An iterated block particle filter for inference on coupled dynamic systems with shared and unit-specific parameters

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Joint work with
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Questions to be addressed

1. When can we carry out full-information likelihood-based inference on a general class of spatiotemporal partially observed Markov process models?
2. When should we want to?
3. Is there an intersection between scientific problems of interest and the capabilities of the `spatPomp` R package?

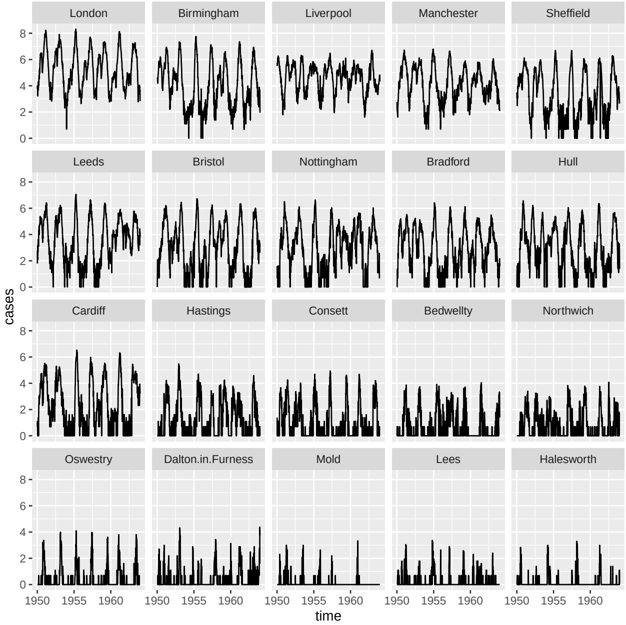
We introduce the **iterated block particle filter** because it is currently the most powerful algorithm available in `spatPomp`.

Inference challenges in population dynamics

1. Combining measurement noise and process noise.
2. Including covariates in mechanistically plausible ways.
3. Continuous time models.
4. Modeling and estimating interactions in coupled systems.
5. Dealing with unobserved variables.
6. **Modeling spatial-temporal dynamics**.
7. Studying population dynamics via genetic sequence data.

1–6 are from Bjornstad & Grenfell (*Science*, 2001).
7 is an active topic, but not the focus of this talk.
1–5 are largely solved, from a methodological perspective.

Example: Pre-vaccination measles in England & Wales



Time series data, panel data & spatiotemporal data

- Looking at one unit (town) is **time series analysis**.
- Joint modeling of a few units (say, 2 or 3) is **multivariate time series analysis**.
- Analysis of many time series, without consideration of dynamic interactions, is **panel data analysis**.
- Allowing for coupling between units, we get **spatiotemporal analysis**, which in our context is **metapopulation analysis**.

Question: When should we avoid inference for spatiotemporal models? When do we need to consider coupling? How?

Desiderata

- We want to be able to fit arbitrary dynamic models. The limitations should be our scientific creativity and the information in the data.
- In practice, that means using **plug-and-play** methods which need a simulator from the model but not nice closed-form expressions for densities.
- We want statistically efficient inference, to extract all the information in the data.
- In practice, that means using likelihood-based methods.
- In the time series case, iterated particle filtering (IF2) implemented in the R package `pomp` enables Masters-level statisticians to do this (`https://ionides.github.io/531w22/`). The science may be hard, but the statistics is becoming routine.

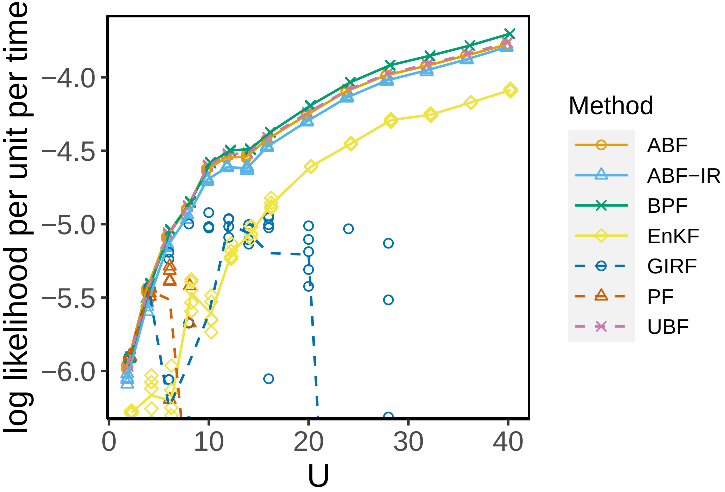
Panel data

- To investigate epidemiological dynamics in multiple cities, one can consider each city independently, perhaps modeling a background immigration rate of infections for each city.
- **Decoupling** leads to panel data analysis, by assumption. Iterated filtering methods extend to panel data (Breto et al, *Journal of the American Statistical Association*, 2019).
- We must decide which parameters should be modeled as **shared** vs **unit-specific**.
- The consequences of decoupling are becoming easier to study with the development of statistical inference methods for coupled systems, i.e., metapopulation dynamics.

The curse of dimensionality

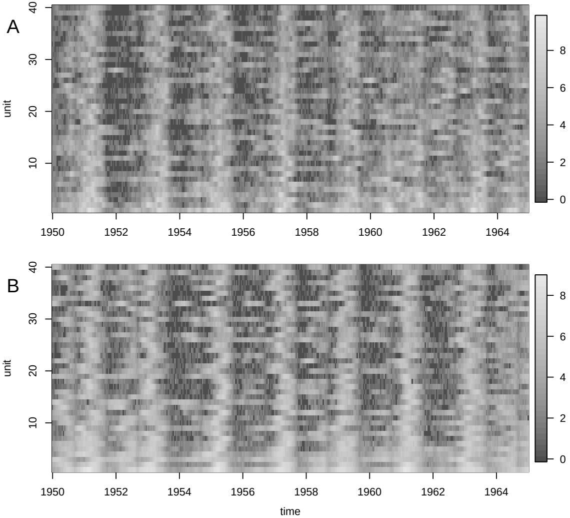
- Particle filter (PF) methods are effective for inference on low-dimensional nonlinear partially observed stochastic dynamic systems. They scale exponentially badly.
- Extending the successes of particle filter methods from time series data to metapopulation data is becoming possible.
- Algorithms under consideration:
  Bagged filters (BF, IBF)
  Ensemble Kalman filter (EnKF, IEnKF)
  Guided intermediate resampling filter (GIRF, IGIRF)
  Block particle filter (BPF, IBPF)
- Filters estimate latent states and evaluate the likelihood.
- Each filter has an iterated version which estimates parameters by repeated filtering using stochastic parameter perturbations.
- These algorithms are all implemented in an R package, `spatPomp`.

Filtering U units of a coupled measles SEIR model



Simulated data using a gravity model with geography, demography and transmssion parameters corresponding to UK pre-vaccination measles (Ionides et al, JASA, 2021).

$U = 40$ units for a coupled measles SEIR model



A. Simulated Susceptible-Exposed-Infected-Recovered dynamics coupled with a gravity model (log of biweekly reported cases).
B. Measles UK pre-vaccination case reports for the 40 largest cities.

Parameters for the measles model

- Seasonal tranmission: mean and amplitude, using school term for contact rate.
- Durations of latency and infectious period.
- Initial values: fraction susceptible, latent and infectious.
- Cohort effect: all births in an age cohort start school in September.
- Inhomogenous mixing coefficient.
- Measurement fraction.
- Transport model gravity constant.
- Dynamic noise (process overdispersion).
- Measurement overdispersion.

More on the block particle filter

- BPF worked quickly, easily and reliably on our measles model filtering experiments.
- This motivated us to develop an IBPF for parameter estimation.
- BPF has theoretical support in some situations (Rebeschini & Van Handel, *Annals of Applied Probability*, 2015).
- BPF was independently proposed as the "factored particle filter" by Ng et al (2002, *Proc. 18th Conference on Uncertainty and Artificial Intelligence*) but not widely popularized.

Particle filter (PF)

Evolutionary analogy

Mutation

$\downarrow$

Fitness

$\downarrow$

Natural selection

Particle filter algorithm

Predict: stochastic dynamics

$\downarrow$

Measurement: weight

$\downarrow$

Filter: resample

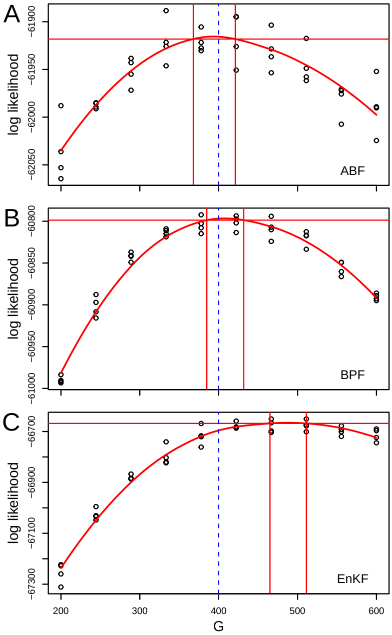
- PF is an evolutionary algorithm with good mathematical properties: an unbiased likelihood estimate and consistent latent state distribution.

Block particle filter (BPF)

Evolutionary analogy	**Block particle filter**
Mutation	**Predict: stochastic dynamics**
$\downarrow$	$\downarrow$
Fitness for each chromosome	**Measurement: weight for each block**
$\downarrow$	$\downarrow$
Natural selection for each chromosome	**Filter: resample for each block**
$\downarrow$	$\downarrow$
Recombine chromosomes	**Recombine blocks**

- Blocks in BPF allow recombination (reassortment of chromosomes in sexual reproduction) in the evolutionary analogy.
- Blocks are a partition of the metapopulation units. Our experiments suggest treating each sub-population (i.e., city) as a block.

Measles likelihood slices for coupling parameter, G



Simulating 15 year of data from $U = 40$ cities for the measles model. Slice likelihood, varying G with other paramters fixed at the truth.

A. Evaluation using adapted bagged filter (ABF).

B. Evaluation using block particle filter (BPF).

C. Evaluation using EnKF.

Results from Ionides et al (2021, *JASA*). We computed a slice due to lack of good optimization algorithms to compute a profile.

Scalability needed for practical inference

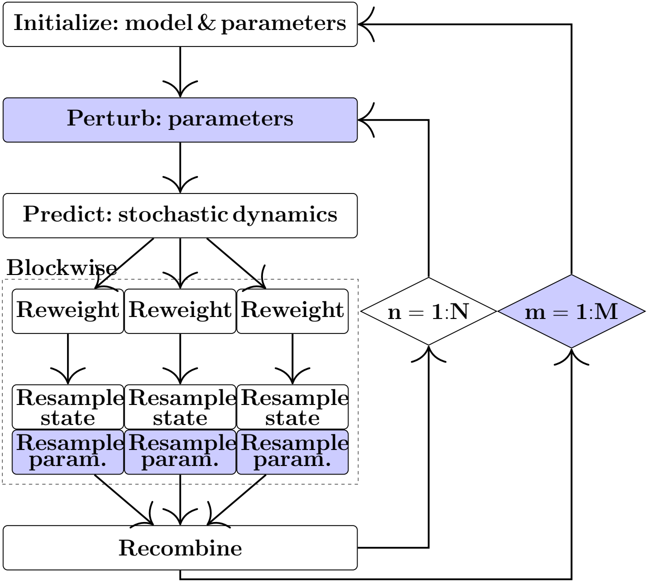
Large numbers of parameters

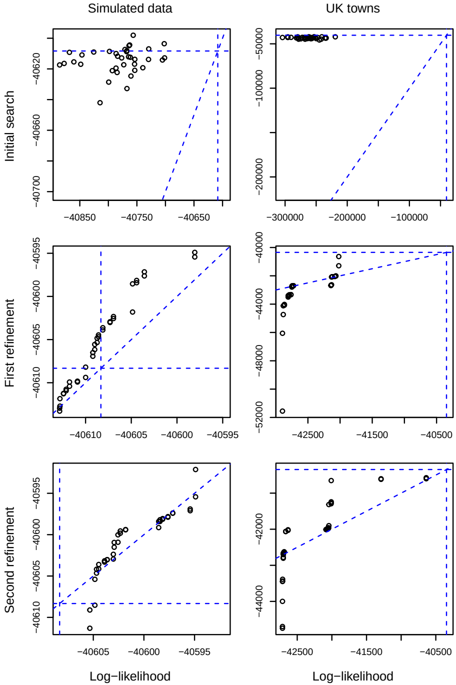
- Initial conditions will typically have to be estimated for each unit.
- Various dynamic parameters and measurement parameters (e.g., reporting rate) may also need to be unit-specific to obtain a statistical fit to the data.
- Working with hundreds of estimated parameters raises additional challenges on top of the high-dimensional coupled dynamics.

A moderate numbers of spatial units is enough to open new possibilities.

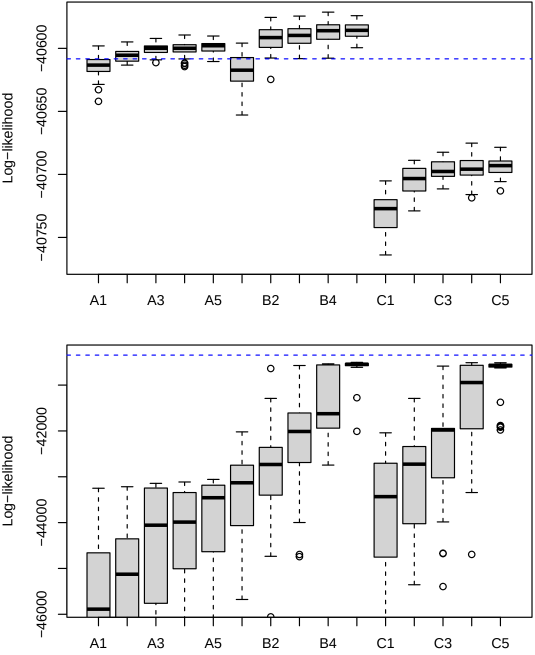
- As soon as dimension exceeds capabilities of a particle filter (say, $U = 5$) we are in situations where likelihood-based inference for general models has been inaccessible.
- 10-100 coupled units is our target problem size.
- Larger problems will need numerical approximations (e.g., EnKF). Exact Monte Carlo methods help study the effect of these approximations.

An iterated block particle filter for parameter estimation





- IBPF applied to simulations and data.
- Multiple searches from random starting points.
- Top 25% of searches are subsequently refined.



- IBPF applied to simulations (top panel) and data (bottom panel).
- Multiple search refinements.

(A) Mostly shared parameters.

(B) All unit-specific parameters

(C) all unit-specific, without coupling

Cholera in Haiti, 2010-2019

- 820,000 reported cases and nearly 10,000 deaths

- Population of 10,000,000 in 10 départements

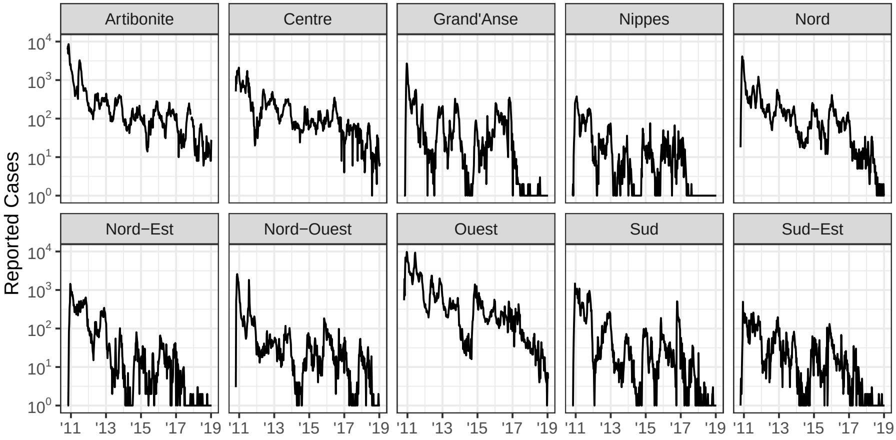
- Lee et al (2020) developed 3 models to guide vaccination plans:

1. stochastic, national
2. ODE, spatial
3. stochastic, spatial

https://doi.org/10.5194/nhess-20-471-2020

- Wheeler et al (2023) continued the data analysis

Haiti cholera weekly reports 2010-2019 (log scale)



Log-likelihoods of models and an ARMA benchmark

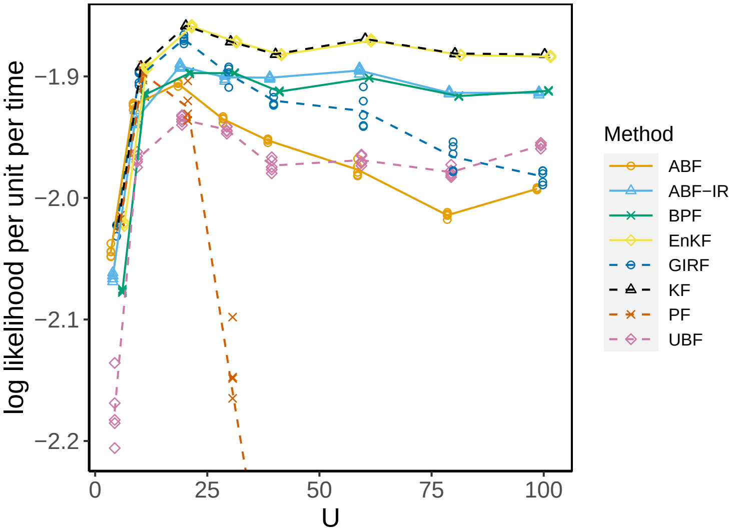
	Model 1	(p)	Model 2	(p)	Model 3	(p)
Wheeler et al	-2731.3	(15)	-21957.3	(6)	-17850.4	(35)
Lee et al	-3030.9	(20)	-29367.4	(6)	-31840.8	(29)
Log-ARMA(2,1)	-2803.7	(4)	-18027.0	(40)	-18027.0	(40)

Model 1 (stochastic, aggregated):
We add process overdispersion, and beat the ARMA benchmark.

Model 2 (deterministic, spatial):
We use a log-normal measurement model. ODE models fall far short of the ARMA benchmark.

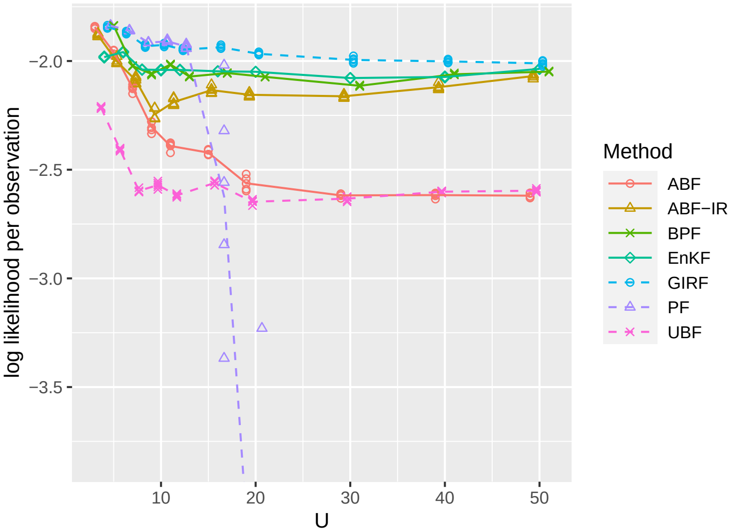
Model 3 (stochastic, spatial):
(We fit the model using IBPF, and beat the ARMA benchmark.

Filtering U-dimensional correlated Brownian motion



$$\mathrm{Cov}\big(X_{u,n} - X_{u,n-1}, X_{\tilde{u},n} - X_{\tilde{u},n-1}\big) \sim 0.4^{|u-\tilde{u}|}$$

Filtering U units of Lorenz 96 toy atmospheric model



$$dX_u(t) = \Big\{X_{u-1}(t)\big(X_{u+1}(t) - X_{u-2}(t)\big) - X_u(t) + F\Big\}dt + \sigma\, dB_u(t)$$

Future work

- We are reaching to the point where we can carry out likelihood-based inference for a flexible class of metapopulation models for measles. Flexibility supports generation and testing of scientific hypotheses.

- Many systems in ecology, epidemiology and elsewhere could be studied in a SpatPOMP framework. Including microbiomes?

- Modeling and inference for nonlinear stochastic dynamics is hard. But, if you can't build a quantitative statistical model then you don't understand it and you can't control it?

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