

Abstract:

In the context of a species sampling problem we discuss a nonparametric maximum likelihood estimator for the underlying probability mass function. The estimator is known in the computer science literature as the high profile estimator. We prove strong consistency and derive the rates of convergence, for an extended model version of the estimator. We also study a sieved estimator for which similar consistency results are derived. Numerical computation of the sieved estimator is of great interest for practical problems, such as forensic DNA analysis, and we present a computational algorithm based on the stochastic approximation of the expectation maximization algorithm. As an interesting byproduct of the numerical analyses we introduce an algorithm for bounded isotonic regression for which we also prove convergence.