

## Individual Reflection

This project reflects my best effort in terms of research, analysis, and the application of bioinformatics techniques. I approached the problem by carefully selecting and applying the most appropriate tools and methods to analyze the structural impact of SCN2A mutations. I invested significant time and effort in understanding the underlying biology of the SCN2A gene and how mutations could affect the structure and function of the encoded protein. The choice of using RMSD and SASA as key metrics was informed by their relevance in structural biology, and I ensured that the methods I employed were both robust and scientifically sound.

However, I could have been more effective in the initial stages of data collection and processing by better anticipating challenges with data integration. One area for improvement would have been to conduct a more thorough initial exploration of the available data, identifying potential issues with data completeness and consistency early on. This would have allowed me to address these challenges more proactively, rather than having to make adjustments later in the project. Additionally, I could have explored alternative data sources or

complementary datasets to enhance the depth and breadth of my analysis.

The most challenging part of this project was ensuring the accuracy of structural predictions. Predicting the structural impact of mutations is inherently complex, as it requires not only a deep understanding of protein folding and dynamics but also the ability to effectively utilize computational tools. To overcome this challenge, I relied on a combination of literature review, expert consultation, and rigorous testing of the analysis pipeline. I spent considerable time refining the model and validating the results against known data, which helped to increase my confidence in the findings. Moreover, I learned to troubleshoot and debug complex bioinformatics tools, which was both a challenging and rewarding experience.

As I was the sole contributor to this project, I took on all roles, including data collection, analysis, and report preparation. While this allowed me to develop a comprehensive understanding of every aspect of the project, it also meant that I missed out on the collaborative learning and idea exchange that often comes from working in a team. In a group setting, I would have appreciated the opportunity to collaborate and discuss the project with peers, which could have led to new insights and potentially more innovative approaches. I also recognize that

working alone can sometimes lead to a narrower perspective, and in future projects, I plan to seek out more collaborative opportunities to broaden my approach.

This project deepened my understanding of bioinformatics and the SCN2A gene. And, in reflecting on the project as a whole, I am quite proud of the work I have accomplished.