**Computational Approaches for Mass**

**Spectrometry-based Characterization**

**of Antibody Repertoires**

Laymans summary

Antibodies are important proteins in our immune system, that help combat diseases. Currently, there is a focus on creating antibody-based drugs for use as medicine. To better understand antibodies, scientists are seeking more ways to study them.

To study antibodies, it’s important to determine their protein sequence: which building blocks are used, and in what order. Traditionally, scientists would look at the genetic code for antibodies, but now they're exploring a protein-level approach. This involves directly analyzing the antibodies in our body in different places and situations. Mass spectrometry is a tool that is often used to analyze proteins directly. However, studying antibodies is challenging because there are trillions of possible antibodies.

In this thesis, I describe computational methods we developed to analyze the antibodies in our bodies. By tracking individual antibodies over time, we can observe how our immune system responds to vaccines or diseases. We were able to detect and quantify the unique antibodies in human blood and milk. We found that our immune system relies on a surprisingly low number of antibodies, despite the trillions of possibilities.

We also developed a way to directly sequence antibodies from blood, by combining several MS approaches. This brings us closer to automatic antibody analysis and to find potential new therapies more efficiently.

*These methods can help researchers better study our antibody responses and identify medicinal antibodies in serum. By sequencing these antibodies, they can be converted to medicine more quickly.*

*We show that MS can be used to study antibody responses. By understanding how our antibodies respond to different situations, we can potentially simplify and speed up drug development and combat diseases more effectively.*