Machine-Learning based sequence analysis, bioinformatics & nanopore transduction detection

Stephen Winters-Hilt

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This is intended to be a simple and accessible book on machine learning methods and their application in computational genomics and nanopore transduction detection. This book has arisen from eight years of teaching one-semester courses on various machine-learning, cheminformatics, and bioinformatics topics. The book begins with a description of ad hoc signal acquisition methods and how to orient on signal processing problems with the standard tools from information theory and signal analysis. A general stochastic sequential analysis (SSA) signal processing architecture is then described that implements Hidden Markov Model (HMM) methods. Methods are then shown for classification and clustering using generalized Support Vector Machines, for use with the SSA Protocol, or independent of that approach. Optimization metaheuristics are used for tuning over algorithmic parameters throughout. Hardware implementations and short code examples of the various methods are also described.

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