8.   Summary

In my thesis work I created efficient tools and data structures that can be used for building molecular networks. Our *MiTab SQLite* format makes it easier to store, transform and analyze molecular network data. I built the *PsimiSQL Python* class that can be used to convert several data formats to MiTab SQL easily. Our research group created a powerful protocol for constructing molecular networks. The protocol proved to be well usable for the establishment of the human-*Salmonella* database.

I also built another *Python class TopologyAnalyser* that can analyze edge-list files. The class can count the TI values for the given network. Edge-list files can be easily obtained from any network.

The reached goals

- I have successfully made a framework and data strucures that can parse molecular networks.

- I have created a host-pathogen network based on *ARN*, *Salmonet* and the human-*Salmonella* predictions.

- I managed to create and test software that can calculate TI an analyze TI.

For the first time I applied TI in the analysis of a host-pathogen molecular network. Although the topological importance is an ecological index, it is proven that it can be used to mark the central proteins of a host-pathogen network. These kind of topological indices are rarely used for the analysis of molecular networks. My thesis reveals that biologically relevant results can be obtained by using indices like this.

In this data set, the predictions and the topological importance marked a protein slpA, that haven't been described in *Salmonella* virulence yet.

Experiments that aim to explore the connections between *Salmonella* and enterocytes have already started based on results that were achieved by my scripts and data structures.