# Protein Bioinformatics Reflection

Starting this course was an unexpected step for me, as I transitioned from a medical background into bioinformatics. I wasn’t sure what to expect, but I’m glad I could rely on my medical and clinical knowledge throughout the journey. This course not only helped me revisit protein biology concepts from my undergraduate years but also introduced me to computational methods and tools that were entirely new to me. While the learning curve was steep at times, I’ve grown to appreciate the computational side of biology and how it complements my clinical understanding.

One of the most meaningful aspects of this course was refining my understanding of how structure determines function in proteins. Although this was a familiar concept, this class gave me a deeper appreciation of the finer details, like chain interactions, residue roles, and how these elements interplay to drive function. Using tools like molecular dynamics (MD) simulations and visualization platforms (PyMOL, Chimera, and VMD) helped solidify these ideas while also teaching me practical skills for structural analysis. For example, working on the N-terminal domain of CCK1R, I analyzed how specific mutations, like S82R and M89V, impacted ligand binding and structural stability. These hands-on experiences tied theory to practice and improved my ability to manipulate and interpret protein data.

The course activities were critical in helping me achieve my learning goals. Learning to use the command line and read coding syntax was one of the most challenging yet rewarding aspects. I started as a beginner, but by the end of the course, I could write and adapt simple scripts for tasks like calculating phi and psi angles or assigning secondary structure types. These coding exercises were particularly valuable because they taught me not just to use tools but also to understand the logic behind them. The challenge project, which involved analyzing CCK1R using various computational techniques, gave me a sense of how these tools can answer complex biological questions. It also showed me how foundational skills like coding and scripting can be applied to solving structural and functional questions, making them feel less intimidating and more approachable over time.

Watching my classmates’ presentations revealed just how many ways there are to approach similar challenges. Some projects focused heavily on structural comparisons, like visualizing mutations and their effects on protein stability with tools like PyMOL, while others explored functional questions, such as the impact of phosphorylation on regulatory mechanisms. A few even combined multiple approaches, blending visualization with docking or interaction analysis. Seeing their work emphasized the flexibility and creativity in this field and showed me that there’s no one “right” way to solve these problems. It also highlighted the breadth of computational tools available and the opportunity to create or refine workflows for more detailed analyses. For example, one presentation explored the role of specific residues in protein-protein interactions, which made me think about how similar methods could be applied to my own project. This exposure encouraged me to think more critically about my own methods and consider how I might expand or adjust them in future projects.

Beyond the technical skills, this course gave me a clearer sense of how to integrate computational biology into my career. I’ve always been interested in leveraging my medical background in the biotech field, and this class has opened new possibilities. By combining computational tools with clinical knowledge, I can explore exciting areas like structural biology, drug design, or biomarker discovery. While I found coding and computational analysis overwhelming at times, I also discovered how much I enjoy this side of science. The practical skills I gained, such as scripting and using advanced visualization tools, have made me more confident in tackling complex biological problems and finding innovative solutions.

On a larger scale, this course highlighted how computational biology can influence not only individual research but also broader applications in medicine and industry. For instance, tools like MD simulations, docking software, and structural alignment methods could play a role in advancing personalized medicine, improving drug discovery pipelines, or even predicting the impacts of mutations on a molecular level in disease contexts. The ability to manipulate and analyze protein data computationally opens opportunities to contribute to projects with significant societal impacts, such as developing therapies for conditions like cancer or metabolic disorders. These applications show how bioinformatics bridges the gap between research and real-world solutions, which is a perspective I hadn’t fully appreciated before this course.

In conclusion, this course was more than just a class, it was a stepping-stone into a new way of thinking about proteins and biology. It challenged me, helped me grow, and left me with skills and knowledge that I’ll carry forward into my academic and professional pursuits. The combination of medical insight and computational analysis has given me a unique perspective, and I’m excited to see where this path takes me next.