

# Perfect Epidemics

## Applied Probability Seminar

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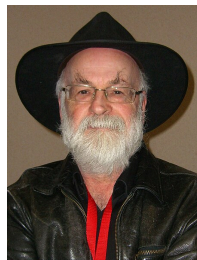
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# Introduction

“Maybe the only significant difference between a really smart simulation and a human being was the noise they made when you punched them.”

([The Long Earth](#), Pratchett & Baxter, 2012)



Handout available on the web: use the QR-code

or visit <https://wilfridskendall.github.io/talks/PerfectEpidemics/>.

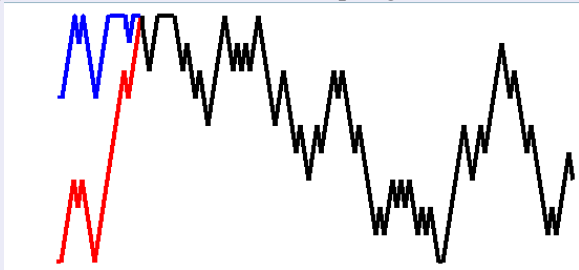
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# 1: Introduction to Perfect Simulation

- Propp & Wilson (1996) invented exact simulation / Coupling from the Past (CFTP) / perfect simulation;
- The term “perfect simulation” (WSK, 1998) should make you suspicious: perfection is never achieved. This is why the term was chosen!
- Key ideas of “*classic CFTP*”:
  - ▶ extend simulation *backwards* through time not forwards;
  - ▶ exploit monotonicity (*couple* maximal and minimal processes);
  - ▶ seek coalescence.
- Simplest possible example: *random-walk-CFTP*  
(can boost to use Ising model to do simple image reconstruction).

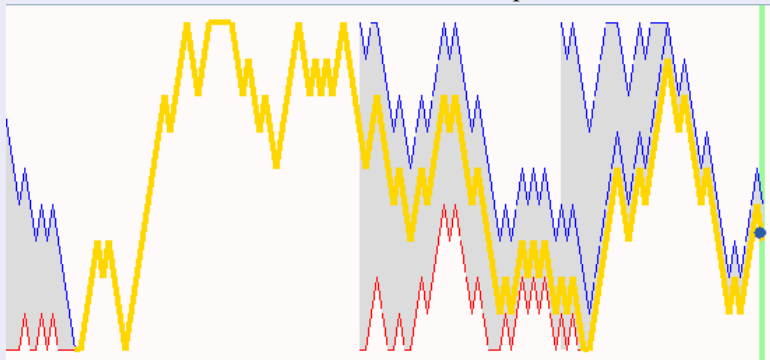
## Classic CFTP for a simple random walk (I)

- Consider a simple random walk on  $\{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$ .
  - ▶  $\mathbb{P}[+1 \text{ jump}] = p \in (0, 1)$ , while  $\mathbb{P}[-1 \text{ jump}] = 1-p$ , **except that**
  - ▶ at state 9 replace  $+1$  jump by staying still, **and**
  - ▶ at state 0 replace  $-1$  jump by staying still.
- Conventional MCMC picks a starting point, then runs the simple random walk for long time till approximate equilibrium.
- How long? One way to *estimate* this is to run two (or several?) coupled copies till they meet. If probability of meeting by time  $T$  is high, then deviation of  $X_T$  from equilibrium is statistically small,
- Generally **not true** that location *at* coupling is a draw from equilibrium.



## Classic CFTP for a simple random walk (I)

- So now start at top (9) and bottom (0) at negative time  $-T$ , run to time 0.
- If not coupled, then back-off to time  $-2T$  and repeat.
- May need to iterate back-off doubling several times.
- When coupled, top and bottom yield a common value at time 0.
- The common value is an exact draw from equilibrium!



## 2: A short section on some theory about CFTP

- What about cases where monotonicity fails? or there isn't a sensible “maximal” process? Ideas (WSK, 1998):
  - ▶ cross-couple upper and lower envelope processes,
  - ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process);
- Theoretical limits: *in principle* we can show that
  - ▶ *Classical CFTP* equivalent to uniform ergodicity (Foss & Tweedie, 1998).
  - ▶ *Dominated CFTP* achievable under geometric ergodicity (WSK, 2004).
  - ▶ Dominated CFTP can work in some **non**-geometrically ergodicity cases (Connor & WSK, 2007a; *nb* corrigendum Connor & WSK, 2007b);
- *Dominated CFTP* can be used to carry out perfect simulation for stable point processes (WSK & Møller, 2000);
- Detailed expositions: WSK (2005), Huber (2015).  
(Want to implement CFTP in R? see WSK, 2015.)

### 3: Perfect Epidemics: a challenge problem for CFTP

Many important inferential questions (Cori & Kucharski, 2024).

Simplest models (versus UK model with  $10^6$  agents!, Fraser & Others, 2023):

**S-I-R deterministic epidemic:** susceptibles  $s$ , infectives  $i$ , removals  $r$  (constant total population  $s + i + r = n$ ):

$$\begin{aligned}s' &= -\alpha s i, \\ i' &= (\alpha s - \beta) i, \\ r' &= \beta i.\end{aligned}$$

**S-I-R stochastic epidemic:** a Markov chain  $(S, I, R)$  with transitions

**Infection:**  $S \rightarrow S - 1, \quad I \rightarrow I + 1$  at rate  $\alpha S I$ ,

**Removal:**  $I \rightarrow I - 1, \quad R \rightarrow R + 1$  at rate  $\beta I$ .

These models make an unrealistic assumption: homogeneous mixing.

# The first question asked about a new epidemic

“What is the R-number?”

The R-number is  $\alpha s_0/\beta$ : mean number of new infectives produced per infective at *start* of epidemic with initially  $s_0$  susceptibles.

Whittle (1955)’s threshold theorem: R-number  $\gg 1$  means positive chance of epidemic infecting significant proportion of the population.

*Wikipedia*: “The British-registered *Diamond Princess* was the first cruise ship to have a major [COVID-19] outbreak on board, with the ship quarantined at Yokohama from 4 February 2020 for about a month. Of 3711 passengers and crew, around 700 people became infected and 9 people died.”

Evidently  $\alpha s_0/\beta \gg 1$  – as was sadly later confirmed, a sorrow for us all.





## 4: Inference on the R-number

Important, because the R-number controls severity of epidemic. However:

- 1 Modelling is **tough**. *Either* massive assumptions (homogeneous mixing) *or* very many parameters;
- 2 Inference is **really tough**: hard to get information about infection times;
- 3 It is all **especially tough** in early stages. Answers are most needed when hardly any information is available (a simplified example for a Warwick UG second-year statistics module shows how tough this can be);
- 4 Markov chain Monte Carlo (MCMC) can be used (see next slide) but what about burn-in?
- 5 Can we use **perfect simulation**?

We are going to try to make headway in using perfect simulation to aid inference.

## 5: An easier question

An absurdly simple variant of contact tracing:

“When did the infections occur, supposing we only observe removals?”

(Gibson & Renshaw, 1998; O'Neill & Roberts, 1999; Gibson & Renshaw, 2001)

- ➊ Thus  $n$ ,  $\alpha$ ,  $\beta$  are known, removal times are observed, but unobserved infection times **must be inferred**.
- ➋ Visualize  $n$  timelines, along which incidents are scattered:
  - ▶ potential removals, activated if timeline is infected;
  - ▶ potential infections, activated if timeline is infected *and* if designated target timeline is lowest uninfected timeline.
- ➌ Poisson point processes of appropriate rates yield an S-I-R epidemic.
- ➍ Evolve whole S-I-R trajectory in *algorithmic time* (alter potential infections and removals using immigration-death in discrete algorithmic time).
- ➎ Result: *trajectory-valued chain*, unconditioned S-I-R as equilibrium.

# From incidents to unconditioned epidemic trajectories (1/3)



Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

# From incidents to unconditioned epidemic trajectories (2/3)

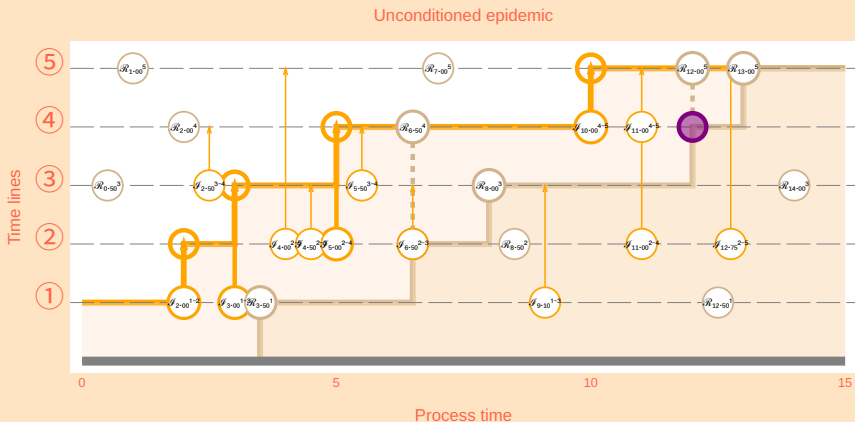


Figure 2: Activate *infection* if target on lowest uninfected timeline. *removal* if in infected region and remove lowest infected (purple disk if different timeline).

# From incidents to unconditioned epidemic trajectories (3/3)

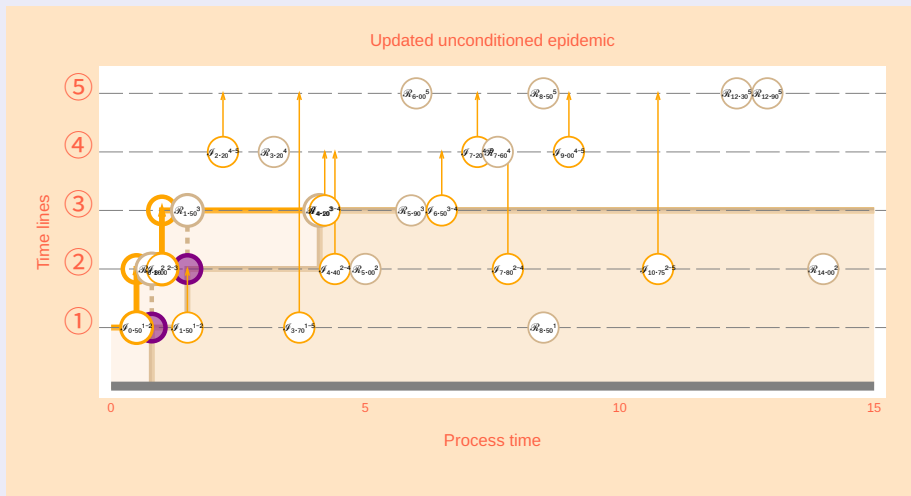


Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing the original incidents by a new set of incidents.

## Crucial technical point

- Updates in algorithmic time  $\tau$  are then (algorithmic-)*time-reversible*: so restriction to subset  $S$  of state-space (in our case, *activated* removals occurring precisely at specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in  $S$ .
- For later purposes it is convenient to stage the replacement as follows:
  - ① Replace removals ( $R$ s);
  - ② Re-sample timelines (though not times) of  $R$ s;
  - ③ Replace infections ( $I$ s).
- Re-express using continuously varying  $\tau$ . Process time runs over  $[0, T]$ .
  - ① For  $2nT < \tau < (2n+1)T$ , update old  $R$ s with times in  $(0, \tau - 2nT)$ ;
  - ② For  $\tau = (2n+1)T$ , resample timelines (not times) of  $R$ s;
  - ③ For  $(2n+1)T < \tau < (2n+2)T$ , update old  $I$ s in  $((2n+2)T - \tau, T)$ .
- Thus the original update is expressible as a (continuous) composition of updates, each of which satisfies detailed balance in equilibrium.
- The connection “restriction=conditioning” is thereby preserved.
- Crucially, step 2 ensures composition action is irreducible over  $S$ !  
(So equilibrium under conditioning is unique.)

# Illustration of technical point (1/8)

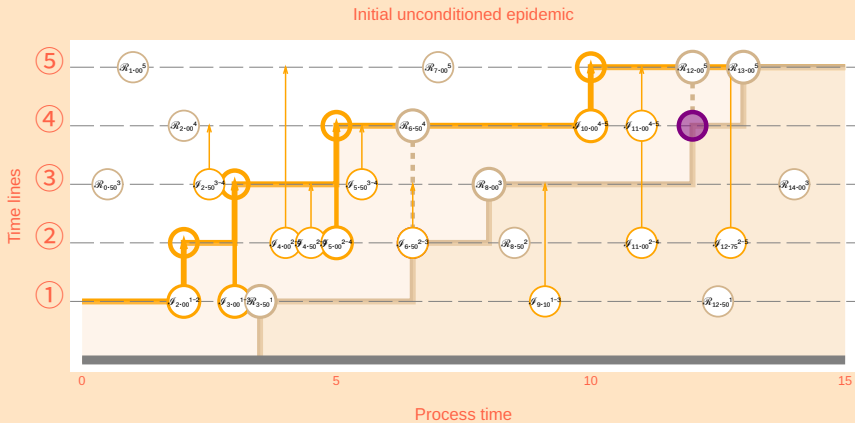


Figure 4: No change to removals or infections

# Illustration of technical point (2/8)

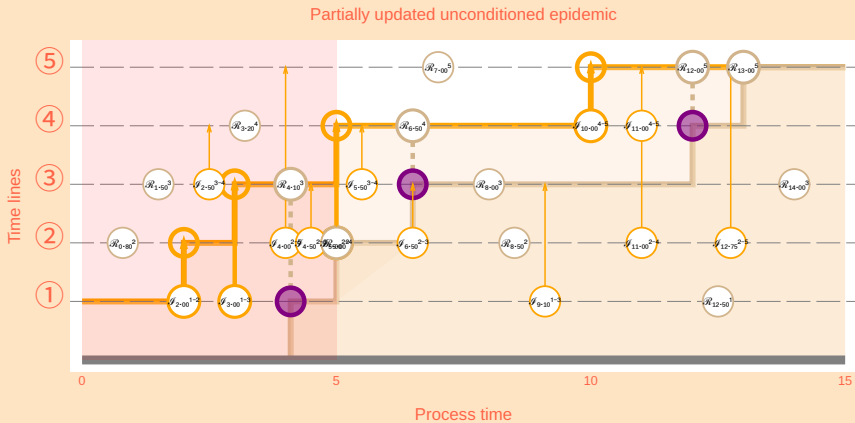


Figure 5: Replace first third of removals, infections unchanged



# Illustration of technical point (3/8)

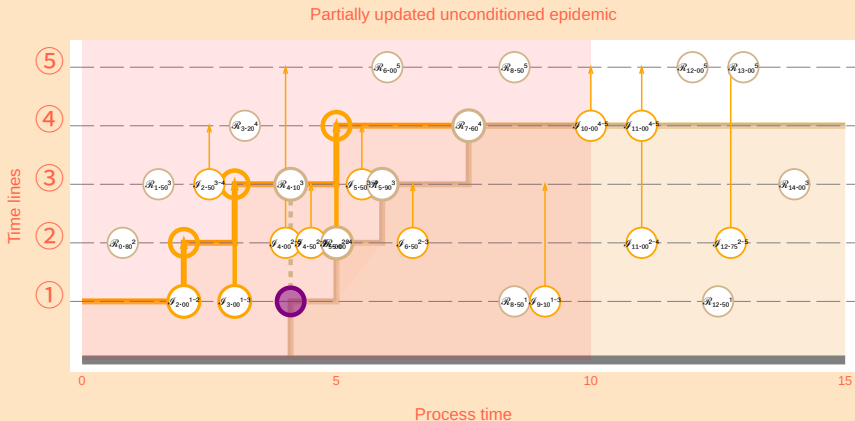


Figure 6: Replace first two-thirds of removals, infections unchanged

# Illustration of technical point (4/8)

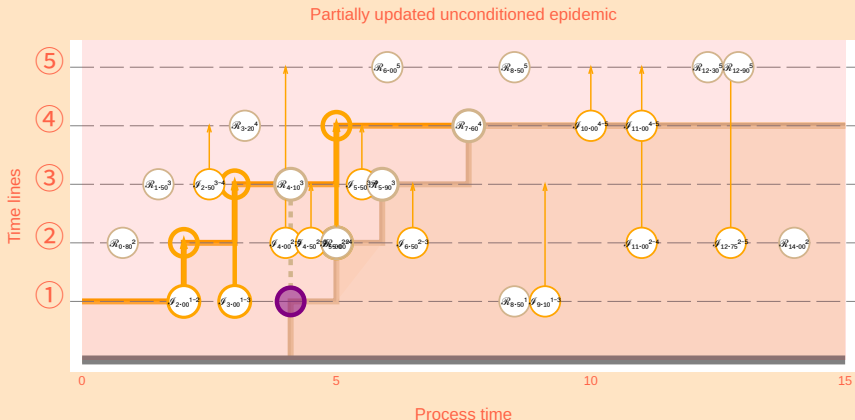


Figure 7: All removals resampled, infections unchanged

# Illustration of technical point (5/8)

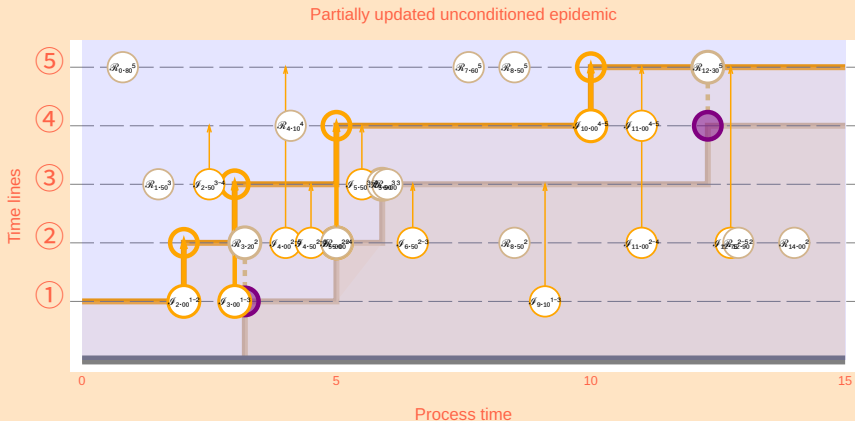


Figure 8: Re-sample all removal timelines, infections unchanged

# Illustration of technical point (6/8)

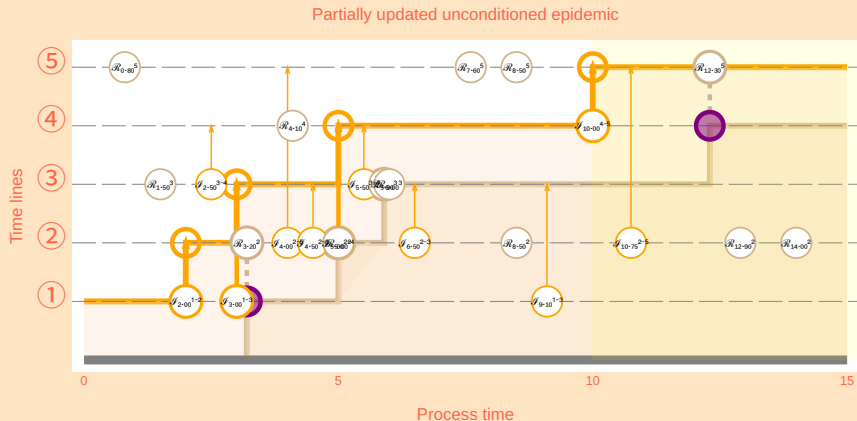


Figure 9: Re-sample last third of infections

# Illustration of technical point (7/8)

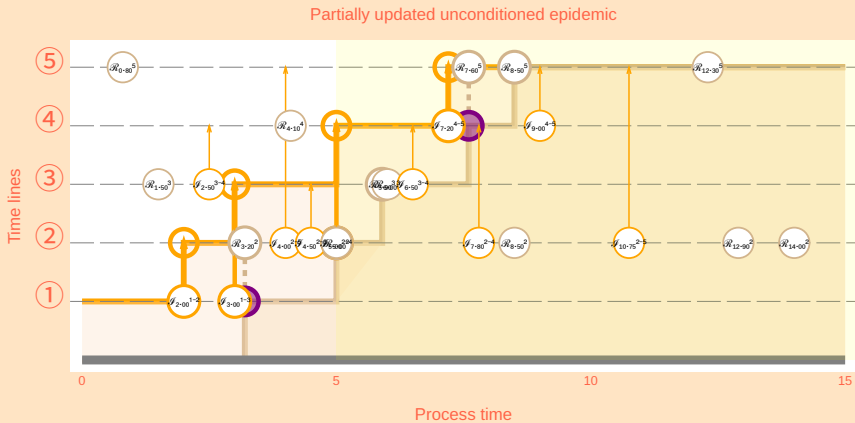


Figure 10: Re-sample last two-thirds of infections

## Illustration of technical point (8/8)

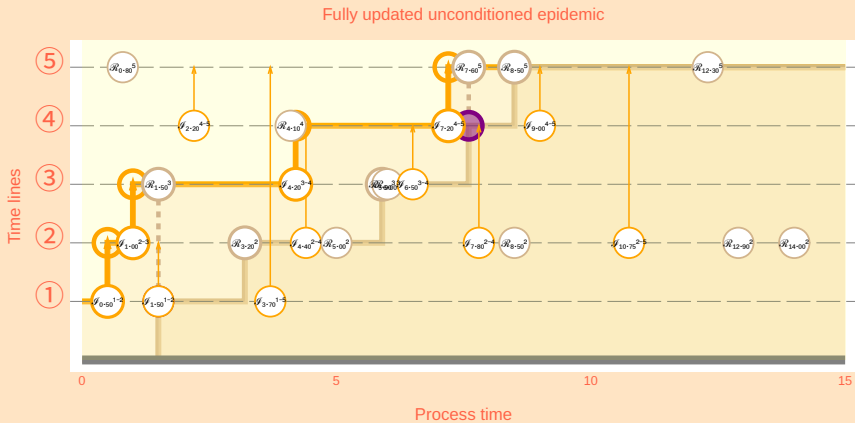


Figure 11: All infections now re-sampled.

# Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point).  
Consequently:
  - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

## Implications:

- ▶ a removal can be introduced only if it doesn't activate;
- ▶ a conditioned removal timeline can be altered only if it doesn't de-activate;
- ▶ an infection cannot be removed if that loses a conditioned removal;
- ▶ an infection can be introduced only if no new observed removals result.
- Does this produce a *feasible* and suitably monotonic algorithm?
- **Housekeeping details** required to establish that monotonicity still works.  
Key notions: *last feasible epidemic* (LFE) and *no-fly zone* (NFZ).

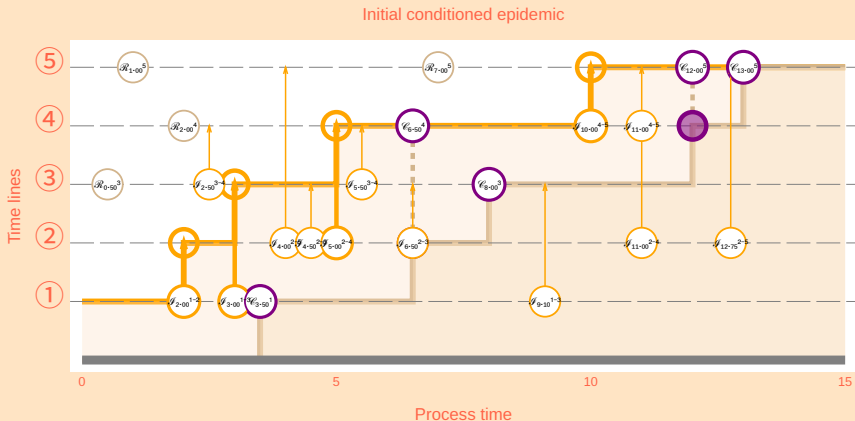


Figure 12: Initial epidemic with conditioned removals indicated using purple circles (and purple disks when different timelines are infected).



# Conditional epidemic update

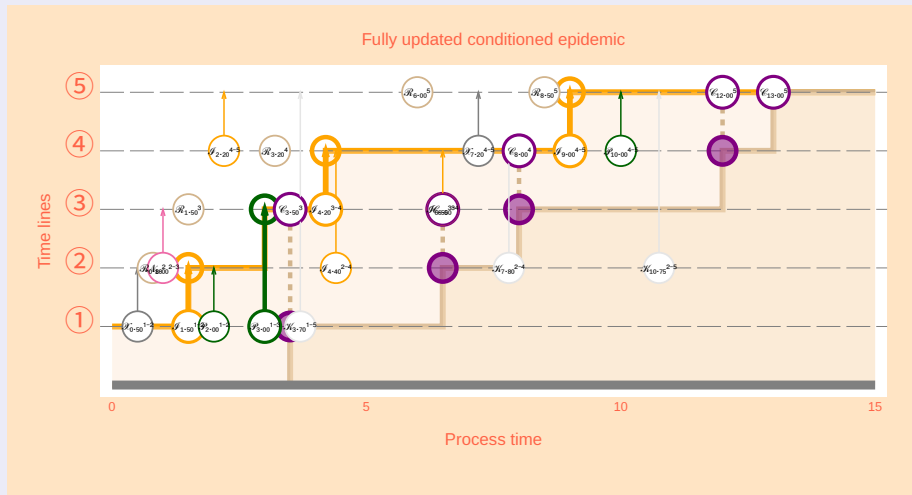


Figure 13: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

# Last feasible epidemic (LFE)

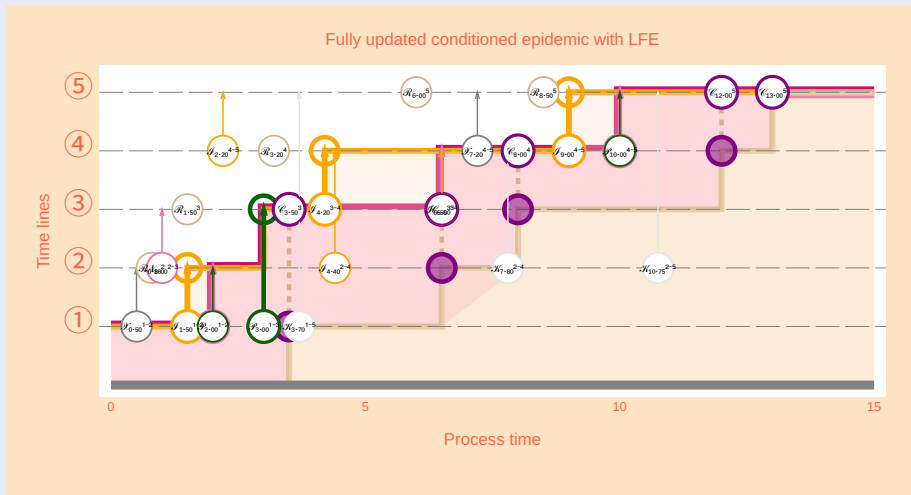


Figure 14: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

## Fully updated conditioned epidemic with NFZ

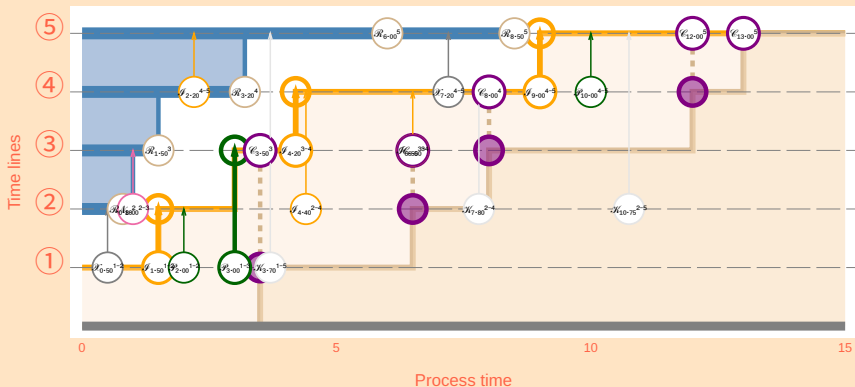
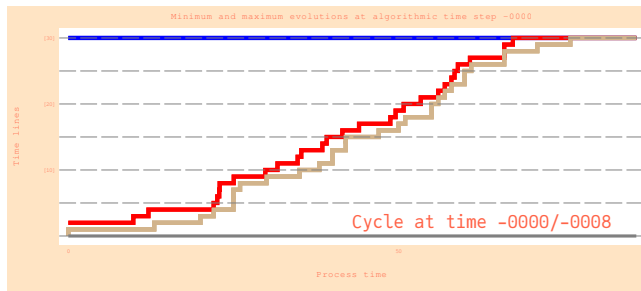


Figure 15: NFZ computed recursively working right-to-left: trace region of timelines that must not be infected if one is not to activate unobserved removals.

# Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see p. 125, [Bailey, 1975](#)).
- **Assume**
  - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives  $I_0$  at time 0;
  - ▶ *all* removals are recorded;
  - ▶ no further removals after last observed removal (makes life easier).
- Coding in *julia* ([Bezanson \*et al.\*, 2017](#)), we can construct a **perfect simulation GIF** yielding a draw from unobserved pattern of infections.



# So what?

- Why this emphasis on unobserved infections given fixed  $\alpha$  and  $\beta$ , when we need inference on R-number  $\alpha n/\beta$  for *unknown*  $\alpha$  and  $\beta$ ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different*  $\alpha$  and  $\beta$ . The perfect simulation provides exact simulation-based computation to integrate out pattern of unobserved infections.
- So (next steps after Connor & WSK, 2024)
  - ▶ estimate likelihood test statistic for specified  $\alpha$  and  $\beta$ ;
  - ▶ construct steepest ascent algorithm (in effect, variant of Robbins-Monro stochastic optimization) to find *maximum a posteriori* estimates of  $\alpha$  and  $\beta$ ;
  - ▶ or even, with some computational effort, compute the entire posterior joint density for  $\alpha$  and  $\beta$ !
- Finally: generalize to other suitable compartment models?

# Conclusion

- If MCMC burn-in is a concern, try to build a perfect simulation!
- CFTP works even for significantly complex and relevant models of real-life phenomena.
- *Of course* detailed models resist perfect simulation (but it will be helpful to compare with a simpler model using fewer parameters).
- Still to be done: statistical estimation of parameters, generalization to other compartment models.
- Thank you for your attention! **QUESTIONS?**



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# Technical information

Image	Attribution	
<i>Terry Pratchett</i> Classic CFTP for a simple random walk	Luigi Novi Result of code written by WSK	<i>CC BY 3.0</i>
<i>Diamond Princess</i> Epidemic CFTP images and animation	Alpsdake Result of code written by WSK	<i>CC BY-SA 4.0</i>

These notes were produced from `PerfectEpidemics.qmd`:

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Date:	Mon Jan 13 17:52:33 2025 +0000
Summary:	Added commentary.