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Exploring next-generation sequencing in clinical microbiology

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Propositions

accompanying the dissertation

Exploring next-generation sequencing approaches in clinical microbiology for identification, characterization and typing of pathogens

by

Nilay Peker

1. An appropriate diagnostic algorithm is essential for infection management. (This thesis)
2. A cgSNP approach relying on reference-based mapping of reads or assemblies results in more reproducible phylogenies and is more robust than a cgMLST approach for long-read sequencing data. (This thesis)
3. The longer the sequencing fragments, the higher the resolution for taxonomical classification and genome reconstruction. (This thesis)
4. One bioinformatics tool does not fit all. (This thesis)
5. Nucleic acid extraction is a persistent bias in NGS protocols. (This thesis)
6. An amplicon-based NGS method can be advantageous for screening to rapidly clear the vast majority of negative samples for outbreak management. (This thesis)
7. Metagenomics next-generation sequencing (mNGS) has the potential to become a cost-competitive option for routine diagnostics as it could be used as a direct “rule in” or “rule out” test to confirm the presence or absence of an infectious aetiology. (This thesis)
8. Every step in the entire (diagnostic) NGS chain, from sampling to processing of sequence reads, can make an important difference for an optimal result. (This thesis)
9. “If we knew what it was we were doing, it would not be called research, would it?” Albert Einstein
10. “Simplicity is the ultimate sophistication.” Leonardo da Vinci