

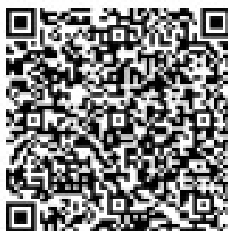
# Perfect Epidemics

Applied Probability Seminar  
Department of Statistics, University of Warwick

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Warwick, York

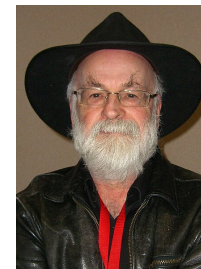
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## Introduction

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

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## Perfect Epidemics

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### 1: Introduction to Perfect Simulation

Here’s a very brief summary of CFTP / perfect simulation.

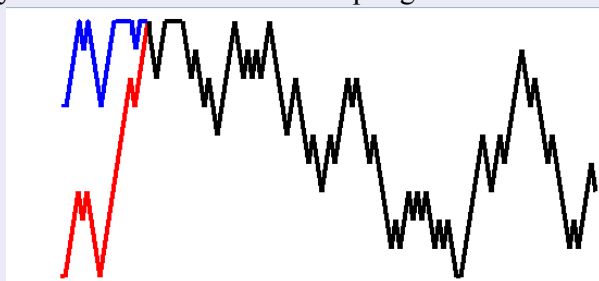
1. Jim Propp described the discovery of CFTP as like walking down the street and suddenly noticing a 50\$ bill lying on the ground.
2. In particular, “exact simulation” cannot somehow miraculously defeat numerical approximation error :-).
3. We will cover these key ideas in a single very specific example.
4. Propp & Wilson (1996) show how to vary random walk CFTP to get exact samples for a *critical* Ising model (Persi Diaconis: “Like seeing the landscape of Mars for the first time”). The Ising model with an external field can be used to model images, hence CFTP can be used for image reconstruction.

#### 1: Introduction to Perfect Simulation

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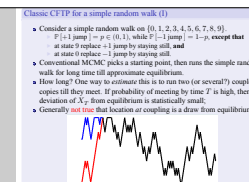
## Classic CFTP for a simple random walk (I)

- 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.



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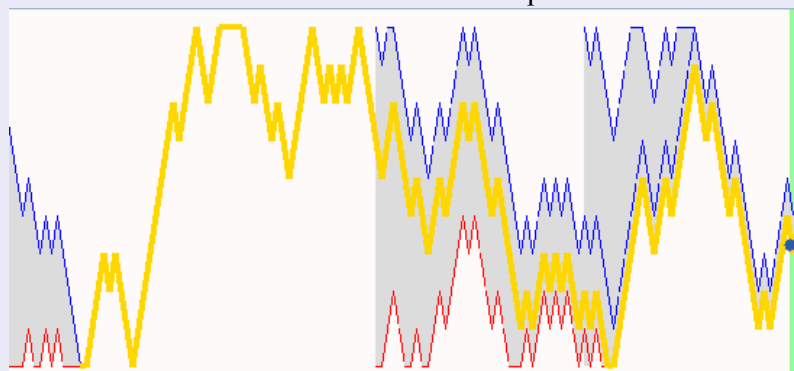


This random process is asymmetric simple random walk on the integers, but forbidding any transitions outside the specified state-space.

- The process is irreducible and aperiodic, so equilibrium is a truncated Geometric distribution (hint: use reversibility to check this!).
- Conventional MCMC is overkill here, of course: we could simulate directly from the equilibrium distribution.
- This observation was originally formalized by Aldous. Here we use 'synchronous coupling – variants are possible but not particularly useful.
- Clearly not true in our case: coupling can only occur at 0 or 9!
- In this case the blue and red evolutions can only couple at a boundary, so self-evidently the value at time of coupling cannot be a draw from the equilibrium!

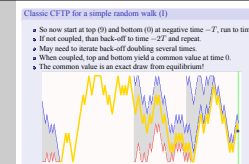
## Classic CFTP for a simple random walk (I)

- So now start at top (9) and bottom (0) at negative time  $-T$ , run to time 0.
- If not coupled, than 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!



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- Ideally one needs to choose  $T$  neither too small nor too large. But the result is not particularly sensitive to this.
- Very important that one doesn't introduce different jumps for the same time  $-t$  in this binary back-off! We must **re-use randomness**.
- The binary back-off procedure means, if  $T$  is initially set to be too small then the extra work that is required is only ever a factor of 4!
- Re-use of randomness means there is now no point in continuing: the common value at time 0 will be the same however far we extend into the past with further back-offs.
- Why is the common value an exact draw from equilibrium? Informally, because one would get the same result however far one backed-off: therefore the draw is effectively a draw from time  $-\infty$ . The golden thread can be viewed as a perfect draw from the last segment of such a simulation (this sort of device is very well-known to ergodic theorists). Remarkably, this can easily be converted into a fully rigorous proof!

## 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.)

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## 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

$$\begin{aligned}\text{Infection: } S &\rightarrow S - 1, \quad I \rightarrow I + 1 & \text{at rate } & \alpha S I, \\ \text{Removal: } I &\rightarrow I - 1, \quad R \rightarrow R + 1 & \text{at rate } & \beta I.\end{aligned}$$

These models make an **unrealistic assumption**: **homogeneous mixing**.

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## Perfect Epidemics

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

(Locally finite) point processes cannot in general be treated using Classic CFTP, because the "top" pattern would have points *everywhere*. More generally, the "in principle" results encourage us to try CFTP out on a wide variety of models (For example, for  $M/G/k$  multiserver queues, Connor & WSK, 2015; Connor, 2020).

1. To be computationally effective, the WSK (1998) fixes still require some associated notion of partial order and (perhaps weak) amenability of the dominating process.
2. Basic ideas: use the notion of regenerative sets ("small sets"), and (Foster-)Lyapunov arguments. Note that the recipes given for these tend not to be computationally practical: they simply show the possibility of (possibly computationally infeasible) CFTP. They are intended as a challenge: when can one find *practical* methods?
3. This is the end of the visual introduction to CFTP. People who are interested in CFTP from a practical point of view may find it useful to work through WSK (2015).

2: A short section on some theory about CFTP

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

Here are two classical models (one deterministic, one stochastic) from mathematical epidemiology. Even the exceedingly simple case of deterministic S-I-R permits only *partial* closed-form solution.

The assumption of homogeneous mixing of population greatly simplifies the mathematics *and* statistics. Without this assumption one ends up with huge numbers of parameters, which is very bad news statistically speaking. A lot of research has been done on how to deal with more realistic models! (For example, the UK model using 1000000 agents mentioned here!)

However in this work we deal only with perfect simulation for homogeneous mixing. Before running, one must learn to walk!

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):

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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.



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## 4: Inference on the R-number

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

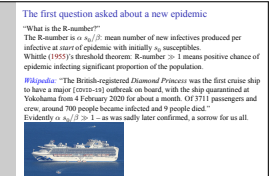
- 1 Modelling is **tough**. *Either* massive assumptions (homogeneous mixing) *or* very many parameters;
- 2 Inference is **really tough**: hard to get information about infection times;
- 3 It is all **especially tough** in early stages. Answers are most needed when hardly any information is available (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**?

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### — The first question asked about a new epidemic



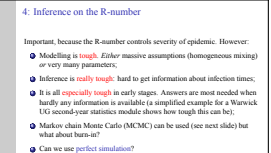
I am skipping over very influential early work on this incident, which particularly focussed on the incubation period (a time when the subject is infectious, perhaps at time-varying rate, before symptoms appear). This is related to drawing inferences about  $\beta$ .

See Mizumoto *et al* (2020) for very early analysis of the *Diamond Princess* outbreak.

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### — 4: Inference on the R-number



The “R-number” was the subject of continuing interest throughout the COVID-19 pandemic!

Notice that the “R-number” is as much a social construct as a biological one, and in real situations will interact in subtle and complicated ways with behaviour.

We will seek 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)

- 1 Thus  $n$ ,  $\alpha$ ,  $\beta$  are known, removal times are observed, but unobserved infection times **must be inferred**.
- 2 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.
- 3 Poisson point processes of appropriate rates yield an S-I-R epidemic.
- 4 Evolve whole S-I-R trajectory in *algorithmic time* (alter potential infections and removals using immigration-death in discrete algorithmic time).
- 5 Result: *trajectory-valued chain*, unconditioned S-I-R as equilibrium.

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

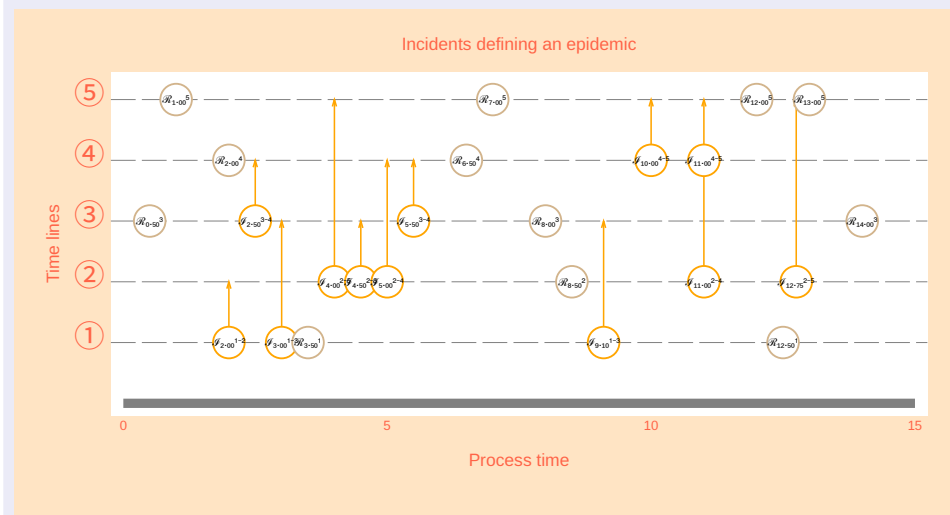


Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

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### 5: An easier question

1. Instead of trying to tackle inference concerning the parameters, let's concentrate on the large number of nuisance parameters provide by (typically unobserved) infection times.
2. This is a compromise: instead of tracking individuals as in the stochastic epidemic model, we effectively track the numbers of individuals in various categories.
3. Poisson point processes generate incidents, which then collectively influence the S-I-R trajectory.
4. I learned the phrase “algorithmic time” from Andrew Stuart. We move from Poisson points spread out along timelines to discrete immigration-death processes producing patterns that evolve in algorithmic time.
5. But we shall quickly move to *continuous* algorithmic time.

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Colour-coding distinguishes infections from deaths. Note that infections need to specify which timeline is going to be infected.

- For an infection incident to be activated, it must sit on an infected portion of its timeline and must point to the least of the uninfected timelines (calculating at the process time of the incident).
- For a removal incident to be activated, it must sit on an infected portion of its timeline.

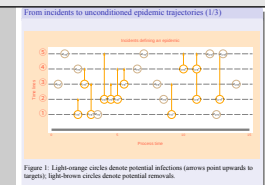


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## From incidents to unconditioned epidemic trajectories (2/3)

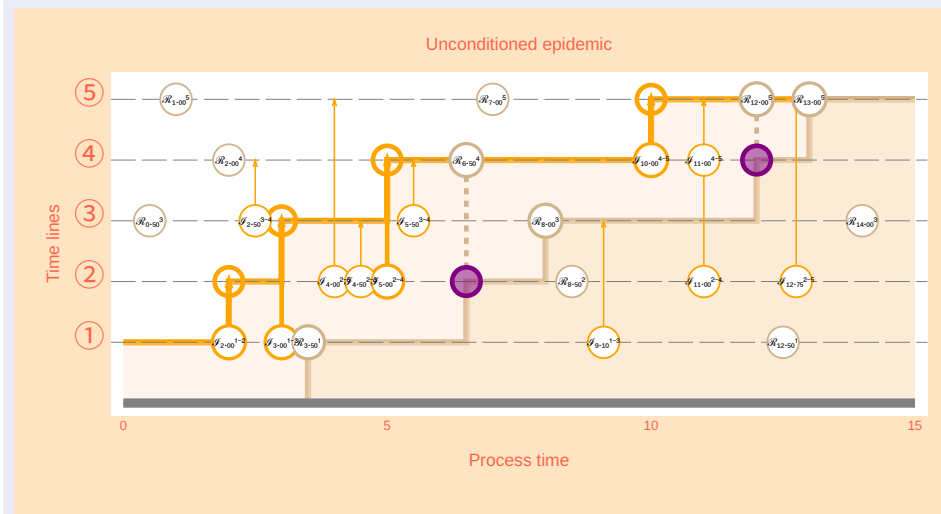
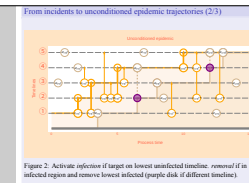


Figure 2: Activate *infection* if target on lowest uninfected timeline. *removal* if in infected region and remove lowest infected (purple disk if different timeline).

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Here is the resulting evolution of an epidemic. Note however that we need to specify the initial number of infectives (here we specify  $I_0 = 1$ ).



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

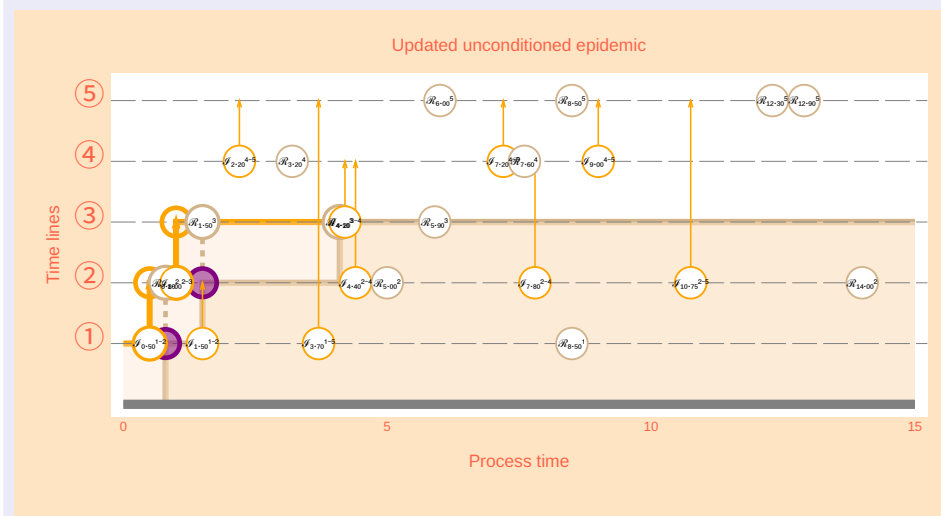
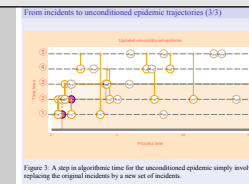


Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing the original incidents by a new set of incidents.

## Perfect Epidemics

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An update in algorithmic time, if there is no conditioning, simply involves replacement of one set of incidents by another.





## 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.)

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## Perfect Epidemics

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### Crucial technical point

In the case of discrete algorithmic time, it seems that arranging for conditioning would involve horrendous computation. Instead we “unroll” into continuous algorithmic time.

Intuitively, we analyze first removals and then infections “pixel-by-pixel” along the process time axis.

It turns out to be convenient to work forwards in time for removals, then backwards in time for infections – and to re-assign random timelines (but not times) for removals in between these two phases.

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  $S$ .
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## Illustration of technical point (1/8)

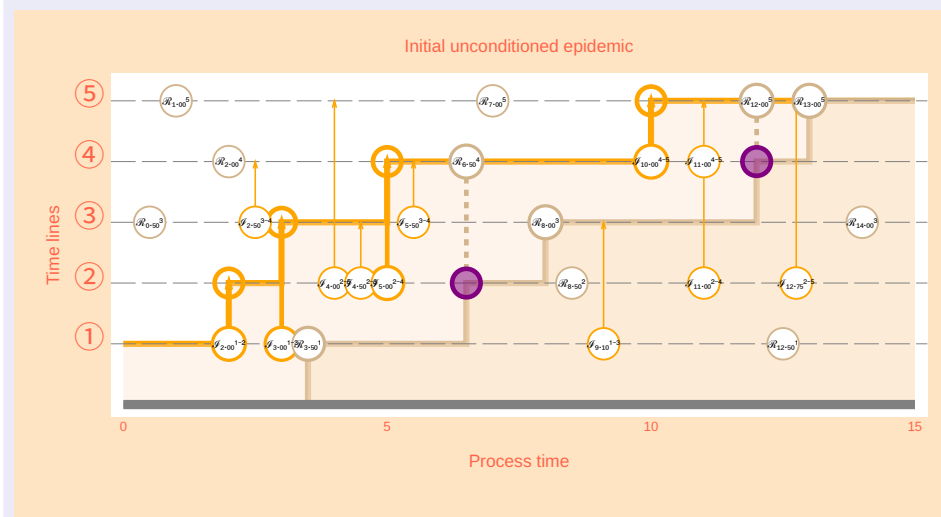


Figure 4: No change to removals or infections

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Here is the initial configuration again.

Illustration of technical point (1/8)

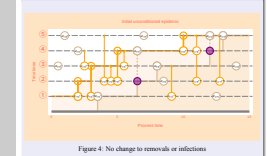


Figure 4: No change to removals or infections

## Illustration of technical point (2/8)

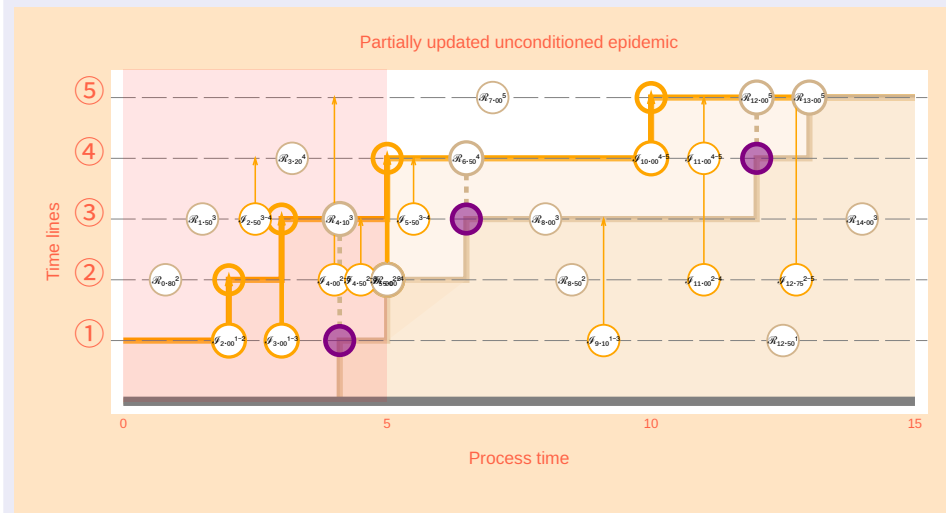
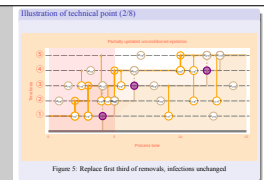


Figure 5: Replace first third of removals, infections unchanged

## Perfect Epidemics

Now we use the immigration-death process of removals to work along the process-time axis removing old removals and adding new ones. At present we are not applying conditioning. Here we are 1/3 of the way through dealing with removals.



## Illustration of technical point (3/8)

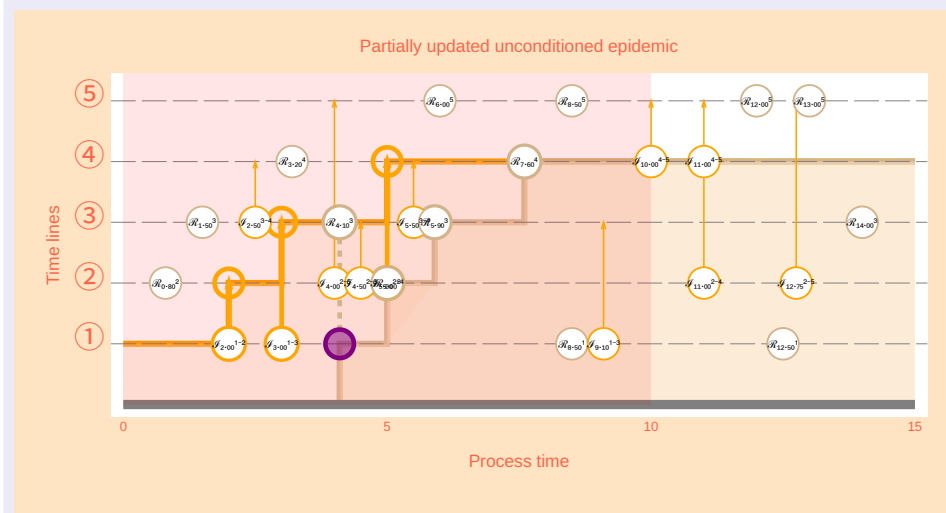
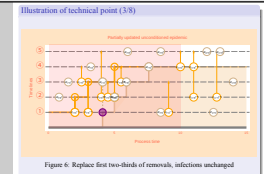


Figure 6: Replace first two-thirds of removals, infections unchanged

## Perfect Epidemics

Here we are 2/3 of the way through dealing with removals.





## Illustration of technical point (4/8)

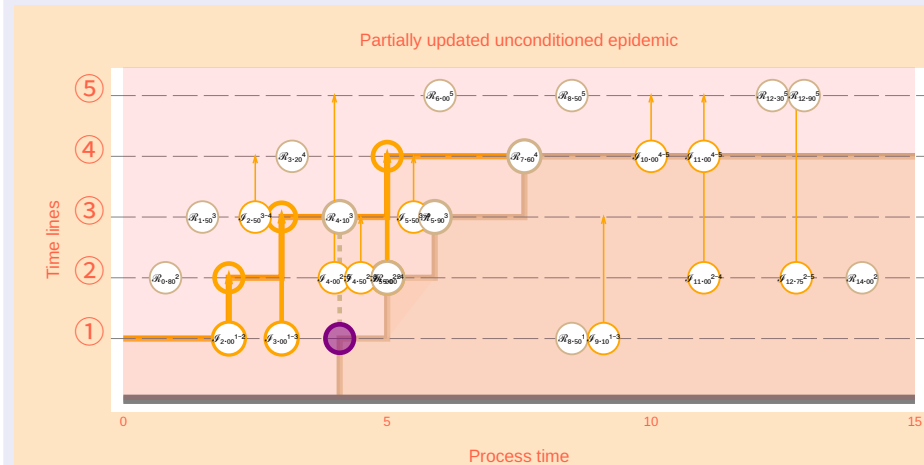


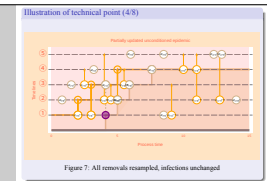
Figure 7: All removals resampled, infections unchanged

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All removals have now been processed. Because we are not yet conditioning, all old removals have now been removed, and all new removals have been added.

Notice that nothing was done for this simulation in the last 1/3 of removal work, not surprising since most timelines were by then removed, and so there isn't much scope for removals to arrive.



## Illustration of technical point (5/8)

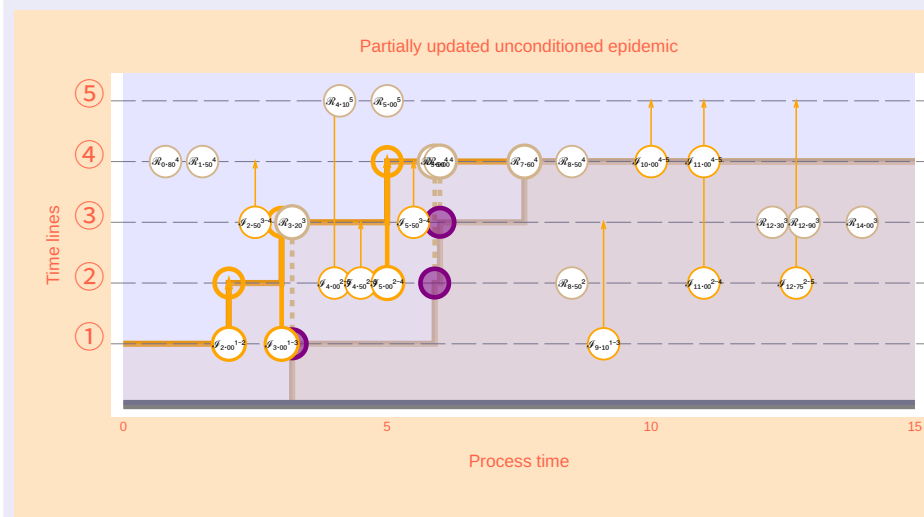


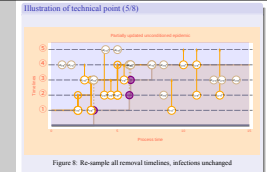
Figure 8: Re-sample all removal timelines, infections unchanged

## Perfect Epidemics

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At this stage we now re-sample the timelines for all removals. Since we are not conditioning, this results in a big change.

1. When we proceed to consider conditioning on observing certain removals, the observed ("conditioned") removals will not have been moved so far (their removal will have been rejected!) but at this stage the change in timeline will be accepted if the dynamics do not then lead to a change in conditioned removals.
2. On the other hand, timeline-resampling for an inactivated removal will be rejected if it leads to that removal being activated, but statistically the effect will be the same as if it wasn't re-sampled.



## Illustration of technical point (6/8)

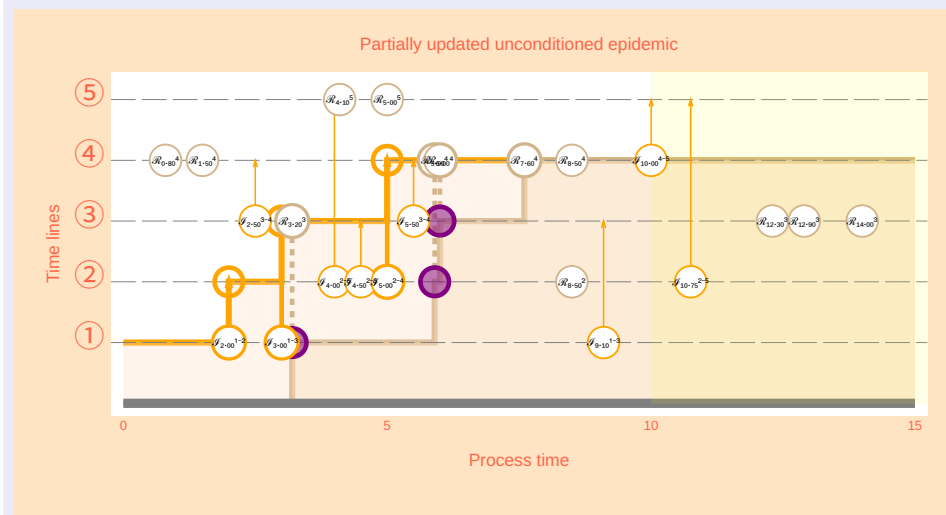
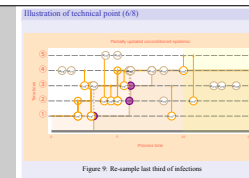


Figure 9: Re-sample last third of infections

## Perfect Epidemics

2025-01-15

Now we resample infections, but this time working backwards through process time. Here is how matters stand after 1/3 of the work is done. Again, there is little scope for anything to be done yet: one infection has been dropped.



## Illustration of technical point (7/8)

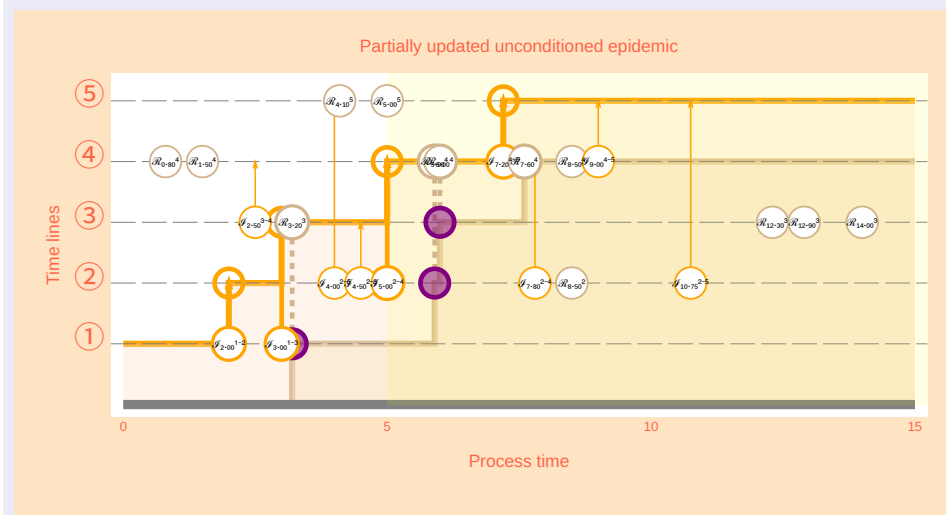
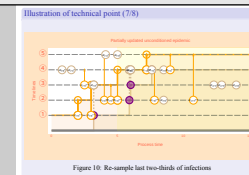


Figure 10: Re-sample last two-thirds of infections

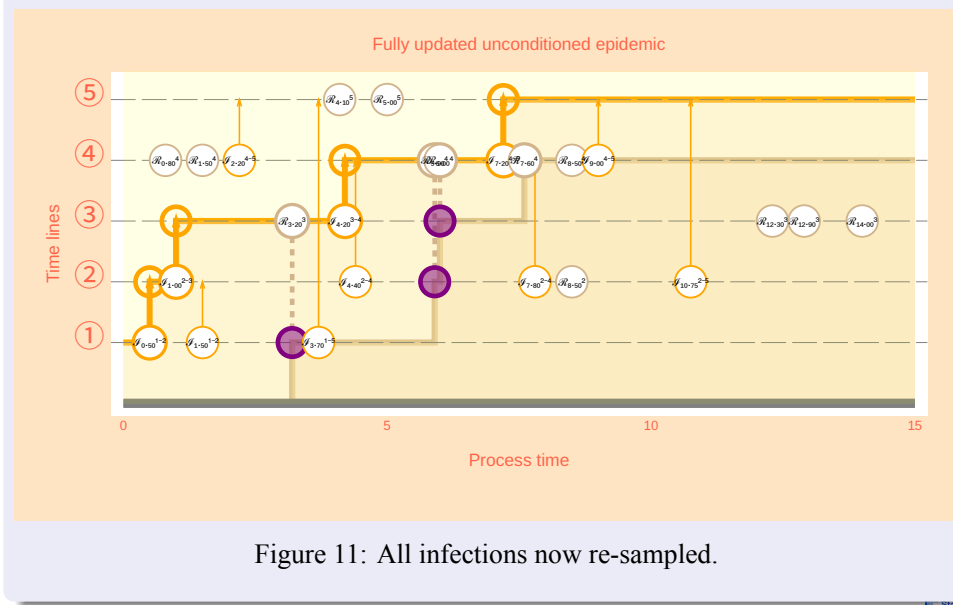
## Perfect Epidemics

2025-01-15

And here is how matters stand after 2/3 of the work is done. There is a lot more change here.

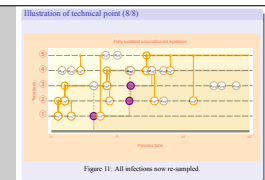


## Illustration of technical point (8/8)



## Perfect Epidemics

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Finally the entire process time range is dealt with. In this unconditioned case all removals and infections are removed and replaced by new ones. Under conditioning, however, each individual decision (to remove, resample, or introduce) has to be tested to see if it affects the pattern of conditioned removals. We now need to consider how to do this efficiently, but also in a manner that allows us to reason about the crucial monotonicity.

## 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)*.

## Perfect Epidemics

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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)*.

Monotonicity is a key concept here. (Note however that we can still sometimes generate perfect simulation algorithms even when monotonicity does not obtain: we don't need to do this here but should bear it in mind for more general problems in the future.)

- We can also deal with "unbounded" sample space using the notion of Dominated CFTP.
- The heart of the matter lies in establishing (some variant of) monotonicity.
- Additionally, for a complicated algorithm such as this one, it is important to test the underlying logic by implementing the algorithm in computer code (which has a way of revealing false hidden assumptions!).

## Initial conditional epidemic

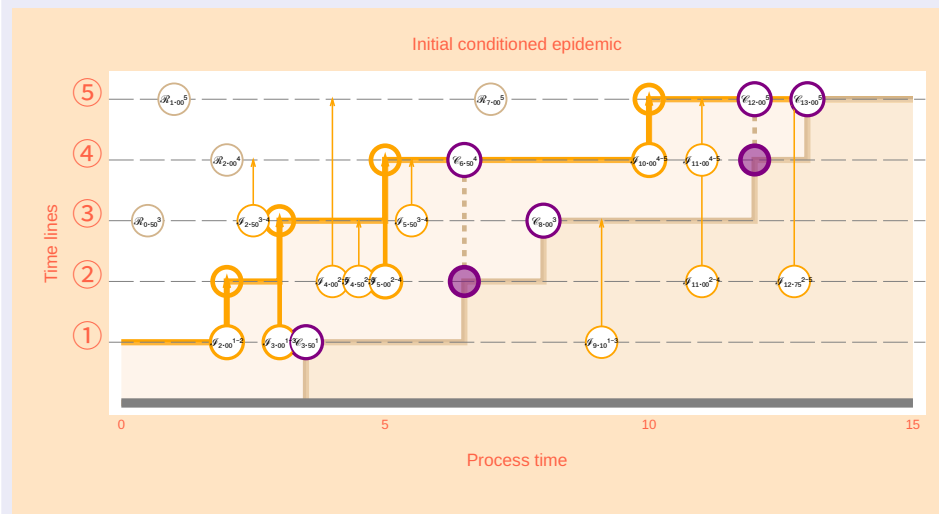


Figure 12: Initial epidemic with conditioned removals indicated using purple circles (and purple disks when different timelines are infected).

## Perfect Epidemics

2025-01-15

Here is a slightly different initial epidemic, which includes *conditional removals*, indicated by purple circles.

- Essentially we change it in the same way as in the unconditioned case (working “pixel-by-pixel”), but forbidding any change if that breaks conditioning.
- Dealing with removals is easy: it amounts to removing all inactivated removals and replacing them with a new bunch, and then resampling the conditional removal timelines, accepting only those changes which do not de-activate the conditional removals.
- But we need to take more care about whether or not we can take away or add in *infections*.

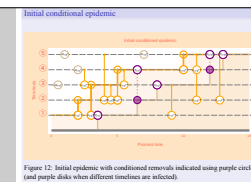


Figure 12: Initial epidemic with conditioned removals indicated using purple circles (and purple disks when different timelines are infected).

## Conditional epidemic update

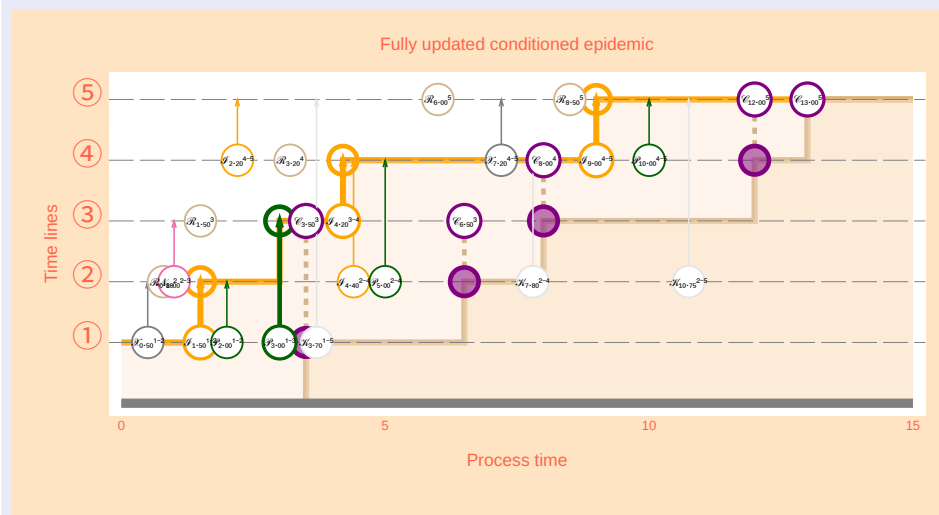


Figure 13: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

## Perfect Epidemics

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Here is the result of the update, which we now explain general terms. We have noted removals are easy. Re-sampling the conditioned removal timelines is a simple accept-reject step for each conditioned removal.

The key to dealing with infections that target the infected region is also rather simple:

1. Always add them (because it won't make a difference).
2. Delete them only if it is clear that this will not result in a conditioned removal falling out of the infected region.
3. Implementation amounts to referring to a recursively-defined *last feasible epidemic* (LFE). The LFE coincides with the actual epidemic trajectory exactly when deletion of the infection in question will lead to a conditioned removal falling out of the infected region; therefore this deletion is rejected and the retained infection is designated as *perpetuated* (coloured green!). Otherwise the infection can be deleted.
4. Infections targetting the susceptible region are trickier, and we will discuss them briefly below.

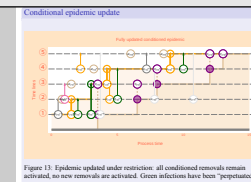


Figure 13: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

## Last feasible epidemic (LFE)

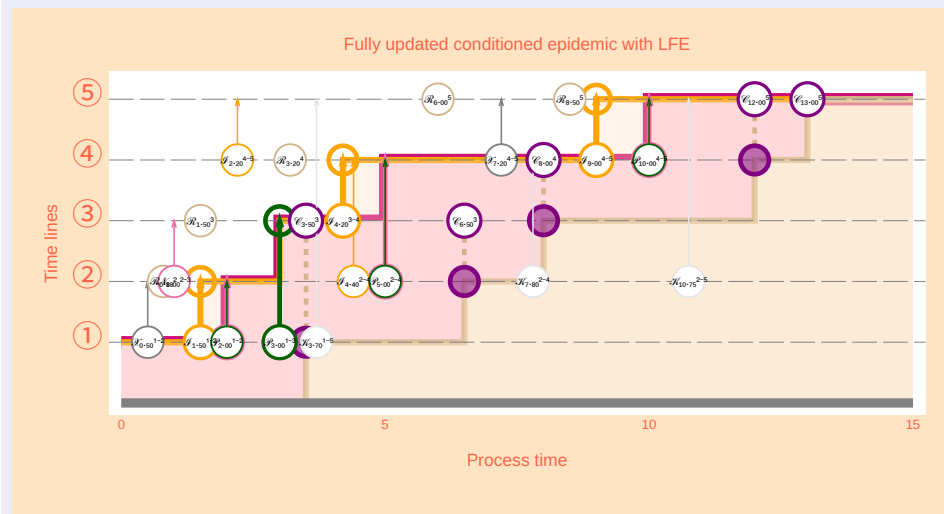


Figure 14: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

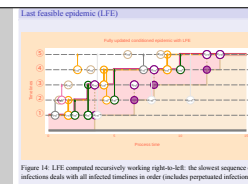
## Perfect Epidemics

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First we draw the LFE. Because it is defined recursively working backwards in process time, it can be computed in entirety from the updated conditional epidemic.

- Of course, when computing the update, we have to compute it set-by-step when working backwards in process time.
- Here there are three discrepancies between LFE and epidemic trajectory, over intervals [1.5, 2.0], 4.2, 6.5, and [9.0, 10.0].
- At times 2.00 and 3.00 there are perpetuations (an old infection has to be retained to ensure conditioning is not broken); at the second time 3.00 the perpetuation ends up forming part of the epidemic trajectory.

A relatively simple induction argument shows that the LFE depends monotonically on the epidemic trajectory!



## No-fly zone (NFZ)

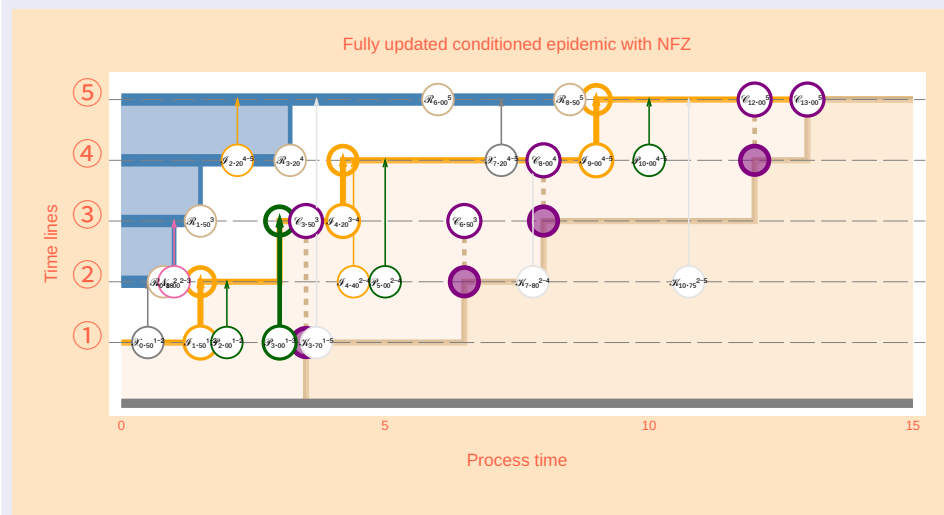


Figure 15: NFZ computed recursively working right-to-left: trace region of timelines that must not be infected if one is not to activate unobserved removals.

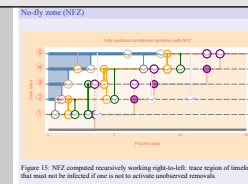
## Perfect Epidemics

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The NFZ applies to determine whether to allow introduction of infections which target the susceptible region. Things are a bit more complicated than for the LFE, as there are two phenomena to bear in mind.

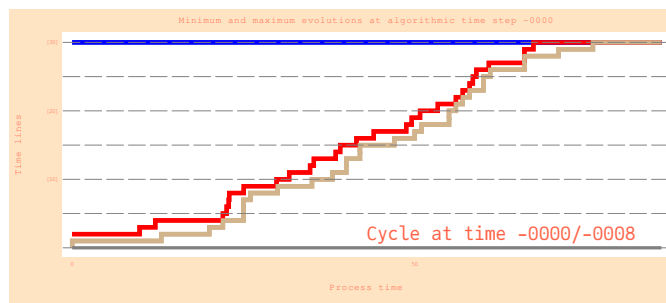
1. An infection rooted in the infection zone must be assessed to see whether its introduction would lead to activating a removal, because it connects the infectious zone to a timeline which would lead to such an activation (a “no-fly” portion of the timeline).
2. An infection rooted in the susceptible zone may be such that it makes a portion of its timeline *before* its time into “no-fly”.

The NFZ is a recursive evaluation of such “no-fly” regions, working backwards in process time. A more involved induction argument shows that the NFZ depends monotonically on the epidemic trajectory. One can then demonstrate that algorithmic-time evolution of the conditioned epidemic is monotonic: hence CFTP is feasible!



## 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.



Statistics

## So what?

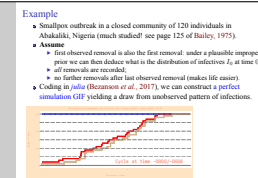
- Why this emphasis on unobserved infections given fixed  $\alpha$  and  $\beta$ , when we need inference on R-number  $\alpha n/\beta$  for *unknown*  $\alpha$  and  $\beta$ ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different*  $\alpha$  and  $\beta$ . 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?

Statistics

## Perfect Epidemics

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### Example



We could vary the assumption concerning the initial and final numbers of infectives while still using essentially the same perfect simulation algorithm! This amounts to presuming some Bayesian prior knowledge.

- How do we allow for the (unobserved) number of initial infectives being unobserved?
- Use an independence sampler: draw from the (unconditioned) number of initial infectives, accept if this leads to observed removals exactly at the list of conditioned removals.
- (One can alternatively employ a random-walk Metropolis sampler, so long as the prior for the initial number of infectives is suitably monotonic.)

### Technical note:

The simulation implementation uses *julia* ([Bezanson et al., 2017](#)), which combines rapid development, an expressive syntax (very useful for involved algorithms), and remarkably fast execution using very good “just in time” compi-

## Perfect Epidemics

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### So what?

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  - ▶ or even, with some computational effort, compute the entire posterior joint density for  $\alpha$  and  $\beta$ !
- Finally: generalize to other suitable compartment models?

In effect, perfect simulation supplies a well-behaved stochastic integration mechanism, reducing an MCMC algorithm to use a technique equivalent to a much more amenable Monte Carlo calculation. Other compartment models presenting varying degrees of challenge:

1. Split population into a small number of interacting sub-populations;
2. (For purposes of insight even if impractical.) Treat each individual as a sub-population on its own;
3. Allow parameters to change at specific times of day or week;
4. Allow for some activated removals to be unobserved!



# 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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## Conclusion

Lots still to do!

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Image information

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

A “near-maximal” configuration

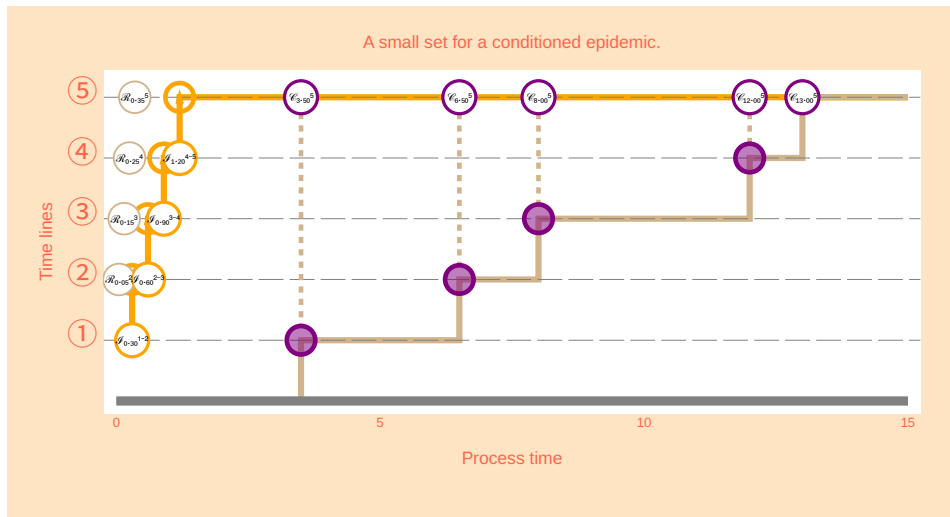
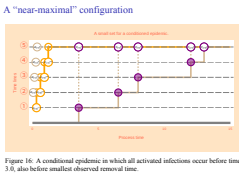


Figure 16: A conditional epidemic in which all activated infections occur before time 3.0, also before smallest observed removal time.

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A “near-maximal” configuration



1. For a “near-maximal configuration”, we set relevant infections to occur in order on or before a fixed small time  $\delta = 1.5 > 0$ , where  $2\delta$  is smaller than any of the conditioned removal times.
2. All inactivated removals have to occur before their respective infections (in order to avoid activation).
3. Variants on this construction can be used to show that CFTP for the perfect epidemic must coalesce in finite time;
4. However to get a sensible stochastic bound on coalescence time would require a lot more work!

# Other technical information

## Software versions

Software used in computations:

Software	Version	Branch	Date of last commit
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	2.2.585	master	Wed Jan 15 16:27:48 2025

## Revision history

These notes were produced from PerfectEpidemics.qmd:

Author:	Wilfrid Kendall <a href="mailto:W.S.Kendall@warwick.ac.uk">W.S.Kendall@warwick.ac.uk</a>
Date:	Wed Jan 15 16:27:48 2025 +0000
Summary:	Editing for style. Added appendix on near-maximal configuration.

Statistics