Course title: **Computational DNA nanotechnology**

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Keywords: DNA self-assembly, DNA nanostructures, DNA computing, precision medicine

Language: English

Course presentation

DNA is the data molecule of biology. Living cells have used DNA for hundreds of millions, potentially billions of years to store the essential information about their proteins which are behind most of the processes of life. DNA is a stable storage medium because it generally consists of two helical strands bound to each other by hydrogen bonds between the complementary nucleotides. This structure allows a single DNA to contain hundreds of millions of pairs of nucleotides—base pairs.

Even though the DNA in a modern cell is typically handled by a variety of proteins, the hydrogen bonds between complementary nucleotides will spontaneously arise in a solution of DNA of sufficient concentration. This process may give rise to richer structures than the classic double helix. In fact, arbitrarily complex aperiodic structures can in theory be obtained by spontaneous associations of carefully designed DNA molecules, referred to as the DNA tiles. In practice these structures tend to accumulate errors and eventually become disorderly, but compliance with theoretical predictions can be ensured on scales sufficient for practical applications. The spontaneous formation of such structures from individual DNA tiles is called *DNA self-assembly*.

DNA self-assembly has sparked interest in using DNA as a substrate for computation, because spontaneous association of tiles can be described as programmed construction of a result from individual DNA sequences. This in turned opened the possibility of using DNA self-assembly in biomedical applications as a relatively cheap and precise way of assembling nanoscale structures, which may facilitate drug delivery, or more generally modulate cellular processes by structural interaction.

In this course we focus on an abstract model of DNA self-assembly—aTAM—formalising the notion of DNA tiles, attaching between themselves via abstract "glues". We formally define aTAM, list examples of structures which may be formed by asynchronous self-assembly, and give some bounds on the complexity of these structures. We then show how to design a tile set producing exactly a set of given shapes. Finally, the students will be asked to design a tile set of their own, which we will then implement in an actual wet lab to also explore the physical and chemical characteristics of the design.

References

1. Paul W. K Rothemund, Nick Papadakis, Erik Winfree: *Algorithmic Self-Assembly of DNA Sierpinski Triangles.* PLOS Biology, December 7, 2004. `https://doi.org/10.1371/journal.pbio.0020424`
2. `https://en.wikipedia.org/wiki/DNA_nanotechnology`

Goals

1. Understand the biological underpinnings of DNA tiles and self-assembly.
2. Understand the theoretical computational theory of self-assembly.
3. Design a set of DNA tiles assembling in a given structure.
4. Test the assembly of the designed tile set in the lab.

Prerequisites

A good understanding of the basics of theory of computing is required for this course. The students should be familiar with at least one abstract model of computing: Turing machines, Boolean networks, Petri nets, etc. Only notions of DNA biochemistry are required.

Plan and schedule

This course is taught over *12 hours* and is structured into four 3-hour sessions:

1. Introduction to DNA computing *(3h)*.
2. Introduction to DNA tile design *(3h)*.
3. Exercise session: design a DNA tile set *(3h)*.
4. Lab session: watch or participate in the self-assembly experiment, depending on the group size and availability of the instruments and benches. *(3h)*.

Grading

The students will be graded according to the quality of their work in the theoretical exercise session on DNA tile design.