

## MASTER-THESIS

# Identification of Patient-Infections by Next-Generation Sequencing

Early detection of infections in patients can not only save the individual life but can also help to detect early stages of pandemics. In the age of the rise of antibiotic-resistant bacteria hospitals are in need for fast and accurate detections of such cases. To identify this infections, blood samples from patients are analysed in laboratories with specified tests and hypothesis. *Next-Generation Sequencing* (NGS) offers a rather new approach to analyse such samples fast, cost-efficient and when applied correct with a less limited set of hypothesis. All *transcripts* within that sample can be analysed in its entirety by NGS. Down-stream analysis assign the transcript back to its human origin or in case of an infection to its bacterial source.

The aim of this thesis is the implementation of a prototypical NGS-pipeline to identify bacterial transcripts within a complex mixture of transcripts. The thesis decompose into three parts: (1) overview and comparison of NGS technologies and algorithms, (2) simulation-based approach for a proof-of-concept and (3) real-life application in an experimental setting.

### Literature:

- **Martin Kircher and Janet Kelso** (2010):  
*High-throughput DNA sequencing – concepts and limitations*
- **Heng Li and Nils Homer** (2010):  
*A survey of sequence alignment algorithms for next-generation sequencing*

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