

Data analytics for personalized genomics and precision medicine**Data & Python & Sequence****Lecturer: YuLI(李煜)fromCSE****Liyu95.com, liyu@cse.cuhk.edu.hk****Friday, 5th September 2025**

Today's agenda

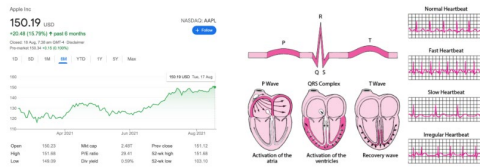
- Different data types
- Introduction to Python programming
- Sequence data
- Sequence comparison and alignment score (Not finished)

Post-course survey results

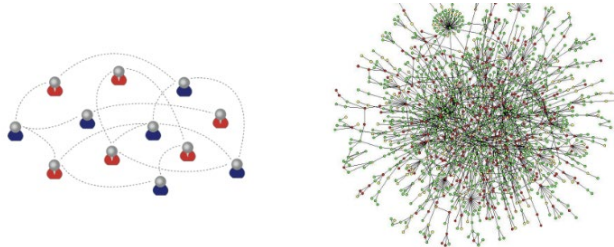
Positive responses: "fun", "clear", "engaging", "humorous and enthusiastic", "Pretty good"	Requests: More rest time, increased student participation, simpler definitions of complex terms
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Recap from Last Lecture

- Overview of multi-scale health data:
 - Molecular: Genome, transcriptome, proteome, metabolome
 - Clinical: Medical imaging, blood tests, ECG
 - Lifestyle: Diet, exercise, social media, environment
 - Other: Drug history, family history, travel history
- Emphasis on genomics in personal health and infectious disease



5. **Graph/Networks:** Objects and connections (e.g., social networks, PPI)



6. **Text:** Short or long documents
7. **Multi-modality Data:** Combined types (e.g., video, EHRs, spatial transcriptomics)
8. **Unknown Data:** Diet and Exercise.

Introduction to Python Programming

What is programming

- Communicating with the computer

What is Python

- Tool for communication with the function like a translator to translate our language to the way computer can understand (like WhatsApp and WeChat)

What is Numpy

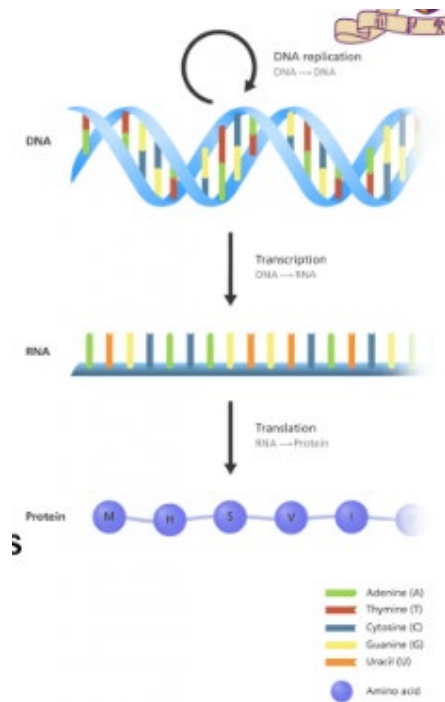
- Additional plug-in library to make Python more powerful usually helpful for math calculation. Usually use for calculate mean, variance, median, max, min and lots of other things.

Homework 0: don't need submit.

Why Sequence Data

Central dogma

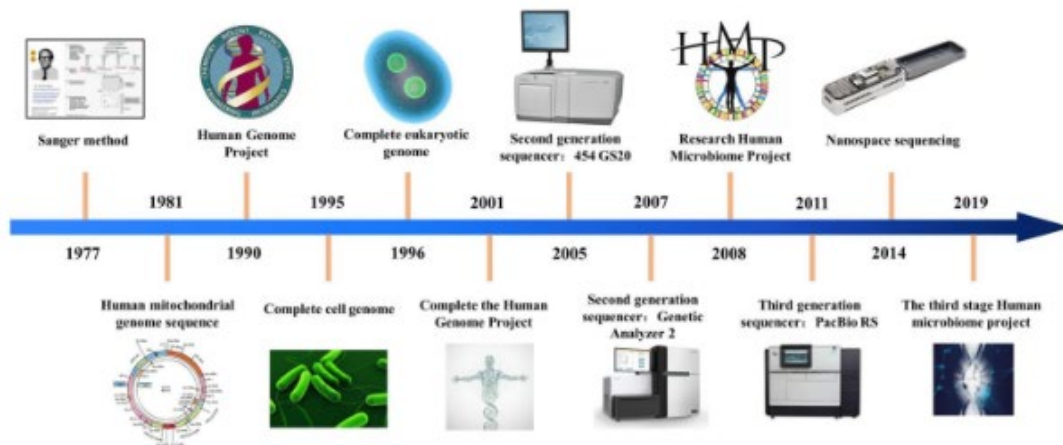
- The genetic information hidden in DNA sequences
- Biologists believe genotypes are determined by the sequences.



DNA, RNA and protein sequences

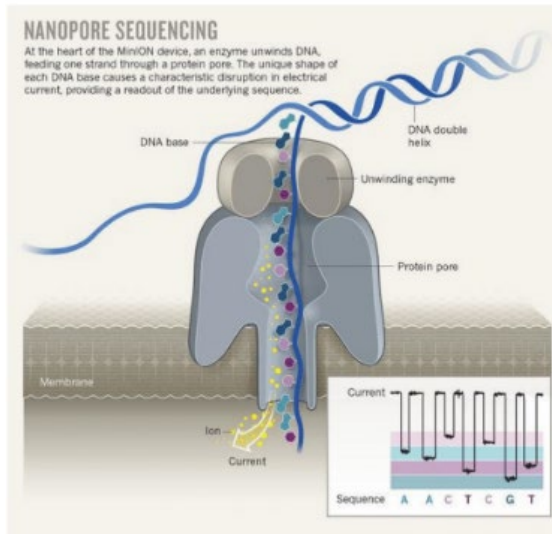
- DNA: composed of ATCG, Complementary double strand
- RNA: composed of AUCG
- Protein usually composed of 20 amino acids

How do we get the sequences



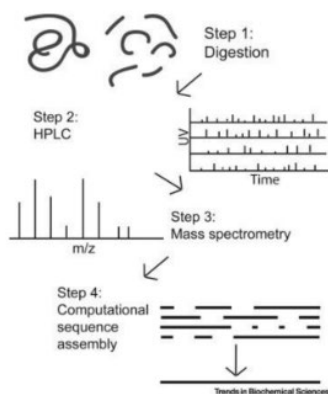
Nanopore sequencing

- DNA goes through a chemical pore
- Able to obtain very long (up to 4Mb VS 1000bp)
- Error rate is high (5% VS 0.001%)
- Using the current change to detect Sequence



Protein sequencing

- Based on mass spectrometry
- Break down the long sequence to short pieces
- Each piece will be detected by mass spectrometry
- Assemble the short pieces into the raw sequence



What are the raw data and what do we do them

DNA Sequence:

1. Reading raw sequences
2. Quality control to delete noises
3. Map reads to reference genome
4. Variant calling for mutation
5. Check the phenotype are associated with variants or not

