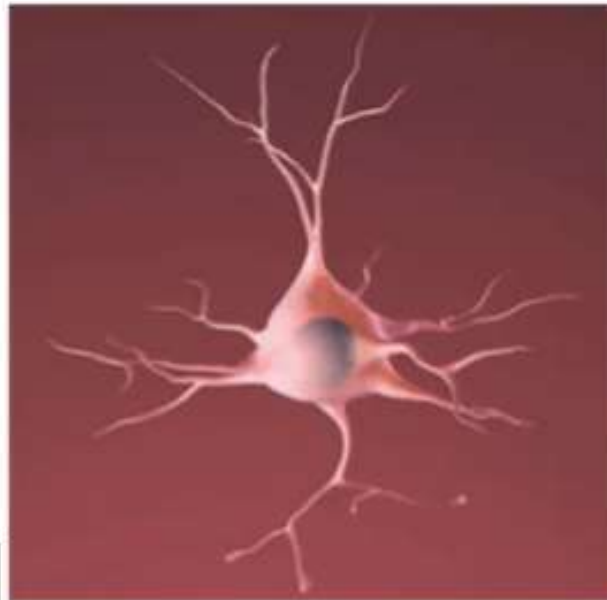
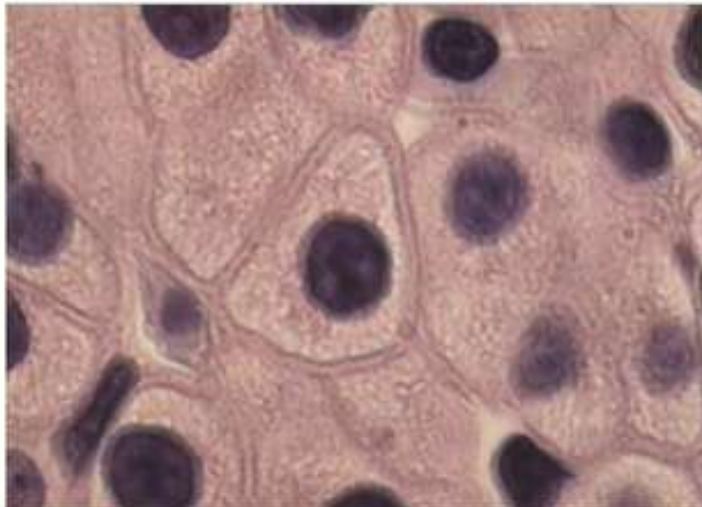


# Why genomics?



Steven Salzberg





slide adapted from Rafael Irizarry







**DNA**

ACTGACCTAGATCAGTGTAGCGATCGTATACGAGACCGATTTCATCGGCAT



transcription

**RNA**

AUCAGUCGAUCACCGAU



translation

**protein**





**DNA**

ACTGACCGTTCGATCGATCGTATACGATTACAAAATCATCGGCAT

↓ transcription

**RNA**

AUCAGUCGAUCACCGAU

↓ translation

**protein**



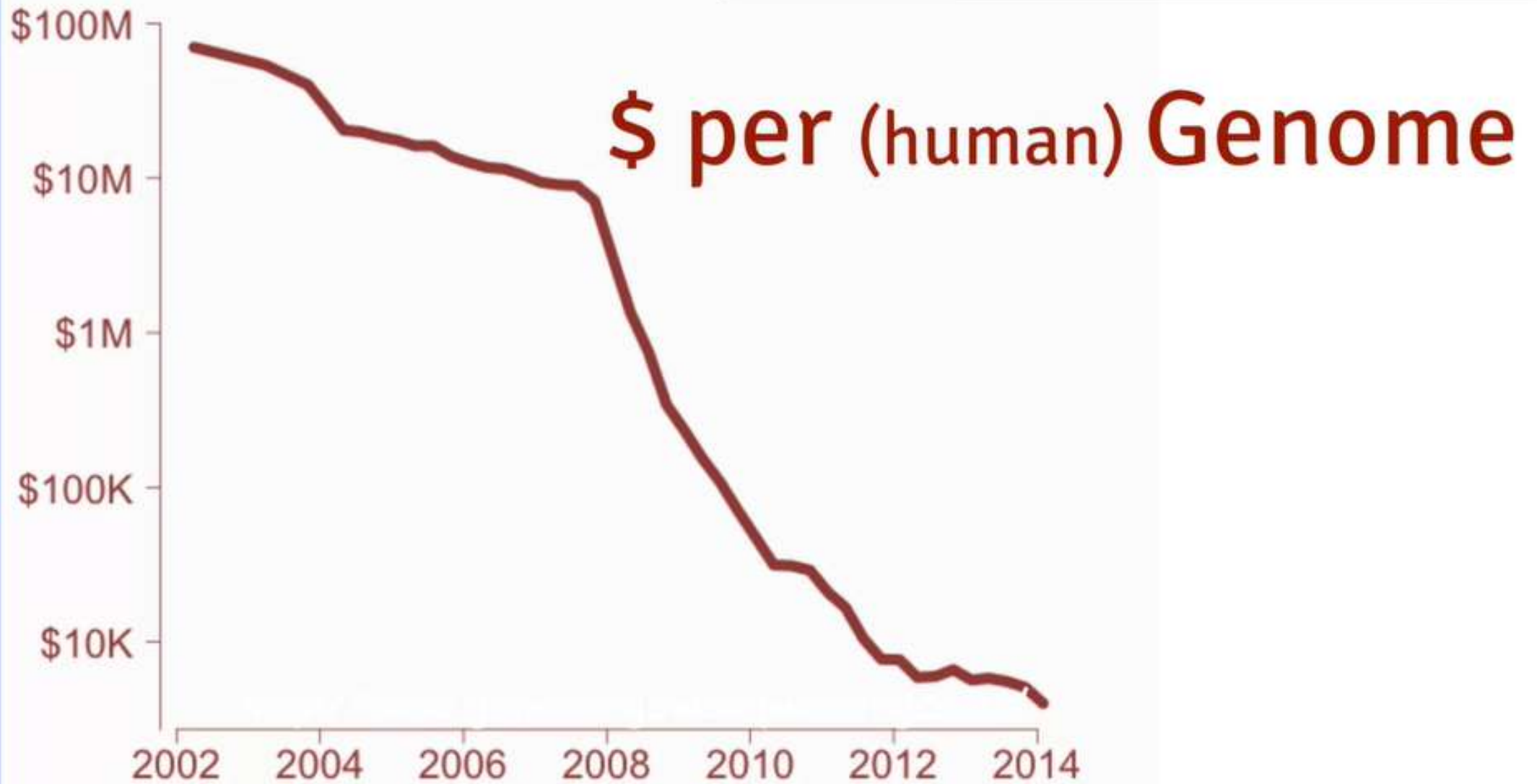


Image via Illumina: <http://goo.gl/y0M01y>



@HWI-EAS121:4:100:1783:550#0/ [http://brianknaus.com/software/srtoolbox/s\\_4\\_1\\_sequence80.txt](http://brianknaus.com/software/srtoolbox/s_4_1_sequence80.txt)  
CGTTACGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGGATCTCGTATGCCGTCTGCTATGCCGTCAGCAAGACAGCGGC  
+HWI-EAS121:4:100:1783:550#0/1  
aaaaa`b\_aa`aa`YaX]aZ`aZM^Z]YRa]YSG[[ZREQLHESDHNDHDHMEEDDMPENITKFLFEEDDDHEJQMEDDD  
@HWI-EAS121:4:100:1783:1611#0/1  
GGGTGGGCATTTCCACTCGCAGTATGGGTGCGGCACGACAGGCAGCGGTCAGCCTGCGCTTTGGCCTGGCCTTCGGAAA  
+HWI-EAS121:4:100:1783:1611#0/1  
a``^`\_`\_`\_`^a``a`^a`\_`\_`]a\_]`]]`a`\_\_\_\_\_`\_`^^`]X]\_]XTV\_`]]NX\_XVX]]\_TTTTG[VTHPN]VFDZ  
@HWI-EAS121:4:100:1783:322#0/1  
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+HWI-EAS121:4:100:1783:322#0/1  
abaa`^aaaaabbbaababbbbbbb`bbbb`bbbbbbbbb`bbbaV^\_a``a``]``aT]a\_\_V\]]\_]`a`]a\_abbaV\_\_  
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@HWI-EAS121:4:100:1783:207#0/1  
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Data source: <http://www.genome.gov/sequencingcosts/>



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## SRA

Sequence Read Archive (SRA) makes biological sequence data available to the research community to enhance reproducibility and allow for new discoveries by comparing data sets. The SRA stores raw sequencing data and alignment information from high-throughput sequencing platforms, including Roche 454 GS System®, Illumina Genome Analyzer®, Applied Biosystems SOLiD System®, Helicos Heliscope®, Complete Genomics®, and Pacific Biosciences SMRT®.

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