

Perfect Epidemics

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

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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.

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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- ➍ Simplest possible example: *random-walk-CFTP*
(can boost to use Ising model to do simple image reconstruction).

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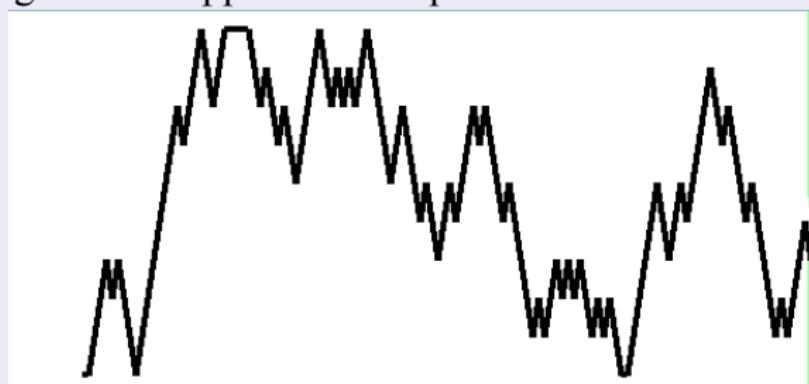
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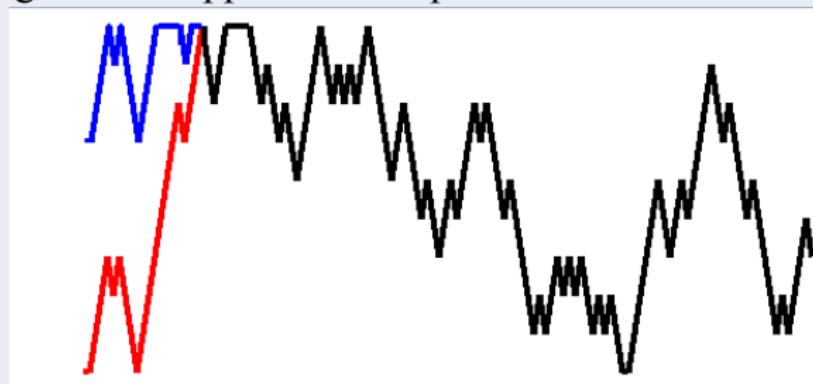
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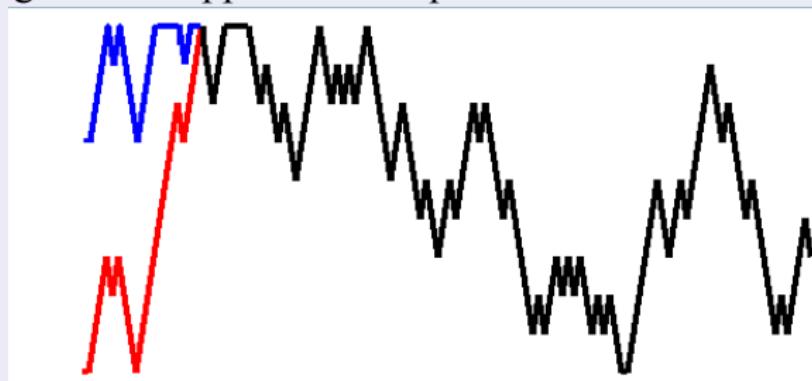
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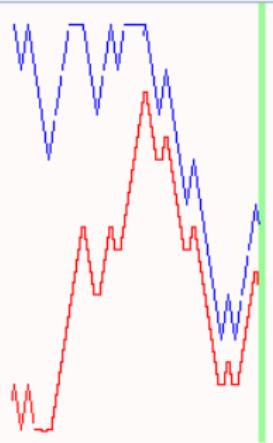
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- ④ Generally **not true** that location *at coupling* is a draw from equilibrium.

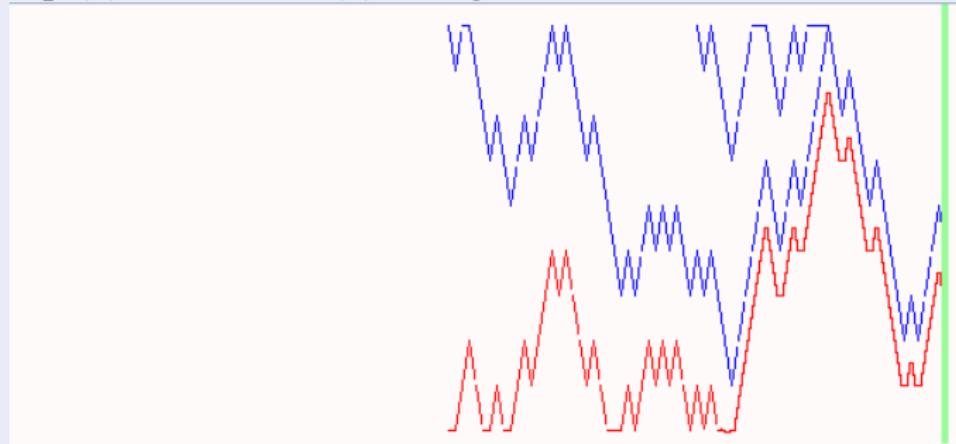
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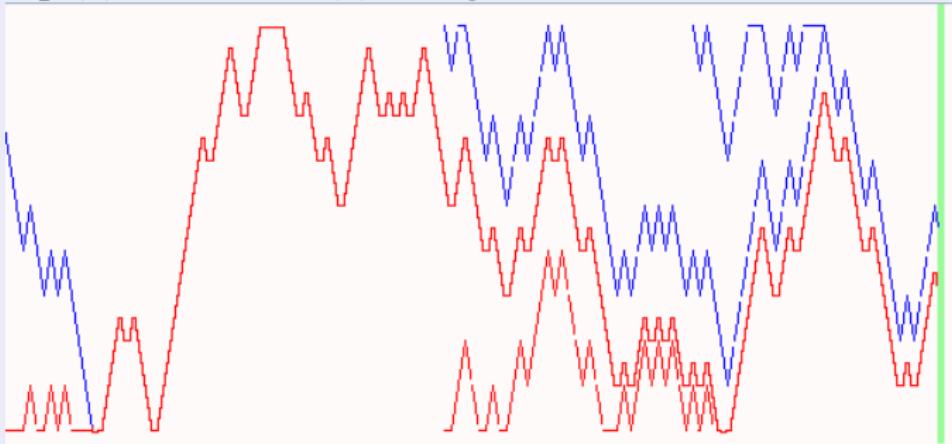


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NB: re-use randomness!

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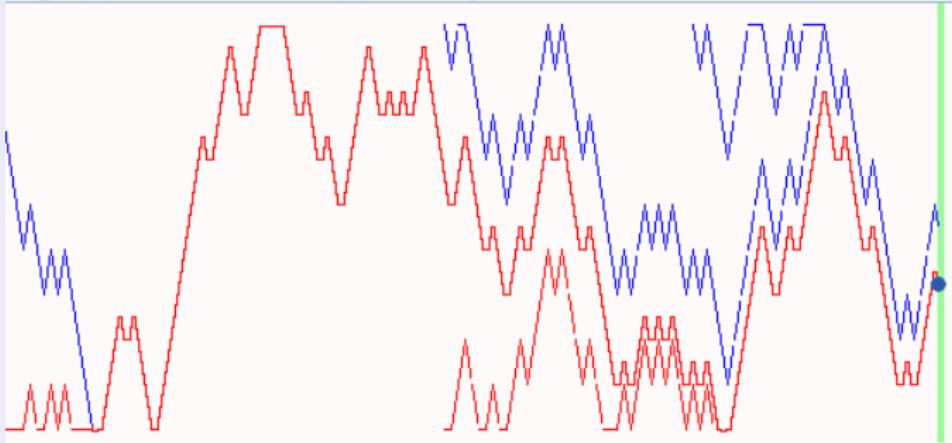
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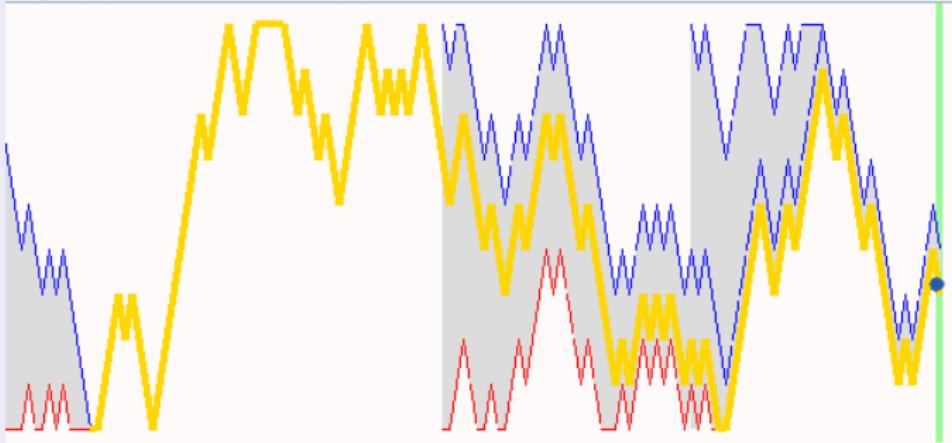
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- ③ May need to iterate back-off doubling several times.
- ④ When coupled, top and bottom yield a common value at time 0.
- ⑤ The common value (golden thread) is an exact draw from equilibrium!

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- ④ Detailed expositions: WSK (2005), Huber (2015).
(Want to implement CFTP in R? see WSK, 2015.)

3. Perfect Epidemics: a challenge problem for CFTP

S-I-R deterministic epidemic:

based on susceptibles s , infectives i , removals r :

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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).



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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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- ➎ Can we use **perfect simulation**?

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- ⑤ Result: *trajectory-valued chain*, unconditioned S-I-R as equilibrium.

From incidents to unconditioned epidemic trajectories (1/3)

Incidents defining an epidemic

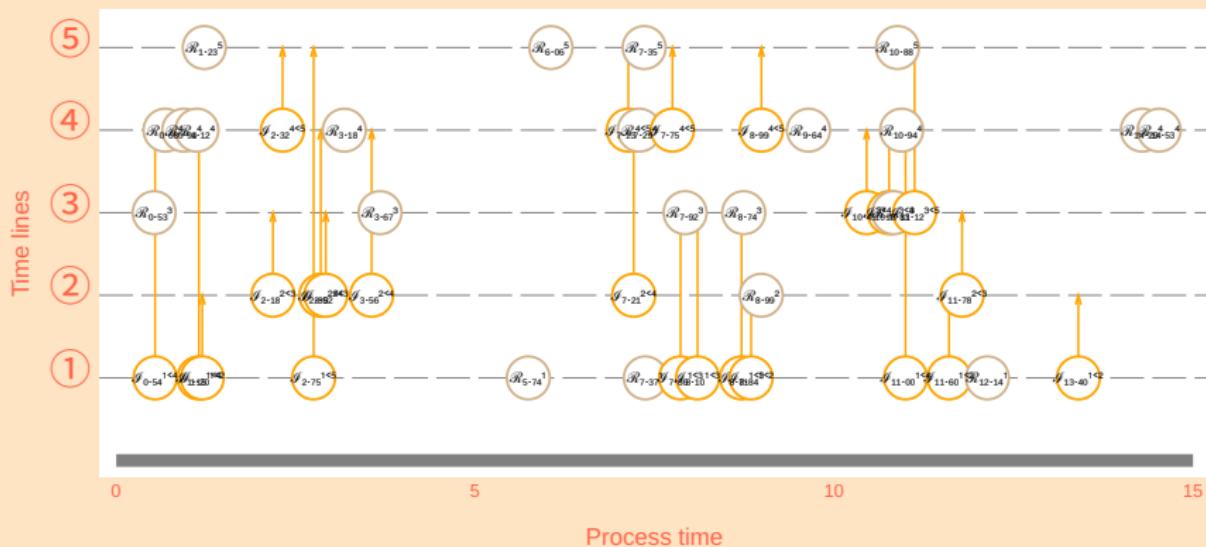


Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

From incidents to unconditioned epidemic trajectories (2/3)

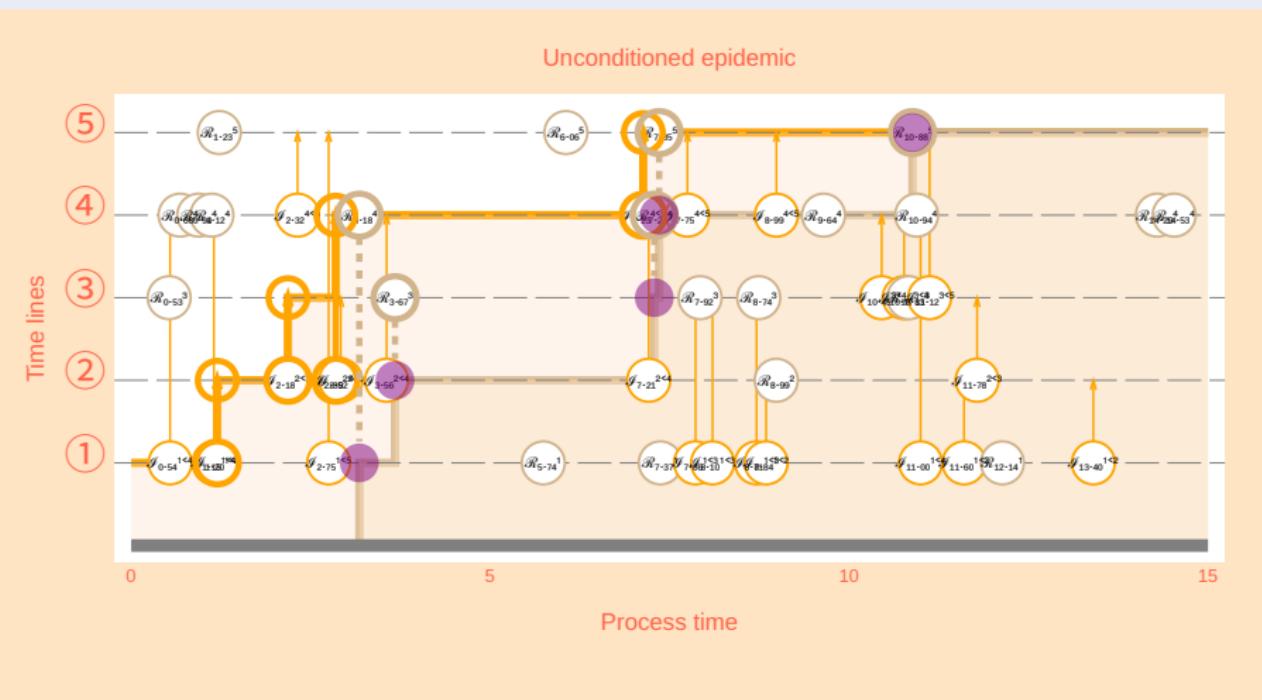


Figure 2: (a) *Infection* activates if target lies on the lowest uninfected timeline; and (b) *removal* activates if on infected timeline; remove lowest infected (purple disk).

From incidents to unconditioned epidemic trajectories (3/3)

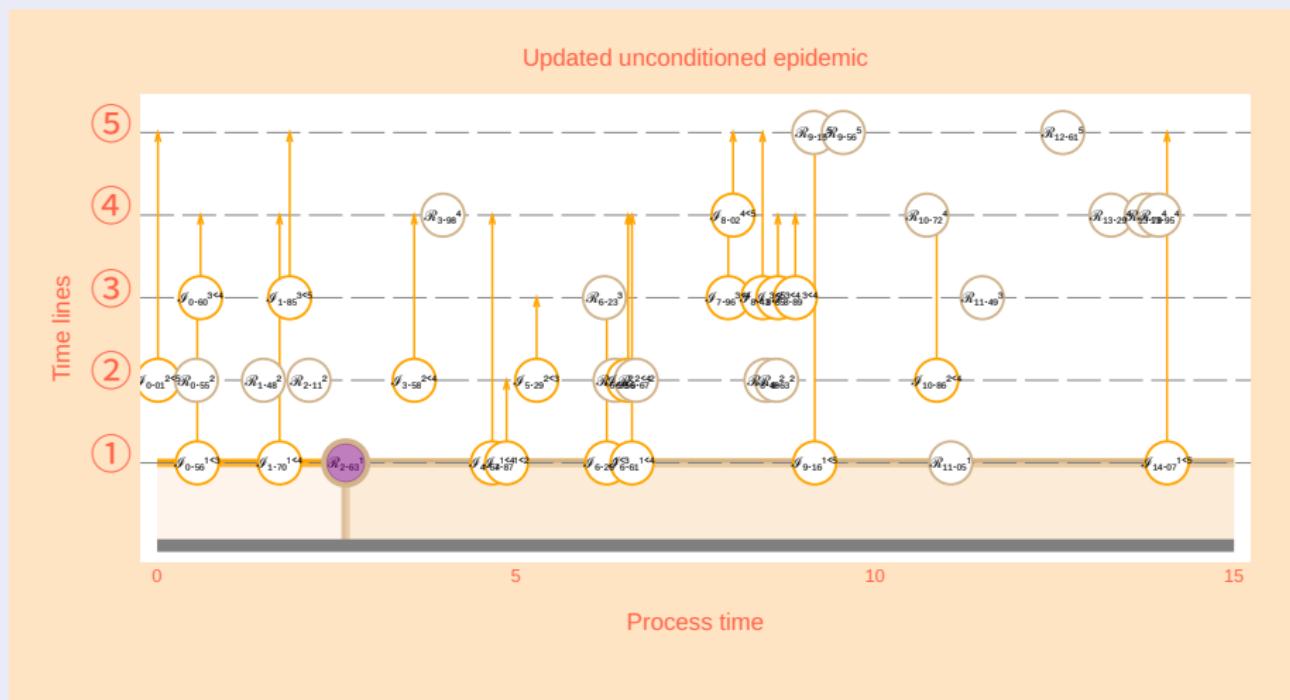


Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing all original incidents by an entirely new set of incidents.

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- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.

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- 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.)

Free evolution evolving in continuous algorithmic time

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- 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)*.

Initial conditioned epidemic

The initial conditioned epidemic

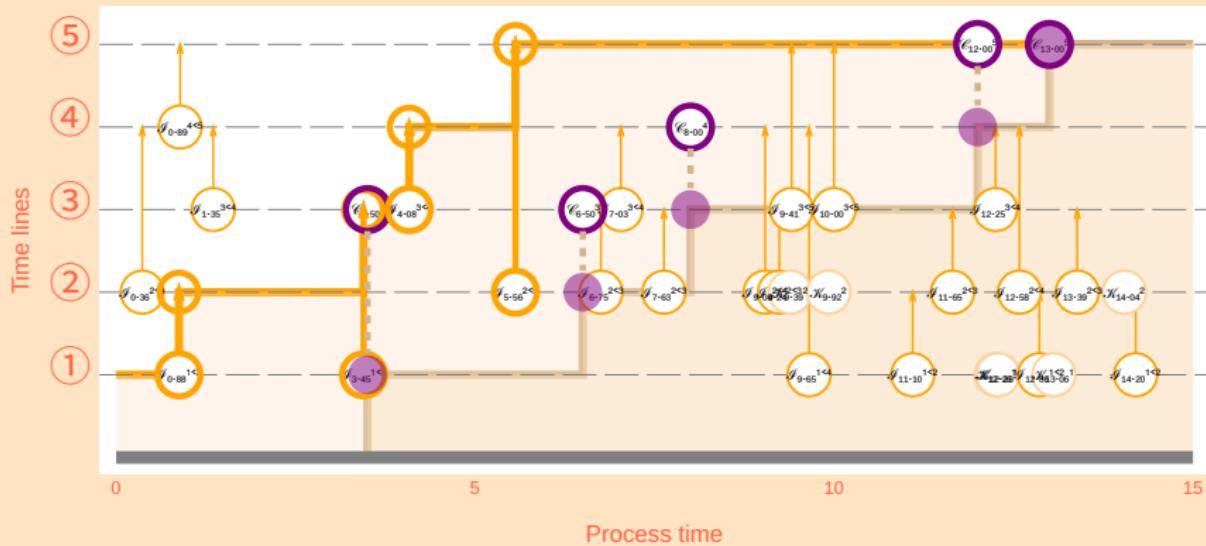


Figure 4: Initial conditioned epidemic, with conditioned removals indicated using purple circles (and purple disks when non-target timelines are infected).

Conditional epidemic update

Fully updated conditioned epidemic

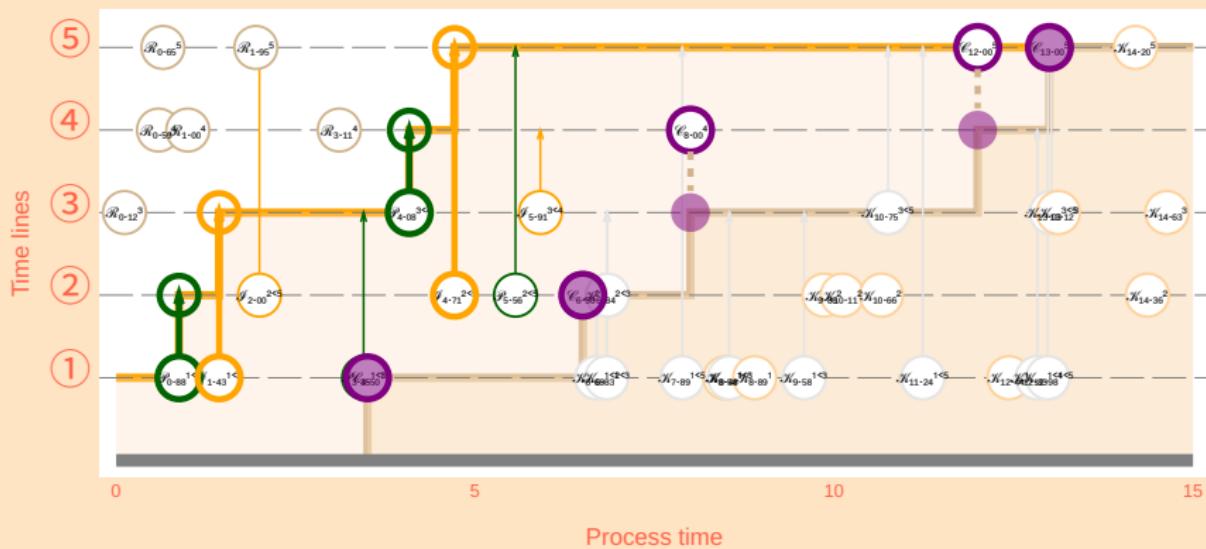


Figure 5: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

Laziest feasible epidemic (LFE)

Fully updated conditioned epidemic with LFE

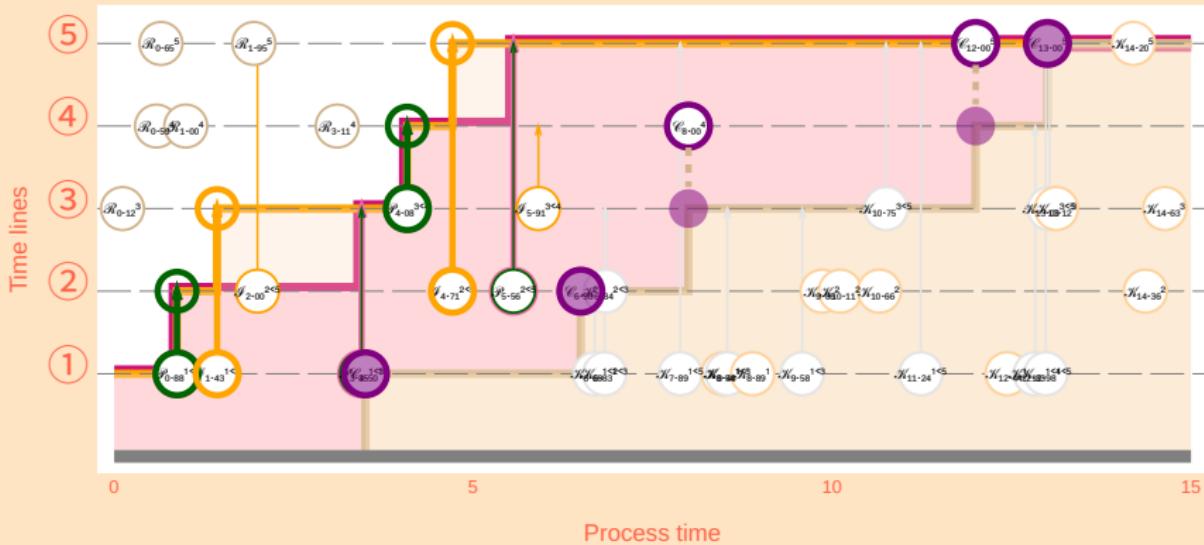


Figure 6: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

No-fly zone (NFZ)

Fully updated conditioned epidemic with 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

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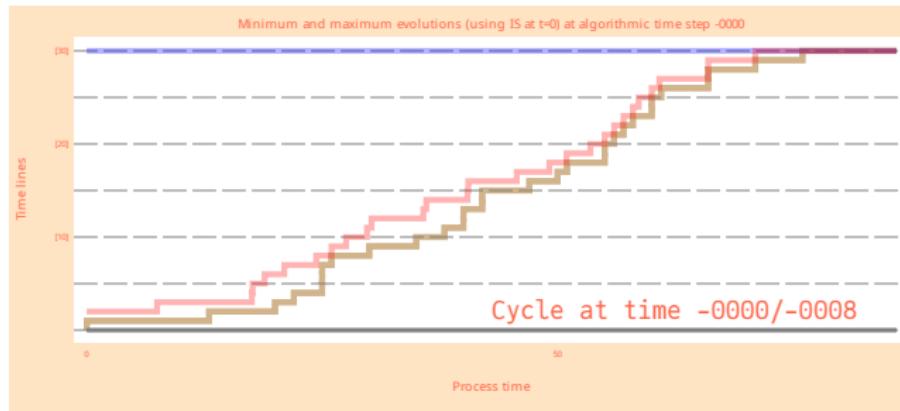
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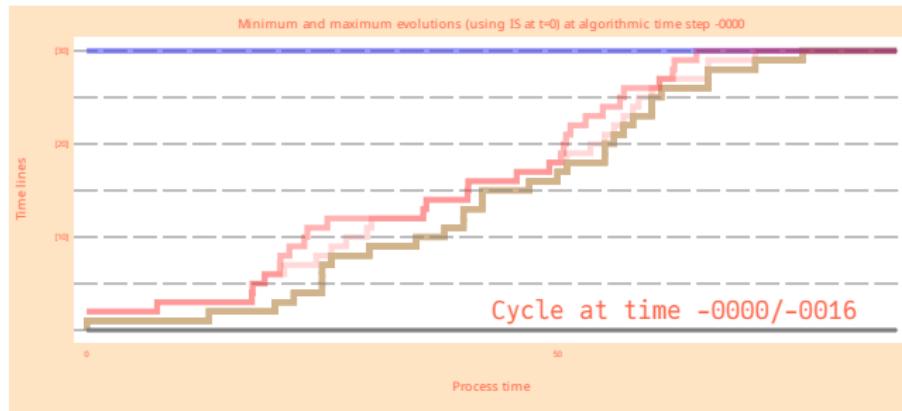
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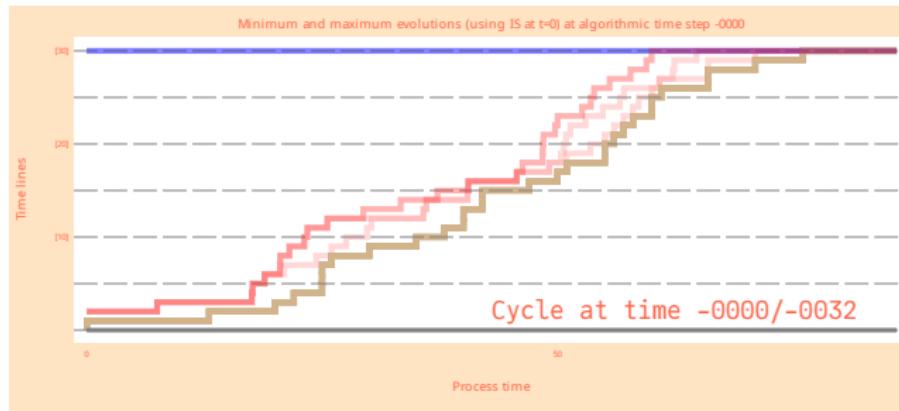
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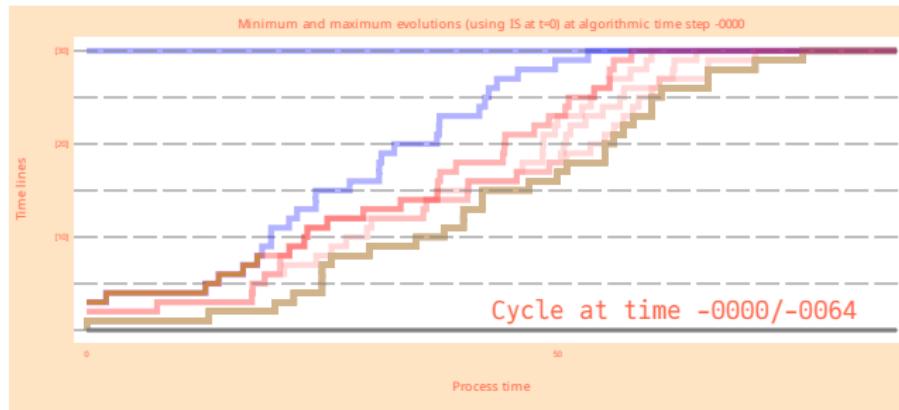
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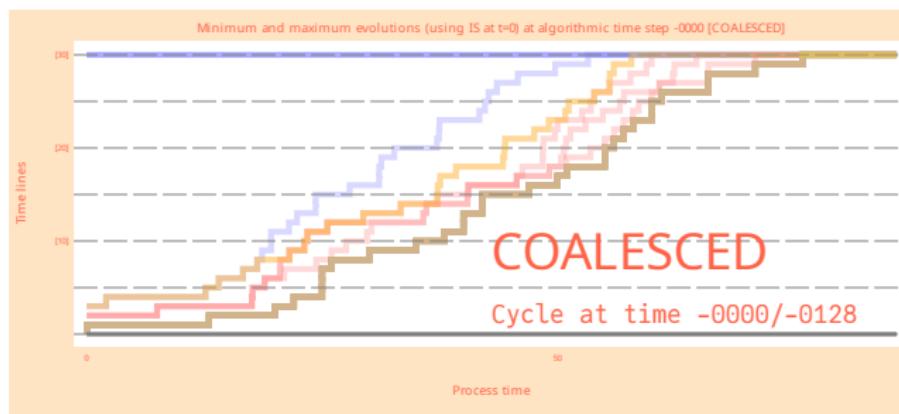
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- Finally: can we generalize to other suitable compartment models?

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



References I

- Bailey, N.T.J. (1975) *The mathematical theory of infectious diseases and its applications*, 2nd Ed. ed. Griffin.
- Bensoussane, H. (2025) Bayesian Individual-level Epidemic Models : Accounting for Missing Data and Utilising Covariate Information (PhD No. January).
- Bezanson, J., Edelman, A., Karpinski, S., & Shah, V.B. (2017) Julia: A Fresh Approach to Numerical Computing. *SIAM Review*, **59**, 65–98.
- Cori, A. & Kucharski, A. (2024) Inference of epidemic dynamics in the COVID-19 era and beyond. *Epidemics*, **48**, 100784.
- Donnelly, P. & Kurtz, T.G. (1996) A countable representation of the Fleming-Viot measure-valued diffusion. *The Annals of Probability*, **24**, 698–742.
- Foss, S.G. & Tweedie, R.L. (1998) Perfect simulation and backward coupling. *Stochastic Models*, **14**, 187–203.
- Fraser, C. & Others (2023) OpenABM-Covid19: Agent-based model for modelling the Covid-19 and Contact-Tracing.
- Gibson, G.J. & Renshaw, E. (1998) Estimating parameters in stochastic compartmental models using Markov chain methods. *Mathematical and Medical Biology*, **15**, 19–40.
- Gibson, G.J. & Renshaw, E. (2001) Likelihood estimation for stochastic compartmental models using Markov chain methods. *Statistics and Computing*, **11**, 347–358.

References II

- Huber, M.L. (2015) *Perfect Simulation*. Boca Raton: Chapman; Hall/CRC.
- Liggett, T.M. (1985) *Interacting Particle Systems*, Grundlehren der mathematischen wissenschaften. Berlin, Heidelberg: Springer Berlin.
- O'Neill, P.D. & Roberts, G.O. (1999) Bayesian Inference for Partially Observed Stochastic Epidemics. *Journal of the Royal Statistical Society Series A: Statistics in Society*, **162**, 121–129.
- Pratchett, T. & Baxter, S. (2012) *The Long Earth*. Doubleday.
- Propp, J.G. & Wilson, D.B. (1996) Exact sampling with coupled Markov chains and applications to statistical mechanics. *Random Structures and Algorithms*, **9**, 223–252.
- Rocklöv, J., Sjödin, H., & Wilder-Smith, A. (2020) COVID-19 outbreak on the Diamond Princess cruise ship: estimating the epidemic potential and effectiveness of public health countermeasures. *Journal of Travel Medicine*, **27**, 7 pp.
- SBC (2020) Omnithermal Perfect Simulation for Multi-server Queues. *ACM Transactions on Modeling and Computer Simulation*, **30**, 1–15.
- SBC & WSK (2007b) Perfect simulation for a class of positive recurrent Markov chains (corrigendum). *Annals of Applied Probability*, **17**, 1808–1810.
- SBC & WSK (2007a) Perfect simulation for a class of positive recurrent Markov chains. *Annals of Applied Probability*, **17**, 781–808.
- SBC & WSK (2015) Perfect simulation of M/G/c queues. *Advances in Applied Probability*, **47**, 1039–1063.

References III

- SBC & WSK (2024) Perfect Epidemics.
- Whittle, P. (1955) The outcome of a stochastic epidemic—a note on Bailey's paper. *Biometrika*, **42**, 116–122.
- WSK (1998) Perfect Simulation for the Area-Interaction Point Process. *Probability towards 2000* (Accardi, L. & Heyde, C.C. eds). Springer-Verlag, pp. 218–234.
- WSK (2004) Geometric ergodicity and perfect simulation. *Electronic Communications in Probability*, **9**, 140–151.
- WSK (2005) Notes on Perfect Simulation. Singapore: World Scientific, pp. 93–146.
- WSK (2015) Introduction to CFTP using R. *Stochastic geometry, spatial statistics and random fields, Lecture notes in mathematics*. Springer, pp. 405–439.
- WSK & Møller, J. (2000) Perfect simulation using dominating processes on ordered spaces, with application to locally stable point processes. *Advances in Applied Probability*, **32**, 844–865.

Image information

<i>Image</i>	<i>Attribution</i>	
<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

<i>Date</i>	<i>Title</i>		<i>Location</i>	
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

A small set for a conditioned epidemic.

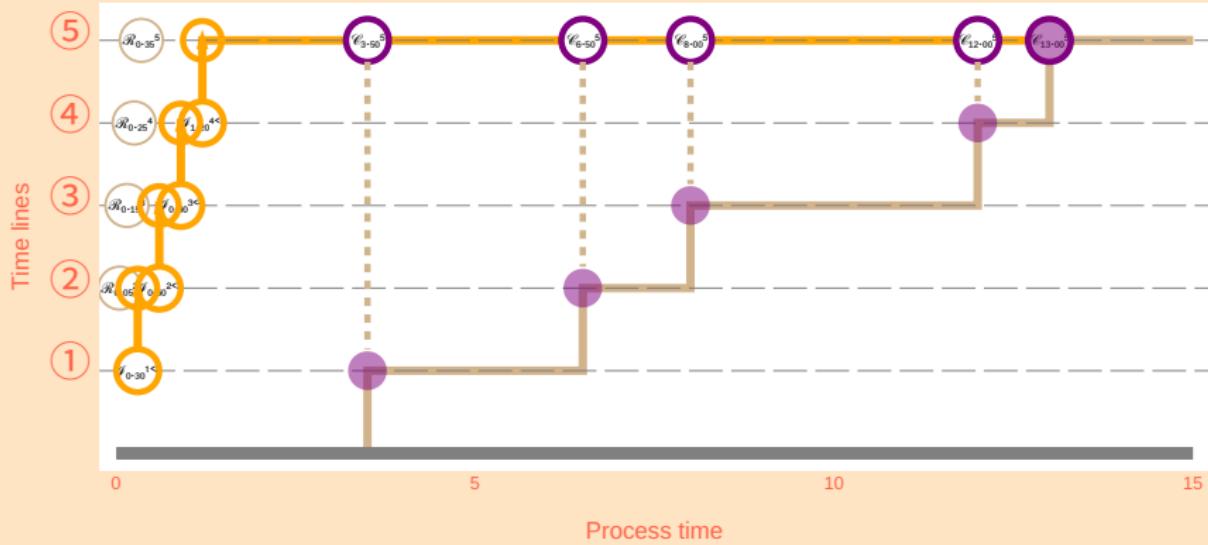


Figure 8: A conditioned epidemic in which all activated infections occur before time 3.0, also before smallest observed removal time.

Appendix B: Notes towards a monotonicity proof

Summary of plan of proof:

- ① Let $EPI_{\tau=0}^{\pm}$ represent two epidemic trajectories (\pm) at algorithmic time $\tau=0$, viewed as subsets of “timeline-space” $\{(k, [0, T)) : k = 1, 2, \dots\}$.

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- ② Suppose at algorithmic time $\tau=0$ the *fast* $\text{EPI}_{\tau=0}^+$ is never later than the *slow* $\text{EPI}_{\tau=0}^-$ so $\text{EPI}_{\tau=0}^+ \supseteq \text{EPI}_{\tau=0}^-$; additionally suppose monotonicity holds for conditional removal marks: if $\mathcal{C}_{\tau=0}^{\pm}$ are conditional removals at fixed process time t then $\mathcal{C}_{\tau=0}^+ \text{ timeline} \geq \mathcal{C}_{\tau=0}^- \text{ timeline}$.

Appendix B: Notes towards a monotonicity proof

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- ③ Then a related monotonicity holds for the laziest feasible epidemics:
 $\text{LFE}_{\tau=1}^+ \leq \text{LFE}_{\tau=1}^-$ at algorithmic time $\tau=1$.

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- ③ Then a related monotonicity holds for the laziest feasible epidemics: $\text{LFE}_{\tau=1}^+ \leq \text{LFE}_{\tau=1}^-$ at algorithmic time $\tau=1$.
- ④ Likewise a similar monotonicity (but reversing the set-theoretic inclusion!) holds for no-fly zones: $\text{NFZ}_{\tau=1}^+ \subseteq \text{NFZ}_{\tau=1}^-$.

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- ① Let $\text{EPI}_{\tau=0}^{\pm}$ represent two epidemic trajectories (\pm) at algorithmic time $\tau=0$, viewed as subsets of “timeline-space” $\{(k, [0, T)) : k = 1, 2, \dots\}$.
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- ③ Then a related monotonicity holds for the laziest feasible epidemics: $\text{LFE}_{\tau=1}^+ \leq \text{LFE}_{\tau=1}^-$ at algorithmic time $\tau=1$.
- ④ Likewise a similar monotonicity (but reversing the set-theoretic inclusion!) holds for no-fly zones: $\text{NFZ}_{\tau=1}^+ \subseteq \text{NFZ}_{\tau=1}^-$.
- ⑤ Now prove $\text{EPI}_{\tau=1}^+ \supseteq \text{EPI}_{\tau=1}^-$ moreover if $\mathcal{C}_{\tau=1}^+$ matches $\mathcal{C}_{\tau=1}^-$ at process time t then $\mathcal{C}_{\tau=1}^+ \text{ timeline} \geq \mathcal{C}_{\tau=1}^- \text{ timeline}$.

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

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

- ① For the top timeline n , $\text{LFE}_{\tau=1}^{\pm}(n)$ must precede any \mathcal{C}^{\pm} on timeline n ; set $\text{LFE}_{\tau=1}^{\pm}(n) = T$ if no such \mathcal{C}^{\pm} .

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

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

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- ② For $k < n$ with LFE _{$\tau=1$} [±]($k+1$) = T , again LFE _{$\tau=1$} [±](k) must precede any \mathcal{C}^\pm on timeline k ; set LFE _{$\tau=1$} [±](k) = T if no such \mathcal{C}^\pm .

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- ③ Suppose n_0 is largest k with $\text{LFE}_{\tau=1}^{\pm}(k) < T$. Working downwards through $\ell = n_0 - 1, \dots, 1$, $\text{LFE}_{\tau=1}^{\pm}(\ell)$ is the time of the latest infection targeting $\ell + 1$ and based in the infected region such that

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 - (a) $\text{LFE}_{\tau=1}^{\pm}(\ell) \leq \text{LFE}_{\tau=1}^{\pm}(\ell + 1)$;

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

- ① For the top timeline n , LFE _{$\tau=1$} [±](n) must precede any C[±] on timeline n ; set LFE _{$\tau=1$} [±](n) = T if no such C[±].
- ② For $k < n$ with LFE _{$\tau=1$} [±]($k+1$) = T , again LFE _{$\tau=1$} [±](k) must precede any C[±] on timeline k ; set LFE _{$\tau=1$} [±](k) = T if no such C[±].
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 - ⓐ LFE _{$\tau=1$} [±](ℓ) ≤ LFE _{$\tau=1$} [±]($\ell + 1$);
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- ② For $k < n$ with $\text{LFE}_{\tau=1}^{\pm}(k+1) = T$, again $\text{LFE}_{\tau=1}^{\pm}(k)$ must precede any \mathcal{C}^{\pm} on timeline k ; set $\text{LFE}_{\tau=1}^{\pm}(k) = T$ if no such \mathcal{C}^{\pm} .
- ③ Suppose n_0 is largest k with $\text{LFE}_{\tau=1}^{\pm}(k) < T$. Working downwards through $\ell = n_0 - 1, \dots, 1$, $\text{LFE}_{\tau=1}^{\pm}(\ell)$ is the time of the latest infection targeting $\ell + 1$ and based in the infected region such that
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LFE _{$\tau=1$} : monotonicity

- ① Re-sample \mathcal{C}^\pm timelines by accept-reject: same proposals for both \pm . As $\text{EPI}_{\tau=0}^+ \supseteq \text{EPI}_{\tau=0}^-$, so \mathcal{C} timelines for $\text{EPI}_{\tau=1}^+$ no lower than for $\text{EPI}_{\tau=1}^-$.

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- ③ Now work inductively. Suppose monotonicity holds for $k+1, \dots, n$. Then $LFE_{\tau=1}^+(k) \leq LFE_{\tau=1}^+(k+1) \leq LFE_{\tau=1}^-(k+1)$. But the set of “times of \mathcal{C}^- on timelines $\ell, \ell+1, \dots, n$ ” is a subset of the set of “times of \mathcal{C}^+ on timelines $\ell, \ell+1, \dots, n$ ”. So if b_k^\pm is the resulting right-constraint on $LFE_{\tau=1}^\pm(k)$ then $b_k^+ \leq b_k^-$.

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- ④ Suppose $EPI_{\tau=0}^\pm$ infects timeline $k+1$ at time a_k^\pm : $a_k^+ \leq a_k^- \leq b_k^-$ by monotonicity for $EPI_{\tau=0}^\pm$. If no $\tau=1$ infections infect timeline $k+1$ in $[a_k^\pm, b_k^\pm]$, then $LFE_{\tau=1}^\pm(k)$ perpetuates a_k^\pm using $EPI_{\tau=0}^\pm(k)$. Then argue case-by-case:

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 - (a) no perpetuation occurs (use fact, all infections are shared);

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- ④ Suppose $EPI_{\tau=0}^\pm$ infects timeline $k+1$ at time a_k^\pm : $a_k^+ \leq a_k^- \leq b_k^-$ by monotonicity for $EPI_{\tau=0}^\pm$. If no $\tau=1$ infections infect timeline $k+1$ in $[a_k^\pm, b_k^\pm]$, then $LFE_{\tau=1}^\pm(k)$ perpetuates a_k^\pm using $EPI_{\tau=0}^\pm(k)$. Then argue case-by-case:
 - (a) no perpetuation occurs (use fact, all infections are shared);
 - (b) $LFE_{\tau=1}^-(k)$ is perpetuated (so no useful infections after perpetuation);

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

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

- ① Set $\text{NFZ}_{\tau=1}^{\pm,*}$ to be union of regions $(k, [0, t])$ for all \mathcal{R} s of $\text{EPI}_{\tau=1}^{\pm}$, for timeline k and time t of \mathcal{R} . Set $\text{NFZ}_{\tau=1}^{\pm,*} = \{(k, [0, t_k^*]) : t_k^* > 0\}$.

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

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- ② Set $\text{NFZ}_{\tau=1}^{\pm,0} = \{(k, [0, t_k]) : t_k > 0\}$ as monotonic envelope of $\text{NFZ}_{\tau=1}^{\pm,*}$: $\{t_k\}$ is smallest non-decreasing sequence majorizing $\{t_k^*\}$.

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- ③ Work backwards through new “*non-removed*” \mathcal{J} s. At step j , time t ,

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 - ④ accept \mathcal{J} if it targets $\text{NFZ}_{\tau=1}^{\pm,j-1}$ at timeline k but infection fails: set $\text{NFZ}_{\tau=1}^{\pm,j} = \text{NFZ}_{\tau=1}^{\pm,j-1} \cup \{(k-1, [0, t])\}$;
otherwise set $\text{NFZ}_{\tau=1}^{\pm,j} = \text{NFZ}_{\tau=1}^{\pm,j-1}$ and

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otherwise set $\text{NFZ}_{\tau=1}^{\pm,j} = \text{NFZ}_{\tau=1}^{\pm,j-1}$ and
 - ④b) **reject** \mathcal{J} if it would infect part of $\text{NFZ}_{\tau=1}^{\pm,j-1}$;

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

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

- ① Set $\text{NFZ}_{\tau=1}^{\pm,*}$ to be union of regions $(k, [0, t])$ for all \mathcal{R} s of $\text{EPI}_{\tau=1}^{\pm}$, for timeline k and time t of \mathcal{R} . Set $\text{NFZ}_{\tau=1}^{\pm,*} = \{(k, [0, t_k^*]) : t_k^* > 0\}$.
- ② Set $\text{NFZ}_{\tau=1}^{\pm,0} = \{(k, [0, t_k]) : t_k > 0\}$ as monotonic envelope of $\text{NFZ}_{\tau=1}^{\pm,*}$: $\{t_k\}$ is smallest non-decreasing sequence majorizing $\{t_k^*\}$.
- ③ Work backwards through new “*non-removed*” \mathcal{J} s. At step j , time t ,
 - ④(a) **accept** \mathcal{J} if it targets $\text{NFZ}_{\tau=1}^{\pm,j-1}$ at timeline k but infection fails: set $\text{NFZ}_{\tau=1}^{\pm,j} = \text{NFZ}_{\tau=1}^{\pm,j-1} \cup \{(k-1, [0, t])\}$;
otherwise set $\text{NFZ}_{\tau=1}^{\pm,j} = \text{NFZ}_{\tau=1}^{\pm,j-1}$ and
 - ④(b) **reject** \mathcal{J} if it would infect part of $\text{NFZ}_{\tau=1}^{\pm,j-1}$;
 - ④(c) **accept** \mathcal{J} if it doesn’t target $\text{NFZ}_{\tau=1}^{\pm,j-1}$.

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

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 - ④(c) **accept** \mathcal{J} if it doesn’t target $\text{NFZ}_{\tau=1}^{\pm,j-1}$.
- ④ Set $\text{NFZ}_{\tau=1}^{\pm} = \text{NFZ}_{\tau=1}^{\pm,j}$ if a total of j new \mathcal{J} s are proposed for $\text{EPI}_{\tau=1}^{\pm}$, so no more \mathcal{J} s remain!

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

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

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

- ① Since $\text{EPI}_{\tau=0}^+ \supseteq \text{EPI}_{\tau=0}^-$ and the set of \mathcal{R} s for $\text{EPI}_{\tau=1}^\pm$ are formed by intersecting the same \mathcal{R} pattern with the complements of $\text{EPI}_{\tau=0}^\pm$, it follows that $\text{NFZ}_{\tau=1}^{+,*} \subseteq \text{NFZ}_{\tau=1}^{-,*}$.

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- ② Monotonicity for $\text{NFZ}_{\tau=1}^{\pm,0}$ is a direct consequence.

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

- ① Since EPI _{$\tau=0$} ⁺ \supseteq EPI _{$\tau=0$} ⁻ and the set of \mathcal{R} s for EPI _{$\tau=1$} [±] are formed by intersecting the same \mathcal{R} pattern with the complements of EPI _{$\tau=0$} [±], it follows that NFZ _{$\tau=1$} ^{+,*} \subseteq NFZ _{$\tau=1$} ^{-,*}.
- ② Monotonicity for NFZ _{$\tau=1$} ^{±,0} is a direct consequence.
- ③ Given NFZ _{$\tau=1$} ^{+,j-1} \subseteq NFZ _{$\tau=1$} ^{-,j-1}, create NFZ _{$\tau=1$} ^{±,j} by proposing \mathcal{J} at time t targeting timeline k , based in EPI _{$\tau=0$} ⁺ infected region. Then $\text{NFZ}_{\tau=1}^{+,j} = \text{NFZ}_{\tau=1}^{+,j-1} \cup \{(k-1, [0, t])\}$ exactly when \mathcal{J} fails to infect in EPI _{$\tau=1$} ⁺. Then

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 - (b) infection fails for EPI _{$\tau=1$} ⁺ because timeline $k-1$ is not infected at t in EPI _{$\tau=0$} ⁺. But we know EPI _{$\tau=0$} ⁺ \supseteq EPI _{$\tau=0$} ⁻, so timeline $k-1$ is not infected at t in EPI _{$\tau=0$} ⁻ either. So infection in EPI _{$\tau=1$} ⁻ also fails.

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

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

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

Consider:

- there is epidemic monotonicity at algorithmic time $\tau=0$
(EPI _{$\tau=0$} ⁺ \supseteq EPI _{$\tau=0$} ⁻, also \mathcal{C} s in EPI _{$\tau=0$} ⁺ are never lower than in EPI _{$\tau=0$} ⁻);

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

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- at algorithmic time $\tau=1$ there is monotonicity of laziest feasible epidemic ($\text{LFE}_{\tau=1}^+(k) \leq \text{LFE}_{\tau=1}^-(k)$ for all timelines k);

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Deduce epidemic monotonicity at algorithmic time $\tau=1$

($EPI_{\tau=1}^+ \supseteq EPI_{\tau=1}^-$).

Two cases to consider. Use ∂NFZ to represent right-most boundary for a NFZ , and similarly use ∂EPI to represent *left*-most boundary for a EPI):

① $\partial NFZ_{\tau=1}^+ \leq LFE_{\tau=1}^+ \leq \partial NFZ_{\tau=1}^- \leq LFE_{\tau=1}^-;$

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

$$\partial NFZ_{\tau=1}^\pm \leq \partial EPI_{\tau=1}^\pm \leq LFE_{\tau=1}^\pm.$$

$EPI_{\tau=1}$: monotonicity (II)

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

- ① If the $EPI_{\tau=1}^-(k)$ infection is perpetuated, it must agree with $LFE_{\tau=1}^-(k)$ and so monotonicity follows.

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- ③ If the $EPI_{\tau=1}^-(k)$ infection is not perpetuated and occurs earlier than $LFE_{\tau=1}^+(k)$ then it is available as a possible candidate for $EPI_{\tau=1}^+(k)$ and so here too $EPI_{\tau=1}^-(k)$ is no earlier than $EPI_{\tau=1}^+(k)$.

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This completes the proof of monotonicity for $EPI_{\tau=1}$.

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- 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.

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- 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).

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

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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.

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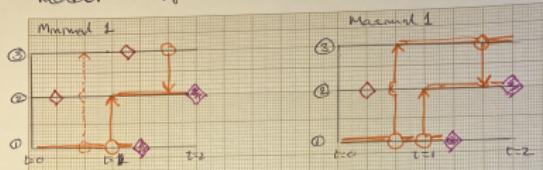
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Then **CFTP** would make sense, and it would only be necessary to show that accessibility of a set of near-maximal configurations guarantees eventual coalescence.

Counterexample to monotonicity

"Observe" generalization to compartmental model can fail to be monotone!

1/2/25



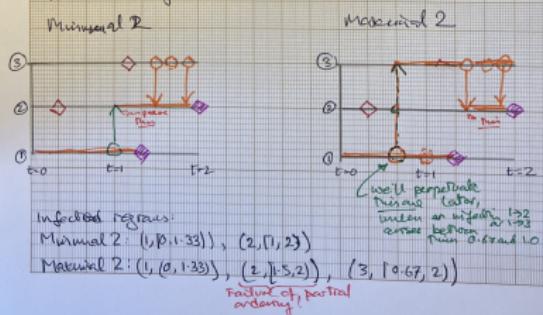
◆ Conditioned removal

◆ Infection

◆ Inactivated removal

This is after deleting all old inactivated removals and replacing by new inactivated removals.

Now work from right-to-left deleting all infections except where so doing would leave a conditioned removal uninfected. (and inactivated removals.)
At $t=1$ we get to:



Other technical information

Software used in computations

<i>Software</i>	<i>Version</i>	<i>Branch</i>	<i>Last commit</i>
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