(Particle) Markov chain Monte Carlo

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Inference and prediction



Once the model is fitted and the model fit assessed, we can use the model / parameter estimates in various ways:

- **Inference**: interpreting the parameter estimates.
- **Prediction**: to predict what might happen if the outbreak were to occur under the same conditions again.
- **Forecasting**: to predict what might happen in the future, based on data available now.

So what's the problem?



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The likelihood for compartmental models relies on having **exact** observations of event **times** and **types**. In practice events are rarely observed in detail:

- **Surveillance**: e.g. under-reporting, imperfect coverage, imperfect diagnosis, mis-diagnosis;
- Rounding error: e.g. data often collated daily / weekly;
- **Hidden states**: some epidemiological processes never observed (e.g. you might know *roughly* when you started feeling sick with flu, but not when you were infected or when you became infectious).

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Dealing with these challenges is **hard**! (But we will have a go!)

Intractable likelihoods



To deal with the **partially observed** data, we can introduce a set of **latent** variables, $\mathbf{x} = (\mathbf{t}, \delta)$, where \mathbf{t} is a vector of **hidden** event *times*, and δ is a vector of **hidden** event *types*.

Then the **likelihood** can be expressed as:

$$f(\mathbf{y} \mid \theta) = \int_{\mathcal{X}} f(\mathbf{y} \mid \mathbf{x}, \theta) f(\mathbf{x} \mid \theta) d\mathbf{x},$$

where

- $f(y \mid x, \theta)$ is an observation process (or measurement error / model discrepancy);
- $f(\mathbf{x} \mid \theta)$ is the **likelihood function** based on the **latent** variables \mathbf{x} .

Intractable likelihoods



$$f(\mathbf{y} \mid \theta) = \int_{\mathcal{T}} f(\mathbf{y} \mid \mathbf{x}, \theta) f(\mathbf{x} \mid \theta) d\mathbf{x},$$

This **marginalises** (averages) across the hidden variables x.

This is a complex integral, over all possible combinations of events, and all possible event times consistent with the data.

It may also be the case that the **number** of hidden events is **unknown**, in which can we have to repeat the integration for every possible number of hidden events.

Data augmentation



One approach is therefore to include the **hidden** variables ${\bf x}$ as **additional parameters** in the model.

We can then estimate the **joint posterior** distribution for (θ, \mathbf{x}) , and then derive the **marginals** for the parameters of interest (θ) numerically.

This is usually done using MCMC methods; an approach known as **data-augmented MCMC** (e.g. Gibson and Renshaw 1998; Philip D. O'Neill and Roberts 1999; Jewell et al. 2009).

It is very powerful, but difficult to code, scale and optimise.

Simulation-based approaches



Alternatively, we can build inference algorithms around **simulating** directly from the model-of-interest, and then searching for parameter sets that are more consistent with the **observed data**.

These **simulation-based methods** are also powerful and flexible:

- Don't have to store all of the latent variables (so memory requirements are lower).
- · Are often straightforward to parallelise.
- Simulation can often be easier than calculating the likelihood.
- Implementation often easier than DA (e.g. "plug-and-play")

However, there are also practical difficulties:

- The probability of matching the data exactly (i.e. getting a non-zero likelihood) is often very low.
- · Often require some form of approximation to obtain a match.

Alternative fitting methods



Examples of latent variable methods:

- Data-augmented MCMC (e.g. Gibson and Renshaw 1998; Philip D. O'Neill and Roberts 1999; S. Cauchemez and Ferguson 2008; Jewell et al. 2009)
- · Sequential Monte Carlo (Simon Cauchemez et al. 2008)

Examples of simulation-based methods:

- · Maximum likelihood via iterated filtering (Ionides, Bretó, and King 2006)
- **Approximate Bayesian Computation** (e.g. Toni et al. 2009; McKinley, Cook, and Deardon 2009; Conlan et al. 2012; Brooks Pollock, Roberts, and Keeling 2014)
- **Pseudo-marginal methods** (e.g. P. D. O'Neill et al. 2000; Beaumont 2003; Andrieu and Roberts 2009; McKinley et al. 2014)
- Particle MCMC (Andrieu, Doucet, and Holenstein 2010; Drovandi, Pettitt, and McCutchan 2016)
- Synthetic likelihood (Wood 2010)
- **History matching** (with **emulation**) (e.g. Andrianakis et al. 2015; McKinley et al. 2018)

Pseudo-marginal MCMC



```
Require: 	heta^{(0)}.

for i=1,\ldots,n do

Propose candidate 	heta'\sim q\left(\cdot\mid\theta^{(i-1)}\right).

Calculate the acceptance probability:
```

$$\begin{split} \alpha &= \min \left({1,\frac{\hat{f}\left({\mathbf{y}} \mid \boldsymbol{\theta}' \right)f\left(\boldsymbol{\theta}' \right)}{\hat{f}\left({\mathbf{y}} \mid \boldsymbol{\theta}^{(i-1)} \right)f\left(\boldsymbol{\theta}^{(i-1)} \right)}} \right. \\ &\times \frac{q\left(\boldsymbol{\theta}^{(i-1)} \mid \boldsymbol{\theta}' \right)}{q\left(\boldsymbol{\theta}' \mid \boldsymbol{\theta}^{(i-1)} \right)} \right) \end{split}$$

```
\begin{array}{l} \text{Sample } u \sim U(0,1) \\ \text{if } u < \alpha \text{ then} \\ \theta^{(i)} = \theta' \\ \text{else} \\ \theta^{(i)} = \theta^{(i-1)} \\ \text{end if} \\ \end{array}
```

One option is to simply plug this **estimate** into a standard Metropolis-Hastings algorithm in place of the true likelihood.

Remarkably, as long as this estimate is **unbiased**, this will still converge to the **true** posterior.

This approach is known as **pseudo-marginal MCMC**.

Beaumont (2003); Andrieu and Roberts (2009).

Simulation-based approximations



One option is to replace the likelihood, $f(\mathbf{y} \mid \theta)$, by a **Monte Carlo** estimate:

$$\begin{split} f(\mathbf{y} \mid \boldsymbol{\theta}) &= \int_{\mathcal{X}} f(\mathbf{y} \mid \mathbf{x}, \boldsymbol{\theta}) f(\mathbf{x} \mid \boldsymbol{\theta}) d\mathbf{x} \\ &\approx \frac{1}{M} \sum_{i=1}^{M} f(\mathbf{y} \mid \mathbf{x}_{i}, \boldsymbol{\theta}), \end{split}$$

where $\mathbf{x}_i \sim f(\mathbf{x} \mid \theta)$ are simulations from the underlying model.

This provides an **unbiased** estimate for $f(\mathbf{y} \mid \theta)$.

Efficiency of pseudo-marginal MCMC



The efficiency (i.e. **mixing**) of pseudo-marginal MCMC relies on the **variance** of the **estimator** $\hat{f}(\mathbf{y} \mid \theta)$.

- If the variance is **small**, then mixing will be **improved**.
- If the variance is **large**, then mixing will be **poor**.

We can reduce the variance by:

- increasing the number of simulations $M \to \text{higher computational}$ burden;
- · improving the estimator.

Particle MCMC



This leads on to the idea of **particle MCMC** (Andrieu, Doucet, and Holenstein 2010).

In essence this aims to use **Sequential Monte Carlo**[†] to produce an **unbiased** estimate of the likelihood that has **lower variance** than a vanilla Monte Carlo estimate.

One of the earliest and most widely used particle filters is known as the **bootstrap particle filter** (Gordon, Salmond, and Smith 1993).

[†]i.e. particle filtering

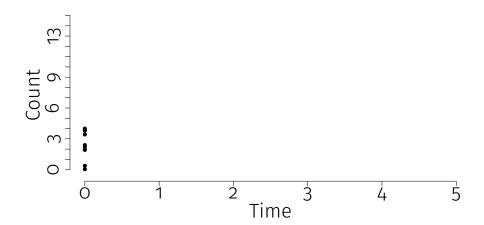
Bootstrap particle filter



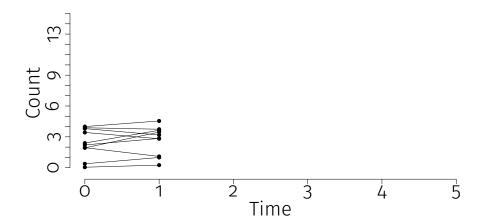
Each **particle** now corresponds to the **unobserved states** of the system at time 0, $\mathbf{x}_0 = (\mathbf{x}_0^1, \dots, \mathbf{x}_0^M)$. The parameters are **fixed**.

- 1. Each particle m is propagated forwards in time by **simulating** from the model $\mathbf{x}_1^m \sim f(\mathbf{x} \mid \mathbf{x}_0^m, \theta)$.
- 2. Each new particle is **weighted** according to the **observation** process, $f(\mathbf{y} \mid \mathbf{x}_1^m, \theta)$.
- 3. These weights are **normalised**, and a **re-sampling** step undertaken.
- 4. The new set of particles are propagated forwards to time t+1 and so on...

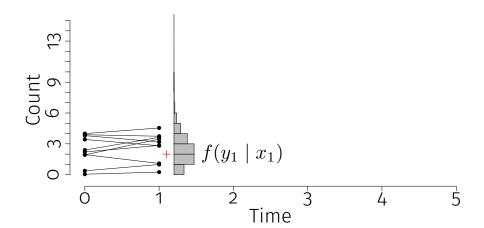




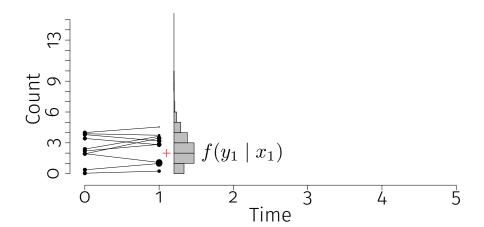




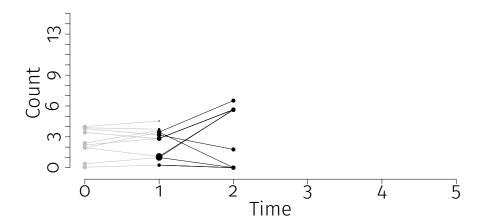




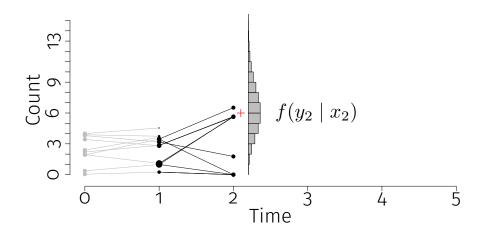




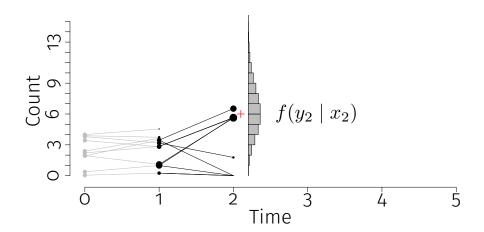




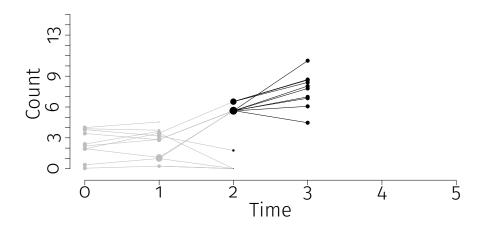




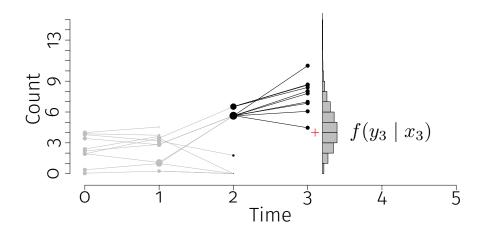




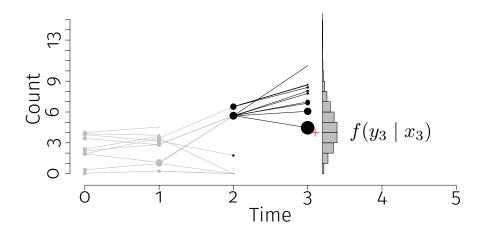






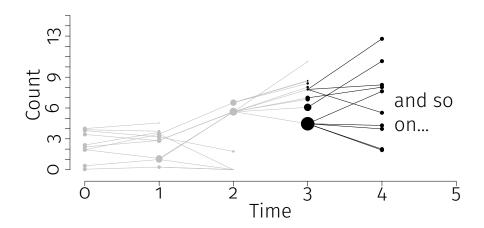






Bootstrap particle filter





Bootstrap particle filter



We can generate an **unbiased estimate** of the conditional densities:

$$\hat{f}\left(y_{t}\mid y_{0:(t-1)}\right) = \frac{1}{M}\sum_{m=1}^{M}f\left(y_{t}\mid \mathbf{x}_{t}^{m},\theta\right),$$

where $y_{0:(t-1)}$ corresponds to the observed time-series counts at time $t_0,t_1,\dots,t_{t-1}.$

It turns out that we can also derive an **unbiased** estimate of the overall **likelihood** as:

$$\hat{f}\left(\mathbf{y}\mid\boldsymbol{\theta}\right) = f\left(y_{0}\right)\prod_{t=1}^{I}\hat{f}\left(y_{t}\mid y_{0:(t-1)}\right).$$

Particle MCMC



Hence we can generate an **unbiased** estimate of the likelihood which **numerically** integrates over the **hidden states**.

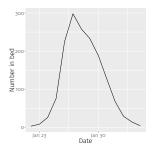
We can then plug this estimate into a standard Metropolis-Hastings algorithm to produce a **pseudo-marginal** MCMC routine that will converge to the *correct posterior distribution in probability*.

This approach only requires a **simulation** model, and an **observation process**.

The bootstrap particle filter we've used is defined for **time-series** counts, and can be extended in various ways.



To illustrate some of these ideas we can use a case study of influenza in a boarding school. These data are from a paper in the BMJ in 1978 (Anonymous 1978) and provided in the outbreaks package. We use a simple $SIRR_1$ model:



The event probabilities are:

$$\begin{split} P\left[S_{t+\delta t} = S_t - 1, I_{t+\delta t} = I_t + 1\right] &\approx \beta SI/N \\ P\left[I_{t+\delta t} = I_t - 1, R_{t+\delta t} = R_t + 1\right] &\approx \gamma I \\ P\left[R_{t+\delta t} = R_t - 1, R_{1,t+\delta t} = R_{1,t} + 1\right] &\approx \gamma_1 R \end{split}$$



Here we will place a Poisson error process around the R curve, such that:

$$R_t \sim \text{Po}(R_t' + 10^{-6}),$$

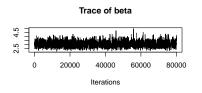
where R_t is the **observed** R count at time t, R_t' is the simulated count[†].

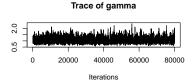
The initial population size is 763 pupils, and we assume an initial introduction of infection of a single child at day o.

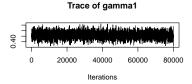
[†]see e.g. Funk et al. (2016) or here for similar ideas in practice



We ran a PMCMC algorithm for 100,000 iterations, discarding the first 20,000 as burn-in. We used 75 particles for the particle filter.



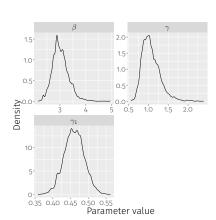






Summaries of the marginal posterior distributions are:

•	Parameter	Mean	2.5%	97.5%
	β	3	2.5	3.7
	γ	1.1	0.73	1.6
	γ_1	0.46	0.41	0.52



Summary



Particle MCMC is a powerful approach for inference in **partially observed** systems (see e.g Wilkinson 2012 or his associated blog for fantastic explanations of these methods).

It is often used when there is some form of **stochastic** discrepancy / observation process mapping the **hidden** states to the **observed** states.

Other particle filters exist, such as the **Alive Particle Filter** (Jasra et al. 2013), and the system can be extended to the **ABC** setting, where approximate matching around data points is used (Drovandi, Pettitt, and Lee 2014; McKinley et al. 2020).

Software



Partially Observed Markov Processes:

- . bomb
- · SimBIID[†]
- · SimInf[‡]
- · nimble§
- · hmer¶

[†]designed mostly for teaching purposes, but should work for simple models

^{*}now implements ABC-SMC (e.g. Toni et al. 2009; McKinley, Cook, and Deardon 2009)

[§]now supports state-space models (although I've not used it for these)

[¶]hot-off-the-press! Implements emulation and history matching for epidemic models

References i



- Andrianakis, Ioannis, Ian Vernon, Nicky McCreesh, Trevelyan J. McKinley, Jeremy E. Oakley, Rebecca N. Nsubuga, Michael Goldstein, and Richard G. White. 2015. "Bayesian History Matching of Complex Infectious Disease Models Using Emulation: A Tutorial and a Case Study on HIV in Uganda." PLoS Computational Biology 11 (1): e1003968.
- Andrieu, Christophe, Arnaud Doucet, and Roman Holenstein. 2010. "Particle Markov Chain Monte Carlo Methods." *Journal of the Royal Statistical Society, Series B (Methodological)* 72 (3): 269–342.
- Andrieu, Christophe, and Gareth O. Roberts. 2009. "The Pseudo-Marginal Approach for Efficient Monte Carlo Simulation." *The Annals of Statistics* 37 (2): 697–725.

References ii



- Anonymous. 1978. "Influenza in a Boarding School." *British Medical Journal* 1: 578.
- Beaumont, Mark A. 2003. "Estimation of Population Growth and Decline in Genetically Monitored Populations." *Genetics* 164: 1139–60.
- Brooks Pollock, Ellen, Gareth O. Roberts, and Matt J. Keeling. 2014. "A Dynamic Model of Bovine Tuberculosis Spread and Control in Great Britain." *Nature* 511: 228–31. https://doi.org/10.1038/nature13529.
- Cauchemez, S., and Neil M. Ferguson. 2008. "Likelihood-Based Estimation of Continuous-Time Epidemic Models from Time-Series Data: Application to Measles Transmission in London." *Journal of the Royal Society Interface* 5 (25): 885–97.

References iii



- Cauchemez, Simon, Alain-Jacques Valleron, Pierre-Yves Boëlle, Antoine Flahault, and Neil M. Ferguson. 2008. "Estimating the Impact of School Closure on Influenza Transmission from Sentinel Data."

 Nature 452: 750–55. https://doi.org/10.1038/nature06732.
- Conlan, Andrew J. K., Trevelyan J. McKinley, Katerina Karolemeas, Ellen Brooks Pollock, Anthony V. Goodchild, Andrew P. Mitchell, Colin P. D. Birch, Richard S. Clifton-Hadley, and James L. N. Wood. 2012. "Estimating the Hidden Burden of Bovine Tuberculosis in Great Britain." *PLoS Computational Biology* 8 (10): e1002730.
- Drovandi, Christopher C., Anthony N. Pettitt, and Anthony Lee. 2014. "Bayesian Indirect Inference Using a Parametric Auxiliary Model." *Statistical Science* 30 (1): 72–95.

References iv



- Drovandi, Christopher C., Anthony N. Pettitt, and Roy A. McCutchan. 2016. "Exact and Approximate Bayesian Inference for Low Integer-Valued Time Series Models with Intractable Likelihoods." *Bayesian Analysis* 11 (2): 325–52.
- Funk, Sebastian, Adam J. Kucharski, Anton Camacho, Rosalind M. Eggo, Laith Yakob & Lawrence M. Murray, and W. John Edmunds. 2016. "Comparative Analysis of Dengue and Zika Outbreaks Reveals Differences by Setting and Virus." *PLoS Neglected Tropical Diseases* 10 (12): e0005173.
- Gibson, Gavin J., and Eric Renshaw. 1998. "Estimating Parameters in Stochastic Compartmental Models Using Markov Chain Methods." *IMA Journal of Mathematics Applied in Medicine and Biology* 15: 19–40.

References v



- Gordon, N. J., D. J. Salmond, and A. F. M. Smith. 1993. "Novel Approach to Nonlinear/Non-Gaussian Bayesian State Estimation." *Radar and Signal Processing, IEE Proceedings F.* 140 (2): 107–13. https://doi.org/10.1049/ip-f-2.1993.0015.
- Ionides, E. L., C. Bretó, and A. A. King. 2006. "Inference for Nonlinear Dynamical Systems." *Proceedings of the National Academy of Sciences USA* 103: 18438–43.
- Jasra, Ajay, Anthony Lee, Christopher Yau, and Xiaole Zhang. 2013. "The Alive Particle Filter." https://arxiv.org/abs/1304.0151.
- Jewell, Chris P., Theodore Kypraios, Peter Neal, and Gareth O. Roberts. 2009. "Bayesian Analysis for Emerging Infectious Diseases." Bayesian Analysis 4 (4): 465–96.

References vi



- McKinley, Trevelyan J., Alex R. Cook, and Robert Deardon. 2009. "Inference in Epidemic Models Without Likelihoods." *The International Journal of Biostatistics* 5 (1). https://doi.org/10.2202/1557-4679.1171.
- McKinley, Trevelyan J., Peter Neal, Simon E. F. Spencer, Andrew J. K. Conlan, and Laurence Tiley. 2020. "Efficient Bayesian Model Choice for Partially Observed Processes: With Application to an Experimental Transmission Study of an Infectious Disease." Bayesian Analysis 15 (3): 839–70. https://doi.org/10.1214/19-BA1174.
- McKinley, Trevelyan J., Joshua V. Ross, Rob Deardon, and Alex R. Cook. 2014. "Simulation-Based Bayesian Inference for Epidemic Models." *Computational Statistics and Data Analysis* 71: 434–47.

References vii



- McKinley, Trevelyan J., Ian Vernon, Ioannis Andrianakis, Nicky McCreesh, Jeremy E. Oakley, Rebecca N. Nsubuga, Michael Goldstein, and Richard G. White. 2018. "Approximate Bayesian Computation and Simulation-Based Inference for Complex Stochastic Epidemic Models." Statistical Science 33 (1): 4–18. https://doi.org/10.1214/17-STS618.
- O'Neill, P. D., D. J. Balding, N. G. Becker, M. Eerola, and D. Mollison. 2000. "Analyses of Infectious Disease Data from Household Outbreaks by Markov Chain Monte Carlo Methods." *Applied Statistics* 49: 517–42.
- O'Neill, Philip D., and Gareth O. Roberts. 1999. "Bayesian Inference for Partially Observed Stochastic Epidemics." *Journal of the Royal Statistical Society. Series A (General)* 162: 121–29.

References viii



- Toni, Tina, David Welch, Natalja Strelkowa, Andreas Ipsen, and Michael P. H. Strumpf. 2009. "Approximate Bayesian Computation Scheme for Parameter Inference and Model Selection in Dynamical Systems." *Journal of the Royal Society Interface* 6: 187–202.
- Wilkinson, Darren J. 2012. Stochastic Modelling for Systems Biology. 2nd ed. Chapman; Hall / CRC.
- Wood, Simon N. 2010. "Statistical Inference for Noisy Nonlinear Ecological Dynamic Systems." *Nature* 466: 1102–4.