

TECHNISCHE UNIVERSITÄT DARMSTADT

Thesis (B.Sc. / M.Sc.) Investigating Virtual Evolution: SELEX Simulator with Generative Models

Background: Systematic Evolution of Ligands by Exponential Enrichment (SELEX) is a powerful method for discovering novel ligands with high affinity and specificity for target molecules. However, the experimental process is time-consuming, resource-intensive, and involves numerous parameters that can significantly impact the outcome. This thesis aims to develop an in-silico SELEX simulator using advanced generative modeling approaches such as flow matching and hidden Markov models. These powerful probabilistic frameworks can capture the complex evolutionary dynamics of the SELEX process, enabling us to model the selection, binding, and amplification stages with high fidelity. By leveraging these generative modeling techniques, we can streamline ligand discovery and optimize experimental conditions through computational exploration.

Department 18

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Schematic representation of the SELEX process for aptamer selection. Starting from a random RNA library, iterative rounds of selection, binding, and amplification are performed to enrich for high-affinity aptamers against a specific target molecule. Image from [1].



Objective: Join our interdisciplinary team and advance ligand discovery through in-silico SELEX simulation. We offer exciting thesis opportunities in the following areas:

- **Simulator Development:** Implement generative modeling techniques (flow matching, hidden Markov models) to simulate the SELEX process with state-of-the-art methods, capturing the complex evolutionary dynamics of sequence populations.
- Virtual Screening: Utilize the simulator to identify promising ligand candidates for experimental validation, optimizing the selection process and reducing experimental iterations.
- **Model Benchmarking:** Compare different generative approaches for their ability to accurately model the evolutionary trajectories observed in experimental SELEX data.
- **Parameter Optimization:** Identify optimal experimental conditions through systematic computational exploration of the parameter space.

Prerequisites:

- Background in medical engineering, electrical engineering, computer science, (computational) biology, mathematics, physics, or related fields.
- Familiarity with Python and machine learning frameworks (e.g., TensorFlow, PyTorch).
- Interest in probabilistic modeling and generative approaches to biological sequence evolution.
- Knowledge in biology is not mandatory, we will give an introduction to the background.

The Self-Organizing-Systems Lab merges practical biological applications of machine learning with a pronounced emphasis on strong theoretical foundations. Within our interdisciplinary team, we actively work towards publications, offering students an opportunity to engage with cutting-edge research.

Fur further information, please contact Philipp Froehlich and Sebastian Wirth.

[1] Kramat, J., Kraus, L., Gunawan, V. J., Smyej, E., Froehlich, P., Weber, T. E., Spiehl, D., Koeppl, H., Blaeser, A., & Suess, B. (2024). Sensing Levofloxacin with an RNA Aptamer as a Bioreceptor. Biosensors, 14(1), 56. https://doi.org/10.3390/bios14010056