|  |
| --- |
|  |
| Mutator : A Framework Towards Thermal Stability Enhancement |
|  |
| Axel Giottonini |
| Bioinformatics and Computational Biology |
| In the quest to enhance protein thermostability, the convergence of cutting edge methodologies from the realms of bioinformatics and language modelling has emerged as a promising avenue. After a large exploration of the capabilities of sequence-to-sequence models, our project focused on a novel strategy named Mutator. Mutator is a framework to improve protein’s thermostability through the simulation of a point mutation mechanism. The two pillars of Mutator are the deterministic and random pipelines, which implement two opposite strategies. In this report, we introduce the basis of the language model theory to understand our novel framework. We pursue with a description of the Mutator, describing its implementation, the data used to train the pipeline model and we present four experiments to measure the framework performances. Finally, we present an overview of the sequence-to-sequence approaches tested and the difficulties laying in their application. |
|  |
| Prof. Dr. Thomas Lemmin thomas.lemmin@unibe.ch |

Sauvez ce document sous le nom : « No d’étudiant » (exemple : 99-999-999.doc)