

First semester report

Botond Kalocsai (kalocsaibotond@gmail.com)

Ph. D. Program: **Statistical Physics, Biological Physics and Physics of
Quantum systems**

Supervisor: **Tibor Vellai**

Ph. D. Thesis title: **Reverse-engineering of molecular biological processes of
ageing**

Contents

1	Introduction	1
2	Research work	2
3	Studies	3

1 Introduction

Our research focuses on the ageing of biological systems, ultimately on human ageing. We want to explore the biochemical processes that lead to ageing. Ageing is the biochemical process that causes a living organism's system to become inoperable, degrade and die over time, even when kept under ideal conditions. Some have even linked the ageing process to the development of cancer.

So far, the theories that best describe ageing are divided into two main groups: genetic and epigenetic. Genetic ageing theories postulate that changes in genetic information drive the ageing process. Epigenetic ageing theories postulate that abnormal gene expression leads to the ageing process.

The most modern theory describes ageing on a genetic basis: transposon proliferation and relocation on the genome. Transposons are segments of DNA that can change their position on the hereditary material through the mechanisms of

the cellular machinery. Retrotransposons are transposons that use the cellular machinery to copy themselves back and forth across the genome, thereby corrupting the information encoded by the genome. The most modern theory postulates that the proliferating retrotransposons that accumulate over time cause the cell to become dysfunctional and cause the exponential ageing process. Meanwhile the relocation of DNA transposons cause slower ageing degradation via the error of their cutting mechanism.

We investigate and develop this theory via classical genetics experiments with *Caenorhabditis elegans* and bioinformatics because *C. elegans* is an excellent model system for the practices of genetics.

2 Research work

Our first investigation was bioinformatical in nature. We got our inspiration from genetics and structural bioinformatics. Experimentally, we know that many retrotransposons have a retroviral origin. They are partially operational retroviral machinery that had accumulated throughout evolutionary history. They even encode viral capsids. In drug engineering, it is a common practice to represent the cellular machinery via networks, especially protein interaction networks, to seek out vulnerabilities in the mechanisms of pathologies. Based on these inspirations, we decided to investigate the machinery of ageing on the interactome of *C. elegans* along the considerations of an online course at [1].

Our main question is how centralised the ageing machinery is. If the ageing machinery is decentralised, do the parallel operating sub-machineries share vulnerability? We did tedious online research for protein interaction and transposon data. We found seemingly usable data at wormbase.org [2] for both the protein interactions [3] and the transposons [4].

When we compiled the interactome, we realised that only a few known transposons were present in the interaction data. This lack of data delimited our research. We could not investigate the structure of the ageing machinery. Unfortunately, our investigation was a preliminary or proof-of-concept, at best. However, the analysis showed that the transposon-coded machinery taps into the host cellular machinery. So, continuing the protein interaction network research might be informative if we had the data.

3 Studies

Because my previous university studies were unrelated to biology, I had to put an untypically heavy effort into studying for my research. Unfortunately, the in-programme announced courses are unrelated or tangentially related at best to my research. So, we chose in-programme courses to somewhat prepare for the theoretical part of the complex examination.

Overall, I had two main objectives this semester: to catch up on my studies for my research and to complete much of my credit obligations. I have participated in the following courses:

- I completed the “Statistical physics of biological systems” (FIZ/3/003E) course.
- I completed the “Statistical physics of polymers and membranes” (FIZ/3/021E) course.
- I completed the “Sensory biophysics” (FIZ/3/010E) course.
- I completed the “Structural Bioinformatics in Drug Design” (BIO/08/27) course.
- I attended the “Genetics I” (genet1b17ea) course.
- I attended the ELTE Department of Genetics seminar.

I attended the structural bioinformatics course, the genetics course and the genetics department seminar to study for my research. My supervisor recommended the attendance of the genetics course and the seminar.

References

- [1] “Network analysis of protein interaction data - an introduction” online course
<https://www.ebi.ac.uk/training/online/courses/network-analysis-of-protein-interaction-data-an-introduction/>
- [2] Wormbase userguide
<https://wormbase.org/about/userguide#32--10>
- [3] Wormbase protein interaction data
https://downloads.wormbase.org/releases/current-production-release/species/c_elegans/PRJNA13757/annotation/c_elegans.PRJNA13758.WS289.interactions.txt.gz
- [4] Wormbase transposon data
https://downloads.wormbase.org/releases/current-production-release/species/c_elegans/PRJNA13757/c_elegans.PRJNA13758.WS289.transposon_cds.pep.gz