

# History of Topology

Semester I, 2009-10

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## History of Topology Outline

- ▶ **Lecture 1:**  
What is topology?  
Euler circuits in graphs
- ▶ **Lecture 2:**  
Topological invariants:  
Euler-Poincaré characteristic
- ▶ **Lecture 3:**  
One recent application of topology in biology

## Some Elementary Biology

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## Some Elementary Biology

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e.g. offspring of a blue eyed mother and brown eyed father has 3/4 chance of having brown eyes.
- ▶ In 1889 Hugo de Vries gave Mendel's inheritance mechanism the name *gene*. Had little understanding of the physical nature of a gene.

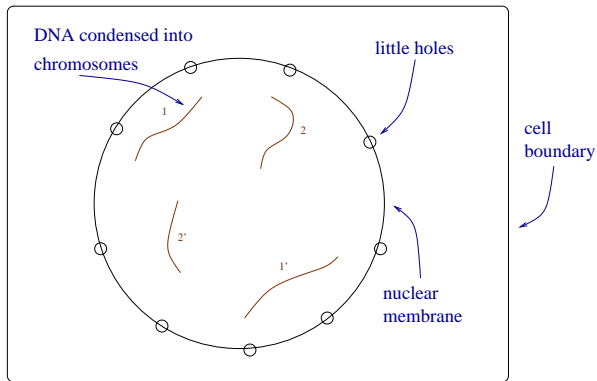
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- ▶ In 1944 it was shown that **Deoxyribonucleic acid**, or DNA, contains the genes of an organism. DNA is a long polymer made from repeating units called *nucleotides*.
- ▶ In 1953 Crick and Watson demonstrated the molecular structure of DNA.



## A typical (animal) cell

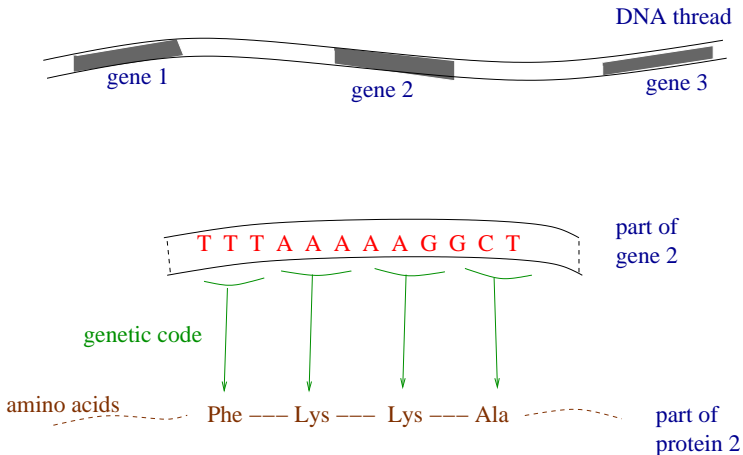


Chromosomes contain a mixture of protein and DNA. They often come in pairs.

Humans cells contain 46 chromosomes in 22 homologous pairs plus the non-homologous X and Y chromosomes that determine sex.

## What is DNA?

DNA is a string of four different nucleotides: **A**denine, **G**uanine, **C**ytosine and **T**hymine.



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## Question

Given a long strand of physical DNA, how can a biologist determine the sequence of letters

*...ACCGATTGCAGTAGC...*

representing the DNA?

## Answer

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Given a long single stranded target thread, the target will bind (or **hybridize**) to precisely those probes which are the Crick-Watson complement of fragments of the target thread.

## Hybridization

For example, the probe

*ACCGTGGA*

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since the probe's Crick-Watson complement is

*TGGCACCT*.

## The upshot

Using arrays of probes of a given length  $L$ , biologists can determine all the letter sequences of length  $L$  contained in a target DNA thread.

## A mathematical question

How can we determine a DNA letter sequence from a knowledge of all  $L$ -letter fragments of the sequence?

## Example of the question

Suppose that a DNA array analysis of a piece of single-stranded target DNA, using probes of length  $L = 3$ , shows that the length 3 fragments of the target DNA are precisely:

$$F = \{ATG, TGG, TGC, GTG, GGC, GCA, GCG, CGT\}$$

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What can we say about the target DNA?

## Some topology

To answer this question let's build the graph whose **vertices** are the  $4^2 = 16$  pairs *AA, AC, AG, AT, CA, ...GT, TT*.

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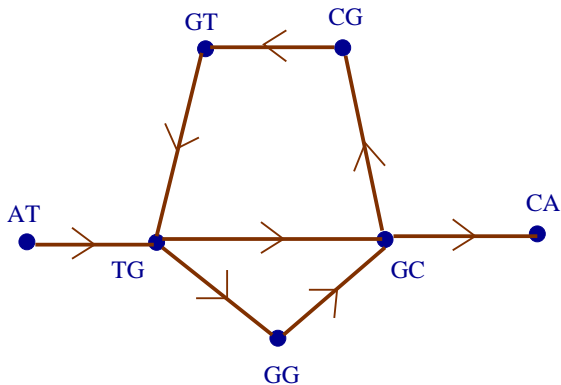
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We'll add an edge between vertex  $XY$  and vertex  $YZ$  if the triple  $XYZ$  is in the collection  $F$  of fragments.

Moreover, we'll place an arrow on the edge going from  $XY$  towards  $YZ$ .

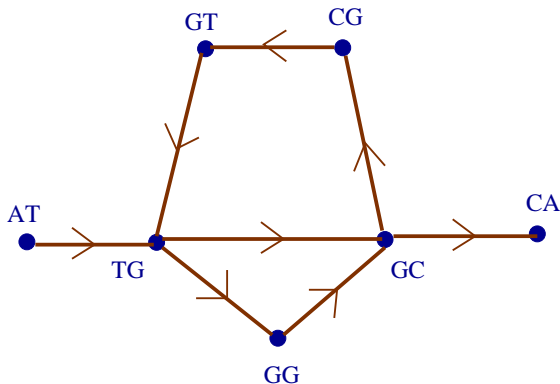
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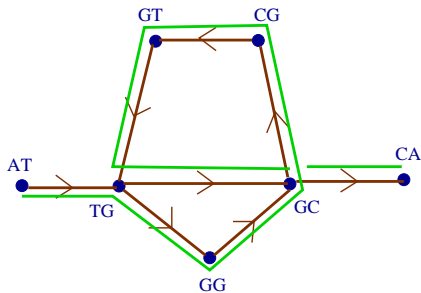
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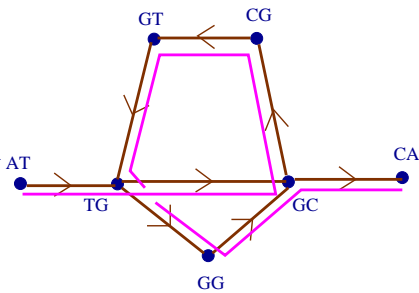
The target DNA corresponds to an Euler path in this graph (where the path direction is given by the arrows in the graph).

## Some topology

There are just two possible Euler paths.



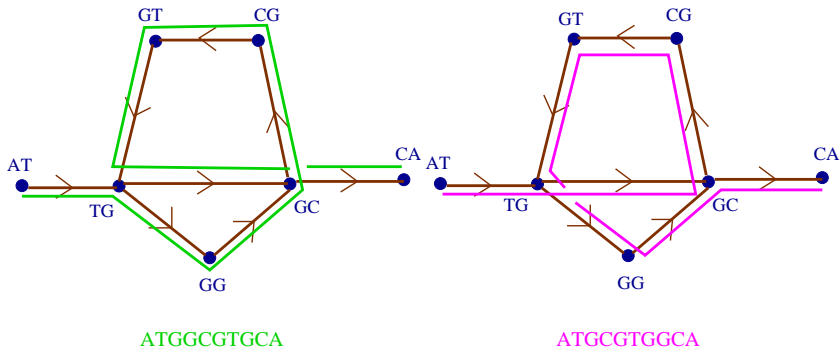
ATGGCGTGCA



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So the possible sequences for the target DNA are: **ATGGCGTGCA** and **ATGCGTGGCA**.

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**Answer:** Euler's proof of his theorem explains how to produce an Euler path.

## Reference

P.A. Prezner, *L*-tuple DNA sequencing: computer analysis,  
*Journal of Biomolecular Structure and Dynamics* 7 (1989), 65-73.