Perfect Epidemics

2nd Workshop, UK Research Network in Stochastics
University of Liverpool

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Introduction

"Once we came to accept the photographic image as reality, the way to its future simulation was open."
[Lev Manovich]

Handout is on the web: use the `QR-code` or visit
`wilfridskendall.github.io/talks/PerfectEpidemics`.

Work on perfect simulation (CFTP) for epidemics, now being written up.
WSK acknowledges the support of UK EPSRC grant EP/R022100.

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1. Introduction to Perfect Simulation

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

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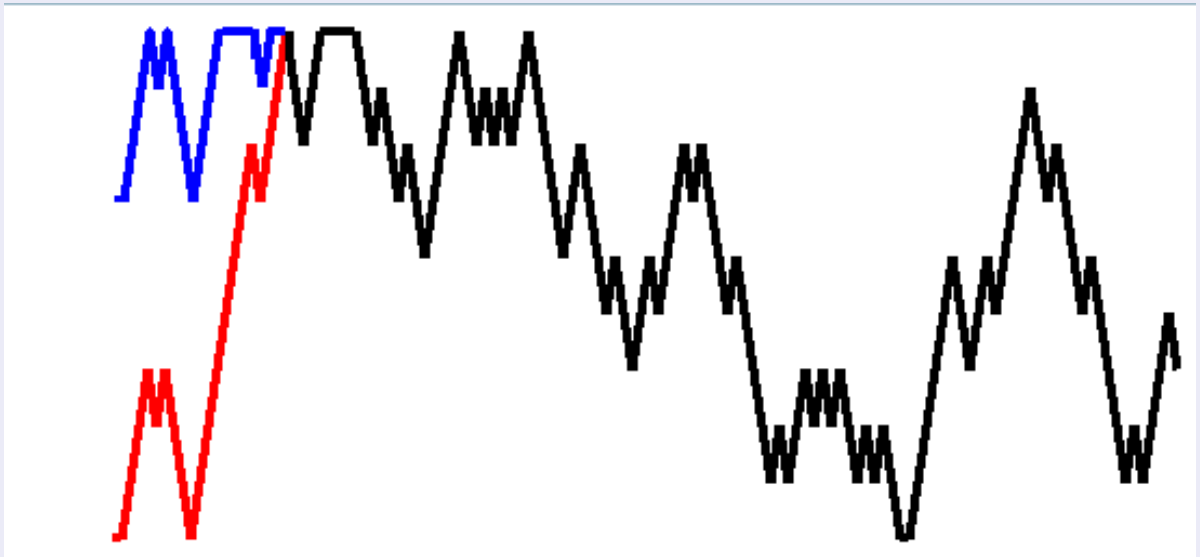
Classic CFTP for a simple random walk (I)

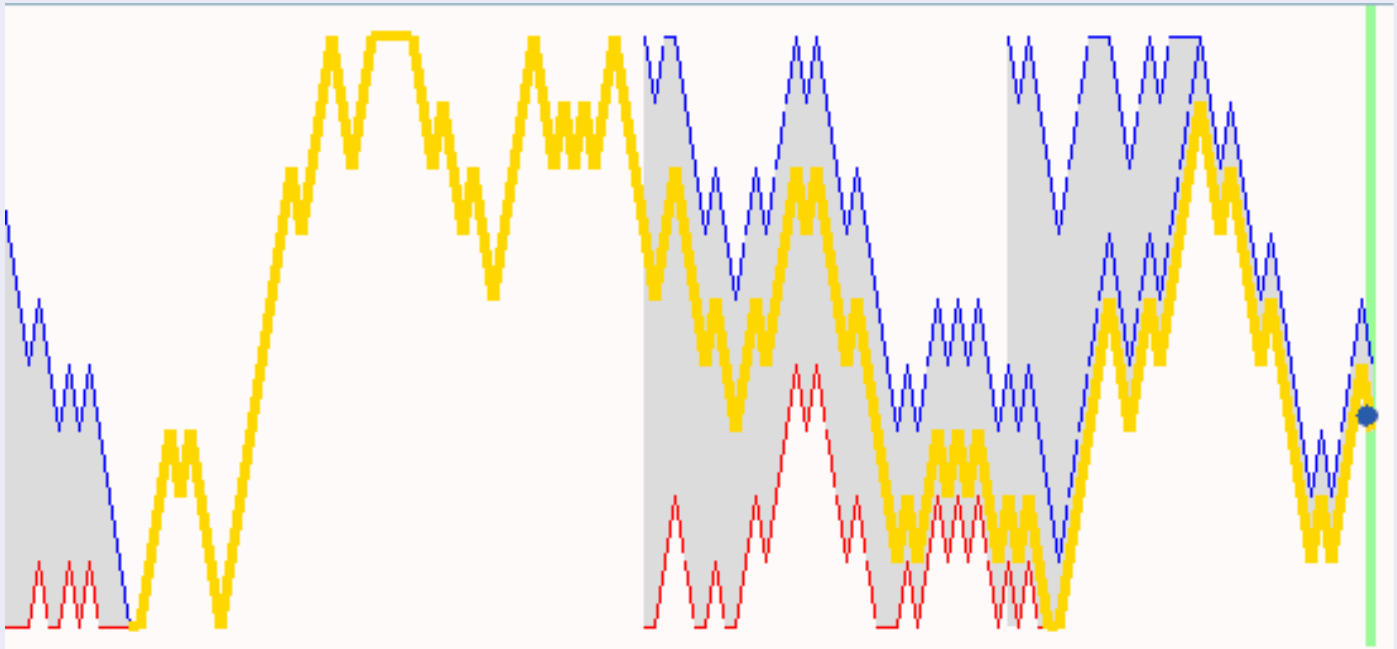
1. Consider a simple random walk on $0{:}9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.
   - $\mathbb{P}[+1 \text{ jump}] = p \in (0, 1)$, while $\mathbb{P}[-1 \text{ jump}] = 1-p$, **except that**
   - at state 9 replace the $+1$ jump by "staying still", **and**
   - at state 0 replace the -1 jump by "staying still".
2. Conventional MCMC picks a starting point, then runs the simple random walk for long time till approximate equilibrium.



3. 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;
4. Generally not true that location *at* coupling is a draw from equilibrium.

Classic CFTP for a simple random walk (I)

1. Start at top (9) and bottom (0) at negative time $-T$, run to time 0.



2. If not coupled by time 0, than back-off to time $-2T$ and repeat.
   NB: re-use randomness!
3. May need to iterate back-off doubling several times.
4. When coupled, top and bottom yield a common value at time 0.
5. The common value (golden thread) is an exact draw from equilibrium!

2. A little theory about CFTP-

1. What if 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).
2. Theoretical limits: *in principle*
   - *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).
3. Dominated CFTP delivers perfect simulation for stable point processes (WSK & Møller, 2000);
4. 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

S-I-R deterministic epidemic:

based on susceptibles s, infectives i, removals r:

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

Constant total population $s + i + r = n$.

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

Infection:	$S \to S - 1\,,$	$I \to I + 1$	at rate	$\alpha\, S\, I\,,$
Removal:	$I \to I - 1\,,$	$R \to R + 1$	at rate	$\beta\, I\,.$

Both make an unrealistic assumption: homogeneous mixing.

In contrast, Fraser & Others (2023) use a UK model with 10^6 agents!

There are *many* important inferential questions (Cori & Kucharski, 2024).

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 strongly 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.

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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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)

Important first step: think about generation of an *unconditioned* epidemic.

1. Suppose n, α, β are known. Eventually 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. First step: 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)

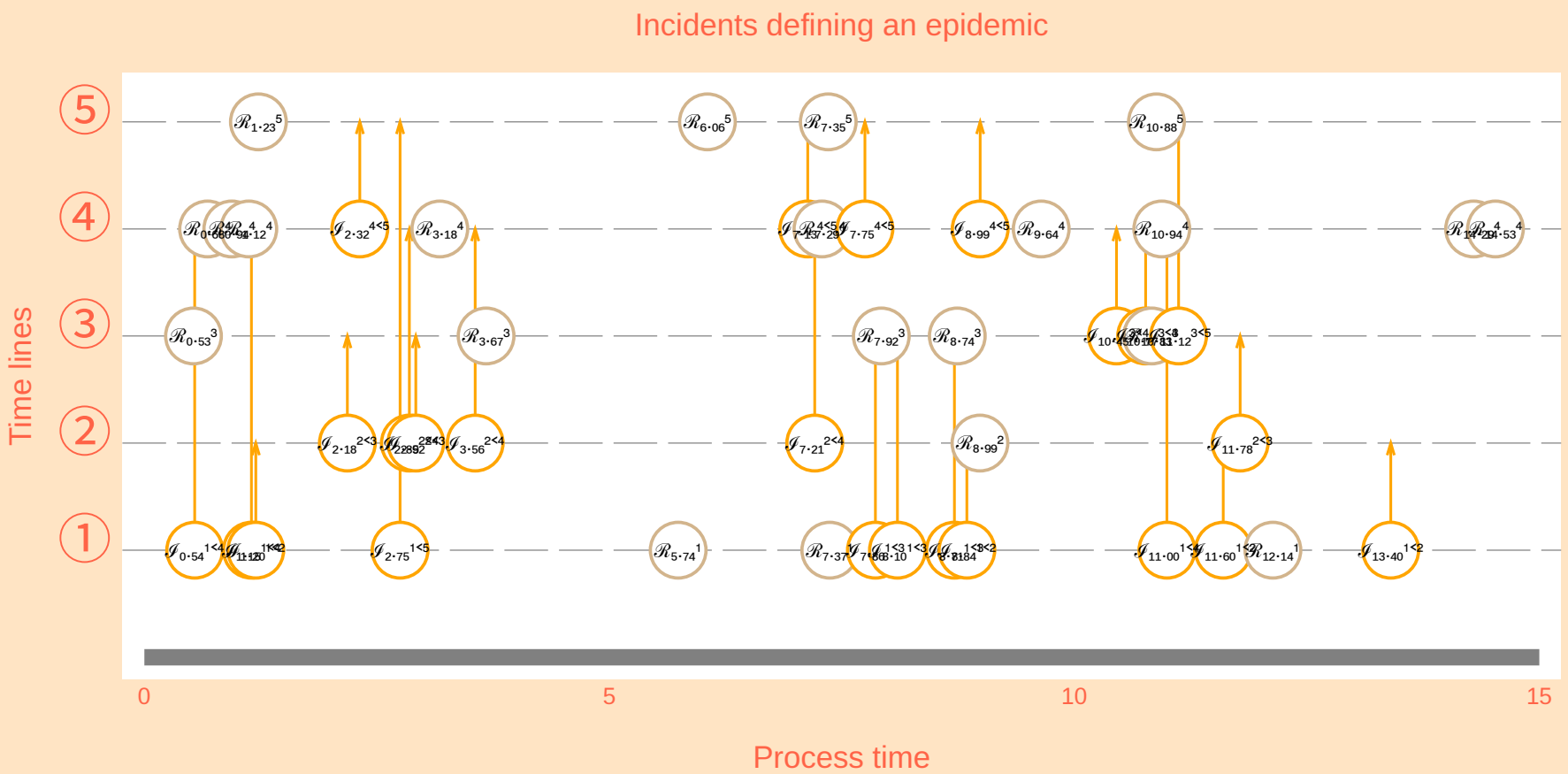

Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

From incidents to unconditioned epidemic trajectories (2/3)

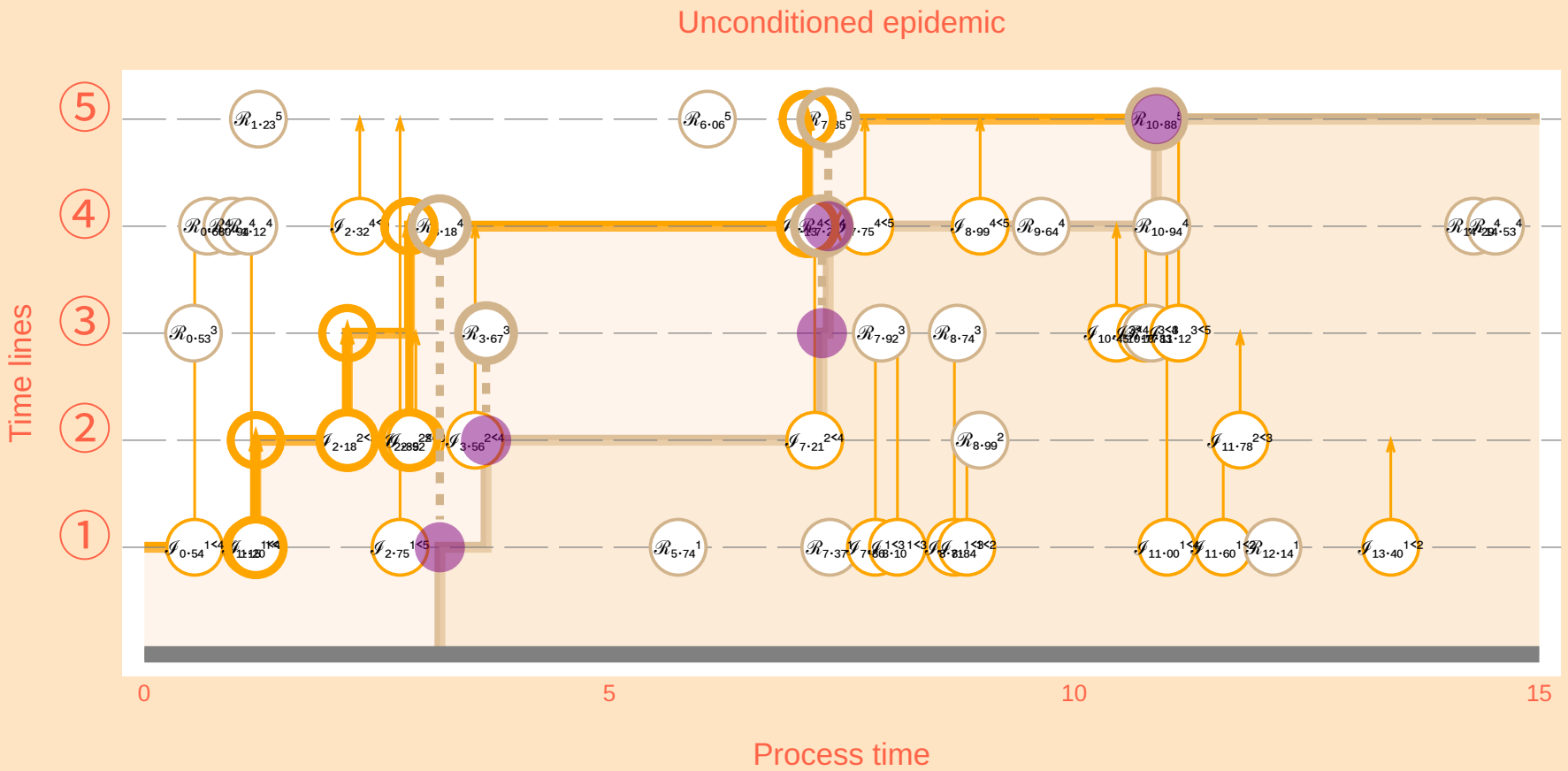

Figure 2: (a) *Infection* activates if target lies on the lowest uninfected timeline; and (b) *removal* activates if on infected timeline; remove lowest infected (purple disk).

From incidents to unconditioned epidemic trajectories (3/3)

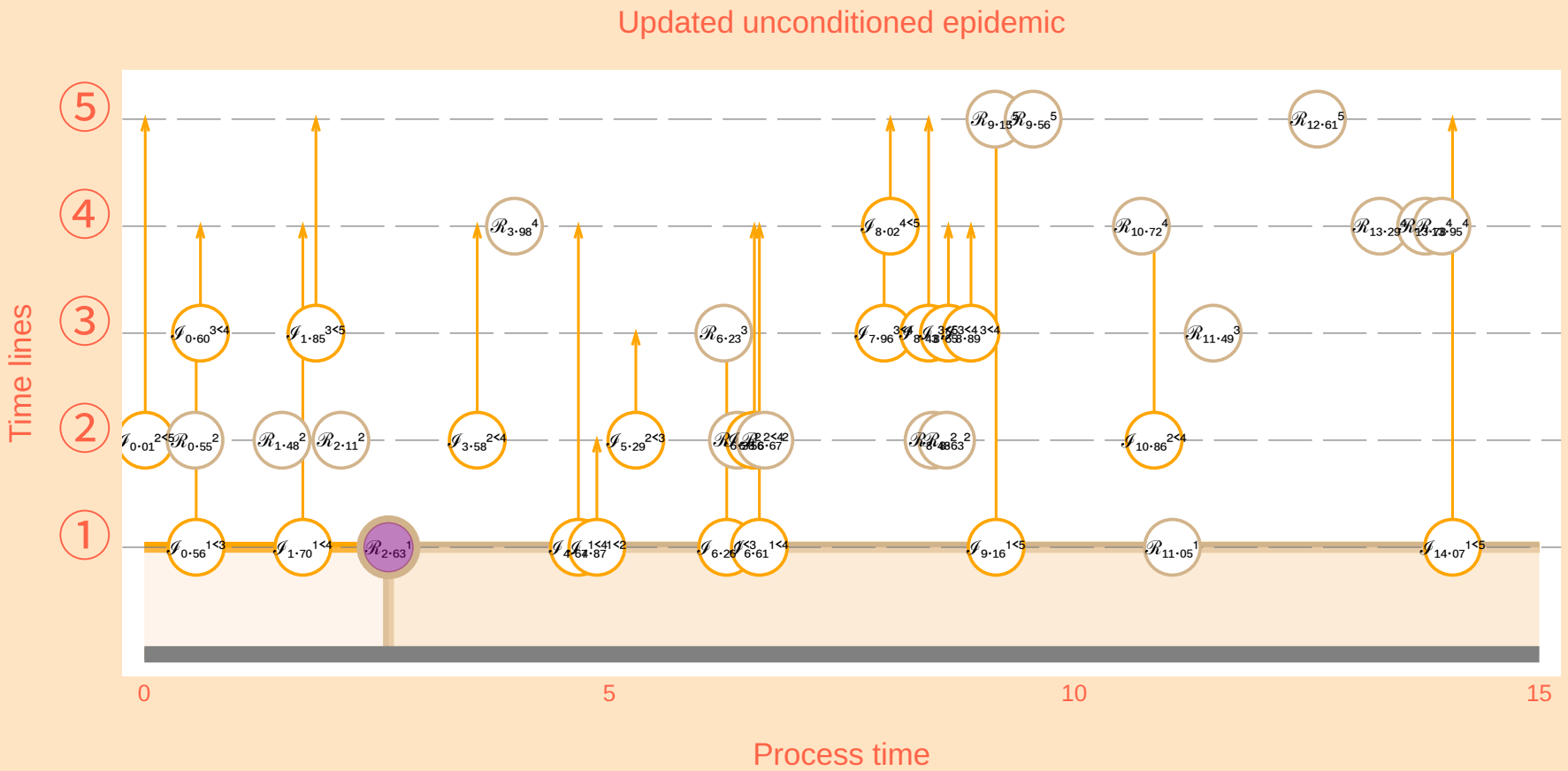

Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing all original incidents by an entirely new set of incidents.

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated* / *conditioned* removals to occur precisely at the 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 ($\mathcal{R}$s);
  2. Re-sample timelines (though not times) of $\mathcal{R}$s;
  3. Replace infections ($\mathcal{I}$s).
- Re-express using *continuously varying* τ. Process time runs over $[0, T]$.
  1. For $2nT < \tau < (2n{+}1)T$, update old $\mathcal{R}$s with times in $(0, \tau - 2nT)$;
  2. For $\tau = (2n{+}1)T$, resample timelines (not times) of $\mathcal{R}$s;
  3. For $(2n{+}1)T < \tau < (2n{+}2)T$, update old $\mathcal{I}$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" holds (needs proof).
- Crucially, re-sampling step 2 ensures composite evolution is irreducible over S! (So equilibrium under conditioning is unique.)

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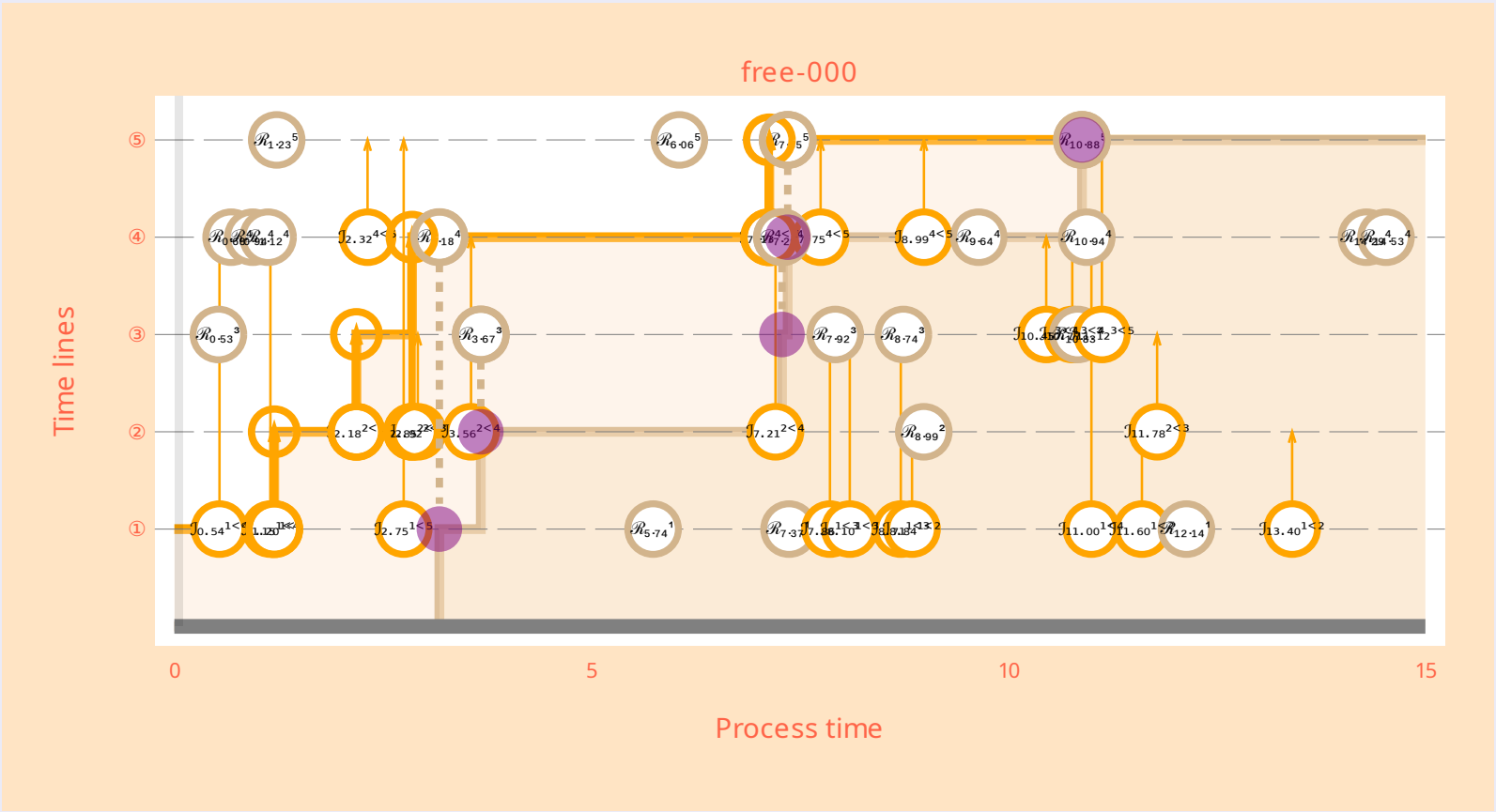
Free evolution evolving in continuous algorithmic time



GIF MP4

4. 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 used to establish that monotonicity still works: *laziest feasible epidemic* (LFE) and *no-fly zone* (NFZ).

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Initial conditioned epidemic

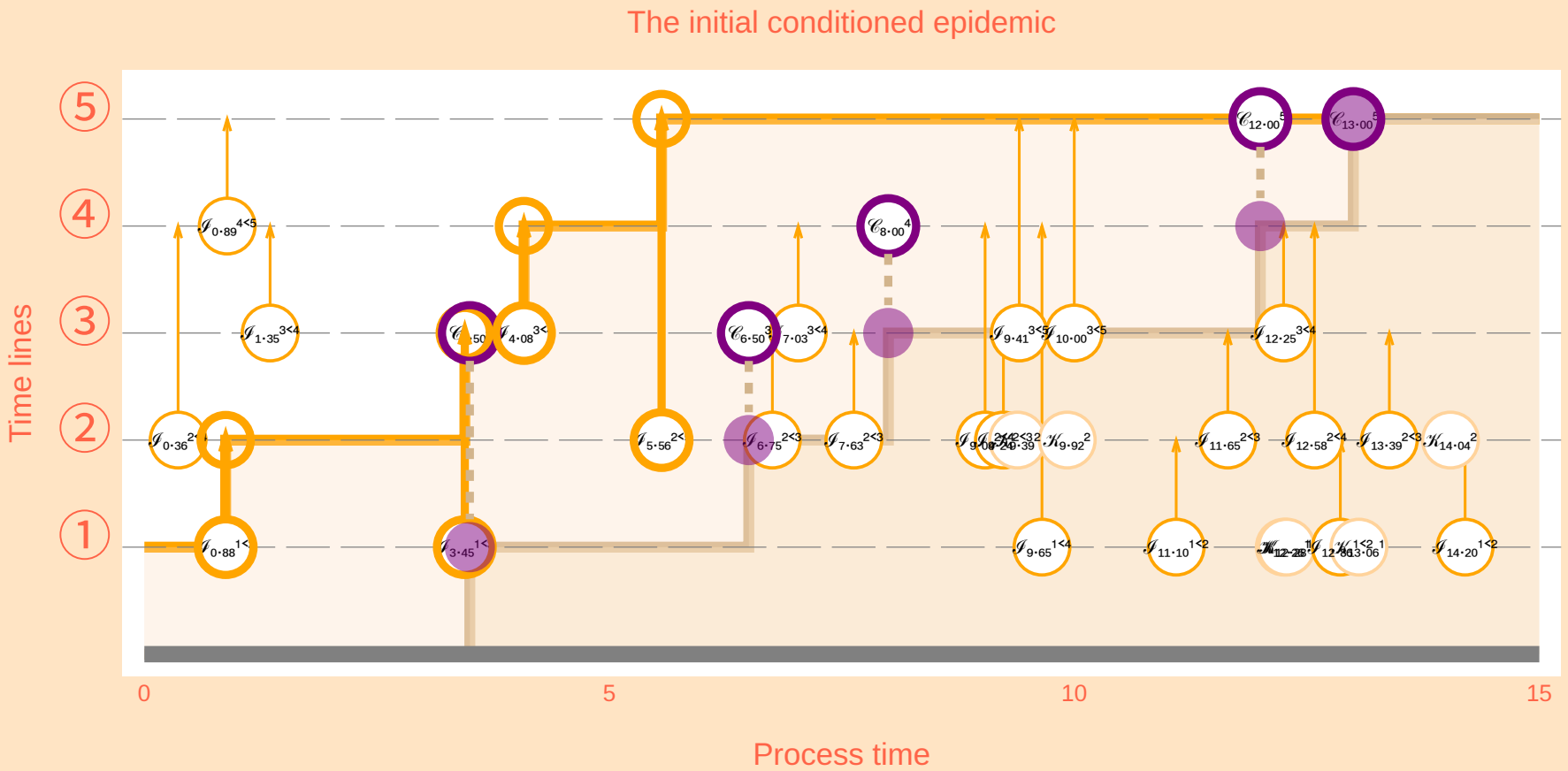


Figure 4: Initial conditioned epidemic, with conditioned removals indicated using purple circles (and purple disks when non-target timelines are infected).

Conditional epidemic update

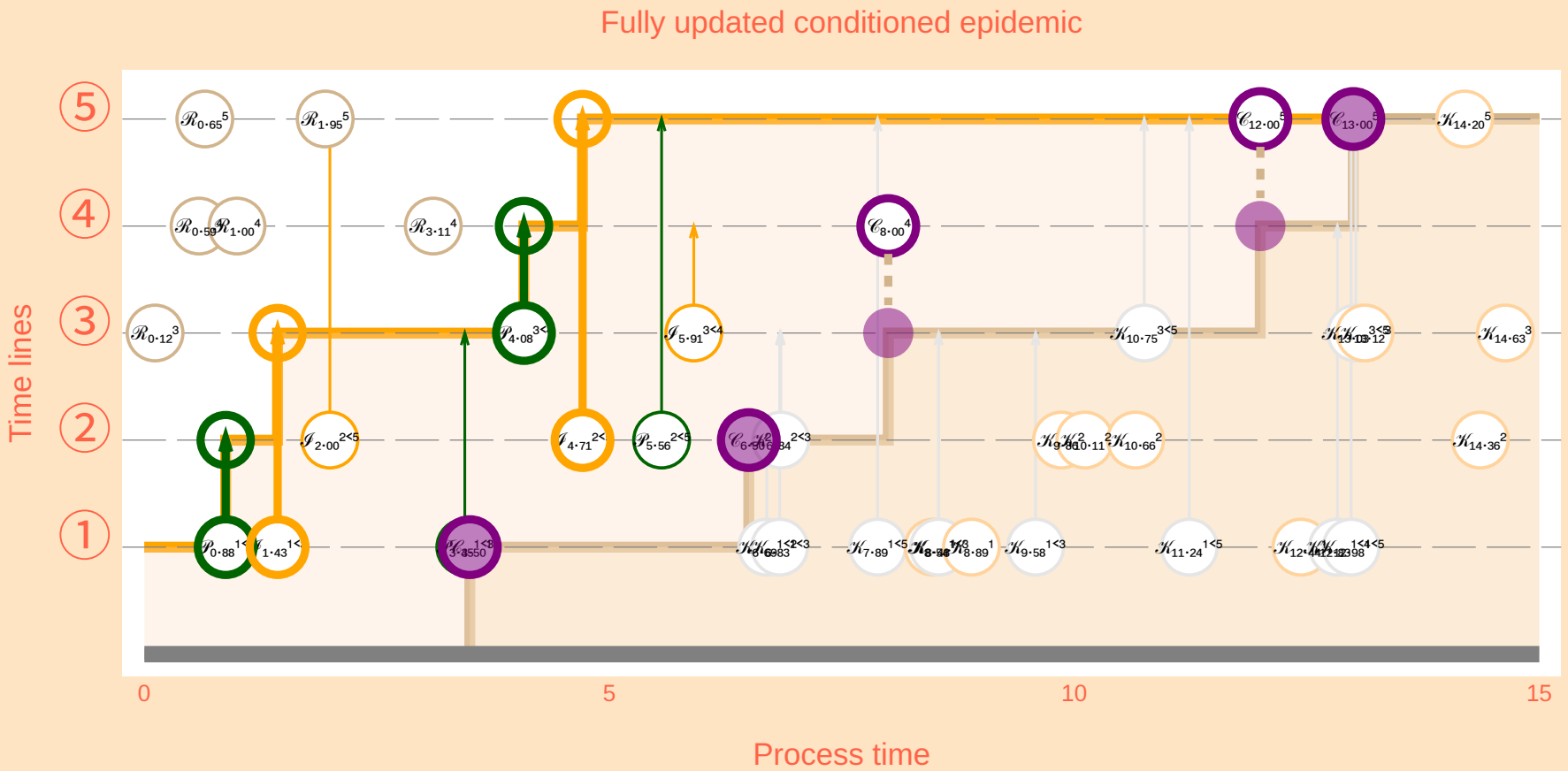


Figure 5: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

Laziest feasible epidemic (LFE)

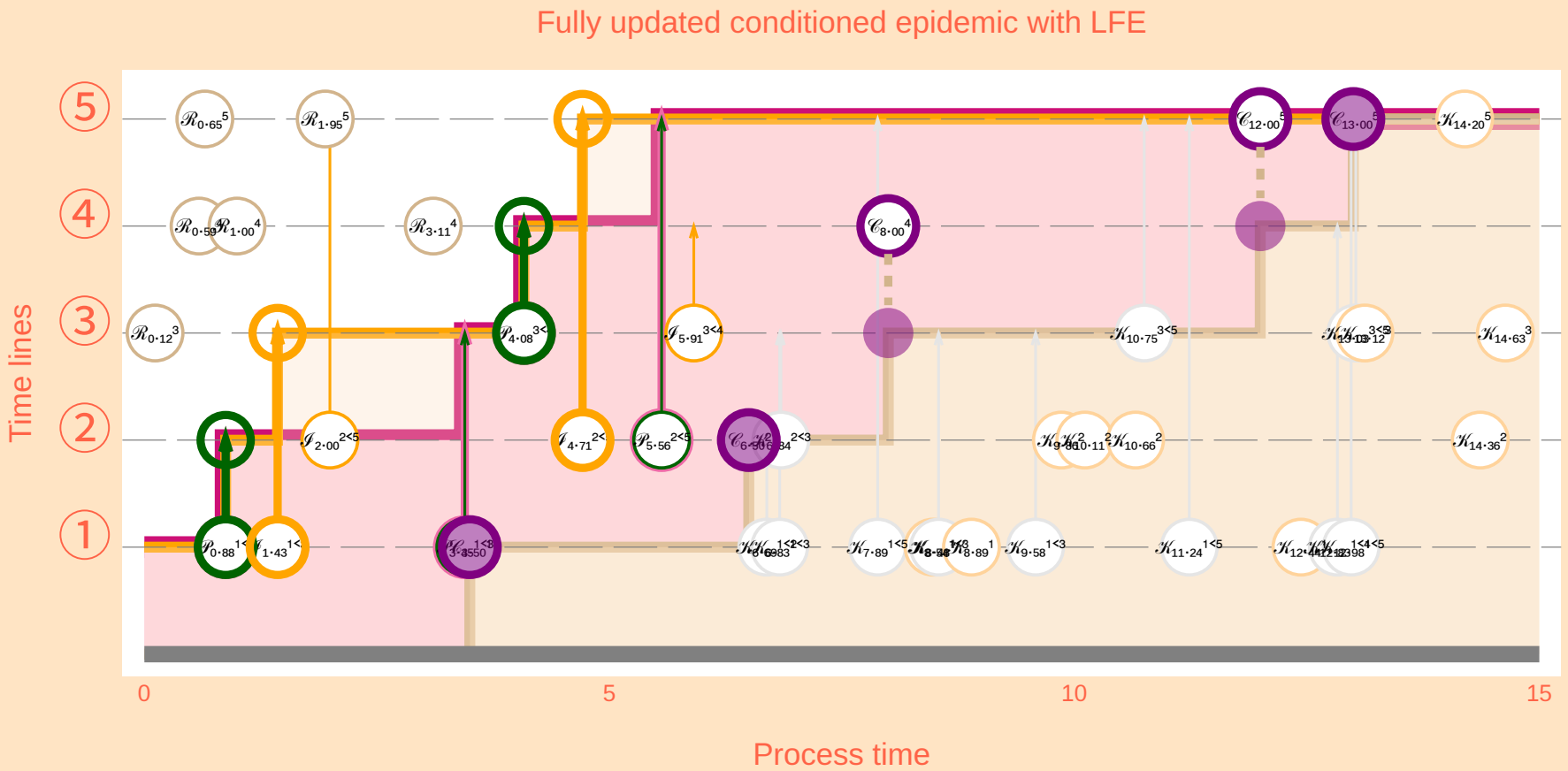


Figure 6: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

No-fly zone (NFZ)

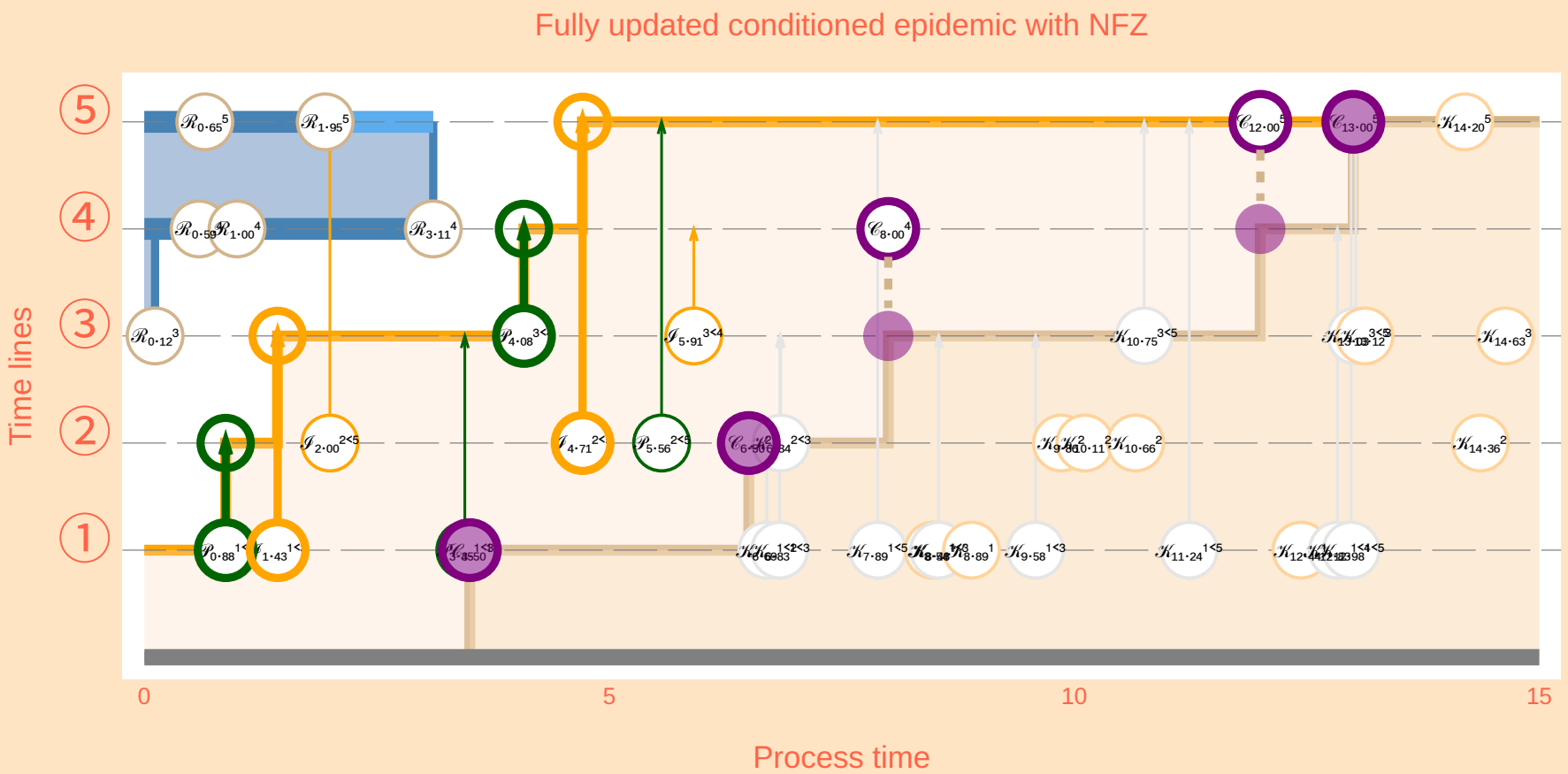
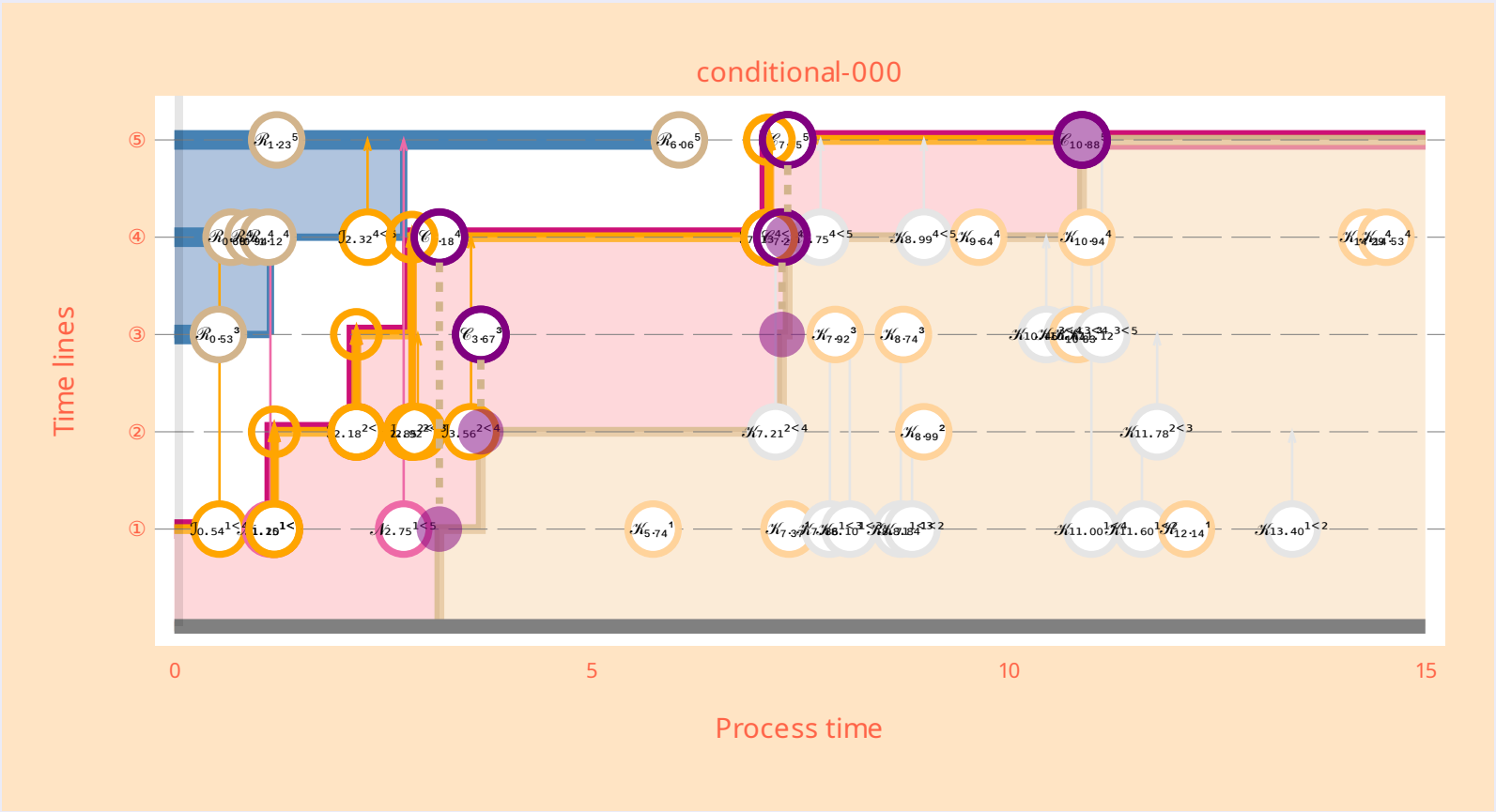


Figure 7: NFZ computed recursively working right-to-left: it traces the region of timelines that must not be infected if one is not to activate unobserved removals.

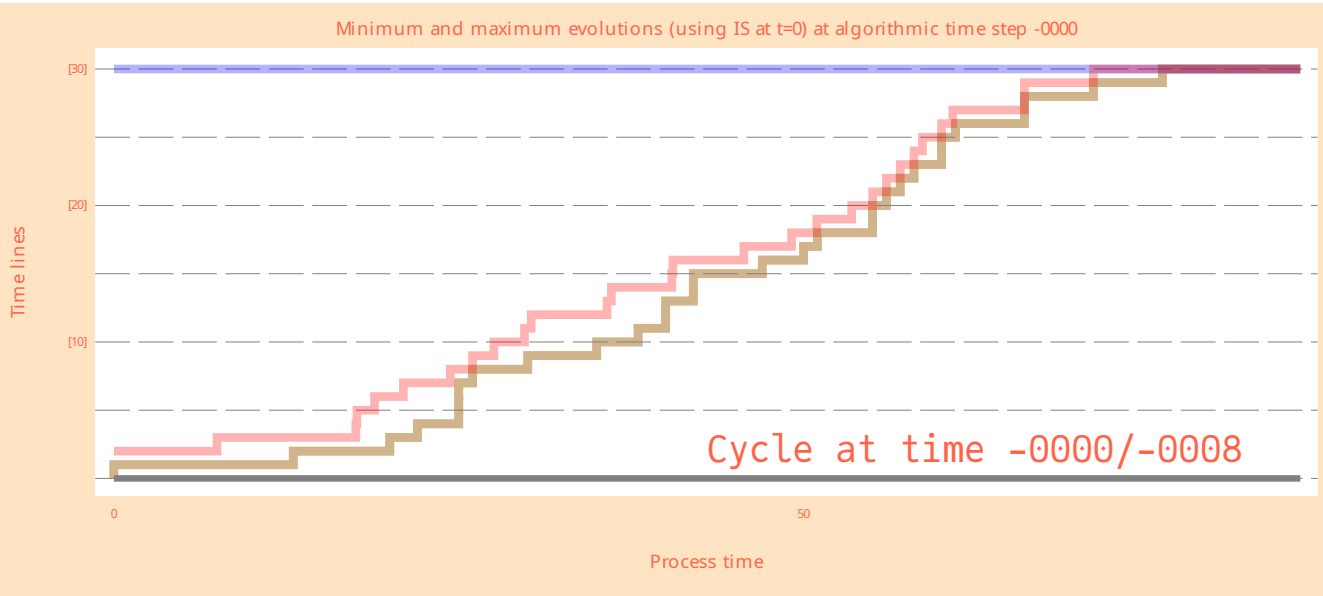
Conditioned evolution evolving in continuous algorithmic time



GIF MP4

5. 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 obtain a GIF or an MP4 of the perfect simulation yielding a draw from unobserved pattern of infections.



So what?

- Why this emphasis on unobserved infections given fixed α and β, when we need inference on R-number $\alpha\, n/\beta$ for *unknown* α and β?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different* α and β. 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 α and β;
  - construct steepest ascent algorithm (in effect, variant of Robbins-Monro stochastic optimization) to find *maximum a posterior* estimates of α and β;
  - or even, with some computational effort, compute the entire posterior joint density for α and β!
- Finally: can we generalize to other suitable compartment models?

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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: seek faster CFTP; statistical estimation of parameters, generalization to other compartment models.
- Thank you for your attention! **QUESTIONS?**

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Image information

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

Previous instances of this talk

Date	*Title*			*Location*
19/04/24	Perfect Epidemics	Short Research Talk	12mn	Warwick
15/05/24	McMC+Perfect Simulation	Graduate Seminar, Aristotle Univ.	50mn	Thessaloniki
17/01/25	Perfect Epidemics	Applied Probability Seminar	50mn	Warwick
27/06/25	Perfect Epidemics	UK Research Network Stochastics	45mn	Liverpool

Appendix A: A “near-maximal” configuration

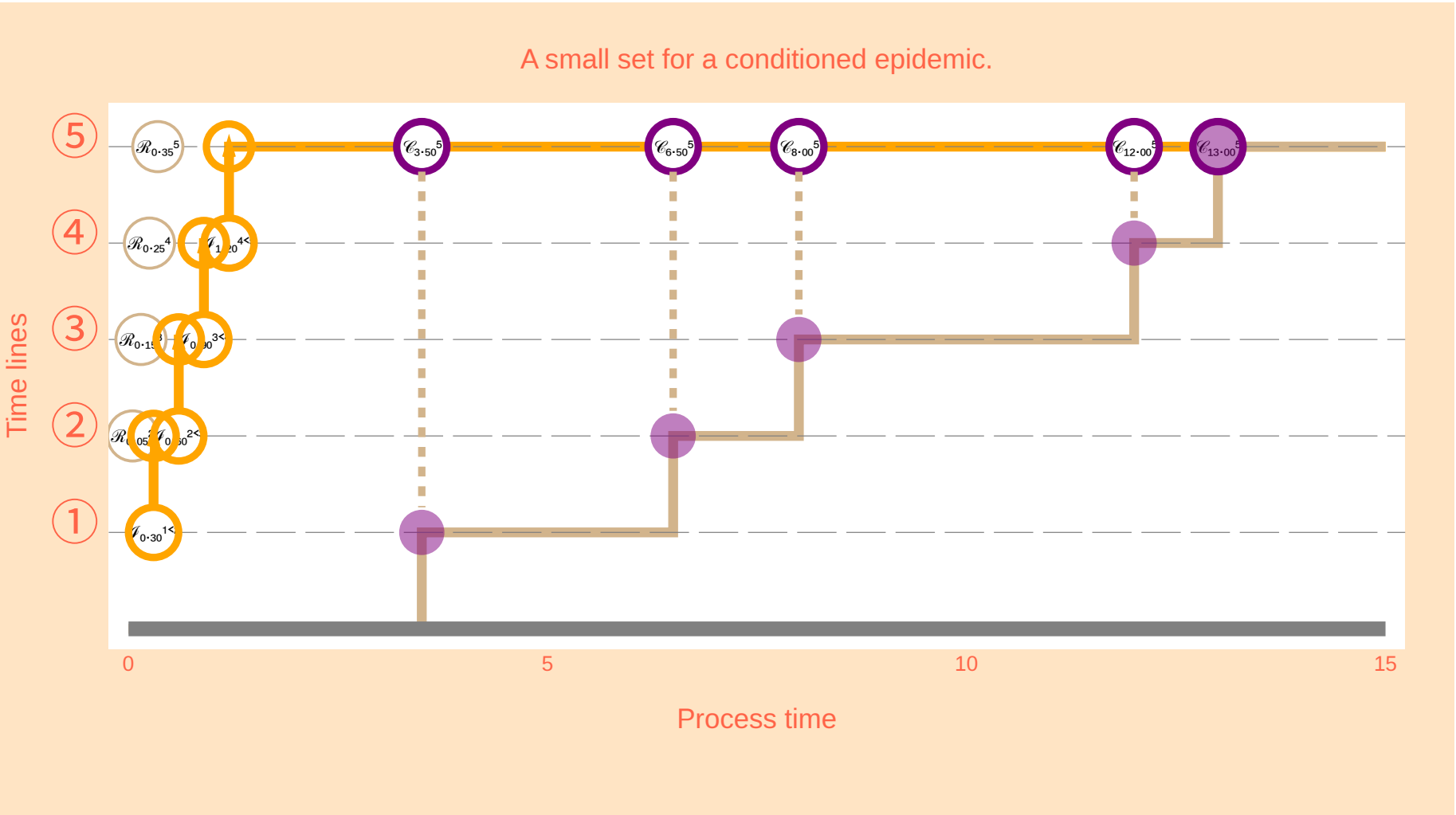

Figure 8: A conditioned epidemic in which all activated infections occur before time 3.0, also before smallest observed removal time.

Appendix B: Notes towards a monotonicity proof

Summary of plan of proof:

1. Let $\mathrm{EPI}^{\pm}_{\tau=0}$ represent two epidemic trajectories ($\pm$) at algorithmic time $\tau{=}0$, viewed as subsets of "timeline-space" $\{(k, [0, T)) : k = 1, 2, \ldots\}$.
2. Suppose at algorithmic time $\tau{=}0$ the *fast* $\mathrm{EPI}^{+}_{\tau=0}$ is never later than the *slow* $\mathrm{EPI}^{-}_{\tau=0}$ so $\mathrm{EPI}^{+}_{\tau=0} \supseteq \mathrm{EPI}^{-}_{\tau=0}$; additionally suppose monotonicity holds for conditional removal marks: if $\mathcal{C}^{\pm}_{\tau=0}$ are conditional removals at fixed process time t then $\mathcal{C}^{+}_{\tau=0}$ timeline $\geq \mathcal{C}^{-}_{\tau=0}$ timeline.
3. Then a related monotonicity holds for the laziest feasible epidemics: $\mathrm{LFE}^{+}_{\tau=1} \leq \mathrm{LFE}^{-}_{\tau=1}$ at algorithmic time $\tau{=}1$.
4. Likewise a similar monotonicity (but reversing the set-theoretic inclusion!) holds for no-fly zones: $\mathrm{NFZ}^{+}_{\tau=1} \subseteq \mathrm{NFZ}^{-}_{\tau=1}$.
5. Now prove $\mathrm{EPI}^{+}_{\tau=1} \supseteq \mathrm{EPI}^{-}_{\tau=1}$ moreover if $\mathcal{C}^{+}_{\tau=1}$ matches $\mathcal{C}^{-}_{\tau=1}$ at process time t then $\mathcal{C}^{+}_{\tau=1}$ timeline $\geq \mathcal{C}^{-}_{\tau=1}$ timeline.

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$\mathrm{LFE}_{\tau=1}$: recursive construction

Let $\mathrm{LFE}^{\pm}_{\tau=1}(k)$ be the (process) time of the latest infection of timeline k needed if all $\mathcal{C}^{\pm}$s of $\mathrm{EPI}^{\pm}_{\tau=1}$ are to be infected.

1. For the top timeline n, $\mathrm{LFE}^{\pm}_{\tau=1}(n)$ must precede any $\mathcal{C}^{\pm}$ on timeline n; set $\mathrm{LFE}^{\pm}_{\tau=1}(n) = T$ if no such $\mathcal{C}^{\pm}$.
2. For $k < n$ with $\mathrm{LFE}^{\pm}_{\tau=1}(k{+}1) = T$, again $\mathrm{LFE}^{\pm}_{\tau=1}(k)$ must precede any $\mathcal{C}^{\pm}$ on timeline k; set $\mathrm{LFE}^{\pm}_{\tau=1}(k) = T$ if no such $\mathcal{C}^{\pm}$.
3. Suppose n_0 is largest k with $\mathrm{LFE}^{\pm}_{\tau=1}(k) < T$. Working downwards through $\ell = n_0{-}1, \ldots, 1$, $\mathrm{LFE}^{\pm}_{\tau=1}(\ell)$ is the time of the latest infection targeting $\ell{+}1$ and based in the infected region such that
   (a) $\mathrm{LFE}^{\pm}_{\tau=1}(\ell) \leq \mathrm{LFE}^{\pm}_{\tau=1}(\ell{+}1)$;
   (b) $\mathrm{LFE}^{\pm}_{\tau=1}(\ell)$ precedes any $\mathcal{C}^{\pm}$ on timeline ℓ.
4. Equivalently, $\mathrm{LFE}^{\pm}_{\tau=1}(\ell)$ is the time of the latest potential infection targeting $\ell{+}1$ such that
   (a) $\mathrm{LFE}^{\pm}_{\tau=1}(\ell) \leq \mathrm{LFE}^{\pm}_{\tau=1}(\ell{+}1)$;
   (b) $\mathrm{LFE}^{\pm}_{\tau=1}(\ell)$ precedes any $\mathcal{C}^{\pm}$ on timelines $\ell, \ell{+}1, \ldots, n$.

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$\mathrm{LFE}_{\tau=1}$: monotonicity

1. Re-sample $\mathcal{C}^{\pm}$ timelines by accept-reject: same proposals for both $\pm$. As $\mathrm{EPI}^{+}_{\tau=0} \supseteq \mathrm{EPI}^{-}_{\tau=0}$, so $\mathcal{C}$ timelines for $\mathrm{EPI}^{+}_{\tau=1}$ no lower than for $\mathrm{EPI}^{-}_{\tau=1}$.
2. In particular, if $\mathrm{LFE}^{+}_{\tau=1}(k) = T$ then $\mathrm{LFE}^{-}_{\tau=1}(k) = T$ also.
3. Now work inductively. Suppose monotonicity holds for $k{+}1, \ldots, n$. Then $\mathrm{LFE}^{+}_{\tau=1}(k) \leq \mathrm{LFE}^{+}_{\tau=1}(k{+}1) \leq \mathrm{LFE}^{-}_{\tau=1}(k{+}1)$. But the set of "times of $\mathcal{C}^{-}$ on timelines $\ell, \ell{+}1, \ldots, n$" is a subset of the set of "times of $\mathcal{C}^{+}$ on timelines $\ell, \ell{+}1, \ldots, n$". So if $b^{\pm}_{k}$ is the resulting right-constraint on $\mathrm{LFE}^{\pm}_{\tau=1}(k)$ then $b^{+}_{k} \leq b^{-}_{k}$.
4. Suppose $\mathrm{EPI}^{\pm}_{\tau=0}$ infects timeline $k{+}1$ at time $a^{\pm}_{k}$: $a^{+}_{k} \leq a^{-}_{k} \leq b^{-}_{k}$ by monotonicity for $\mathrm{EPI}^{\pm}_{\tau=0}$. If no $\tau{=}1$ infections infect timeline $k{+}1$ in $[a^{\pm}_{k}, b^{\pm}_{k})$, then $\mathrm{LFE}^{\pm}_{\tau=1}(k)$ perpetuates $a^{\pm}_{k}$ using $\mathrm{EPI}^{\pm}_{\tau=0}(k)$. Then argue case-by-case:
   (a) no perpetuation occurs (use fact, all infections are shared);
   (b) $\mathrm{LFE}^{-}_{\tau=1}(k)$ is perpetuated (so no useful infections after perpetuation);
   (c) only $\mathrm{LFE}^{+}_{\tau=1}(k)$ is perpetuated (then use $\tau{=}0$ monotonicity).

$\mathrm{NFZ}_{\tau=1}$: iterative construction

1. Set $\mathrm{NFZ}^{\pm,*}_{\tau=1}$ to be union of regions $(k,[0,t])$ for all $\mathcal{R}$s of $\mathrm{EPI}^{\pm}_{\tau=1}$, for timeline k and time t of $\mathcal{R}$. Set $\mathrm{NFZ}^{\pm,*}_{\tau=1} = \{(k,[0,t^*_k]) : t^*_k > 0\}$.
2. Set $\mathrm{NFZ}^{\pm,0}_{\tau=1} = \{(k,[0,t_k]) : t_k > 0\}$ as monotonic envelope of $\mathrm{NFZ}^{\pm,*}_{\tau=1}$: $\{t_k\}$ is smallest non-decreasing sequence majorizing $\{t^*_k\}$.
3. Work backwards through new *"non-removed"* $\mathcal{I}$s. At step j, time t,
   (a) **accept** $\mathcal{I}$ if it targets $\mathrm{NFZ}^{\pm,j-1}_{\tau=1}$ at timeline k but infection fails: set $\mathrm{NFZ}^{\pm,j}_{\tau=1} = \mathrm{NFZ}^{\pm,j-1}_{\tau=1} \cup \{(k-1,[0,t])\}$; otherwise set $\mathrm{NFZ}^{\pm,j}_{\tau=1} = \mathrm{NFZ}^{\pm,j-1}_{\tau=1}$ and
   (b) **reject** $\mathcal{I}$ if it would infect part of $\mathrm{NFZ}^{\pm,j-1}_{\tau=1}$;
   (c) **accept** $\mathcal{I}$ if it doesn't target $\mathrm{NFZ}^{\pm,j-1}_{\tau=1}$.
4. Set $\mathrm{NFZ}^{\pm}_{\tau=1} = \mathrm{NFZ}^{\pm,j}_{\tau=1}$ if a total of j new $\mathcal{I}$s are proposed for $\mathrm{EPI}^{\pm}_{\tau=1}$, so no more $\mathcal{I}$s remain!

NB: ignore $\mathcal{I}$ proposals targeting $\mathrm{NFZ}^{\pm,j-1}_{\tau=1}$: either these are rejected ((b) above) or $\mathrm{NFZ}^{\pm,j}_{\tau=1}$ is modified ((a) above) so they aren't relevant! *Relevant* accepted $\mathcal{I}$s are exactly those *not* targeting the final $\mathrm{NFZ}^{\pm}_{\tau=1}$.

$\mathrm{NFZ}_{\tau=1}$: monotonicity

Establish monotonicity for $\mathrm{NFZ}^{\pm,*}_{\tau=1}$, $\mathrm{NFZ}^{\pm,0}_{\tau=1}$, $\mathrm{NFZ}^{\pm,1}_{\tau=1}$, $\mathrm{NFZ}^{\pm,2}_{\tau=1}$, ... in turn:

1. Since $\mathrm{EPI}^{+}_{\tau=0} \supseteq \mathrm{EPI}^{-}_{\tau=0}$ and the set of $\mathcal{R}$s for $\mathrm{EPI}^{\pm}_{\tau=1}$ are formed by intersecting the same $\mathcal{R}$ pattern with the complements of $\mathrm{EPI}^{\pm}_{\tau=0}$, it follows that $\mathrm{NFZ}^{+,*}_{\tau=1} \subseteq \mathrm{NFZ}^{-,*}_{\tau=1}$.
2. Monotonicity for $\mathrm{NFZ}^{\pm,0}_{\tau=1}$ is a direct consequence.
3. Given $\mathrm{NFZ}^{+,j-1}_{\tau=1} \subseteq \mathrm{NFZ}^{-,j-1}_{\tau=1}$, create $\mathrm{NFZ}^{\pm,j}_{\tau=1}$ by proposing $\mathcal{I}$ at time t targeting timeline k, based in $\mathrm{EPI}^{+}_{\tau=0}$ infected region. Then $\mathrm{NFZ}^{+,j}_{\tau=1} = \mathrm{NFZ}^{+,j-1}_{\tau=1} \cup \{(k{-}1, [0,t])\}$ exactly when $\mathcal{I}$ fails to infect in $\mathrm{EPI}^{+}_{\tau=1}$. Then
   (a) we know k timeline at t is in $\mathrm{NFZ}^{-,j-1}_{\tau=1} \supseteq \mathrm{NFZ}^{+,j-1}_{\tau=1}$;
   (b) infection fails for $\mathrm{EPI}^{+}_{\tau=1}$ because timeline $k{-}1$ is not infected at t in $\mathrm{EPI}^{+}_{\tau=0}$. But we know $\mathrm{EPI}^{+}_{\tau=0} \supseteq \mathrm{EPI}^{-}_{\tau=0}$, so timeline $k{-}1$ is not infected at t in $\mathrm{EPI}^{-}_{\tau=0}$ either. So infection in $\mathrm{EPI}^{-}_{\tau=1}$ also fails.

Thus $\mathrm{NFZ}^{+,j}_{\tau=1} = \mathrm{NFZ}^{+,j-1}_{\tau=1} \cup \{(k{-}1, [0,t])\}$ implies $\mathrm{NFZ}^{-,j}_{\tau=1} = \mathrm{NFZ}^{-,j-1}_{\tau=1} \cup \{(k{-}1, [0,t])\}$ and so $\mathrm{NFZ}^{+,j}_{\tau=1} \subseteq \mathrm{NFZ}^{-,j}_{\tau=1}$.

$\mathrm{EPI}_{\tau=1}$: monotonicity (I)

Consider:

- there is epidemic monotonicity at algorithmic time $\tau=0$ ($\mathrm{EPI}^{+}_{\tau=0} \supseteq \mathrm{EPI}^{-}_{\tau=0}$, also $\mathcal{C}$s in $\mathrm{EPI}^{+}_{\tau=0}$ are never lower than in $\mathrm{EPI}^{-}_{\tau=0}$);
- at algorithmic time $\tau=1$ there is monotonicity of laziest feasible epidemic ($\mathrm{LFE}^{+}_{\tau=1}(k) \leq \mathrm{LFE}^{-}_{\tau=1}(k)$ for all timelines k);
- and there is monotonicity of no-fly zone ($\mathrm{NFZ}^{+}_{\tau=1} \subseteq \mathrm{NFZ}^{-}_{\tau=1}$).

Deduce epidemic monotonicity at algorithmic time $\tau=1$ ($\mathrm{EPI}^{+}_{\tau=1} \supseteq \mathrm{EPI}^{-}_{\tau=1}$).

Two cases to consider. Use $\partial\mathrm{NFZ}$ to represent right-most boundary for a NFZ, and similarly use $\partial\mathrm{EPI}$ to represent *left*-most boundary for a EPI):

1. $\partial\mathrm{NFZ}^{+}_{\tau=1} \leq \mathrm{LFE}^{+}_{\tau=1} \leq \partial\mathrm{NFZ}^{-}_{\tau=1} \leq \mathrm{LFE}^{-}_{\tau=1}$;
2. $\partial\mathrm{NFZ}^{+}_{\tau=1} \leq \partial\mathrm{NFZ}^{-}_{\tau=1} \leq \mathrm{LFE}^{+}_{\tau=1} \leq \mathrm{LFE}^{-}_{\tau=1}$;

In the first case there is nothing to be done: simply use the remark

$$\partial\mathrm{NFZ}^{\pm}_{\tau=1} \quad \leq \quad \partial\mathrm{EPI}^{\pm}_{\tau=1} \quad \leq \quad \mathrm{LFE}^{\pm}_{\tau=1}\,.$$

$\mathrm{EPI}_{\tau=1}$: monotonicity (II)

In the second case argue as follows. Localize to particular timeline k:

1. If the $\mathrm{EPI}^{-}_{\tau=1}(k)$ infection is perpetuated, it must agree with $\mathrm{LFE}^{-}_{\tau=1}(k)$ and so monotonicity follows.
2. If the $\mathrm{EPI}^{-}_{\tau=1}(k)$ infection is no earlier than $\mathrm{LFE}^{+}_{\tau=1}(k)$ then again monotonicity follows.
3. If the $\mathrm{EPI}^{-}_{\tau=1}(k)$ infection is not perpetuated and occurs earlier than $\mathrm{LFE}^{+}_{\tau=1}(k)$ then it is available as a possible candidate for $\mathrm{EPI}^{+}_{\tau=1}(k)$ and so here too $\mathrm{EPI}^{-}_{\tau=1}(k)$ is no earlier than $\mathrm{EPI}^{+}_{\tau=1}(k)$.

This completes the proof of monotonicity for $\mathrm{EPI}_{\tau=1}$.

Appendix C: Naïve approach to compartment models fails

- Consider a modification of this approach to the case of compartmentalized populations.
- Focus on the extreme case in which every individual j has infectivity (outgoing to individual k) $\alpha_{j,k}$ and removal parameter β_j.
- Suppose the conditioning on removals is specifically about named individuals j being removed at specified times r_j;
  suppose also there are no "occult" (unobserved) removals for any other individuals.
- This would apply, for example, in the case of the *Diamond Princess* if α, β depended on age and location of cabin on the ship.

Warwick Statistics

Timelines and incidents for the compartmental generalization

1. Individuals no longer exchangeable, so S-I-R state space is unsuitable.
2. Given population $N \in \mathbb{N}$, the ground space is a tuple of n timelines $(i, [0, T))$, one timeline per individual i, where T is the final time of observation of the epidemic.
3. Typical element of state-space: a locally-finite point pattern of
   - infections $\mathcal{I} = \mathcal{I}_{i,j}(t)$, marked by timelines i at various times t, each infection marked by a target timeline j other than its mark k;
   - (inactivated) removals $\mathcal{R} = \mathcal{R}_i(t)$, marked by timelines i at times t;
   - conditioned removals $\mathcal{C} = \mathcal{C}_i(t)$, marked by timelines i at times t.
4. Initial stipulations:
   - the $\mathcal{I}$s, $\mathcal{R}$s and $\mathcal{C}$s all occur at different times;
   - there is at most one $\mathcal{C}$ per timeline;
   - for convenience, no $\mathcal{I}$ or $\mathcal{R}$ occur after a $\mathcal{C}$ on the same timeline;
5. Epidemic can be viewed as a union of intervals on different timelines;
   - intervals end at the $\mathcal{C}$ in the timeline or at time T;
   - intervals on initially infected timelines start at time 0;
   - intervals on eventually infected timelines start at the first time t an $\mathcal{I}$ targets the timeline while marked by a timeline infected at t.

Process dynamics

Recall that infections and removals *after* a conditioned removal have been censored out. A valid configuration must satisfy the following, derived from the process dynamics:

1. initially infected timelines i possess no $\mathcal{R}_i$: if they possess a (single) $\mathcal{C}_i(t)$ then they contribute $(i, [0, t))$ to the epidemic, otherwise $(i, [0, T)$;
2. other timelines k only contribute if they possess $\mathcal{I}_{k,i}(s)$ such that timeline k is infected at time s, in which case the earliest s is chosen and the contribution is $(i, [s, t))$ when $\mathcal{C}_i(t)$ is the conditioned removal of the timeline, otherwise $(i, [s, T))$;
3. every inactivated removal $\mathcal{R}_i(t)$ satisfies $t < s$, where s is the time of first infection of the timeline i.
4. every conditioned removal $\mathcal{C}_i(t)$ is at the right t of an infected interval.

So each timeline is divided into a *susceptible interval* (empty if it is initially infected), an *infected interval* (empty if it is never infected), and a *removed interval* (empty if it has no conditioned removal).

Dynamics in algorithmic time

This closely corresponds to the evolution of the S-I-R epidemic above, but does not resample the mark i for each conditioned removal $\mathcal{C}_i$;

1. Remove all $\mathcal{R}$s, and re-sample inactivated removals on the susceptible intervals of each timeline. Recompute NFZ as a union of $(i, [0, t_i))$ using the latest time $t_i = t$ of re-sampled $\mathcal{R}_i(t)$.
2. List in *time-reverse order* original infections together with sampled *new* candidate $\tilde{\mathcal{I}}$s in complements of the removed intervals.
3. Work iteratively through this list. Would discarding original $\mathcal{I}_{i,j}(t)$ result in failure to infect a conditioned removal?. If so, retain $\mathcal{I}_{i,j}(t)$ as *perpetuated infection* $\mathcal{P}_{i,j}(t)$, otherwise discard.
4. Otherwise, at $\tilde{\mathcal{I}}_{a,b}(u)$, consider the latest update of NFZ.
   - If a infected at u and u is in b component of latest NFZ, discard $\tilde{\mathcal{I}}_{a,b}(u)$;
   - If a is not infected at u but u lies on b component of latest NFZ, update NFZ by adding/replacing interval of NFZ at a using $(a, [0, u))$;
   - Otherwise retain $\tilde{\mathcal{I}}_{a,b}(u)$ as $\mathcal{I}_{a,b}(u)$.

As in S-I-R case, the conditioned epidemic is the unique equilibrium.

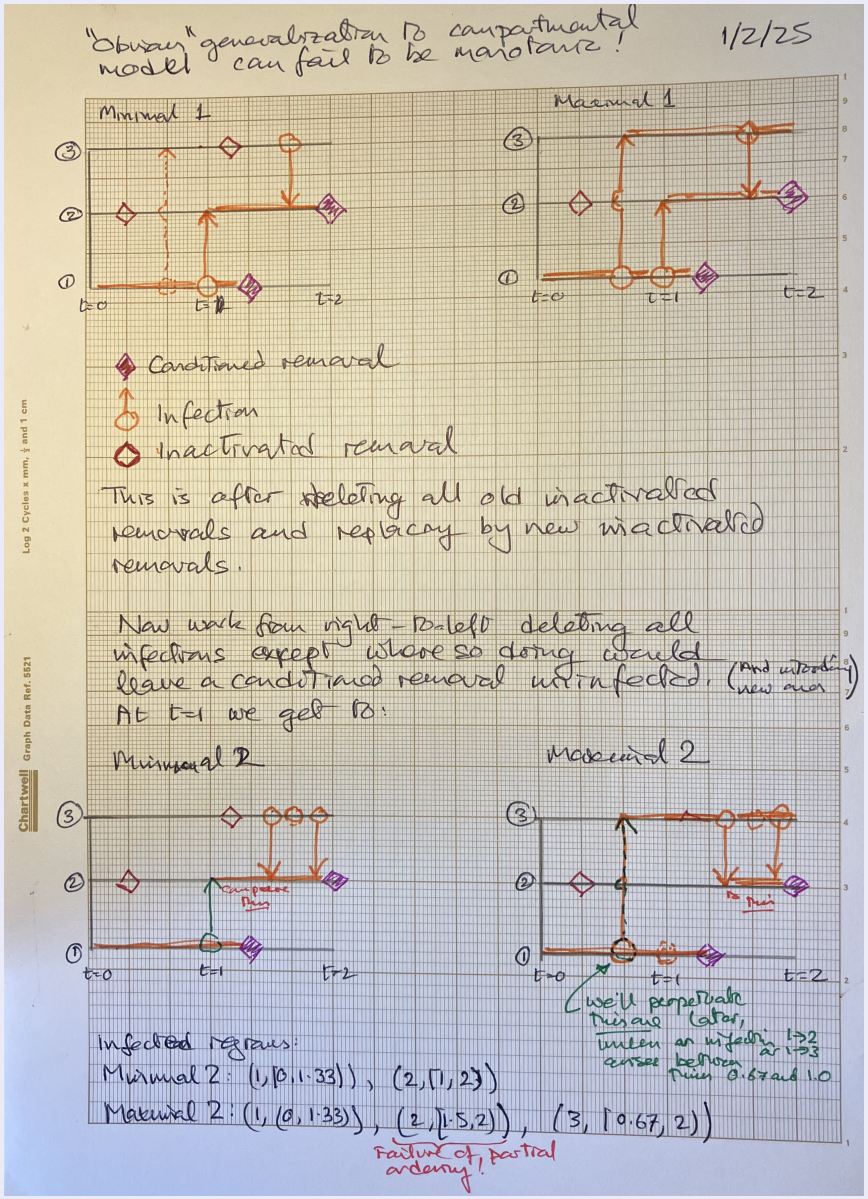
Requirements for monotonicity

For CFTP we need to know that, for coupled iterations (using the same pattern of innovations of new $\mathcal{I}$s and $\mathcal{R}$s), if two variants are started so that the infected region of one contains the other, then this persists through development of the algorithmic time.
It would suffice to prove two technical results:

1. If the old infected region of one contains the other, then the NFZ of the one is contained in the NFZ of the other;
2. If the old infected region of one contains the other, and the NFZ of the one is contained in the NFZ of the other, then the new infected region of the one is contained in the other.

Then CFTP would make sense, and it would only be necessary to show that accessibility of a set of near-maximal configurations guarantees eventual coalescence.

Counterexample to monotonicity



Other technical information

Software used in computations

Software	*Version*	*Branch*	*Last commit*
`quarto`	`1.6.39`	—	
Running under `julia`	`1.11.5`	—	
`EpidemicsCFTP`	`2.2.514`	`develop`	`Fri Mar 21 10:43:55 2025`
`EpidemicsUtilities`	`0.1.2.174`	`main`	`Tue Mar 4 16:32:10 2025`
This `quarto` script	`0.2.2.713`	`develop`	`Wed Mar 12 14:27:50 2025`

Project information

Version:	`0.2.2.715` (`develop`)
Author:	Wilfrid Kendall <`W.S.Kendall@warwick.ac.uk`>
Date:	Fri Jun 20 15:42:30 2025 +0100

Comment:
Preparation for Liverpool seminar

Warwick Statistics