

# Perfect Epidemics

## Applied Probability Seminar

Department of Statistics, University of Warwick

W S Kendall   S B Connor

Warwick, York

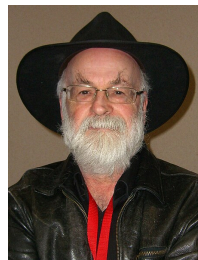
17 January 2025



# 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 is on the web: use the QR-code or visit  
[wilfridskendall.github.io/talks/PerfectEpidemics](https://wilfridskendall.github.io/talks/PerfectEpidemics).

This is initial work on using perfect simulation (CFTP) for epidemics.  
WSK acknowledges the support of UK EPSRC grant EP/R022100.

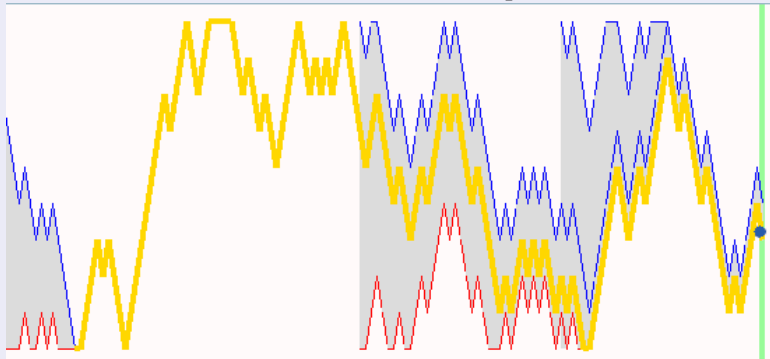
# 1: Introduction to Perfect Simulation

- 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)

- So now start at top (9) and bottom (0) at negative time  $-T$ , run to time 0.
- If not coupled by time 0, 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 (SBC & WSK, 2007a; *nb* corrigendum SBC & 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  $\beta I$ .

Both 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**?

## 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)

An important step on the way: generating an *unconditioned* epidemic.

- 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 First step: 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)

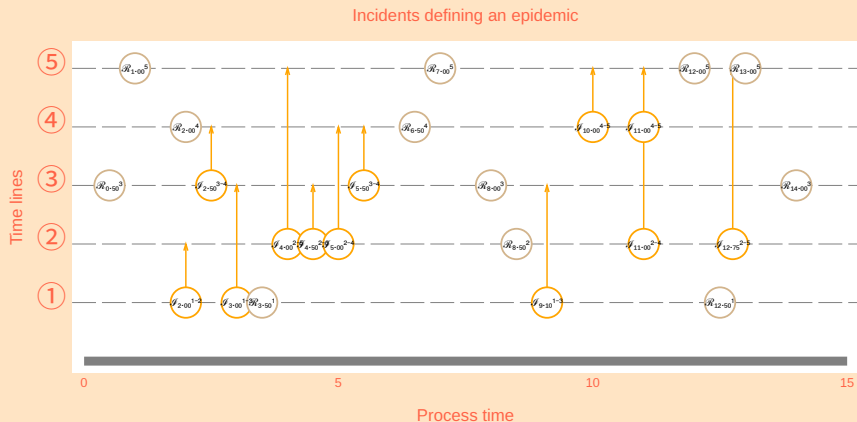


Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

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

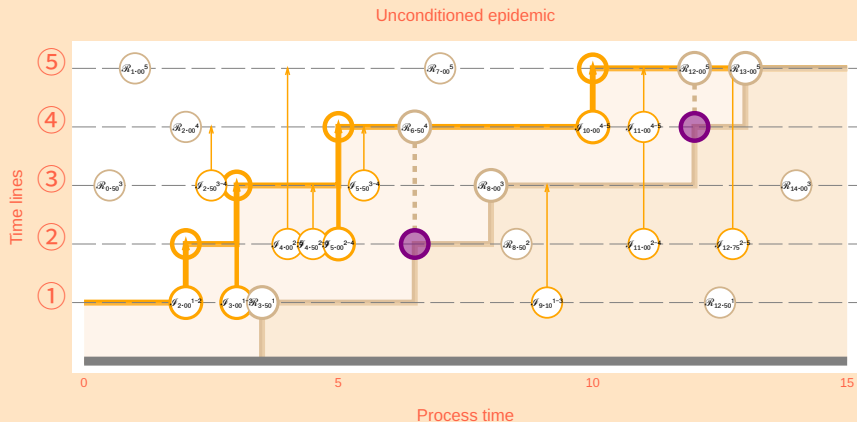


Figure 2: Activate (a) *infection* if target on lowest uninfected timeline; (b) *removal* if in infected region, then remove lowest infected (purple disk if different timeline).

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

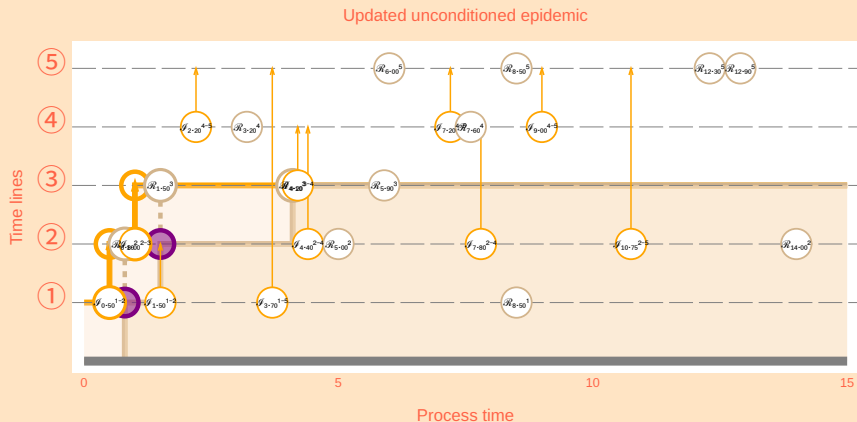


Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing the original incidents by a new set of incidents.

## Crucial technical point

- Updates in algorithmic time  $\tau$  are then (algorithmic-)*time-reversible*: so restriction to subset  $S$  of state-space (of *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:
  - ➊ Replace removals ( $R$ s);
  - ➋ Re-sample timelines (though not times) of  $R$ s;
  - ➌ Replace infections ( $I$ s).
- Re-express using continuously varying  $\tau$ . Process time runs over  $[0, T]$ .
  - ➊ For  $2nT < \tau < (2n+1)T$ , update old  $R$ s with times in  $(0, \tau - 2nT)$ ;
  - ➋ For  $\tau = (2n+1)T$ , resample timelines (not times) of  $R$ s;
  - ➌ 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)

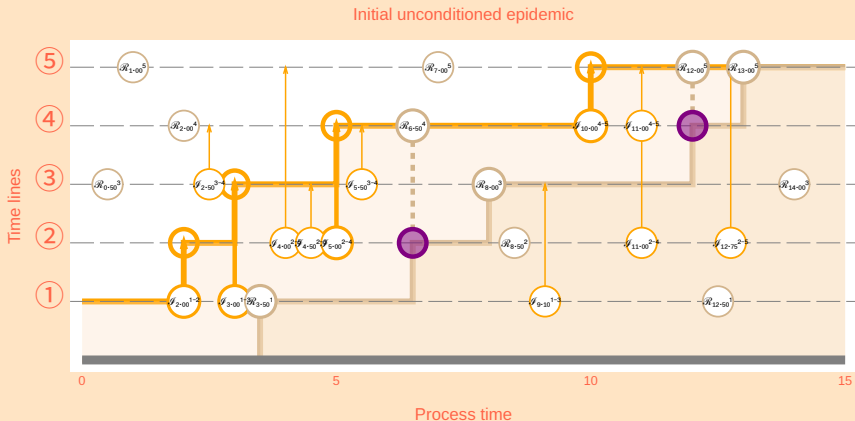


Figure 4: No change yet to removals or infections;

## Illustration of technical point (2/8)

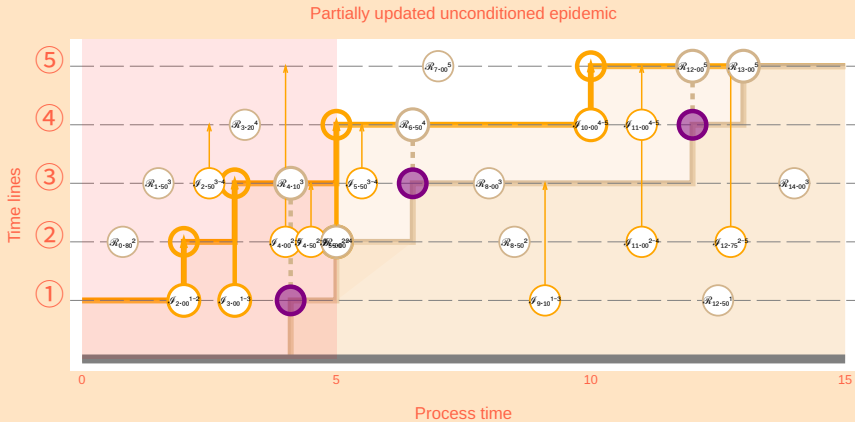


Figure 5: Replace first third of removals, infections unchanged;



## Illustration of technical point (3/8)

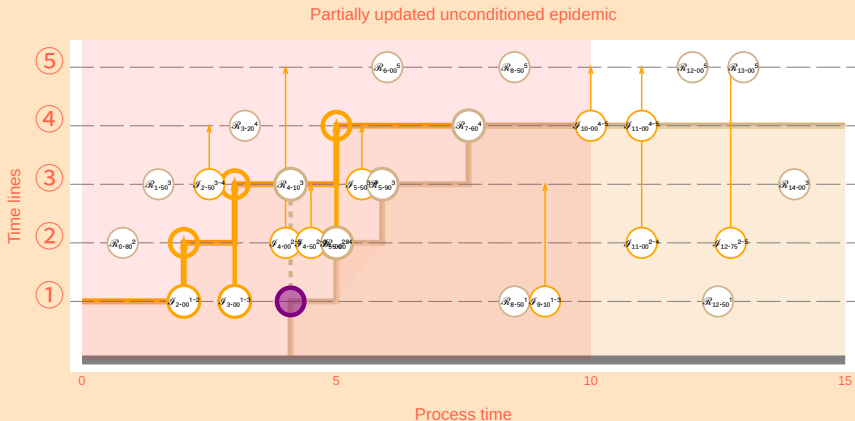


Figure 6: Replace first two-thirds of removals, infections unchanged;

## Illustration of technical point (4/8)

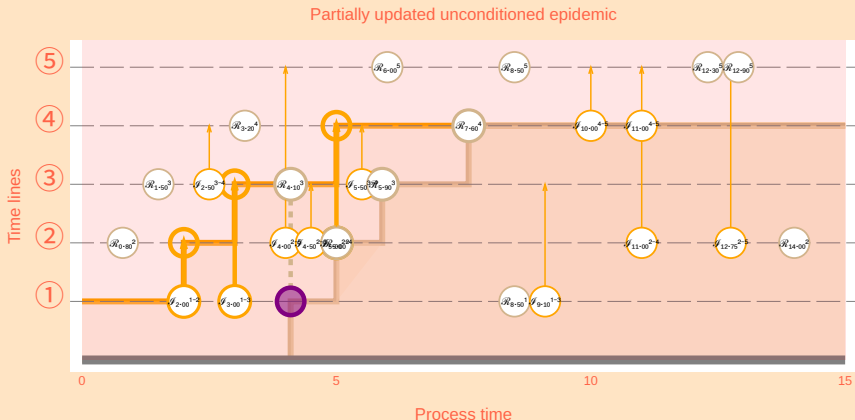


Figure 7: All removals resampled, infections as yet unchanged;

# Illustration of technical point (5/8)

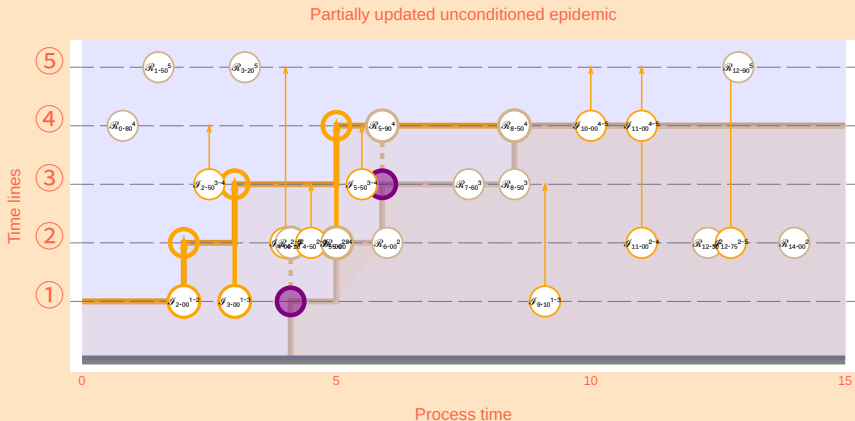


Figure 8: Re-sample all removal timelines, infections as yet unchanged;

# Illustration of technical point (6/8)

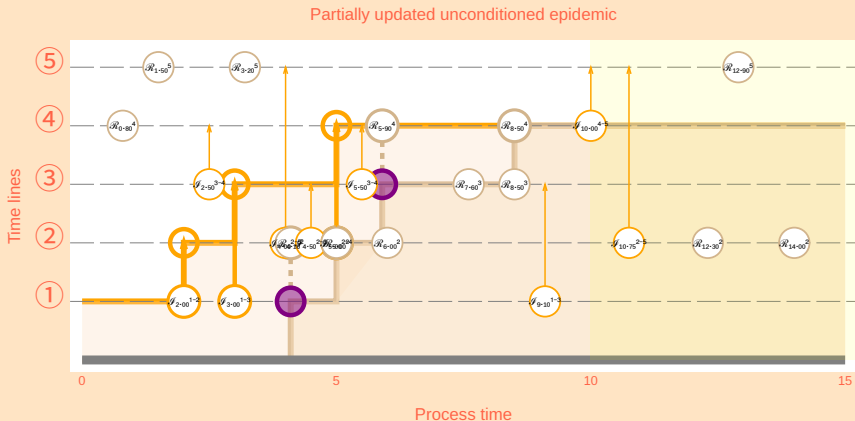


Figure 9: Re-sample last third of infections;

# Illustration of technical point (7/8)

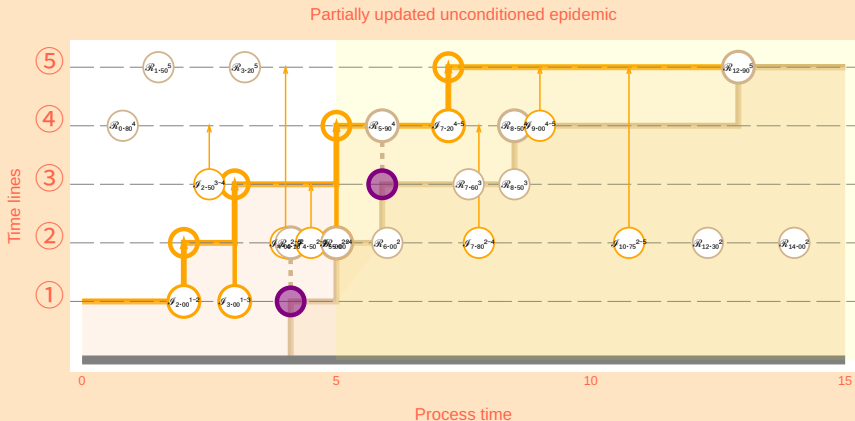


Figure 10: Re-sample last two-thirds of infections;

## Illustration of technical point (8/8)

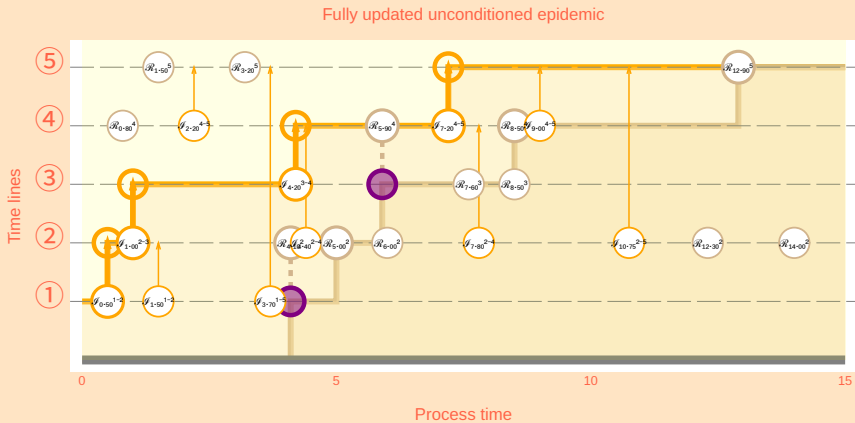


Figure 11: All infections now re-sampled.

# 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 action 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).

# Initial conditional epidemic

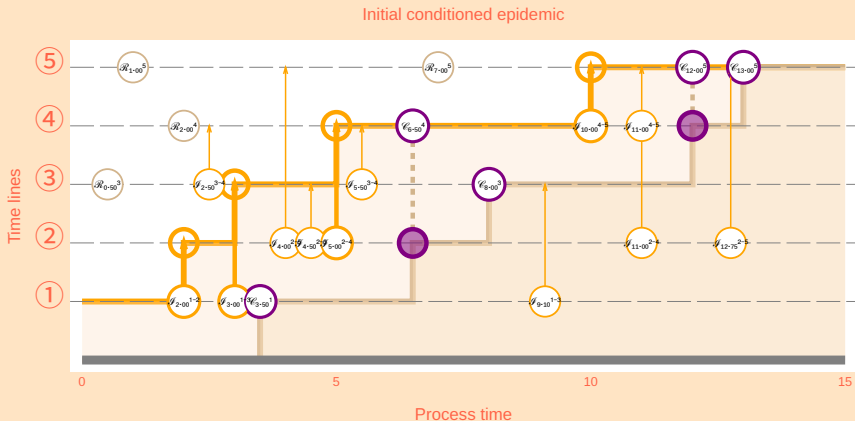


Figure 12: Initial epidemic with conditioned removals indicated using purple circles (and purple disks when different timelines are infected).



# Conditional epidemic update

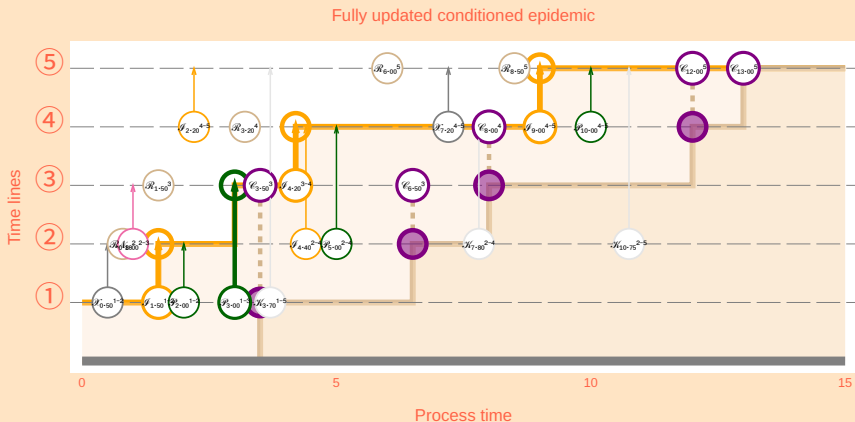


Figure 13: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

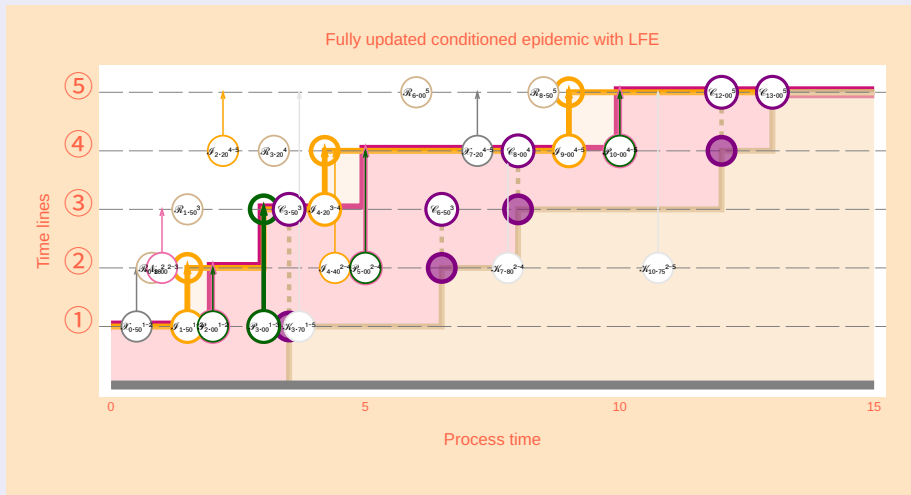


Figure 14: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

## Fully updated conditioned epidemic with NFZ

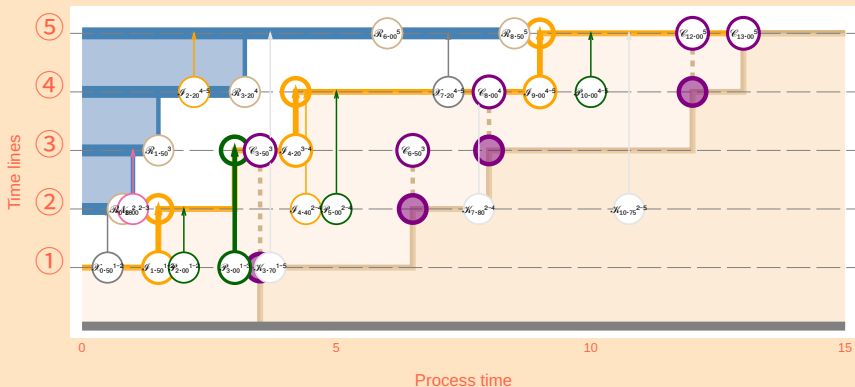
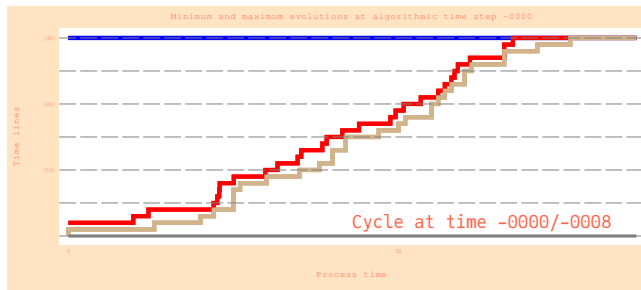


Figure 15: NFZ computed recursively working right-to-left: it traces the region of timelines that must not be infected if one is not to activate unobserved removals.

# Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of [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 **SBC & 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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## Image 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>

## Previous instances of this talk

Date	Title		Location
19/04/24	Perfect Epidemics	Short Research Talk (12min)	Warwick
15/05/24	McMC and Perfect Simulation	Graduate Seminar, Aristotle Univ. (50min)	Thessaloniki
17/01/25	Perfect Epidemics	Applied Probability Seminar (50min)	Warwick

# A “near-maximal” configuration

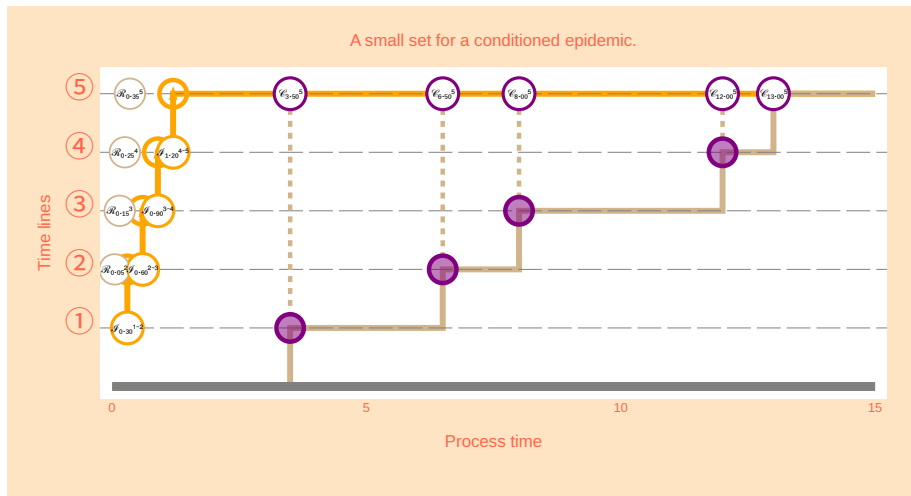


Figure 16: A conditional epidemic in which all activated infections occur before time 3.0, also before smallest observed removal time.

# Other technical information

## Software versions

Software used in computations:

<i>Software</i>	<i>Version</i>	<i>Branch</i>	<i>Date of last commit</i>
Quarto	1.6.39	—	
Running under julia	1.11.2	—	
Module EpidemicsCFTP	2.2.487	main	Fri Jan 10 20:17:28 2025
Module EpidemicsUtilities	0.1.2.154	main	Wed Jan 15 13:23:36 2025
This Quarto script	2.2.589	master	Fri Jan 17 16:59:04 2025

## Revision history

These notes were produced from PerfectEpidemics.qmd:

Author: Wilfrid Kendall [W.S.Kendall@warwick.ac.uk](mailto:W.S.Kendall@warwick.ac.uk)

Date: Fri Jan 17 16:59:04 2025 +0000

Summary: This version has edits arising from the 17/1/2025 talk in Warwick.  
2.2.589