



SYNTHETIC BIOLOGY AND GENETICS

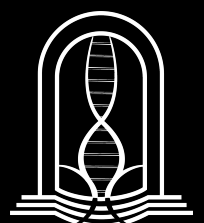
CATEGORY GUIDELINE



Introduction

Synthetic Biology and Genetics is a rapidly developing area that combines ideas from biology, genetics, engineering, and computer science to create new biological systems or improve existing ones. This subcategory in the BioGate Competition embodies the innovative spirit of scientific inquiry, where participants explore diverse applications spanning human, plant, animal, microorganism, energy, food, and environmental domains. The realm of synthetic biology and genetics offers boundless opportunities, spanning from pioneering new medications and sustainable biofuels to genetically enhancing crop productivity, crafting drought-resistant plants, and combating infectious diseases. Project ideas in this category are virtually limitless as they often result in accomplishments in other domains, all of which are equally significant for advancing knowledge.

In the subject of computational biology, our collaboration with ZYMVOL has provided new opportunities for creative research and development. Participants can choose to participate on projects that investigate innovative solutions about synthetic biology and genetics, or they may participate with a Zymvol case scenario that is provided.

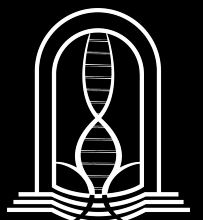


Synthetic Biology

Synthetic biology is described as a growing field of research that creates new biological systems through the combination of biology, engineering, and computer science. The main aim of the field is to design and construct new artificial biological systems that are not found in nature or redesign an existing natural biological systems. The development of such systems allows the scientific community to better understand biological processes proceed.

What do we expect ?

Our expectation from the competitors is that they propose a solution to global problems using synthetic biology. This problem may include a possible treatment or diagnosis for a disease, a research gap in the literature, improvement of an existing technique, or the introduction of a new technique. Regardless of the problem chosen, we expect competitors to use synthetic biology techniques in their projects for the solution in theoretical design and experimentation sections.



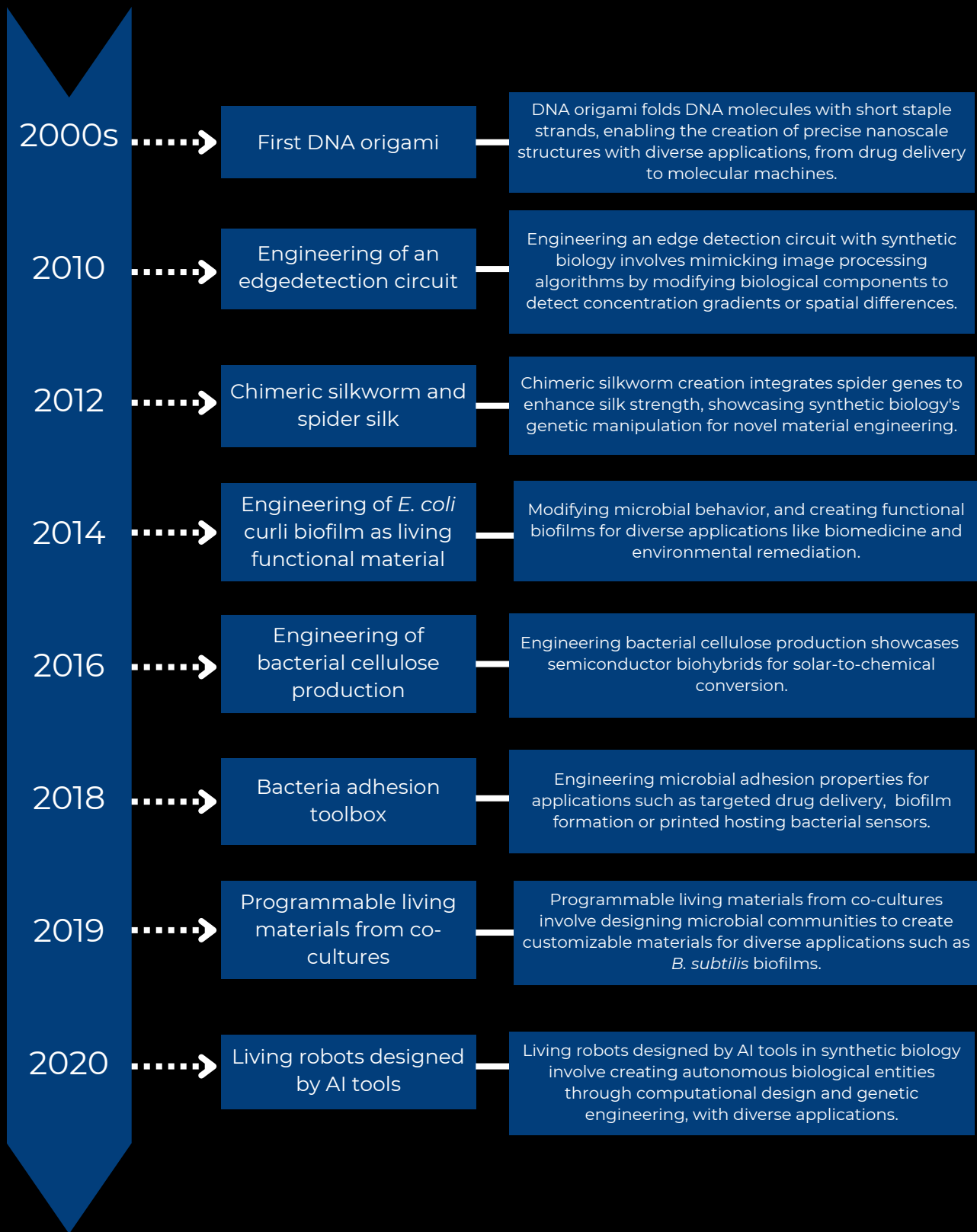
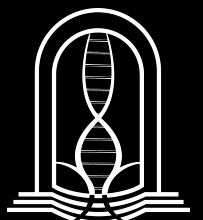


Figure 1. Timeline of major milestones in synthetic biology.

Tang, T. C., An, B., Huang, Y., Vasikaran, S., Wang, Y., Jiang, X., ... & Zhong, C. (2021). Materials design by synthetic biology. *Nature Reviews Materials*, 6(4), 332-350.

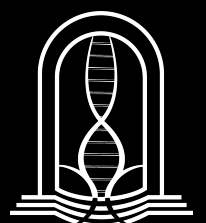


Genetics

Genetics is the study of genes, heredity, and variation in living organisms. It involves the analysis of DNA, RNA, and protein to understand how traits are passed from one generation to the next. It is a multidisciplinary domain, incorporating principles from biology, bioinformatics, and molecular genetics. The primary objective of this field is to decipher the genetic code, paving the way for advancements in medicine, agriculture, and biotechnology.

What do we expect ?

In this competition, we anticipate participants to tackle pressing global challenges through innovative applications in the field of genetics. Competitors are encouraged to address diverse issues, such as devising diagnostic methods for diseases, identifying research gaps within the literature, enhancing existing techniques, or introducing new methodologies. We expect participants to integrate genetic principles and methodologies into their projects. This approach aligns with the competition's emphasis on leveraging the power of genetics to propose comprehensive and impactful solutions to real-world problems.



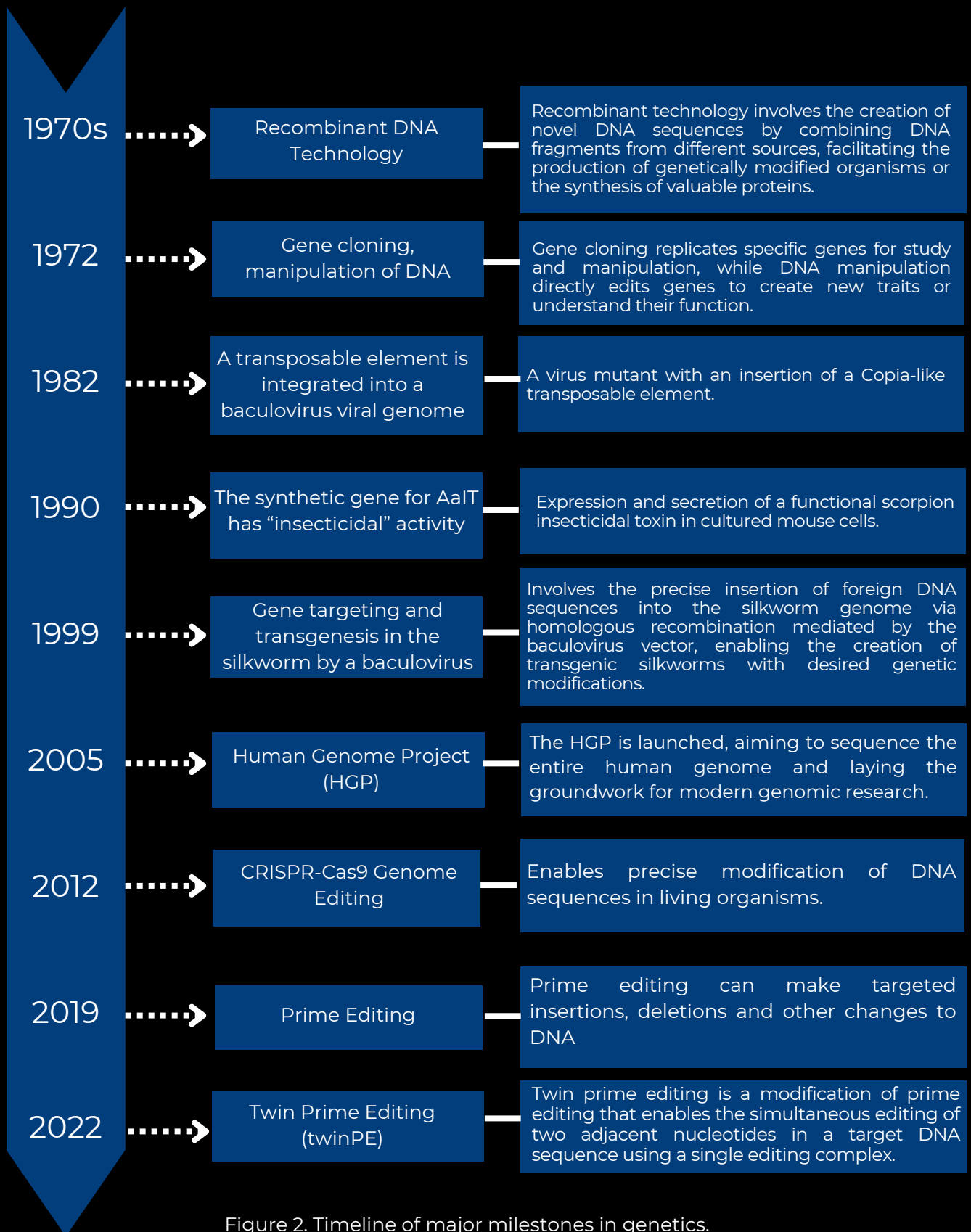
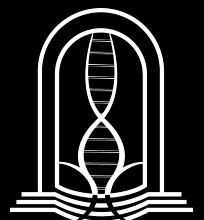


Figure 2. Timeline of major milestones in genetics.

Summers, M. D. (2006). Milestones leading to the genetic engineering of baculoviruses as expression vector systems and viral pesticides. *Advances in virus research*, 68, 3-73.

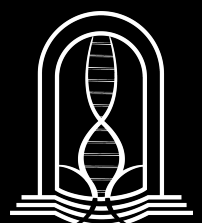


Computational Methods

Computational methods in biology and chemistry involves the use of computational tools such as bioinformatics (i.e. shotgun method and next-generation sequencing), molecular dynamics simulations and molecular docking. These are used to analyze genetic data, simulate biological processes, investigate physicochemical properties (i.e. docking and stability) of biomolecule complexes. The primary goal is to enhance our understanding of biological processes and contribute to fields such as synthetic biology and genetics.

What do we expect ?

For computational methods, we expect participants to utilise these methods in their projects as **tools**. With the power of computers, competitors can add more content to their project via genomic analyses and binding analysis of ligands to receptors. While the participants do not have to include molecular dynamics simulations in the project, it would be useful to include docking studies. With the usage these methods, we expect participants to present more realistic and comprehensive solution(s) to the problems they identified in the areas of synthetic biology and/or genetics.

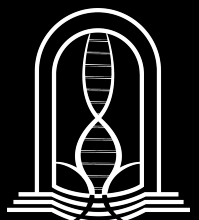


Collaboration with ZYMVOL

Zymvol is a biotechnology company in the Green Chemistry sector, specialising in computer-driven biocatalyst discovery and engineering. The vision of the company is to catalyze the replacement of unsustainable chemical processes, which often use expensive and contaminating metal catalysts by clean and sustainable biocatalysts.

Biocatalysts are used in manufacturing processes where they reduce energy consumption and resources but also cut costs. They also have impactful applications in recycling processes, recovery of raw materials, and water bioremediation. However, tuning the enzyme properties (such as their stability or activity) is often essential to suit the industrial process requirements.

Although participants are welcome to pursue their own project ideas, those who would like assistance or motivation might choose to work on a project scenario that Zymvol has provided.



Case Scenario

This project is designed to mimic the real-life scenarios and challenges encountered in Zymvol company's research and development endeavours.

The goal of this project is to improve the properties of heme-dependent L-tyrosine hydroxylase from *S. sclerotialis* (the X-ray structure can be found at the Protein Data Bank (PDB) with the ID 7kqr) through computational engineering techniques. The project can be focused on two categories*;

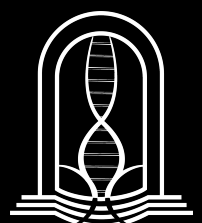
1. Engineering the enzyme to enhance its thermostability.
2. Modifying the enzyme to exhibit activity on a non-natural substrate (pyridine).

*Participants must choose a category for their project from option 1 and 2.

Additionally, Zymvol is offering prizes for the best projects in both categories!

Project Contributions

By participating in this project, participants will gain valuable experience in computational protein engineering techniques, which are essential for designing enzymes with improved properties for various industrial and biomedical applications.



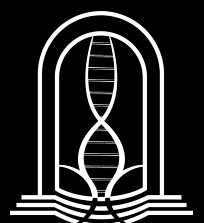
What do we expect?

We expect participants to introduce mutations in the original sequence, in order to improve the target property. Each participant can submit up to 5 different sequences, each representing a unique combination of mutations (maximum 20 mutations per sequence).

To accomplish this, participants will utilize computational tools to introduce mutations into the original enzyme sequence. These mutations should be strategically selected to enhance specific properties of the enzyme. By modifying key amino acids in the sequence, participants can influence the enzyme's behaviour and performance.

Tips for the project

- Bioinformatic tools and public databases can provide useful information by sequence comparison, with minimal computational cost.
- The enzyme behaviour can be modelled computationally: check molecular docking and molecular dynamics, among other algorithms.
- There are plenty of servers out there, give them a try!
- Scientific information is mostly shared through articles. You can check what has been already published, or get inspiration from similar projects in other enzymes.
- Artificial intelligence algorithms are the state-of-the-art.



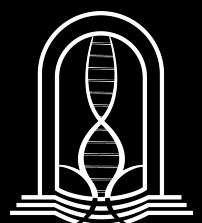
Evaluation

The projects will be evaluated in four contexts and the teams will be entitled to receive gold, silver, and bronze medals according to the scoring. The four contexts include project value, theoretical design**, experimentation, and novelty. Competitors' projects will be evaluated through a submitted report. The report must contain two parts; the first part is where the project value, theoretical design*, and novelty contexts are expressed and explained, and the second part is a formal research report format which includes an introduction, materials & methods, results, discussion and conclusion. Also, a poster presentation is expected during the days of the competition.

Teams joining the competition without making experiment must prepare their reports as a project proposal. Participants must write their expected results and must write a hypothetical discussion.

Teams joining with experimentation (include computational methods) must prepare their reports as formal report format. Experimentation and computational methods will be evaluated as extra credits.

****Participants must choose a topic for their project from options including human being, food, plants, animals, microorganisms, energy and the environment.**



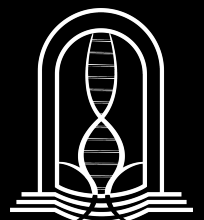
Project value

A detailed explanation of the problem, unmet need, or research gap in the literature must be included in the project report. The project's goal should be clear, explicit, and complementary to the technique chosen. The significance of the chosen issue must be stated in the report.

Theoretical Design

Participants are encouraged to investigate topics related to human beings, animals, plants, foods, microorganisms, energy, or the environment. Each topic will be evaluated equally. Every project topic must be effective, sustainable, and easily accessible.

The theoretical design will be evaluated through the report. We anticipate that material& method section will give a clear hypothetical experimental procedure. In the result and discussion section, both expected and unexpected results should be written and discussed.

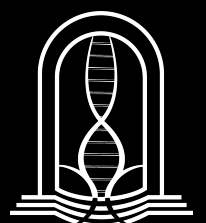


Experimentation

We request participants to carry out their study through actual experimentation using a range of instruments and techniques, including laboratory procedures, bioinformatics, computer analysis, and any other relevant methods. Controls and replicants should be used and stated to ensure the accuracy of the experimental results. Experimentation will be regarded as extra credit, and the utilization of computational methods will also be deemed as extra credit.

Novelty

In the report we expect competitors to write how their project has differed from previous studies and/or their approach was better in terms of efficiency, applicability, accuracy.



Evaluation Chart

