

# SELF: Self Evaluating Learning Framework

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**Abstract:** SELF: self evaluating learning framework is the paper, where students evaluate themselves scientifically. It should be scientific paper based on student's learning progress of this course. Students need to identify whole their works related to genomic topic and fairly make a judgement.

In this paper, I tried to critically rate myself, bring as evidences my works, which had done during the fall semester. It consists from introduction part, where I explained in detail about SELF and about the course description, and further includes problem part, results, discussion sessions. According accomplished works, particularly my research paper shows that I am good candidate for the excellent grade. In my opinion, the aim of the course was to deliver genome understanding to the students, develop their interest to that, encourage them for further development in that field. As a student taking this course can say confidently that professor successfully accomplish his aims, since this course influenced me a lot, and want to continue or do other researches related to genomics.

**Introduction:**

Students, who are taking Genomic course from the professor Jong Bhak in Ulsan National Institute of Science and Technology (UNIST) required to submit Self Evaluating Learning Framework (SELF) to the professor at the end of the semester. The main aim of the SELF is that students evaluate themselves, while providing scientific evidences or reasonable justifications. In addition, it should be scientific paper based on student's learning progress of this course.

Genomic course is the fall semester course of the UNIST, provides lecture once a week for two and half hour, applies three credits. During the semester, students have tasks with clear goals, but for those assignments no assigned deadlines, also students are not asked to provide specific results to the professor or teacher assistants. It all designed for student's self-interests, and further accomplishments totally depends on themselves. Moreover, students provided with a chance to present their investigation about scientific problems in genomics. However, it should not be a review papers, or summary of published researches, rather student's own idea to the current problems in the world. Alike in all courses, students encouraged to participate actively in the classes, and have a critical thinking, also motivated to ask at the same time provide answers to the professor.

Course do not conduct any exams, like midterm or finals. Exams are not enough rewarding method to check student's knowledge. Thereby, professor does not want rank students only according to the exam score, instead he insisting students to evaluate themselves critically.

## Problem:

Now as an undergraduate student of the UNIST, I need to evaluate myself with scientific evidences and with honest logics. What kind of evidences can I provide? Could I love this course? Is this course encouraged me to learn more and motivated to study further? Did I complete professor's all requirements? Could I develop new ideas? Did I try to look for problems and find solutions to them? Was I able to learn main aspects of the course? Those are the main questions, which first of all, I should answer in order to evaluate myself. Furthermore, with results and discussions would proof that why I evaluate myself as A+ student.

## Results:

Below figure shows my first essay on topic "What is sequencing in Genomics and Omics?"

The screenshot shows a Wikipedia article page. At the top, there are navigation tabs: 'page', 'discussion', 'view source', 'history', and 'purge'. The article title is 'What is Sequencing in Genomics and Omics? (as an approach of understanding life) Sequencing'. Below the title, it says 'Madina Seiduly' and '20132023 09/09/2016'. The article text begins with 'First of all, I would like to describe my point of view about life. What is life? Actually, this word correlated with verb "live", which can be expressed in diverse words like breath, staying alive, surviving, reproducing. "Live your life", where only living organisms can achieve that. Thereby, Life is noun state of live, only living things own life. All living organisms distinguished from material things as they were constructed from cells, the basic unit of life. All cells are consisted of variety functional organelles or particles, those give priority to survive. The special thing that exist in all cells of entire organisms is DNA, which carrier with their live survival instructions. It is proved scientifically that DNA in chromosomes of living organisms own information about whole function in the cell, and any mismatch in their structure will lead fall in the function of appropriate organelle or another cell blocks. DNA is the molecule consists of two antiparallel strands of four nucleic acids, which coiled forming double helix. Those four nucleic acids are the monomers of this huge molecule and their base pair were distinguished, either Thymine (T), Cytosine (C), Adenine (A) and Guanine (G). These bases forms with each other, like A-T, G-C, parallel strands. According to the researches, number of base pairs in one cell of human is around 6x10<sup>9</sup>, and fascinating fact is that 2.5 m of DNA coiled in so tiny cell nucleus. Every cell of the human organism equally have that number and length of DNA molecule, however according cell's function only several sections of the DNA could be read and transcribed and translated. Consequently, whole cell DNA molecule have information of life of that organisms, and variety part of organism cells only read pieces they required and save other parts condensed in nucleus. Genomics, if we simplify, want to read those whole DNA base pairs in a cell, so that they could understand their function, effect on, place in and response for their whole genome networks. Moreover, reading possible only by Sequencing DNA, which make scientist to list whole 6 billion codes, consists of A, T, C, G. Until nowadays, most famous and efficient way of Sequencing DNA were Sanger sequencing and Next-generation sequencing. In following two paragraphs I will describe shortly about above two sequencing methods. In 1977 - 80 years first Fred Sanger introduced this method to the world, and have been used till mid 2000s. In any sequencing it is impossible to read it without cutting long DNA or interested gene to tiny splices, by restriction enzymes after isolating gene. Afterwards, we have to amplify it to thousands strands, which it possible by PCR (polymerase Chain reaction). Now we have extreme numbers of single strands, the thing we have to do now copy or make its second strands. For that, we require polymerase to start the polymerization, and polymerase, enzyme that makes that action, and a quantity of dNTP: building blocks of DNA. In addition, we need the crucial feature of this method is ddNTP: terminator nucleotides. If ddNTP binds to the elongating strands it stops elongation, and terminated strand at that position. Correspondingly, all four ddNTP will be labelled with different colors, so later we detect them with UV. This experiment should done four times for the same spice of the strand with four ddATP, ddGTP, ddCTP, ddTTP. As a result, different strands terminated at different strands. Those strands we will run on electrophoresis gel, where short sequences run first, the longest ones run as latest. Thereby, that splice's or gene's DNA code will be sequenced by analyzing result of the gel electrophoresis.

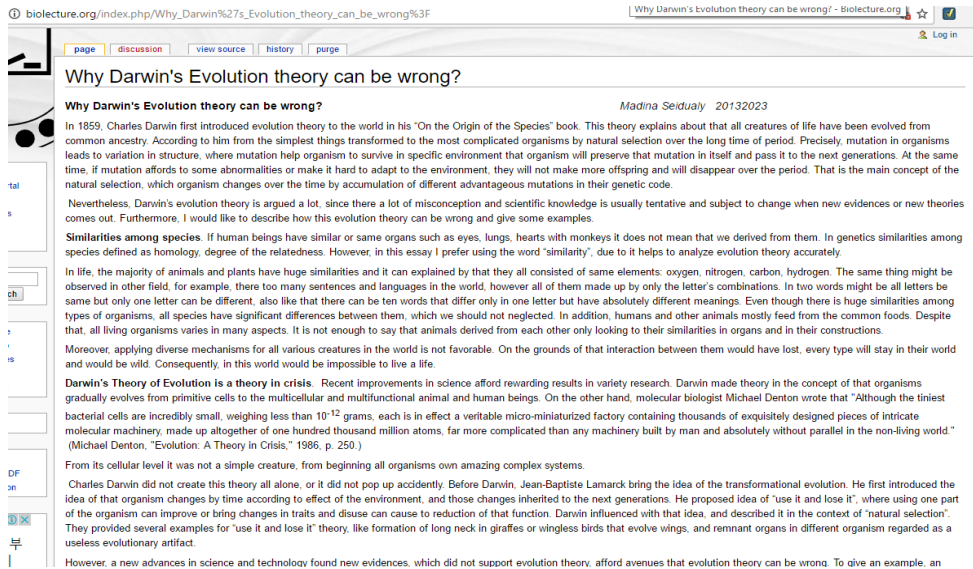
1. Amplification (by cloning) → 2. Primer extension in presence of blocked and labeled nucleotides → 3. Separation by electrophoresis & read out of labels

Target sequence: 5' - ACTGCTACGAGGAGGAGTACCG - 3'

3' - TGCATGACG - 5' (Blocked)

At first, I submit its hard copy to the professor, then I received a lot of correction, since there were things I have to improve, like adding pictures and references.

Further I try to follow professor's instruction and wrote second essay, which was about "Why Darwin's evolution theory can be wrong?" (below fig.2)

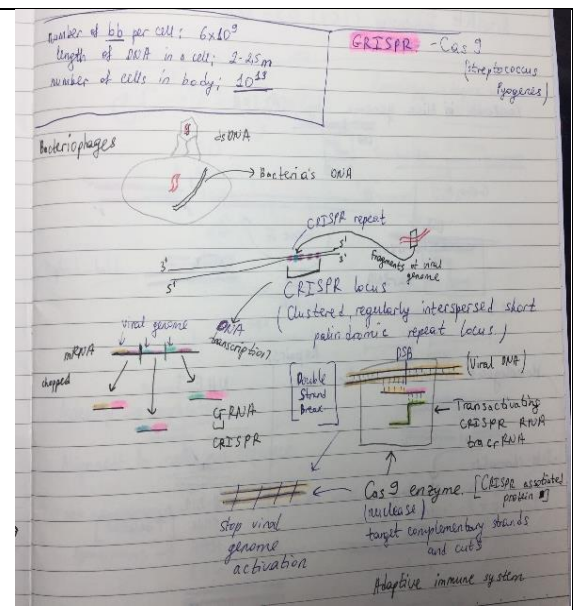
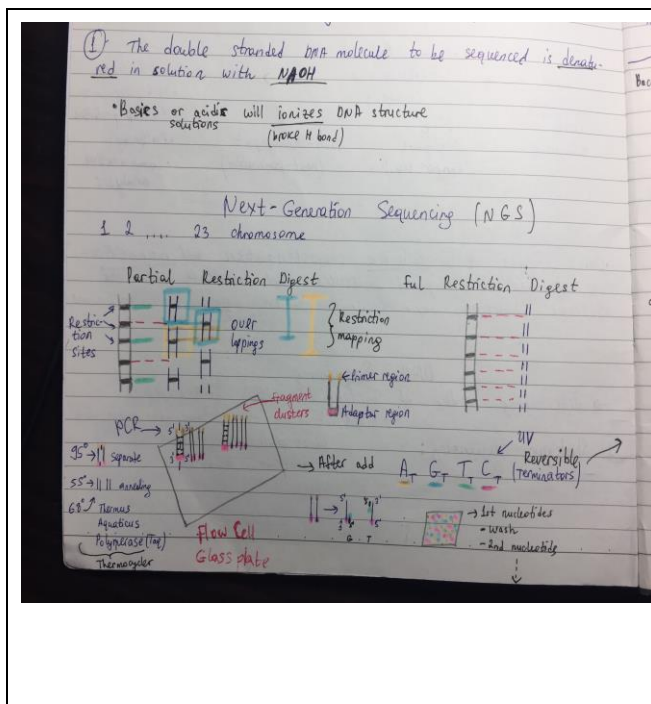


Afterwards, professor gave a special lecture about how to write scientific paper, and emphasized specific aspects, which should be included in scientific papers.

I wanted be able to properly write a satisfying research paper. Initially, it took several times to find specific problem, where you can provide or suggest adequate solution, and also it was not an easy thing.

My interest to genomics increased day by day. I not only read scientific papers, but also try to understand every single words there. Especially, after reading I looked for all technologies, which conduct variety experiments while sequencing DNA.

In following pictures, shown my notebook, where I thoroughly described and tried to understand how sequencing technologies, CRISPR-cas9 works.



In the end, I succeeded to write research paper, which I wished. Now looking forward to professor's feedback. ([http://biolecture.org/index.php/Research\\_paper](http://biolecture.org/index.php/Research_paper))

#### Research paper

### Title: Solving the puzzle about Bowhead whale longevity and its low risk to cancer

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#### Abstract:

Bowhead whale is the longest living organism and have enormous body size, body mass. According hypothesis, their cells have to proliferate plenty times, in the long run this organism should have high risk to cancer, but it is surprisingly vice versa. There is should be regulation involved in Bowhead whale, which is contributes to repress cancer in their body.

Deep diving of the whale in bottom of ocean, induces hypoxia in the organism. Remarkably, in tumor same condition occurs, and in the human body they succeed to induce angiogenesis, in outcome formed vessels supply cancer cell, which will further grow and increase migratory and metastasis. This paper suggest that Bowhead whale angiogenesis process that manage hypoxia condition in whale body may play important role in repressing cancer. Moreover, paper includes current anti-angiogenesis drugs in clinical approaches, and tries to find solution to their side effects.

#### Introduction:

One of the longest – living animals of the earth is the Bowhead whale (*Balaena mysticetus*), which is estimated to live over 200 years. These animals can weigh from 75 to 100 tons, and live entirely in Arctic and sub-Arctic waters. [1]

Before there was assumption about that, if body size and mass big, the greater chance to get mutations in the cell and high risk to the cancer, due to large number of cell replication in the body. Although, the bowhead whale lives more than 200 years and have huge body size, hardly ever gets cancer. Thereby they should maintain protective molecular adaptations relevant to age-related diseases, particularly cancer. [2]

In 2015, Michael Keane, Jeremy Semeiks and several scientists together published a paper in Cell Press Reports about mapping the bowhead whale genome, with the title "Insights into the Evolution of Longevity from the Bowhead Whale Genome", where they reported the sequencing and comparative analysis of the bowhead whale genomes. In paper, scientists after sequencing, identified positive selected genes and bowhead-specific mutations, and tried to correlate them with aging and cancer. Especially, in that paper more focus were given to DNA repair, cancer, cell –cycle linked gene's modifications. Moreover, researchers made an available online data on the website (<http://www.bowhead-whale.org>) for other interested ones to conduct research further within their information.

My research facilitated from this scientific article, with the aid from their whale genome portal. Close look to the condition and structure of the Bowhead whale might give rewarding solutions to the current issues, related to diseases, against cancers or aging. To be specific, my current focus is on the behavior of the cancer and linking it to the Bowhead whale metabolism, and find how whale able to manane the same condition.

In addition, I gave a talk for two times in a class. In a first one, it was about cancer genome remodeling. I presented with Kaznagul, who is taking this course with me, and before presenting we go through a lot scientific papers and tried to understand its nonstable genome. Interested ones can find our presentation on following website:

[http://biolecture.org/index.php/Trying\\_to\\_understand\\_cancer](http://biolecture.org/index.php/Trying_to_understand_cancer)

However, this talk more was like review of the scientific paper, and we emphasized our solution or correction to the paper less. After getting professor's feedback, I presented one more time. This time with clear problem and suggested own solutions with opinions. ([http://biolecture.org/index.php/How\\_come\\_Bowhead\\_whale\\_life\\_long\\_and\\_transfer\\_cancer\\_resistance%3F](http://biolecture.org/index.php/How_come_Bowhead_whale_life_long_and_transfer_cancer_resistance%3F))

Moreover, I never missed the classes and actively participate in every class discussion. Tried ask all interested and I am concerned questions during the lecture.

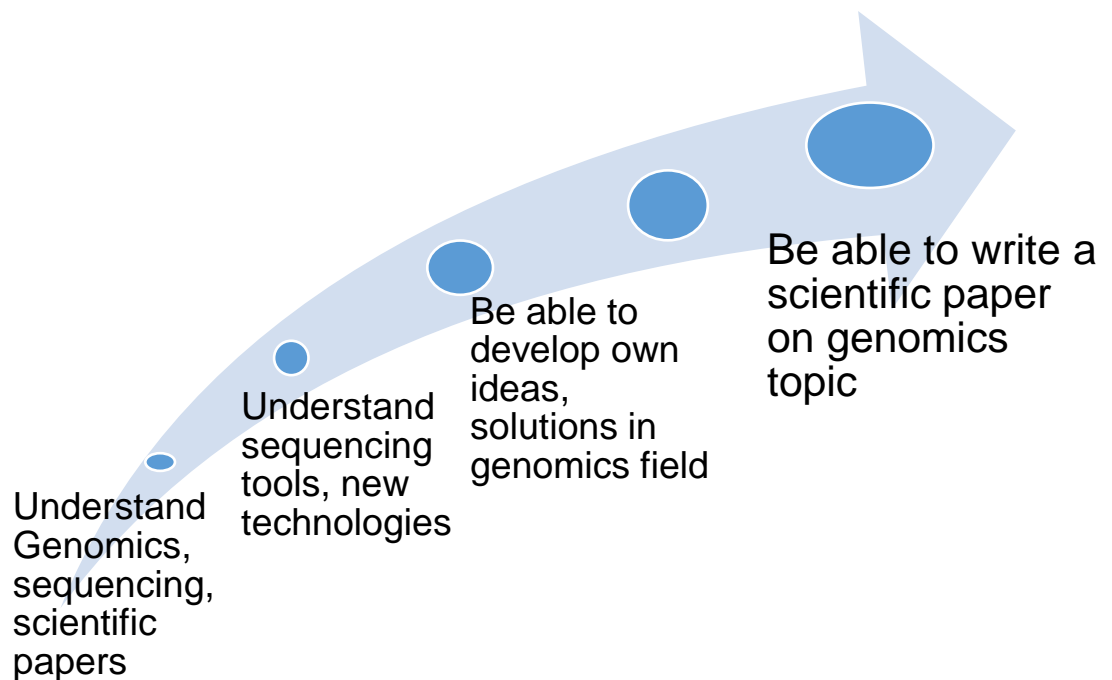
### **Discussion:**

To be honest, before I had interests in genetics, had thoughts that we can find answer about every disease and body condition, about all if we look to the gene of the organisms thoroughly.

After taking Genomics course this semester, my interests to genes increased dramatically. Professor could make me love this course, and I became so enthusiastic about genes. After professor introduces his researches about sequenced genomes, I went home and started to search about that in detail. Primarily, majority of the time spent to search and understand about technologies, which scientists used during the sequencing. At the beginning, it was hard to understand genomics papers, so I spent weeks to understand how they conduct all of experiments, their result data also was difficult to analyze. All topics concerning to genomics were interesting, and I was encouraged by asking various questions during the class, I did not want to miss any opportunity, so every class of the genomics was valuable for me. As shown in results above, I did assignments and usually had pleasure of doing them, every time try to follow feedbacks of the professor. Enthusiasm in me forwarded me to the 2<sup>nd</sup> Genome Korea International Conference, which was organized by UNIST on November 30 in 2016. In the conference, I was introduced with recent researches in genomic field, after that emerged a strong desire about contribution to this field in future.

In diagram below, I wanted to show how my level of genomics increased during this course, if I will rank it in letter grade, my final grade for this course will be A+, in my opinion.

The main essence of the course is to evolve interest to the subject in students and encourage them for further self-learning. Consequently, professor Jong Bhak could success it.



## References:

[1] SELF is a concept formalized by Jong Bhak

[http://biolecture.org/index.php/SELF: Self\\_evaluating\\_learning\\_framework](http://biolecture.org/index.php/SELF: Self_evaluating_learning_framework)

[2] Madina Seidualy's biolecture website, where all of her works uploaded:

[http://biolecture.org/index.php/Madina\\_Seidualy\\_20132023](http://biolecture.org/index.php/Madina_Seidualy_20132023)