

Genetics v Genomics

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Overview

1 Genetics v. Genomics

- Goals
- Genomics: Why We're Here
- Sequencing Technologies

2 In-Class Activity

Today's Goals

- What is/are Genomics?
- How have techniques changed?
- What impact has that had on biological questions?

What is/are Genomics?

- What is Genomics?
- How is it different than Genetics?
- What allows us to do genomics instead of genetics?

What is/are Genomics?

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- 4 Vote on other answers

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What is/are Genomics?

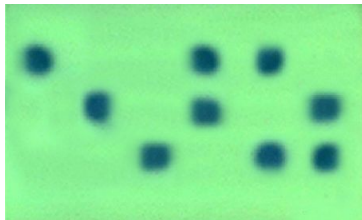
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- In contrast to genetics, which refers to the study of individual genes and their roles in inheritance, genomics uses high throughput DNA sequencing and bioinformatics to assemble, and analyze the function and structure of entire genomes.

Brief History of Sequencing

- Allozymes
- Sanger Sequencing
- Next Generation Sequencing - NGS

Allozymes

- 1960's
- Electrophoresis separates different proteins by amino acid makeup
- First (limited) look at DNA composition

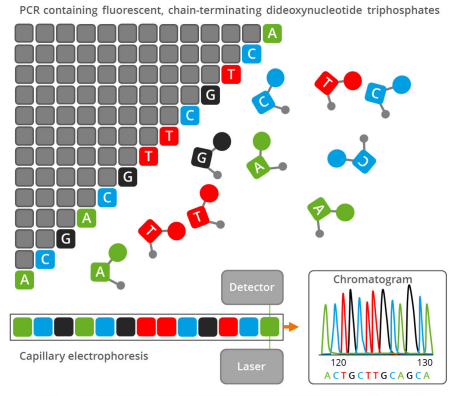


Sanger Sequencing

- 1977
- Determines the sequences a single piece of DNA up to 500bp
- Highly accurate but slow

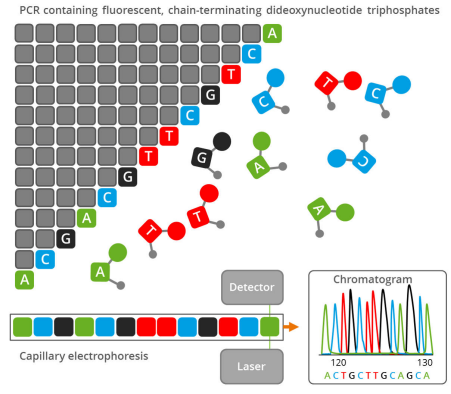
Sanger Sequencing

- Design a primer
- Run a PCR
- Chain-terminating dideoxynucleotide triphosphates



Sanger Sequencing

- Run results on a gel
- Read with a laser, determines which base ended the PCR
- Color order is sequence order



NGS Sequencing

- mid-2000's
- Many different companies and methods
- All generate far more data than Sanger

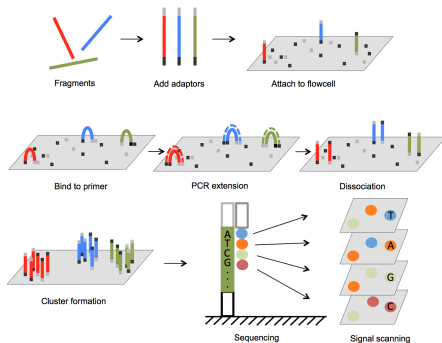
NGS Sequencing - Illumina

- Library Preparation

- Fragment a sample of whole genomic DNA
- Add adaptors for the specific machine

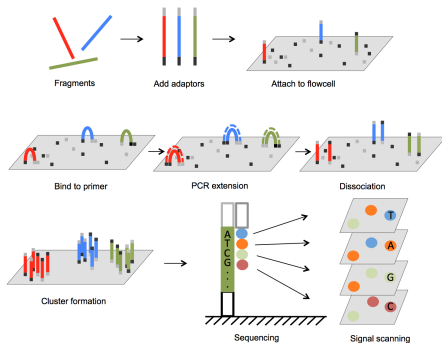
- Amplify with PCR

- Read on machine (next slide)



NGS Sequencing - Illumina

- Machine attaches adapter and DNA to a fixed surface
- Amplifies single strand
- Adds a new base each cycle and images for ID



NGS Sequencing - PacBio

- Library Preparation
 - Fragment a sample of whole genomic DNA
 - Add adapters for the specific machine
- Amplify with PCR
- Read on machine

HOW IT WORKS

DNA is copied by an enzyme in PacBio's machine

The DNA letters used to make the copy have been tagged to emit tiny flashes of colored light.

A camera can catch these tiny flashes thanks to a 50-nanometer hole that screens out other light.



NGS Sequencing - PacBio

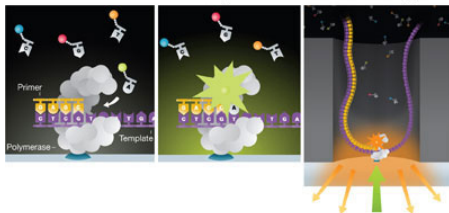
- A copy is made on the machine by an enzyme
- The bases used for the copy are fluorescent
- As a new base is incorporated the color shows the identity

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Next Generation Sequencing vs. Sanger

- Output for Quality Tradeoff
 - NGS = VERY High Output / Good Quality
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- Allozymes
 - 1960's
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 - 1977
- NGS - Next Generation Sequencing
 - 2000



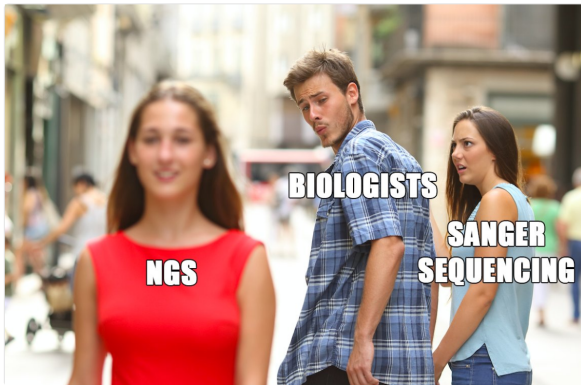
Miles Zhang

@ymilesz

Following

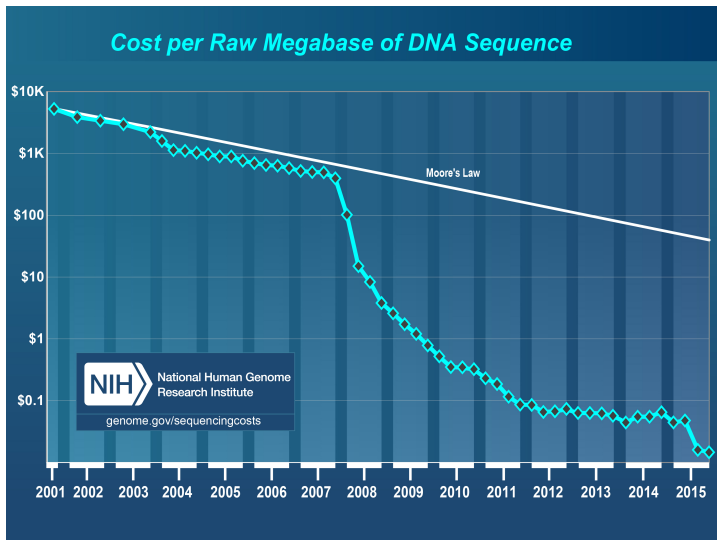


This meme is everywhere, so I thought I'd add a biology twist to it.

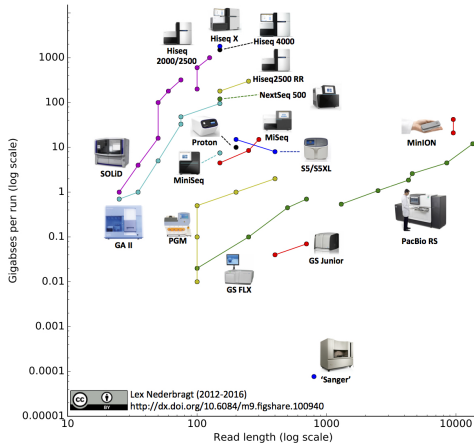


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Sequencing Cost



Sequencing Output



Generational Shift

- More and more data can be generated

Generational Shift

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- Data length and quality are both improving

Generational Shift

- More and more data can be generated
- Data length and quality are both improving
- How does this change the scope of research?

In-Class Activity

- 1 Make 4 groups (rearrange desks)

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 - Transcription Factors
 - CpG islands
 - DNA Methylation

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 - What genes underlie a specific function?
 - What is the code of the human genome?
 - Group's Choice:
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- 3 How would your group assess this question
 - in 1997?
 - in 2017?

- Group Choice Order:

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- 3,234.83 Mb

Function

- 2017
- easily ask question bc you can completely sequence the genome
- RNAseq
- knockout screen - knock sections out and see changes
- 1997
- ask the question in a limited way - how does a single gene alter a single function

Transcription Factor

- Transcription Factor - protein that regulates the transcription of a gene
- feedback loops in gene pathways
- 1997
- knockouts and broad genetic methods
- ask about a known TF
- 2017
- CHIPseq - chromatin immunoprecipitation seq
- digest DNA, protect areas that are bound to protein
- assess which TFs are present
- correlative but guides future research

Genome Assembly

- 1997
- broke down the genome into 150k bp frags
- cloned fragments
- broke down again
- cloned and Sanger sequenced
- 2017
- easy to get a lot of data
- hard to assess repetitive regions
- combine illumina and pacbio data

- 1997
- sanger sequence conserved genes
- 2017
- whole genome seq
- RADseq - focus on shared areas across species

The End