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Enrico Bibbona is associate professor of Statistics at the Department of Mathematical Sciences (DISMA), Politecnico di Torino.

He graduated in Physics at Università di Torino slightly after the extinction of dinosaurs, got a PhD in Mathematics at the same institution and worked at Università di Milano, INRiM, University of Copenhagen and Università di Torino.

His current research interest are in using mathematical modeling to interpret several phenomena in biology and industry and in using advanced statistical tools to tune and validate the models against real data and to draw conclusions from data about questions of practical relevance.



Multiple latent clustering model for the inference of RNA life-cycle kinetic rates from sequencing data

ABSTRACT

We propose a hierarchical Bayesian model to infer RNA synthesis, processing, and degradation rates from sequencing data, based on an ordinary differential equation system that models the RNA life cycle.

We parametrize the latent kinetic rates, that rule the system, with a novel functional form, and estimate their parameters through 6 Dirichlet process mixture models. We simultaneously perform inference, clustering, and model selection. We apply our method to investigate transcriptional and post-transcriptional responses of murine fibroblasts to the activation of proto-oncogene Myc. Our approach uncovers simultaneous regulations of the rates, which had not previously been observed in this biological system.



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