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José M. Ponciano* (josemi@ufl.edu), Carr Hall 882 Newell Dr, Gainesville, FL 32611. A *population biology interpretation of Bayesian Nonparametric Inference from Gene Genealogies*. Preliminary report.

Using a nonparametric Bayesian approach Palacios and Minin (2013) dramatically improved the accuracy, precision and biological adequacy of Bayesian inference of population size trajectories from gene genealogies. These authors proposed an extension of a Gaussian Process (GP) nonparametric inferential method for the intensity function of non-homogeneous Poisson processes. The authors' prior does not assume a form on the population trajectory. Their approach works so well and provides such a profound understanding of the biological process, that the question arises as to how truly 'biology-free' their approach really is. Using well-known concepts of stochastic population dynamics, here I demonstrate that in fact, Palacios and Minin's GP model can be cast as a stochastic, parametric population growth model with density dependence and environmental noise. Making this link between population genetics and stochastic population dynamics modeling provides novel insights into eliciting biologically meaningful priors for the trajectory of the effective population size. The results presented here also bring new understanding of GP as models for the evolution of a trait. Thus, our ecological interpretation of their prior adds to the conceptual and scientific value of these authors' approach. (Received September 22, 2015)