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Hidden Markov models for the analysis of next-generation-sequencing data

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Hidden Markov Models for the Analysis of Next-Generation-Sequencing Data

1. Hidden Markov Models are an appropriate and useful technique for the analysis of Next-Generation-Sequencing data. (This thesis)

2. The following points are important for open and distributable scientific software: Quality of the analysis, ease-of-use, computational resource requirements, flexibility. Each point has to receive considerable attention during software development for the tool to become a success.

3. Simulation studies are useless for the purpose of showing the predictive superiority of one method over others. They are useful, however, for sanity checks, debugging, and comparison of computational resource requirements.

4. Science would benefit from a discussion about scientific success. Focusing on journal impact factors gives an incomplete picture, because other important aspects of scientific work are neglected.

5. Publication bias towards positive results leads to redundant work and a waste of resources (e.g. experiments with negative results that need to be repeated because they are not reported). A solution could be that journals accept to publish results before they are produced, based on the study design.

6. Scientific work requires creative thinking. Because long-term stress and creative thinking are negatively correlated, regulations that try to enforce scientific productivity ("publication pressure") are likely to have an adverse effect on the quality of the science produced.

Aaron Taudt, october 2018