Advancing Evolutionary Biology

Genomics, Bayesian Statistics, and Machine Learning

During the recent decades the field of evolutionary biology has entered the era of big data, which has transformed the field into an increasingly computational discipline. In this thesis I present novel computational method developments, including their application in empirical case studies. The presented chapters are divided into three fields of computational biology: genomics, Bayesian statistics, and machine learning. While these are not mutually exclusive categories, they do represent different domains of methodological expertise. The empirical results presented in this thesis shed new light onto our understanding of the evolutionary dynamics of different organism groups and showcase the utility of the methods and workflows developed in this thesis. To make these methodological advancements accessible for the whole research community, I embed them into well documented open-access programs. This will hopefully foster the use of these methods in future studies, and contribute to more informed decision-making when applying computational methods to a given biological problem.

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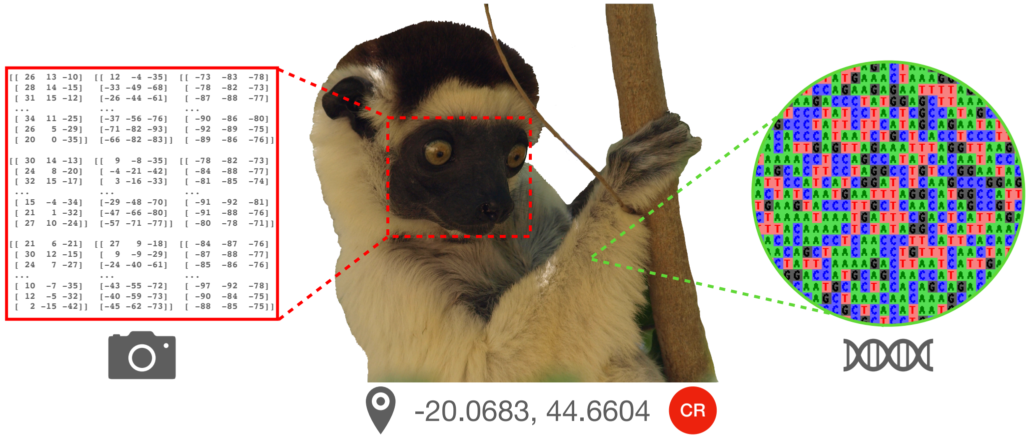

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