Change-point modelling in biological sequences via the bayesian adaptive independent sampler

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Abstract

The change-point problem arises in wide variety of fields, including biomedical signal processing, speech and image processing, seismology, industry (e.g., fault detection) and financial mathematics. Multiple change-point models are also important in many biological applications and,particularly, in analysis of biomolecular sequences. We model genome sequences as a multiple change-point process, that is, a process in which the sequential data are separated into segments by an unknown number of change-points, with each segment supposed to have been generated by a different process. The parameters of the model are estimated by Adaptive Independent Samplers, which are adaptive Markov chain Monte Carlo methods based on the Independent Metropolis-Hastings algorithm. We discuss results of numerical experiments comparing different computing schemes.

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Fingerprint

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Hierarchical Bayesian models are a mainstay of the machine learning and statistics com-munities. Exact posterior inference in such models is rarely tractable, however, and so researchers and practitioners must usually resort to approximate statistical inference meth-ods. new point via the leapfrog integrator. A standard procedure for drawing M samples via Hamiltonian Monte Carlo is described in Algorithm 1. I denotes the identity matrix and N (μ, Σ) denotes a multivariate normal. distribution with mean μ and covariance matrix Σ. For each sample m, we rst resample. the momentum variables from a standard multivariate normal, which can be interpreted as. The No-U-Turn Sampler. Figure 1: Example of building a binary tree via repeated doubling. Independent Metropolis (IM). Propose a new point independently of the current location: k(y |x) = K (y). Encapsulate your sampler: Create an MCMC posterior sampling algorithm for model M that takes data D as input and produces posterior samples {θi }, and a 100 P% credible region ΔP (D) Initialize counter Q = 0 Repeat N ≫ 1 times: 1 Sample a “true” parameter value θ∗ from π(θ) 2 Sample a dataset Dsim from p(D|θ∗) 3 Use the encapsulated posterior sampler to get ΔP (Dsim) from. selection): Shotgun stochastic search, Bayesian adaptive sampling. This is just a small sampling! 42 / 42. Change-point problems arise in a wide variety of fields, including biomedical signal processing, speech and image processing, climatology, industry (e.g. fault detection) and financial mathematics. In this paper, we apply the Cross-Entropy method to a sequential change-point problem. @article{Sofronov2012SequentialCD, title={Sequential change-point detection via the Cross-Entropy method}, author={Georgy Y. Sofronov and Tatiana V. Polushina and Madawa Priyadarshana}, journal={11th Symposium on Neural Network Applications in Electrical Engineering}, year={2012}, pages={185-188} }. Change-point modelling in biological sequences via the bayesian adaptive independent sampler. G. Sofronov. Computer Science.