Marburg University
Department of Computer Science
Prof. Dr. Sebastian Wild

Date: 2025-10-24
Version: 2025-10-24 01:40

Exercise Sheet 2 for Algorithms of Bioinformatics (Winter 2025/26)

Hand In: *Until 2025-10-31 18:00, on ILIAS.*

Problem 1

20 points

Pick a topic in molecular biology, for example one of the famous experiments in the list below, and create an entry about it in our shared Infinity Map (link on ILIAS). The goal is to explain the significance and meaning of the topic to your fellow students on the project in the most fun and accessible way (while remaining factual and scientifically accurate), so be sure to include both a "translation" into non-expert language and the correct terminology.

Feel free to link any type of sources and use AI to help you finding and distilling sources. Your mindmap box has to include your names and has to list all sources.

The exercise sheet submission must contain a copy / summary / screenshot of your contribution.

- **Meselson and Stahl Experiment (1958) on DNA Replication**
  - Often called the **"most beautiful experiment in molecular biology,"** this work settled the debate on how a double helix precisely copies itself.
- **The Hershey-Chase Experiment (1952) on Genetic Material**
  - Using nothing but a kitchen blender and two radioactive elements, these scientists definitively proved which molecule carries genetic instructions.
- **Nirenberg and Matthaei Poly-U Experiment (1961) on Genetic Code**
  - This simple test was the first to crack the three-letter code of life, translating a single synthetic RNA sequence into its corresponding amino acid.
- **Jacob and Monod's Discovery of the *lac* Operon (1961)**
  - This groundbreaking model explained how a bacterium uses a simple molecular switch to decide which energy source to metabolize.
- **Frederick Sanger's Dideoxy Method (1977) for DNA Sequencing**

  - This Nobel Prize-winning chemical method uses chain-terminators to turn the complex task of “reading” DNA into a simple size-sorting problem.

- **Griffith’s Experiment (1928) and Avery-MacLeod-McCarty (1944) on Transformation**
  - Find out how dead bacteria can magically transform harmless living bacteria into lethal pathogens, and what the magical ingredient turned out to be.
- **Discovery of Split Genes and RNA Splicing (Roberts & Sharp, 1977)**
  - This discovery showed that the genes of complex organisms are not continuous, but are **interrupted by "junkßequence** that must be edited out.
- **The Use of Reporter Genes (e.g., Luciferase, GFP)**
  - Learn how scientists attach a gene that makes a cell glow or change color to measure **when and where other genes turn on** in real-time.
- **Elizabeth Blackburn’s & Carol Greider’s Work on Telomerase (1980s)**
  - Discover the specialized enzyme that solves the ënd replication problem,"protecting chromosomes from shortening with every cell division, a key factor in aging and cancer.

Problem 2

40 points

Consider the following variation of the Turnpike Problem with measurement errors:

INEXACT-TURNPIKE-PROBLEM

- **Given:** A list of $\binom{n}{2}$ *intervals* $[\underline{d}_i, \overline{d}_i]$, $i = 1, \ldots, \binom{n}{2}$ with $\underline{d}_i, \overline{d}_i \in \mathbb{N}$.
- **Goal:** Is there a sequence $S[0..n)$ of prefix sums, $0 = S[0] < S[1] < \cdots < S[n-1]$, such that $\Delta(S)$ is covered by the given intervals, i.e., there is a bijective mapping I assigning each pair (ℓ, r) with $0 \le \ell < r < n$ to a unique $i \in [1..\binom{n}{2}]$ such $S[r] - S[\ell] \in [\underline{d}_i, \overline{d}_i]$?

Show that the INEXACT-TURNPIKE-PROBLEM is NP-hard.

Hint: Consider a reduction from the following variant the classic 3-PARTITION-PROBLEM, which you may assume to be NP-hard (actually even strongly NP-hard) without proof.

“$A + B = C$”-3-PARTITION

- **Given:** Integers $\mathcal{X} = x_1, \ldots, x_{3n}$
- **Goal:** Is there a way to *partition* $\mathcal{X}$ into triples $(x_{i_{j1}}, x_{i_{j2}}, x_{i_{j3}})$ for $j = 1, \ldots, n$ such that $x_{i_{j1}} + x_{i_{j2}} = x_{i_{j3}}$?

  Partition here means that $\{i_{j\ell} : j \in [1..n], \ell \in [1..3]\} = [1..3n]$.