Statistica Sinica **34** (2024), 1-22
doi:https://doi.org/10.5705/ss.202022.0188

# AN ITERATED BLOCK PARTICLE FILTER FOR INFERENCE ON COUPLED DYNAMIC SYSTEMS WITH SHARED AND UNIT-SPECIFIC PARAMETERS

Edward L. Ionides*[1], Ning Ning[2] and Jesse Wheeler[1]

[1] *University of Michigan and* [2] *Texas A&M University*

*Abstract:* We consider inference for a collection of partially observed stochastic interacting nonlinear dynamic processes. Each process is identified with a label, called its unit. Here, our primary motivation arises in biological metapopulation systems, in which a unit corresponds to a spatially distinct sub-population. Metapopulation systems are characterized by strong dependence over time within a single unit, and relatively weak interactions between units. These properties make block particle filters effective for simulation-based likelihood evaluation. Iterated filtering algorithms can facilitate likelihood maximization for simulation-based filters. Here, we introduce an iterated block particle filter that can be applied when parameters are unit-specific or shared between units. We demonstrate the proposed algorithm by performing inference on a coupled epidemiological model describing spatiotemporal measles case report data for 20 towns.

*Key words and phrases:* Maximum likelihood estimation, metapopulation, partially observed Markov process, sequential Monte Carlo, spatiotemporal.

## 1. Introduction

Statistical inference for high-dimensional partially observed nonlinear dynamic systems arises in various scientific contexts. Massive models and data sets are considered in the geophysical sciences, carried out under the name of data assimilation (Evensen (2009)). Population models in ecology and epidemiology can be characterized by high levels of stochasticity, nonlinearity, measurement error, and model uncertainty, leading to challenges of a somewhat different nature to those of geophysical models. In addition, biological population systems may have a low population count, owing to a local introduction or fade-out of one or more constituent species. Such situations may require models with integer-valued counts, rather than continuous population approximations. Collections of biological populations measured at different spatial locations may have spatial interactions in addition to local population dynamics; such collections are called a metapopulation. The study of spatiotemporal disease dynamics has motivated research into inference for metapopulation systems (Xia, Bjørnstad and Grenfell (2004); Li et al. (2020); Park and Ionides (2020); Ionides et al. (2021);

*Corresponding author