

# A Bayesian hidden Markov model for the intensity of violence in internal armed conflicts

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Why (and when) do small conflicts become big wars? We develop and explore a Bayesian hidden Markov modeling framework for the intensity and dynamics of violence in civil wars. Using event-level data for all civil wars from 1989 to the present, this framework allows us to study transitions in the latent intensity, e.g. from stable to escalatory and/or de-escalatory, in these conflicts. In particular, we examine the effect of UN Peacekeeping Operations (PKOs) and ceasefire agreements on this underlying intensity seen in civil wars.

# Hidden Markov Model in Multiple Testing on Dependent Count Data

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Multiple testing on dependent count data faces two basic modeling elements: the choice of distributions under the null and the non-null states and the modeling of the dependence structure across observations. A Bayesian hidden Markov model is constructed for Poisson count data to handle these two issues. The proposed Bayesian method is based on the posterior probability of the null state and exhibits the property of an optimal test procedure, which has the lowest false negative rate with the false discovery rate under control. Furthermore, the model has either single or mixture of Poisson distributions used under the non-null state. The extension to Poisson regression models is also discussed. Model selection methods are employed here to decide the number of components in the mixture. Different approaches of calculating marginal likelihood are discussed. Extensive simulation studies and a case study are employed to examine and compare a collection of commonly used testing procedures and model selection criteria.

# A Bayesian hidden Markov model framework for monitoring and diagnosing critically ill hospital patients

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The impact of this research is to push the capabilities of data-driven methodologies and tools to the edge of what is possible for the application of monitoring and diagnosing critically ill hospital patients. HMMs are an ideal tool, providing a very flexible, unique, and interpretable framework for statistical inference in that they allow for the quantification and interpretation of unobservable state spaces. Such state spaces often naturally align with domain expert intuition for the progression of biological processes. Namely, it is readily understood by clinicians that the health of a patient, at any point in time, is characterized by the presence and progression of particular conditions, and the job of the clinician is to infer the mostly likely condition(s) of the patient from exhibited symptoms and data. An HMM will precisely define such conditions as latent states, and quantify the progression of the conditions with rates of transitions between the latent states. Moreover, we demonstrate that in contrast to the current status quo of “black-box” machine learning and artificial intelligence approaches, estimation of an HMM can be understood as a transparent learning algorithm. Important domain knowledge can be accounted for via prior distributions within a Bayesian framework, and uncertainty quantification of the HMM parameters is conveniently provided by credible regions.