

Technological advances in DNA sequencing along with the emergence of new informatics approaches have created new possibilities in many biological fields. In this bachelor thesis, I will focus on the informatics approaches used in speciation genomics, that is research field focused on the problematics of the origin of new species. I will introduce some statistical methods used by these approaches for parameter estimation. The four particular methods I will write about are Maximum likelihood estimation, Bayesian model, Markov chain Monte Carlo and Iterative approach. I will describe several methods used for the detection of interspecific hybrids and recent as well as historical interspecific gene flow. These methods include NewHybrids, the hybrid index, genomic and spatial clines and coalescent-based methods. The thesis demonstrates the usefulness of the connection of applied mathematics and genomics for addressing general biological issues, and speciation particularly.