Research Interests

- Algorithmics
  - Design and analysis of algorithms & data structures
  - Analytic combinatorics

- Bioinformatics
  - RNA secondary structure prediction
  - Algorithms for huge sequence data sets
Thesis Topics

- Experimental evaluation of *median-of-k jumplists*

- *C++ implementation* (adapting existing JAVA implementation), compare with library red-black trees, …
Comparative methods for (huge) immune receptor profiles (similar to metagenome communities, each receptor corresponds to a species), mostly for multiple sclerosis probes;

Visualisation of huge immune receptor sequence data sets (representing the status of human immune system, e.g., healthy vs. infected or disease). Visualisation of multiple probe comparisons, probe specific statistics and clustering of disease specific profiles;

Data-storage concepts for immune receptor sequence data (1 data set ~1 million sequences, each about 250bp), one experiment yields ~100 - 100,000 data sets;
• **Succinct data structures** processing massive sequence data (implementation and evaluation);

• **Own ideas/concepts** for the analysis of huge sequence data sets, RNA structure prediction, … (algorithms or tool implementation).