Tentative project topics

DS202: Algorithmic Foundations of Big Data Biology

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Today’s agenda

1. Projects
    1. Guidelines
    2. Deliverables
    3. Tentative topics
2. Discussion of midterm questions

Timeline

Feb 22 — Guidelines & tentative topics

Feb 22 — Finalise topic & team

Mar 6 — Submit report 1
- Problem description
- Application(s)
- Deliverables
- References

Apr 1 - Apr 10 — Presentations
- One lecture per project
- Teach what you learnt (new algorithms + results)

Apr 10 — Final report, code hosted on your GitHub account, presentation slides

Expectations

1. Self-learn a new research topic (related to big-data biology)
2. Teach the class what you learnt (1 hour lecture)
3. Oral-presentation and submit written-report
    1. Problem description
    2. Significance
    3. Algorithms (design and analysis)
    4. Experiments using real biological data (okay to use open-source software)
    5. Identify scope for further research

Expectations

1. Work as a team (2 members) or solo - your choice
2. All project work must be your own
3. https://sites.google.com/view/ds202/policy

Weightage

1. 10% - Preliminary report
2. 40% - Overall quality of oral presentation (content + communication + Q/A)
3. 25% - Final written report
4. 25% - Efforts towards experimenting with real biological data

Topic-1: Edit distance algorithms with good average-case behaviour

1. We have seen a quadratic-time $O(n^2)$ dynamic programming algorithm to solve edit distance
2. Running $O(n^2)$ algorithm for long sequences can be extremely slow
    1. We may need 95 CPU years to align human genome to mouse genome.
3. Conditional lower bounds suggest that $O(n^{1.99})$ algorithm cannot exist.
4. The runtime of these algorithms is decided by “worst-case” inputs
    1. This makes it necessary to compare every part of one string to every part of another string
5. This serves as a motivation for “average-case analysis”

Topic-1: Edit distance algorithms with good average-case behaviour

Near-Linear Time Edit Distance for Indel Channels

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[WABI 2020] https://doi.org/10.4230/LIPIcs.WABI.2020.17

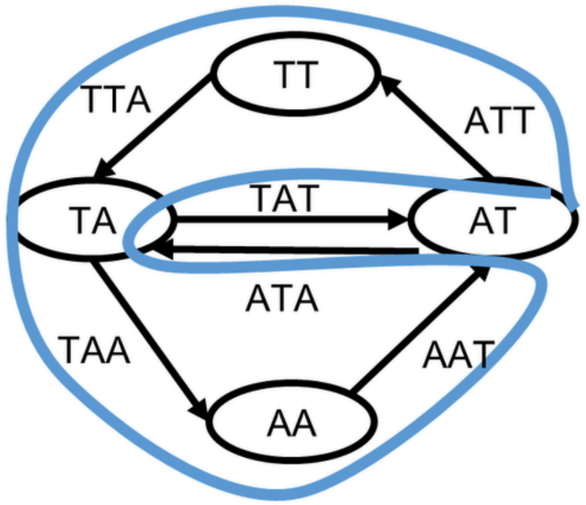
Other references that may be useful
- Paul Medvedev, “Theoretical analysis of edit distance algorithms: an applied perspective”
- Sosic and Sikic, “Edlib: a C/C++ library for fast, exact sequence alignment using edit distance”
- https://github.com/Martinsos/edlib

Topic-2: Solving genome assembly via Eulerian Path

An Eulerian path approach to DNA fragment assembly

Pavel A. Pevzner*, Haixu Tang†, and Michael S. Waterman†‡§

1. Genome reconstruction from short fragments of the genome
2. The above paper inspired several new algorithms and software for genome assembly.
3. Blogs / videos available online



reads *R = {TATTA, TAATA}*

Figure source: [1]

Other references that may be useful
[1] Medvedev and Pop, “What do Eulerian and Hamiltonian cycles have to do with genome assembly?”

Topic-3: Algorithm to construct phylogenetic trees using maximum likelihood

Sequence alignment

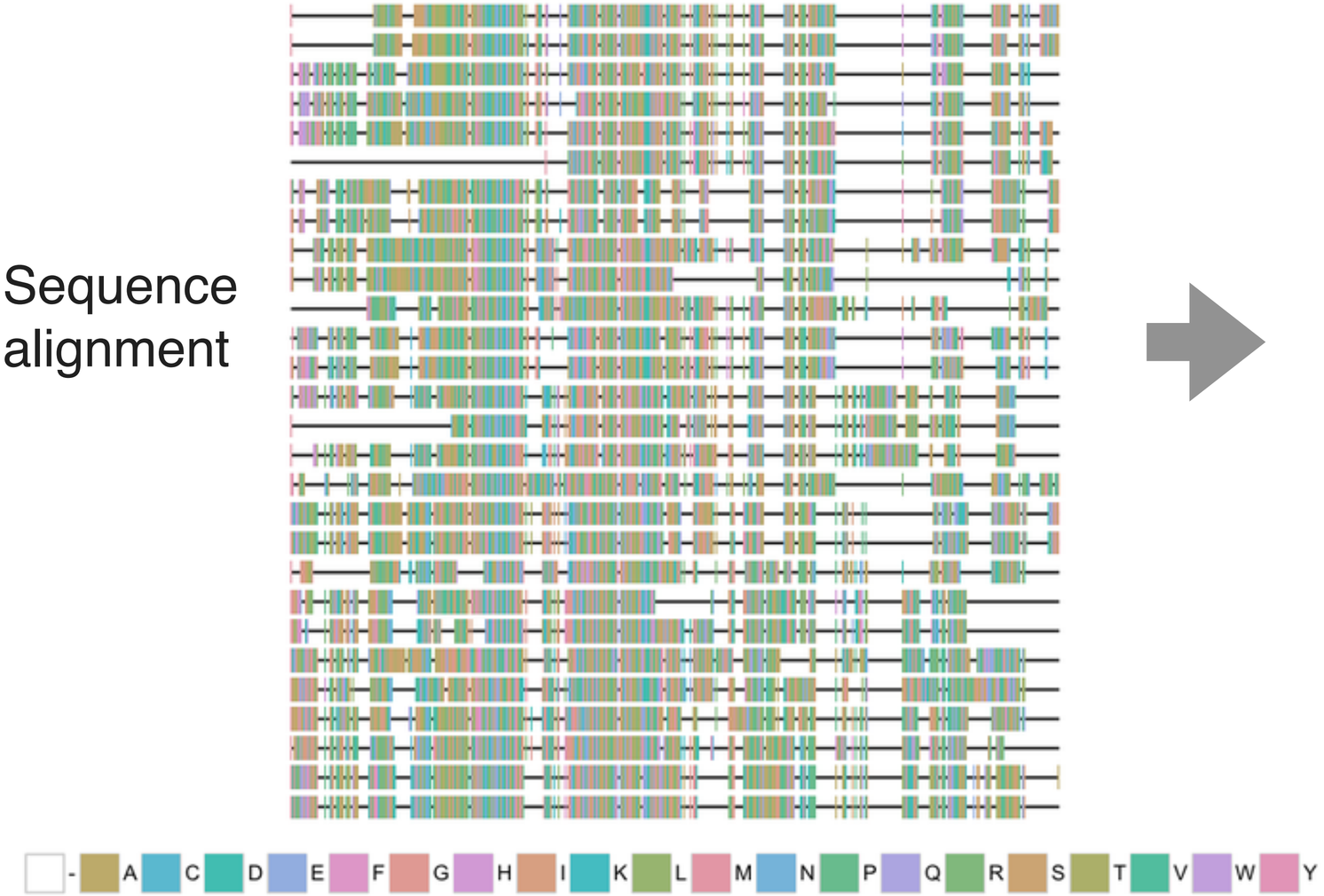


Figure source: Twitter

Evolutionary tree

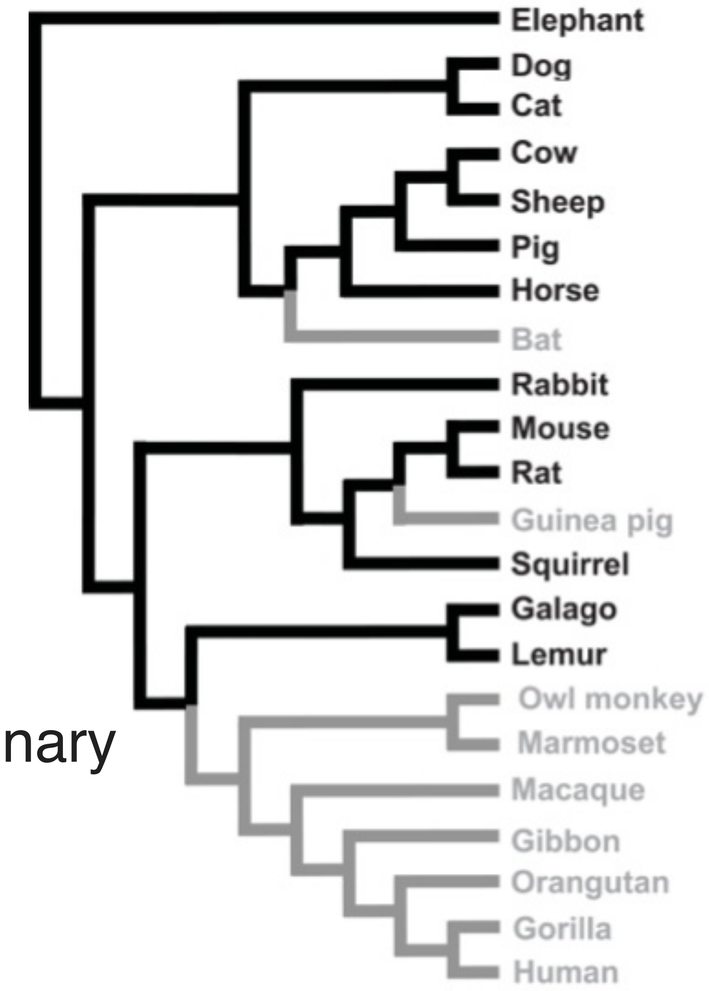


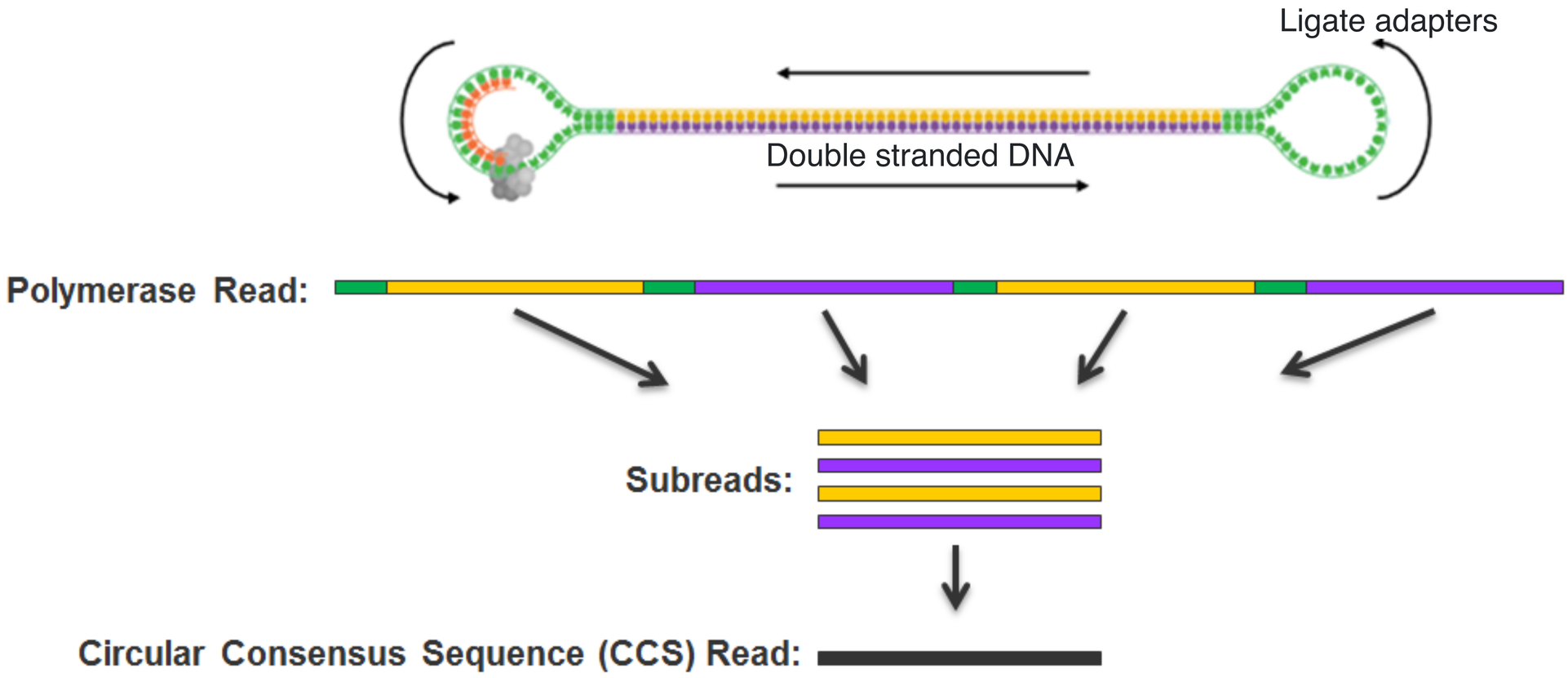
Figure source: realclearscience.com

Topic-3: Algorithm to construct phylogenetic trees using maximum likelihood

1. There are multiple methods to construct phylogenetic trees; maximum likelihood-based methods are most popular and robust
2. Key references:
    1. Durbin textbook (link on course page)
        1. Introduction in section 7.1 and 7.2
        2. Algorithm described in 8.1 - 8.4
3. Pre-requisite: Probability

Topic-4: Transformer-based deep learning model to predict sequence consensus

Developed by Google for PacBio CCS sequencing technology



Topic-4: Transformer-based deep learning model to predict sequence consensus

Developed by Google for PacBio CCS sequencing technology

ARTICLES
https://doi.org/10.1038/s41587-022-01435-7
nature biotechnology
Check for updates

DeepConsensus improves the accuracy of sequences with a gap-aware sequence transformer

https://github.com/google/deepconsensus

Topic-5: Compressibility of Burrows-Wheeler-Transform

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Resolution of the Burrows-Wheeler Transform Conjecture

By Dominik Kempa and Tomasz Kociumaka

https://doi.org/10.1145/3531445