A new iterated filtering algorithm

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Overview

- Introduction to iterated filtering methodology.
- A new iterated filtering algorithm (IF2).
- Theoretical justification of IF2.
- Applications of IF2.

POMP models

- Data y_1^*, \dots, y_N^* collected at times t_1, \dots, t_N are modeled as noisy and incomplete observations of a latent Markov process $\{X(t)\}$.
- This is a **partially observed Markov process (POMP)** model, also known as a hidden Markov model (HMM) or state space model.

SMC methods for POMP models

- **Filtering** is estimation of the latent dynamic process $X(t_n)$ given data y_1^*, \ldots, y_N^* for a fixed model, parameterized by θ .
- Sequential Monte Carlo (SMC) is a numerical method for filtering and evaluating the likelihood function.
- SMC is also called a "particle filter."
- Filtering has extensive applications in science and engineering. Over the last 15 years, SMC has become popular for filtering non-linear, non-Gaussian POMP models.

What is iterated filtering?

- ullet Iterated filtering algorithms adapt SMC into a tool for inference on heta.
- We call IF1 the iterated filtering algorithm of Ionides, Bretó & King (2006). IF1 uses an extended POMP model where θ is replaced by a time-varying process $\theta(t)$ which follows a random walk. SMC filtering on this model can approximate the derivative of the log likelihood.
- Two naive approaches that fail in all but simple problems:
 - Apply a black-box optimizer such as Nelder-Mead to the SMC evaluation of the likelihood.
 - \bullet Carry out Bayesian inference by SMC with θ added to the POMP as a static parameter.

IF2: iterated SMC with perturbed parameters

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For m in 1: M [M filtering iterations, with decreasing \sigma_m]
          \Theta_{0,i}^{F,m} \sim h_0(\cdot \mid \Theta_{i}^{m-1}; \sigma_m) \text{ for } j \text{ in } 1:J
          X_{0,i}^{F,m} \sim f_{X_0}(x_0; \Theta_{0,i}^{F,m}) \text{ for } j \text{ in } 1:J
          For n in 1: N [SMC with J particles]
                      \Theta_{n,i}^{P,m} \sim h_n(\cdot \mid \Theta_{n-1,i}^{F,m}, \sigma_m) \text{ for } j \text{ in } 1:J
                     X_{n,i}^{P,m} \sim f_{X_n|X_{n-1}}(x_n | X_{n-1,i}^{F,m}; \Theta_i^{P,m}) for j in 1:J
                      w_{n,i}^m = f_{Y_n|X_n}(y_n^* \mid X_{n,i}^{P,m}; \Theta_{n,i}^{P,m}) for j in 1:J
                      Draw k_{1:J} with \mathbb{P}(k_j = i) = w_{n,i}^m / \sum_{u=1}^J w_{n,u}^m
                     \Theta_{n,i}^{F,m} = \Theta_{n,k}^{P,m} and X_{n,i}^{F,m} = X_{n,k}^{P,m} for j in 1: J
           End For
          Set \Theta_i^m = \Theta_{N,i}^{F,m} for j in 1:J
End For
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IF2: iterated SMC with perturbed parameters

End For

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For m in 1:M \Theta_{0,j}^{F,m} \sim h_0(\cdot \mid \Theta_j^{m-1}; \sigma_m) \text{ for } j \text{ in } 1:J X_{0,j}^{F,m} \sim f_{X_0}(x_0; \Theta_{0,j}^{F,m}) \text{ for } j \text{ in } 1:J [carry out SMC on an extended model, with the time-varying parameters included in the latent state, intialized at (X_{0,j}^{F,m}, \Theta_{0,j}^{F,m})] Set \Theta_j^m = \Theta_{N,j}^{F,m} for j in 1:J
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Simulator for latent process initial density, $f_{X_0}(x_0; \theta)$ Simulator for latent process transition density, $f_{X_n|X_{n-1}}(x_n \mid x_{n-1}; \theta)$, n in 1:NEvaluator for measurement density, $f_{Y_n|X_n}(y_n \mid x_n; \theta)$, n in 1:NData, $y_{1\cdot N}^*$ Number of iterations, M Number of particles, J Initial parameter swarm, $\{\Theta_i^0, j \text{ in } 1: J\}$ Perturbation density, $h_n(\theta \mid \varphi; \sigma)$, n in 1: NPerturbation sequence, $\sigma_{1\cdot M}$ $\textbf{output:} \ \, \mathsf{Final} \ \, \mathsf{parameter} \ \, \mathsf{swarm}, \ \, \{\Theta^M_i, \ \, j \ \, \mathsf{in} \ \, 1:J\}$ For *m* in 1 : *M* $\Theta_{0,i}^{F,m} \sim h_0(\cdot \mid \Theta_i^{m-1}; \sigma_m) \text{ for } j \text{ in } 1:J$ $X_{0,i}^{F,m} \sim f_{X_0}(x_0; \Theta_{0,i}^{F,m}) \text{ for } j \text{ in } 1:J$ For *n* in 1 : *N* $\Theta_{n,i}^{P,m} \sim h_n(\cdot \mid \Theta_{n-1,i}^{F,m}, \sigma_m) \text{ for } j \text{ in } 1:J$ $X_{n,i}^{P,m} \sim f_{X_{n}|X_{n-1}}(x_{n}|X_{n-1}^{F,m};\Theta_{i}^{P,m})$ for j in 1:J $w_{n,i}^{m} = f_{Y_{n}|X_{n}}(y_{n}^{*} | X_{n,i}^{P,m}; \Theta_{n,i}^{P,m})$ for j in 1:JDraw $k_{1:J}$ with $\mathbb{P}(k_j = i) = w_{n,i}^m / \sum_{u=1}^J w_{n,u}^m$ $\Theta_{n,j}^{F,m} = \Theta_{n,k_i}^{P,m} \text{ and } X_{n,j}^{F,m} = X_{n,k_i}^{P,m} \text{ for } j \text{ in } 1:J$

Set $\Theta_i^m = \Theta_{N,i}^{F,m}$ for j in 1:J

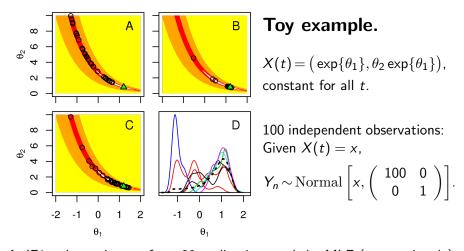
End For

End For

input:

Numerical examples

- We compare IF1, IF2 and the particle Markov chain Monte Carlo (PMCMC) method of Andrieu et al (2010).
- PMCMC is an SMC-based plug-and-play algorithm for full-information Bayesian inference on POMPs.
- Computations were carried out using the pomp R package (King et al, 2009).
- Data and code reproducing our results are included in a supplement to an article in review (Ionides, Nguyen, Atchadé, Stoev & King).



A. IF1 point estimates from 30 replications and the MLE (green triangle). B. IF2 point estimates from 30 replications and the MLE (green triangle). C. Final parameter value of 30 PMCMC chains.

D. Kernel density estimates from 8 of these 30 PMCMC chains, and the true posterior distribution (dotted black line).

Why is IF2 so much better than IF1 on this problem?

- IF1 updates parameters by a linear combination of filtered parameter estimates for the extended model with time-varying parameters.
- Taking linear combinations can knock the optimizer off nonlinear ridges of the likelihood function.
- IF2 does not have this vulnerability.

Application to a cholera model

The study population P(t) is split into susceptibles, S(t), infecteds, I(t), and k recovered classes $R_1(t), \ldots, R_k(t)$. The state process $X(t) = (S(t), I(t), R_1(t), \ldots, R_k(t))$ follows a stochastic differential equation driven by a Brownian motion $\{B(t)\}$,

$$dS = \{k\epsilon R_k + \delta(S - H) - \lambda(t)S\}dt + dP + (\sigma I/P)dB,$$

$$dI = \{\lambda(t)S - (m + \delta + \gamma)I\}dt,$$

$$dR_1 = \{\gamma I - (k\epsilon + \delta)R_1\}dt,$$

$$\vdots$$

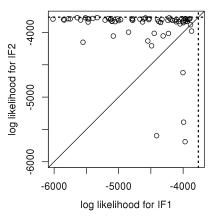
$$dR_k = \{k\epsilon R_{k-1} - (k\epsilon + \delta)R_k\}dt.$$

The nonlinearity arises through the force of infection, $\lambda(t)$, specified as

$$\lambda(t) = \bar{\beta} \exp \Big\{ \beta_{\text{trend}}(t - t_0) + \sum_{j=1}^{N_s} \beta_j s_j(t) \Big\} I + \bar{\omega} \exp \Big\{ \sum_{j=1}^{N_s} \omega_j s_j(t) \Big\},$$

where $\{s_j(t), j=1,\ldots,N_s\}$ is a periodic cubic B-spline basis. The data are monthly counts of cholera mortality, modeled as

$$Y_n \sim \text{Normal}(M_n, \tau^2 M_n^2)$$
 for $M_n = \int_{t_{n-1}}^{t_n} m I(s) ds$.



Comparison of IF1 and IF2 on the cholera model.

Algorithmic tuning parameters for both IF1 and IF2 were set at the values chosen by King et al (2008) for IF1.

- Log likelihoods of the parameter vector output by IF1 and IF2, both started at a uniform draw from a large hyper-rectangle.
- 17 poorly performing searches are off the scale of this plot (15 due to the IF1 estimate, 2 due to the IF2 estimate).
- Dotted lines show the maximum log likelihood.

IF2 as an iterated Bayes map

• Each iteration of IF2 is a Monte Carlo approximation to a map

$$T_{\sigma}f(\theta_{N}) = \frac{\int \check{\ell}(\theta_{0:N})h(\theta_{0:N}|\varphi;\sigma)f(\varphi)\,d\varphi\,d\theta_{0:N-1}}{\int \check{\ell}(\theta_{0:N})h(\theta_{0:N}|\varphi;\sigma)f(\varphi)\,d\varphi\,d\theta_{0:N}},\tag{1}$$

where $\check{\ell}(\theta_{0:N})$ is the likelihood of the data under the extended model with time-varying parameter $\theta_{0:N}$.

- f and $T_{\sigma}f$ in (1) approximate the initial and final density of the IF2 parameter swarm.
- When the standard deviation of the parameter perturbations is held fixed at $\sigma_m = \sigma > 0$, IF2 is a Monte Carlo approximation to $T_{\sigma}^M f(\theta)$.
- Iterated Bayes maps are not usually contractions.
- We study the homogeneous case, $\sigma_m = \sigma$.
- Studying the limit $\sigma \to 0$ may be as appropriate as an asymptotic analysis to study the practical properties of a procedure such as IF2, with σ_m decreasing down to some positive level $\sigma>0$ but never completing the asymptotic limit $\sigma_m\to 0$.

IF2 as a generalization of data cloning

- In the case $\sigma=0$, the iterated Bayes map corresponds to the data cloning approach of Lele (2007, 2010).
- For $\sigma=0$, Lele et al (2007, 2010) found central limit theorems. For $\sigma\neq 0$, the limit as $M\to\infty$ is not usually Gaussian.
- Taking $\sigma \neq 0$ adds numerical stability, which is necessary for convergence of SMC approximations.

Theorem 1. Assuming adequate mixing conditions, there is a unique probability density f_{σ} with

$$\lim_{M\to\infty} T_{\sigma}^M f = f_{\sigma},$$

with the limit taken in the total variation or Hilbert projective norms. The SMC approximation to $T_{\sigma}^{M}f$ converges to $T_{\sigma}^{M}f$ as $J\to\infty$, uniformly in M.

- The Hilbert projective metric has the nice property that T_{σ}^{M} is a contraction.
- Theorem 1 follows from existing results on filter stability.

Theorem 2. Under regularity conditions, $\lim_{\sigma\to 0} f_{\sigma}$ approaches a point mass at the maximum likelihood estimate (MLE).

Outline of proof.

- Trajectories in parameter space which stray away from the MLE are down-weighted by the Bayes map relative to trajectories staying close to the MLE.
- As σ decreases, excursions any fixed distance away from the MLE require an increasing number of iterations and therefore receive an increasing penalty from the iterated Bayes map.
- Bounding this penalty proves the theorem.

Conclusions

- IF1 enabled previously infeasible likelihood-based inference for non-linear, non-Gaussian POMP models.
- We have not yet found a situation where IF2 performs substantially worse than IF1. In complex nonlinear models, we have found IF2 always substantially better.
- In addition, IF2 is simpler. Some extensions are easier: IF2 can readily handle parameters for which the information in the data is concentrated in a sub-interval.
- If you like IF1, you'll love IF2.

- J. R. Stat. Soc. B, 72:269–342.

 Ionides, E. L., Bhadra, A., Atchadé, Y., and King, A. A. (2011).

 Iterated filtering.

 Ann. Stat., 39:1776–1802.
- Inference for nonlinear dynamical systems.

 Proc. Natl. Acad. Sci. USA, 103:18438–18443.

King, A. A., Ionides, E. L., Pascual, M., and Bouma, M. J. (2008).

Andrieu, C., Doucet, A., and Holenstein, R. (2010).
Particle Markov chain Monte Carlo methods

- Inapparent infections and cholera dynamics.

 Nature, 454:877–880.

 Lele, S. R., Dennis, B., and Lutscher, F. (2007).
 - Lele, S. R., Dennis, B., and Lutscher, F. (2007).

 Data cloning: easy maximum likelihood estimation for complex ecological models using Bayesian Markov chain Monte Carlo methods. *Ecology Letters*, 10(7):551–563.
- Lele, S. R., Nadeem, K., and Schmuland, B. (2010).
 Estimability and likelihood inference for generalized linear mixed models using data cloning.

 J. Am. Stat. Assoc., 105:1617–1625.

More iterated filtering references can be found on Wikipedia wikipedia.org/wiki/Iterated_filtering

Thank You!

The End.