Khan Inan

BI-GY 7633 Transcriptomics

Excercise 6

Give three different applications of Next-generation sequencing technologies.

Arguably the most important application is to sequence large-scale genomes or more specific target genomes in order to obtain a reference point or area of study. Two other applications are using them to identify mutations within sequences that may result in cancer or other genetic defects and observing DNA-protein interactions in various organisms.

Why is it important to know the structure of the gene?

Because a gene being in the form of a helix or bundle within a cell tells a lot about its specific stage in the replication/transcripting process

Why are important parts of the genome less likely to contain changes?

This is because these parts of the genome are essential to the roles of cells within organisms and are less likely to be dormant genes that don't affect any kind of cell behavior or protein synthesis

What can we learn by comparing the human genome to the mouse genome?

We can learn about how mammalian cells can respond to various targeted drugs or treatments because an interesting fact to keep in mind is that humans and mice share about 70% of the same gene sequences

What are SNPs and how can they be used to improve our health?

SNP are essentially a genetic list of predispositions to certain diseases, poisons or drugs. It looks at genetic data relating to an individual's lineage and what health problems they are susceptible to. This can be used in the medical field to provide individualized treatments or regimens in order to improve someone's health.

What do we hope to learn by sequencing 1 million individuals?

The information that we would have on record from sequencing 1 million individuals would be extremely useful for tracing ancestry as well as for forensics work. Having DNA information for individuals on record is important for use as a reference point in other fields.

Do we have more human cells or bacteria cells on our bodies?

It used to be believed that bacteria cells outnumber human cells by a massive amount, but modern consensus is that they are relatively similar in number and the ratio is one to one

How did Next-generation sequencing technology change the way we do biology?

It hugely increased the rate at which we can sequence genomes and collect information. Prior to NGS, sequencing even a single genome of a human or organism was a massive project, but after NGS technologies were developed we can sequence thousands of genomes a year.

Explain how Dr. Sanger used the properties of DNA replication to sequence DNA. What is the difference between the dNTPs and ddNTPs?

Sanger further developed various sequencing methods using electrophoresis and he utilized properties of dna replication by using enzymes similar to dna replication within our bodies. These enzymes can manipulate and slice the DNA into sizes that are easier to work with. dNTPs are the nucleotides/building blocks of dna while ddNTPs are the nucleotides that result from sanger sequencing, which is an important distinction to make

How was the sequencing automated?

Instead of just visually reading each band of the gel after electrophoresis, computers were utilized to more quickly and accurately read sanger sequencing data. This was done using fluorescence as well as radioactive chemicals

At which step of the sequencing workflow do the Next-generation sequencing technologies capitalize to increase the throughput?

The parallel sequencing step or the step where fragments are rearranged is when higher throughput results can be obtained. This is the step where automation as well as machine learning can be utilized to increased workflow efficiency

What is bridge amplification?

Bridge amplification is the replication of dna via exposure to artificial nucleotides they are related to. These artificial foreign nucleotides are known as oligonucleotides

What does the number of clusters and number of cycles mean in terms of Illumina?

The number of cycles or cluster essentially indicates the number of bases that can be sequenced, or the scale of the illumina system

Why may it be beneficial to sequence both ends of the fragment?

It created data that is higher quality and can be aligned with each other. Since sequencing both ends of the dna mirrors results, any sort of errors in the sequences can quickly be pinpointed and corrected since the sequences theoretically should match