illumina/Solexa (\$17,000)	reversible terminator	100	0.2	30	3	10 days
AB SOLiD days (\$30,000)	oligo ligation	50	1	50	3.5	14
Helicos days	reversible terminator single molecule	35	1	35	4.5	8
Complete Genomics	probe-anchor ligation	10?	50?	2000?	?	30 days?



# Applications

Unlike previous DNA sequencing technology, these new methods sample very large numbers of single molecules (or ensembles generated from single molecules), enabling new biological insights:

- genomes – re-sequencing, *de novo*
- sequence variation (SNP, indel, and larger)
  - rare variants, not just the common ones
- haplotypes (with difficulty)
- rearrangements (with difficulty)
- methylation status
- expression analysis – counting rather than ratios
- allele-specific expression analysis
- alternative splicing
- small RNAs
- ChIP-seq (proteins bound to DNA)
- rare samples (e.g., in mixtures) – high dynamic range

# Resequence 1 Human Genome

## Capillary Array Electrophoresis (2003)

96 channels x 24 runs/day x 800 bp per run  $\approx$  1.8 Mb/day  
6x coverage of 3 Gb genome takes 26 years with 1 machine,  
 **$\sim$  3 months with 100 machines**

## Sequencing by synthesis on array (2007)

1 Gb/run, 2.5 days/run,  
30x coverage of 6 Gb genome takes 1.5 year  
these are very early days for this collection of emerging  
technologies  $\rightarrow$  e.g., 4-6x improvement over next year  
 **$\sim$  3-4 months with one machine**



# Resequence 1 Human Genome

## Capillary Array Electrophoresis (2003)

96 channels x 24 runs/day x 800 bp per run  $\approx$  1.8 Mb/day

6x coverage of 3 Gb genome takes 26 years with 1 machine

**$\sim$  3 months with 100 machines**

## Sequencing by synthesis on array (Sept 2009)

30 Gb/run,  $\sim$  6 days/run

30x coverage of 6 Gb genome takes 3 runs

**< 1 month with one machine**

# Resequence 1 Human Genome

## Capillary Array Electrophoresis (2003)

96 channels x 24 runs/day x 800 bp per run  $\approx$  1.8 Mb/day

6x coverage of 3 Gb genome takes 26 years with 1 machine

**$\sim$  3 months with 100 machines**

## Sequencing by synthesis on array (end of 2010, projected)

200-300 Gb/run,  $\sim$  7-14 days/run

30x coverage of 6 Gb genome takes  $\sim$  0.5 run

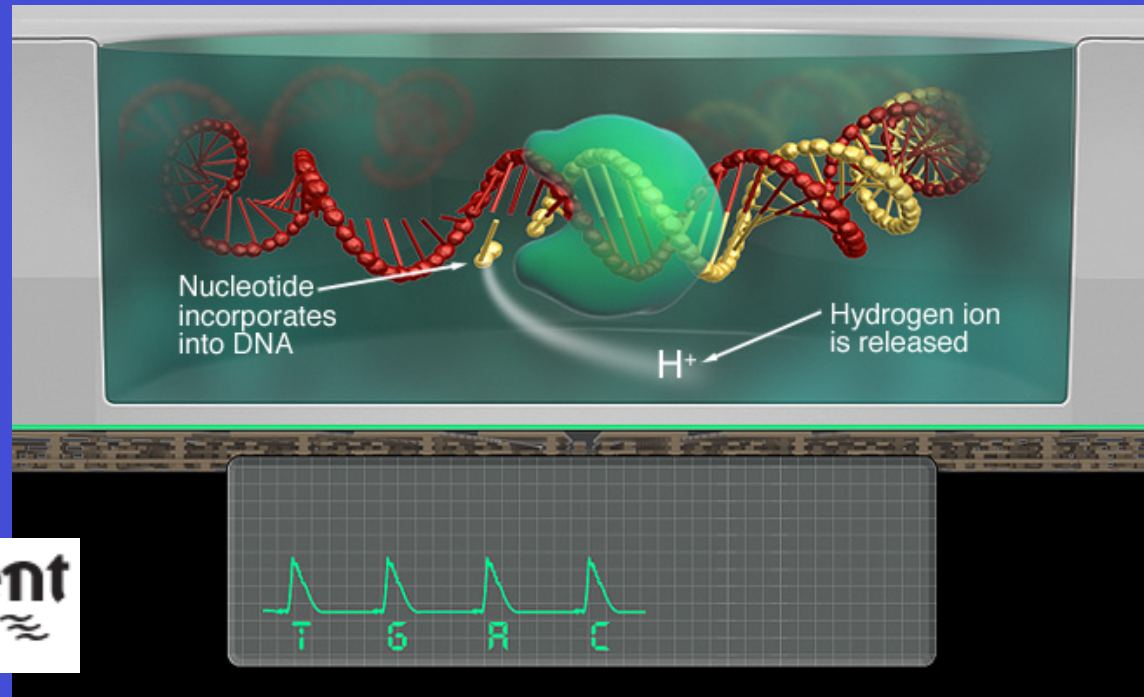
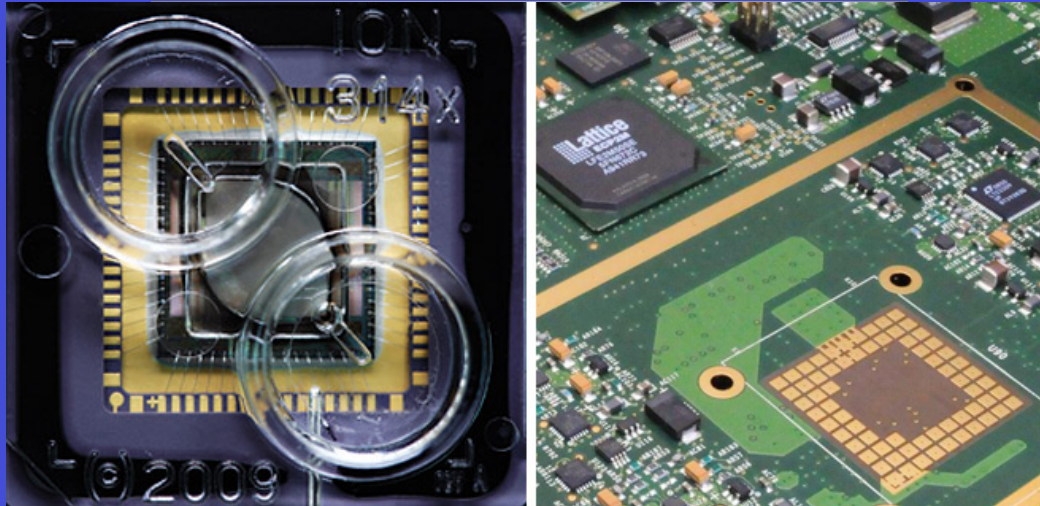
**$\sim$  1 week with one machine ( $\sim$  2 genomes)**

# **Emerging sequencing technologies**

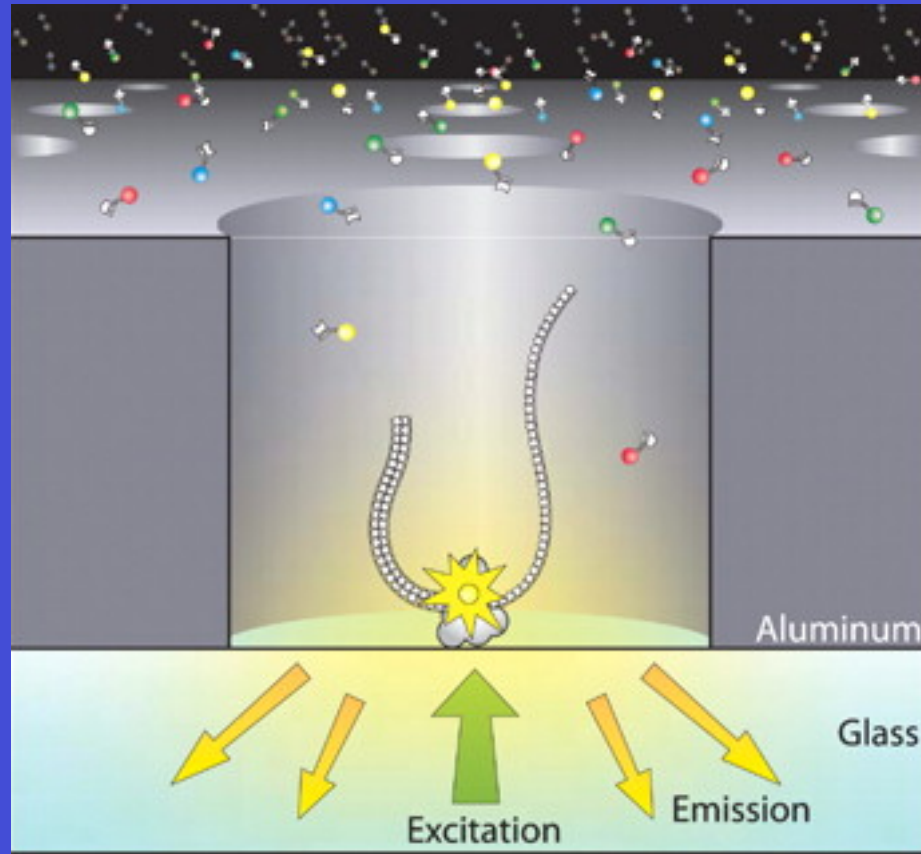


# Sequencing-by-synthesis, native DNA pol/dNTPs, pH detection

1.5 million  
pH meters

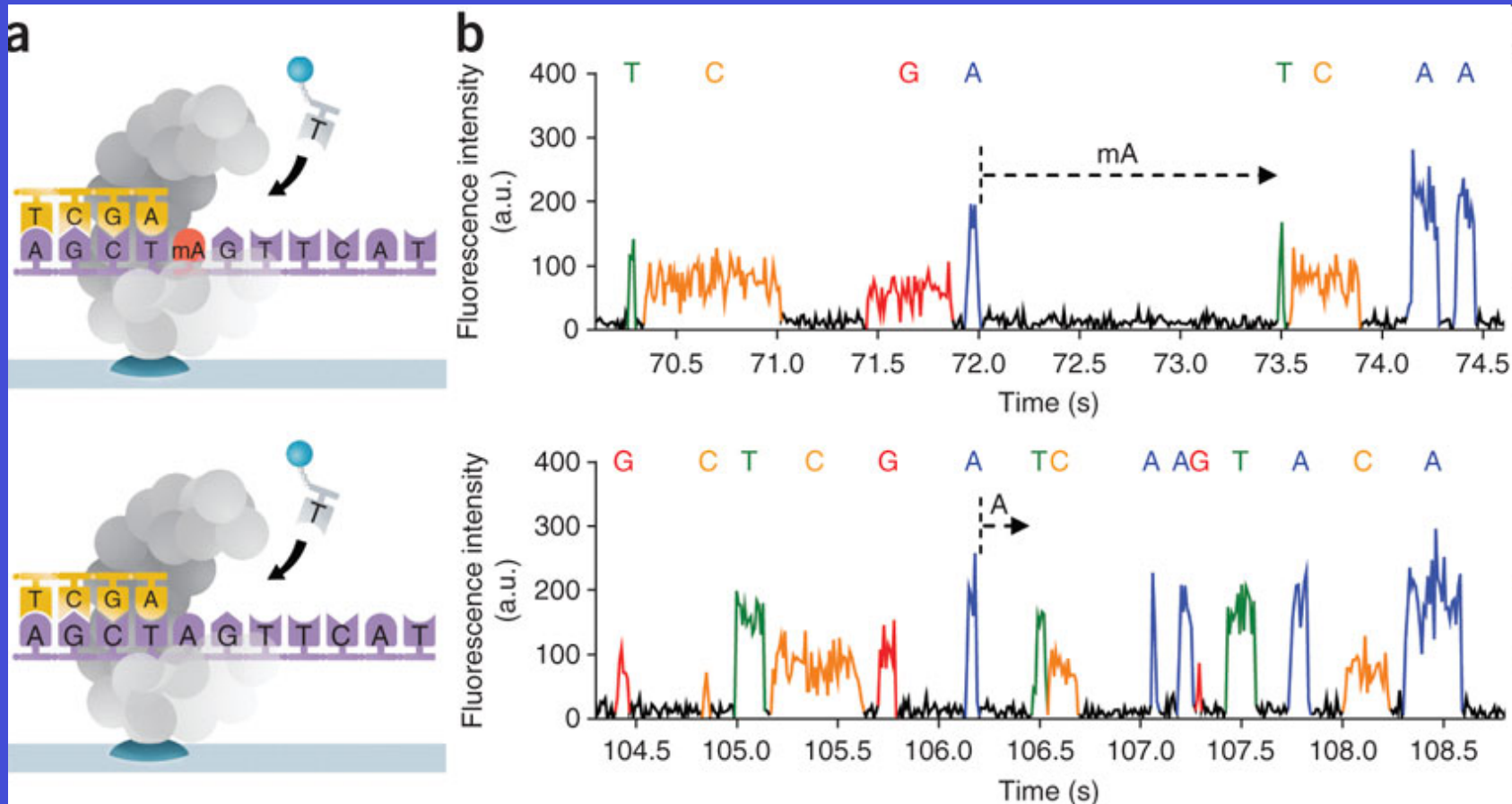


# Free-running polymerase





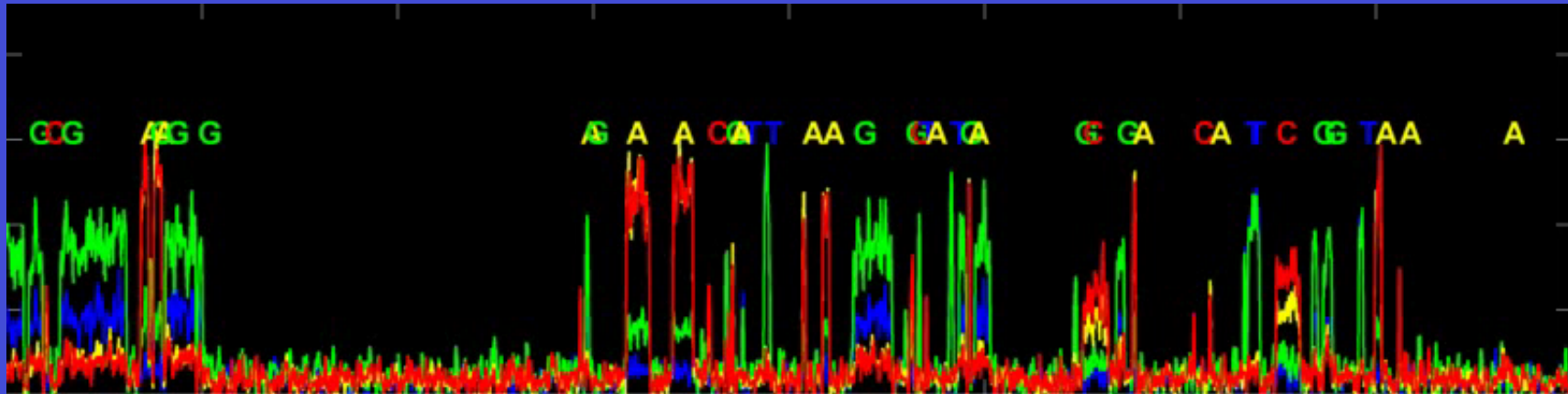
# DNA polymerase as a sequence and methylation reader



Direct detection of DNA methylation during single-molecule, real-time sequencing.  
B Flusberg, *et al.*, Nature Methods online 9 May 2010

# Example of a very long read

10,351 Bases...

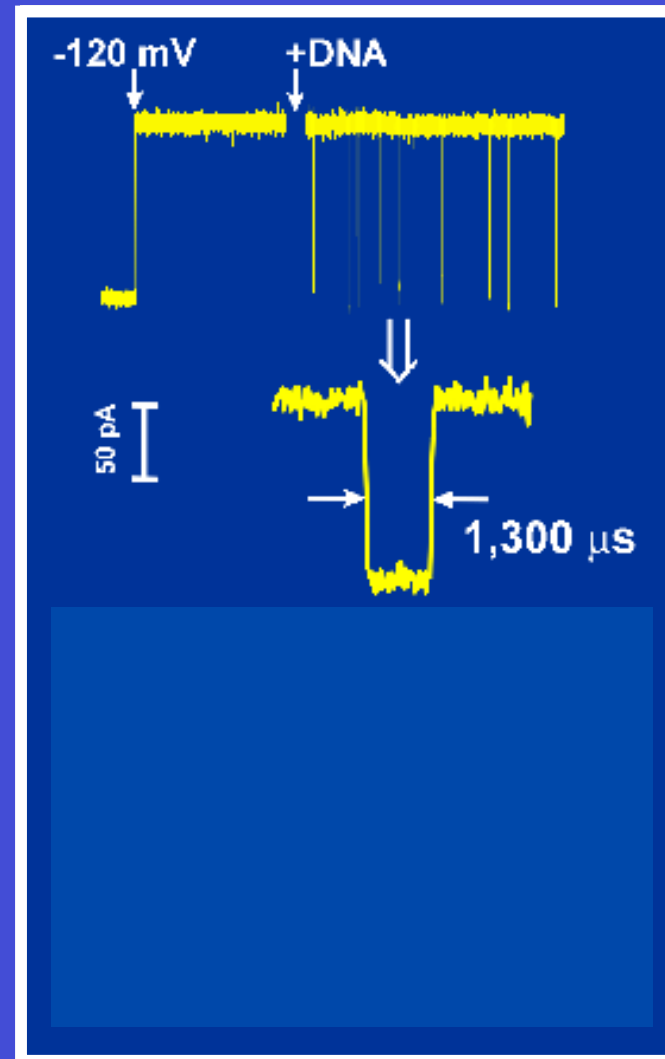
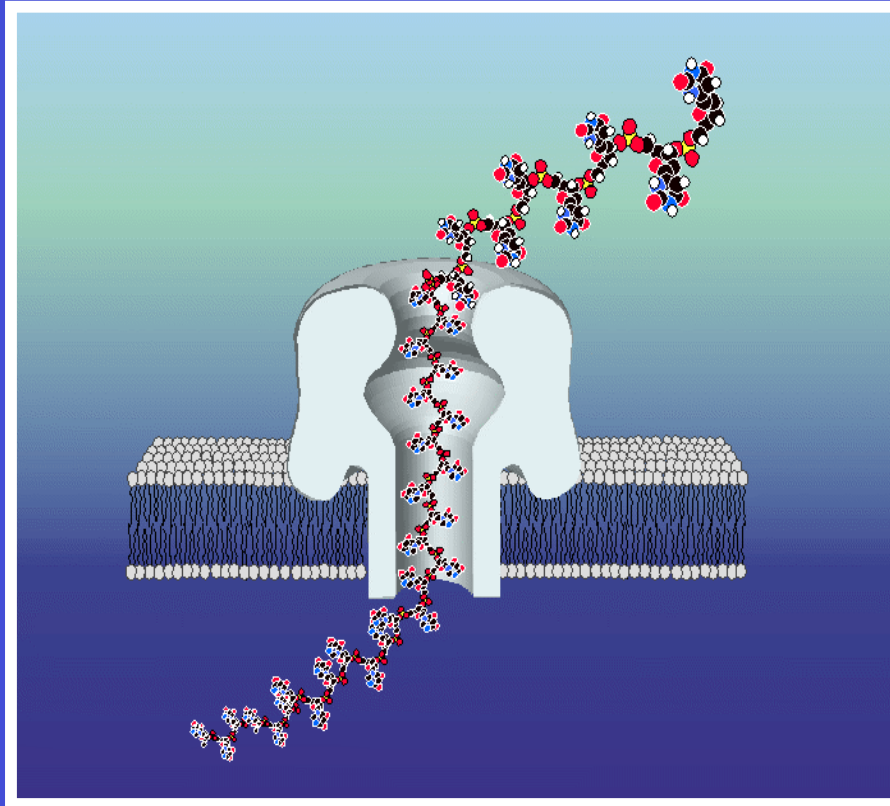


From the *E.coli* genome

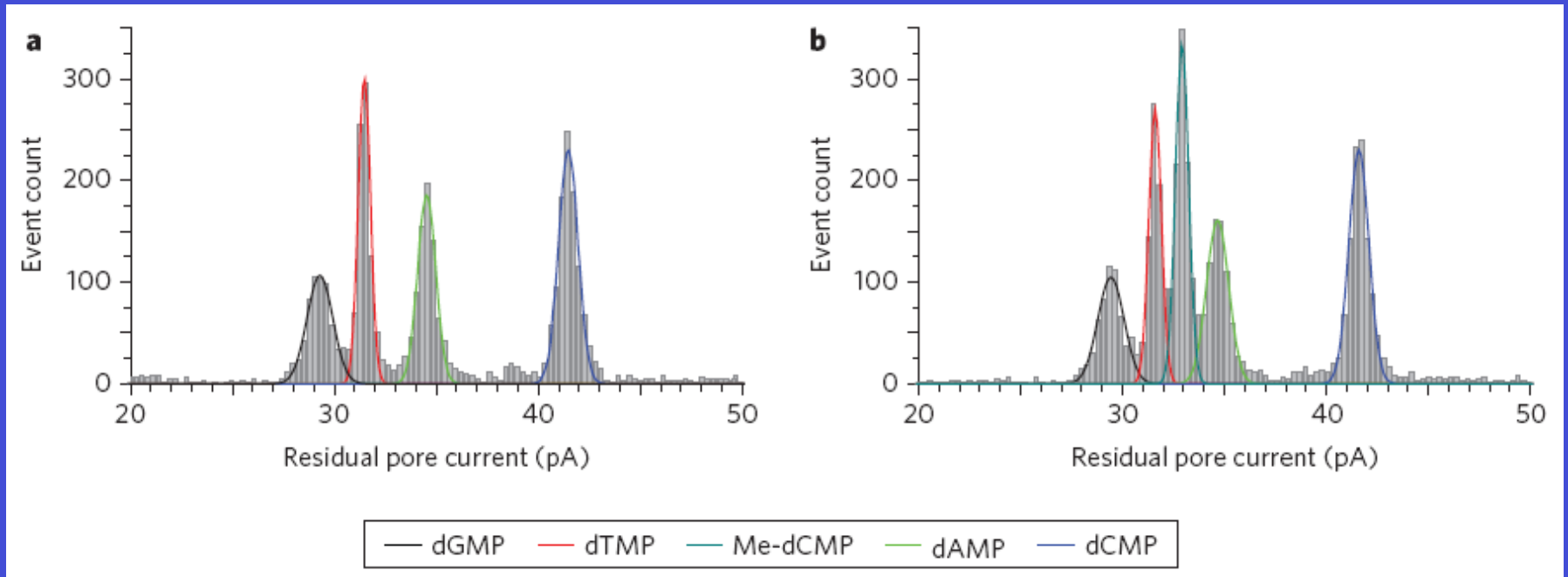
# Nanopore sequencing



# Nanopore sequencing concept



# Direct electronic readout of A, C, G, T and methyl-C



# Nanopore sequencing advantages

- Sequence genomic DNA directly – no conversion or amplification; no reagent costs except extraction
- Very long reads – assembly, haplotype information, structural variants. De novo sequencing
- Microbiome sequencing would be immensely simplified
- Non-destructive of the DNA sample
- A, C, G, T and modified bases
- RNA, too? Gene Expression, allele-specific G.E., splice variants, small RNAs, ...
- Digital (gene expression, copy number variants)
- Very fast
- Fully electronic; takes advantage of integrated chip technology infrastructure
- Portable, hand-held devices



# Resequence 1 Human Genome

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30x coverage of 6 Gb genome takes  $\sim$  0.5 run

**$\sim$  1 week with one machine ( $\sim$  2 genomes)**

## Nanosensor (future)

1 msec per base  
10x coverage of 6 Gb genome takes  
 $\sim$  2 years with single nanopore  
 **$<$  1 day with 1000 nanopore array – assembled?**