IS GOD THE ULTIMATE SOFTWARE ENGINEER?

CHRIS KUNARD





MY JOURNEY



Born in Minnesota



- **BS** Computer Science
- **BS Electrical Engineering**



- 5 years in defense
- Javelin missile

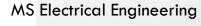




- 10 years in biotech
- Instrument SW
- **Customer Collaboration**











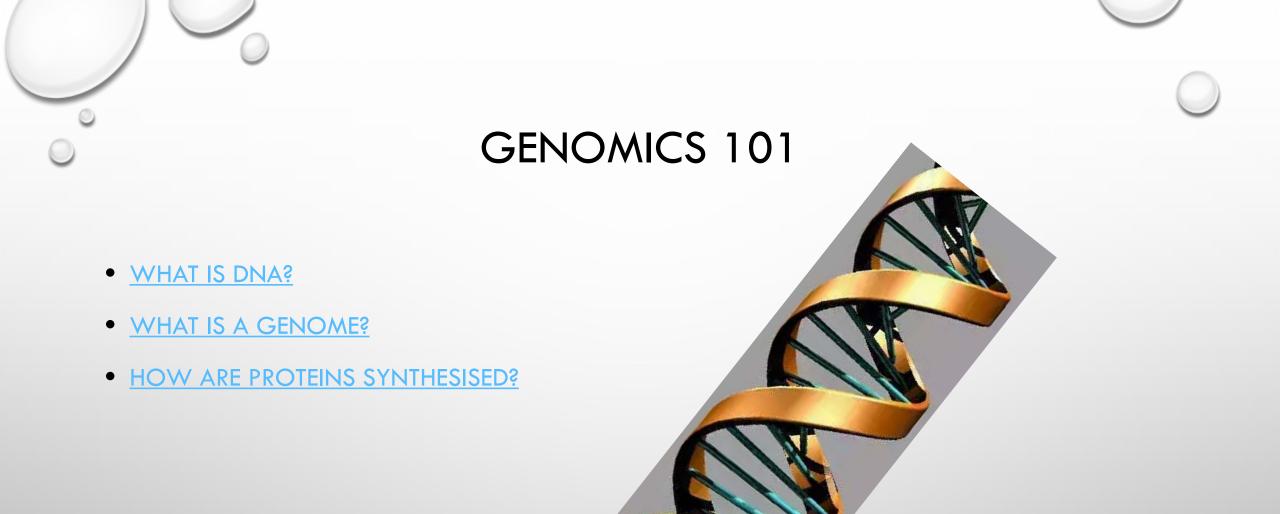
- 15 years in telecom
- Progressed to leadership













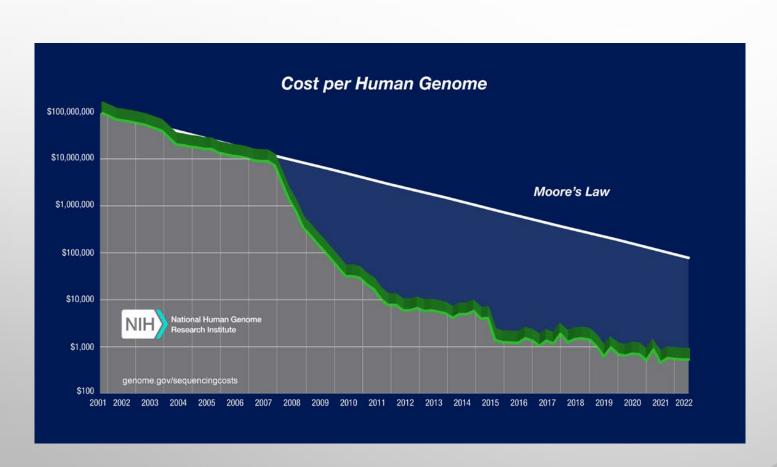
ILLUMINA SEQUENCERS



 ILLUMINA MAKES INSTRUMENTS OF VARIOUS SIZES AND CAPACITIES, ALL OF WHICH ARE DESIGNED TO SEQUENCE DNA

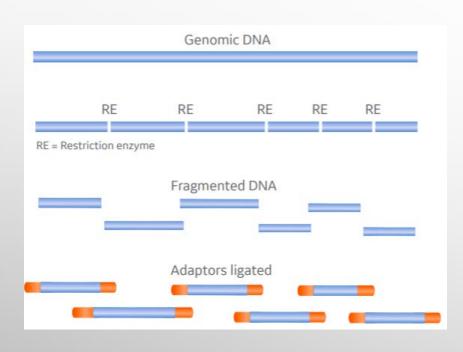


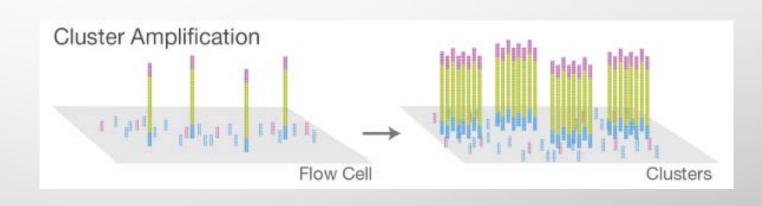
ILLUMINA SEQUENCERS



THE TREMENDOUS
 REDUCTION IN THE COST OF
 SEQUENCING A WHOLE
 HUMAN GENOME HAS
 ALLOWED GENETIC
 INFORMATION TO BE USED
 IN MANY APPLICATIONS

ILLUMINA SEQUENCING – FRAGMENTATION & CLUSTERING

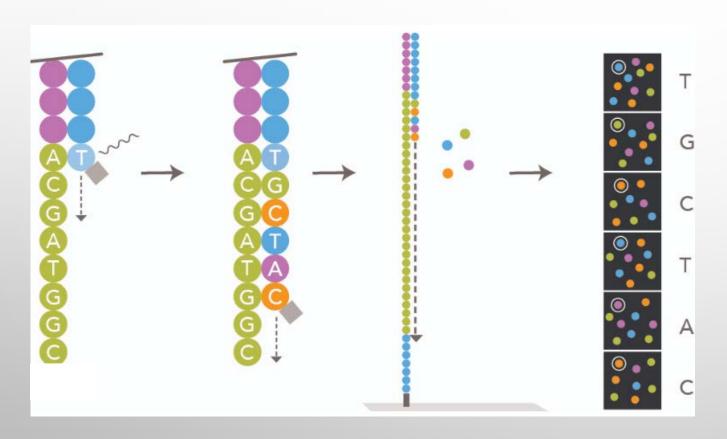




DNA is fragmented so that we can process the millions of fragments in parallel. Each fragment is bonded to the flow cell surface and replicated many times into what is known as a cluster, which allows us to "see" the results of the subsequent reactions.



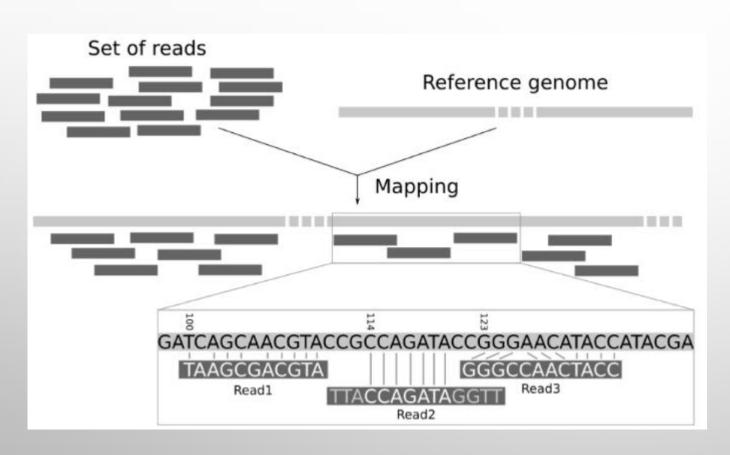
ILLUMINA SEQUENCING



Each strand of DNA is "read" by allowing a polymerase substance containing free-floating elements (A, C, G, T) with fluorescent dye elements attached to them to interact with the strand.

Each round of chemistry allows the next base pair of the strand to bond with its partner base pair. Exposing the fluorescent element to light allows to determine which pair bonded, and therefore the original base pair in the chain.

ILLUMINA SEQUENCING - MAPPING & ALIGNING



Since we chopped up the complete DNA into many strands, we now have to reassemble them back into the original sequence.

This is computationally challenging but is the price we pay for the speed we gain by parallelizing the sequencing process.



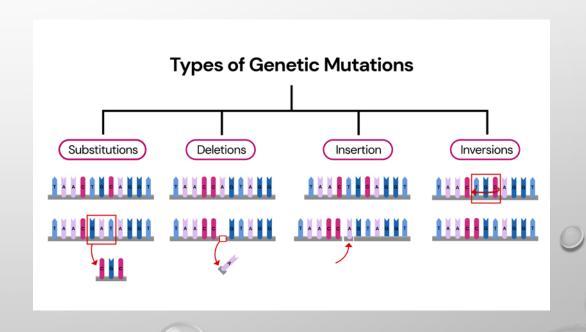
GENETIC VARIATIONS

The most interesting information about a person's genome is how it differs from that of others. We call those differences "variants", and they come in different types. Variants are what make us unique!

Single nucleotide variants (SNVs)

Reference ATCATTCTCCTAGAAGAGAGAATGGGGAGGGTGAGG
Patient ATCATTCTGCTAGAAGAGAGAATGGGGAGGGTGTGG

► Single base changes between reference and patient genomes





SOME APPLICATIONS OF GENOME SEQUENCING



CANCER SCREENING AND DIAGNOSIS



MICROBIOME ANALYSIS



RARE DISEASE IDENTIFICATION



GENETIC ANCESTRY



• AGRICULTURE



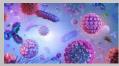
FOOD SAFETY



DRUG DISCOVERY



REPRODUCTIVE HEALTH



INFECTIOUS DISEASE MONITORING



PRECISION MEDICINE



A BIT ABOUT MY "WHY?"

• SHARE YOUR WHY | WHAT ARE THE REAL IMPACTS OF YOUR WORK IN GENOMICS?



IN WHAT WAYS DOES DNA RESEMBLE SOFTWARE?



WHAT QUESTIONS DOES GENOME SEQUENCING RAISE FOR US AS CHRISTIANS?





HOW CAN WE CONNECT FAITH INTO OUR WORKING LIVES?



THANK YOU!

CHRIS KUNARD