Perfect Epidemics

Applied Probability Seminar
Department of Statistics, University of Warwick

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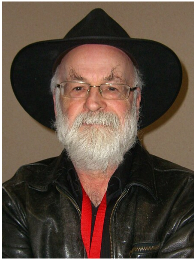
Warwick, York

1 February 2025

Introduction

"Maybe the only significant difference between a really smart simulation and a human being was the noise they made when you punched them."
(The Long Earth, Pratchett & Baxter, 2012)



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

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

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

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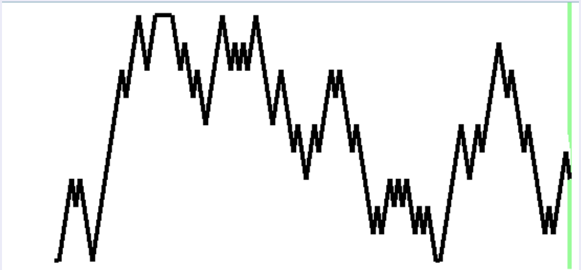

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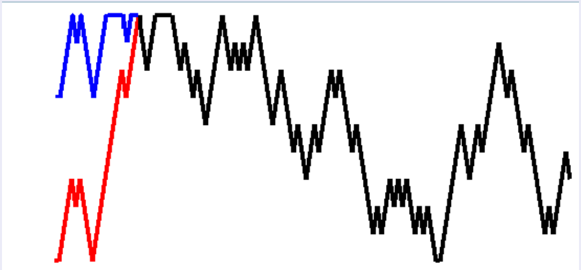

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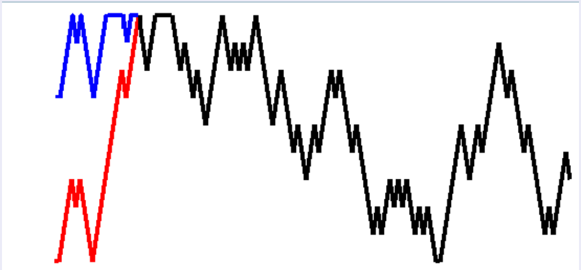
- Generally not true that location *at* coupling is a draw from equilibrium.



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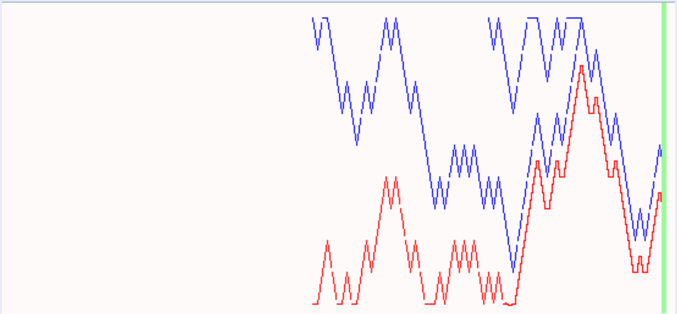

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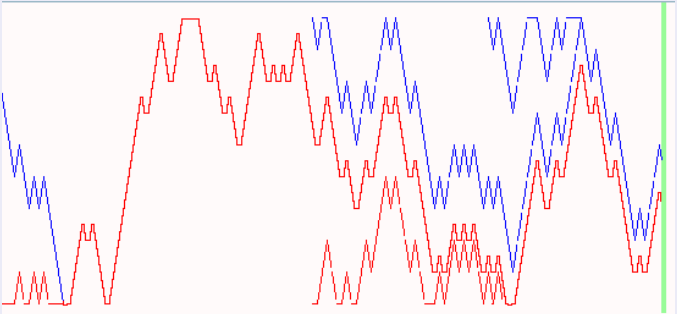

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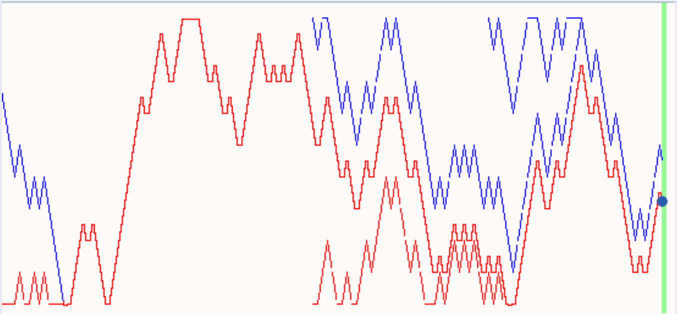

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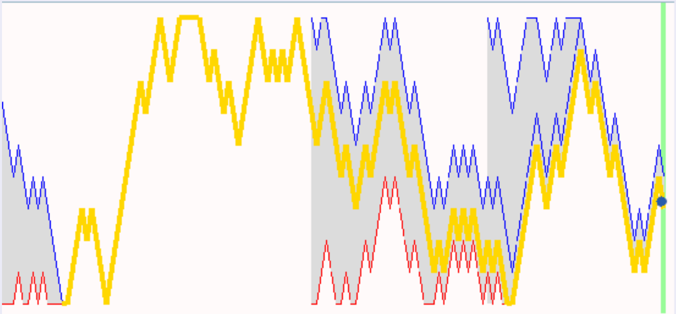
- When coupled, top and bottom yield a common value at time 0.
- The common value is an exact draw from equilibrium!



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

2. 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 $s + i + r = n$):

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

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Both models make an unrealistic assumption: homogeneous mixing.

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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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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 absurdly simple variant of contact tracing:

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

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

From incidents to unconditioned epidemic trajectories (1/3)

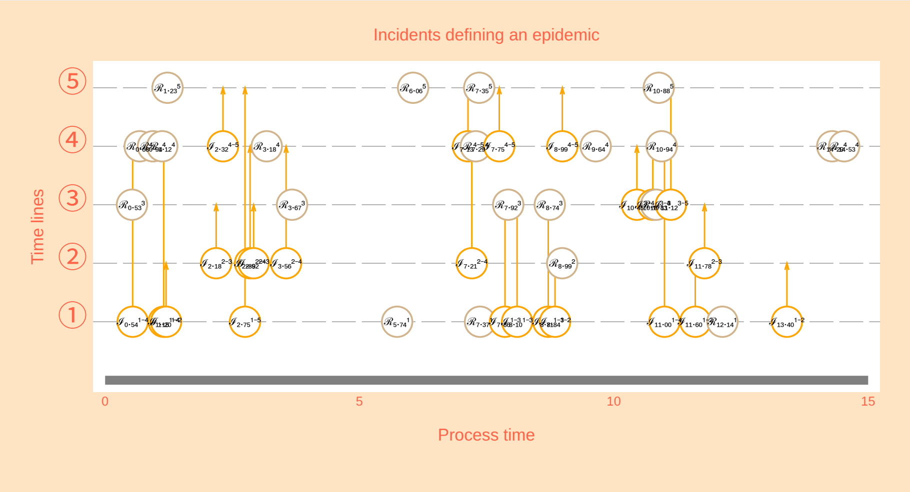

Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

From incidents to unconditioned epidemic trajectories (2/3)

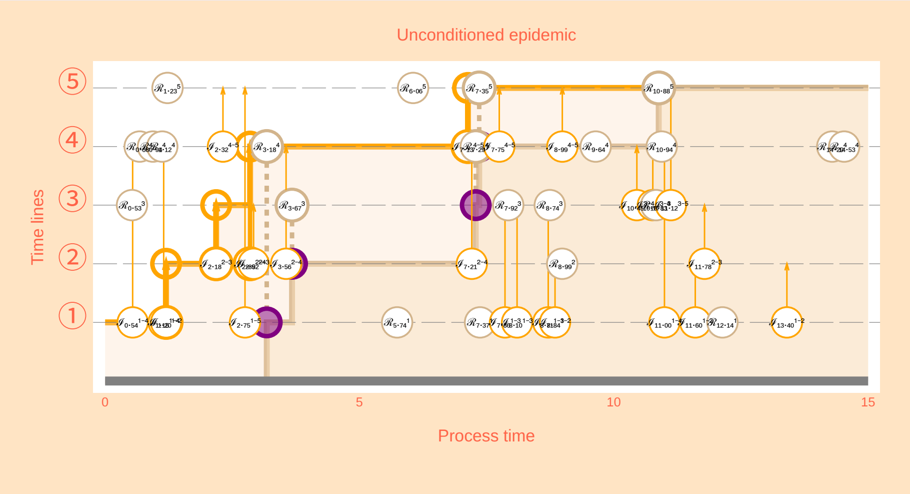

Figure 2: Activate (a) *infection* if target on lowest uninfected timeline; (b) *removal* if in infected region, then remove lowest infected (purple disk if different timeline).

From incidents to unconditioned epidemic trajectories (3/3)

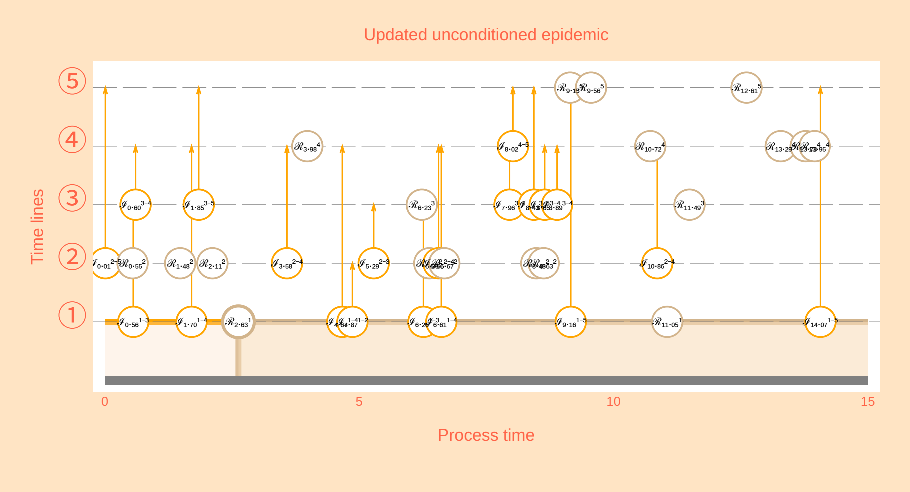

Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing the original incidents by a new set of incidents.

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to subset S of state-space (of *activated* removals occurring precisely at specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S.

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

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- 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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Illustration of technical point (1/8)

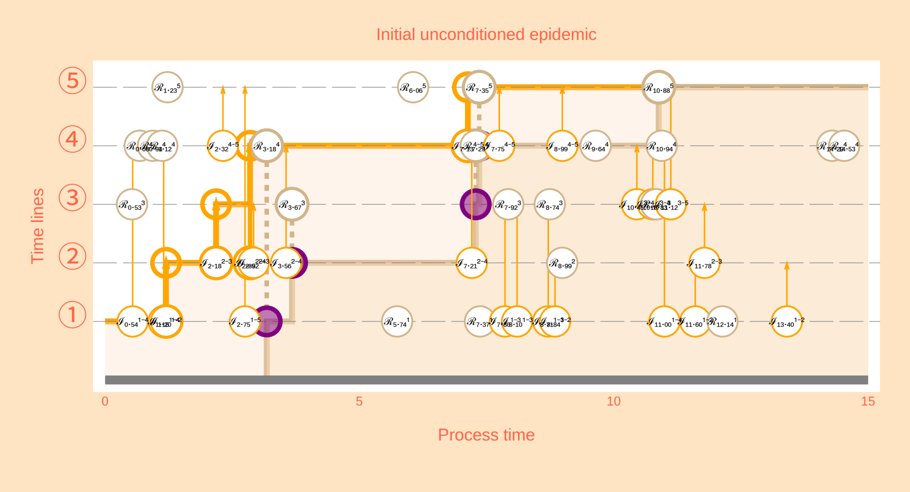

Figure 4: No change yet to removals or infections;

Illustration of technical point (2/8)

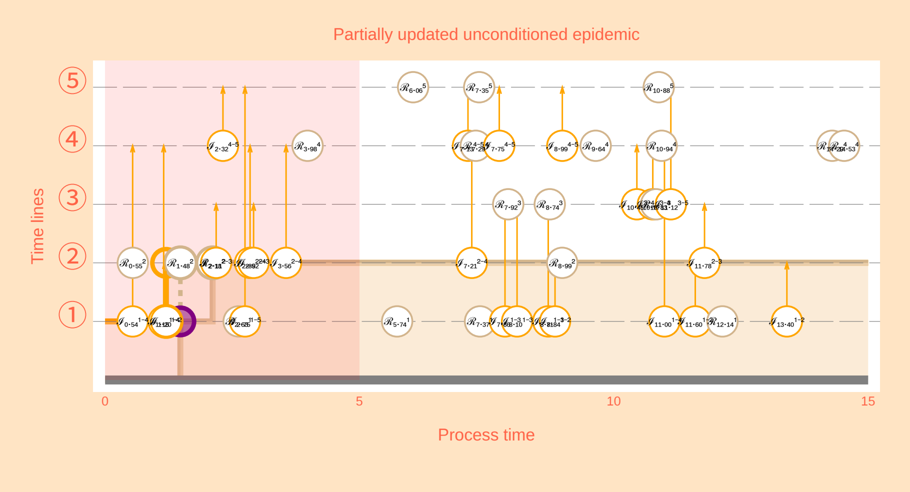

Figure 5: Replace first third of removals, infections unchanged;

Illustration of technical point (3/8)

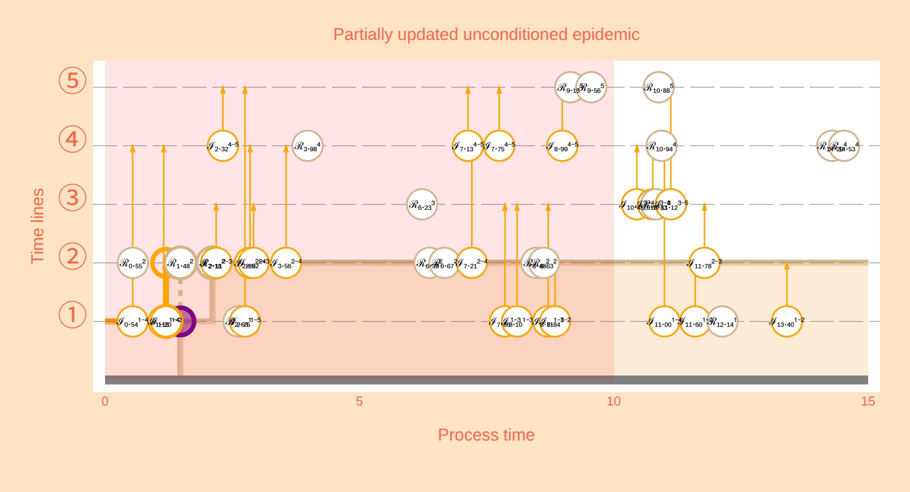

Figure 6: Replace first two-thirds of removals, infections unchanged;

Illustration of technical point (4/8)

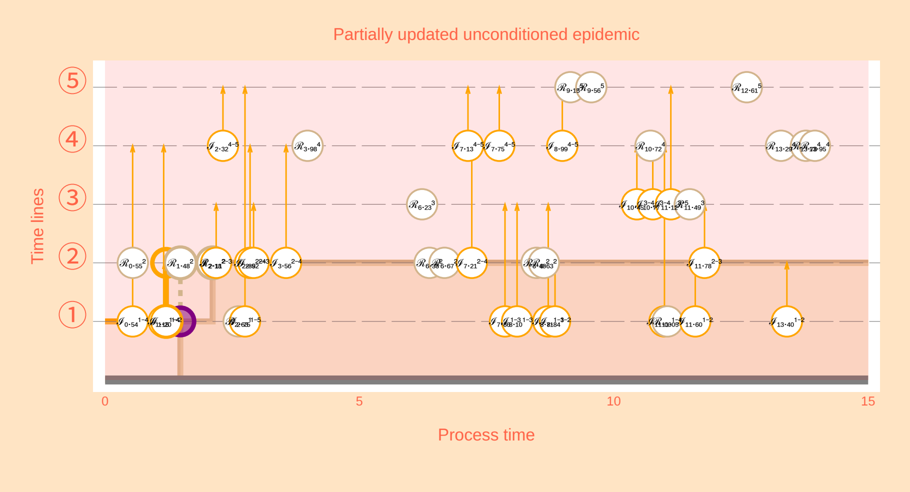

Figure 7: All removals resampled, infections as yet unchanged;

Illustration of technical point (5/8)

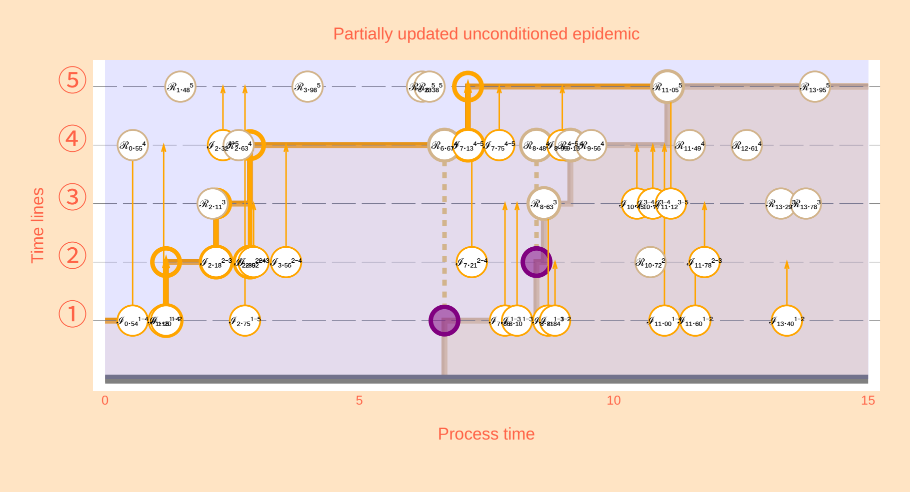

Figure 8: Re-sample all removal timelines, infections as yet unchanged;

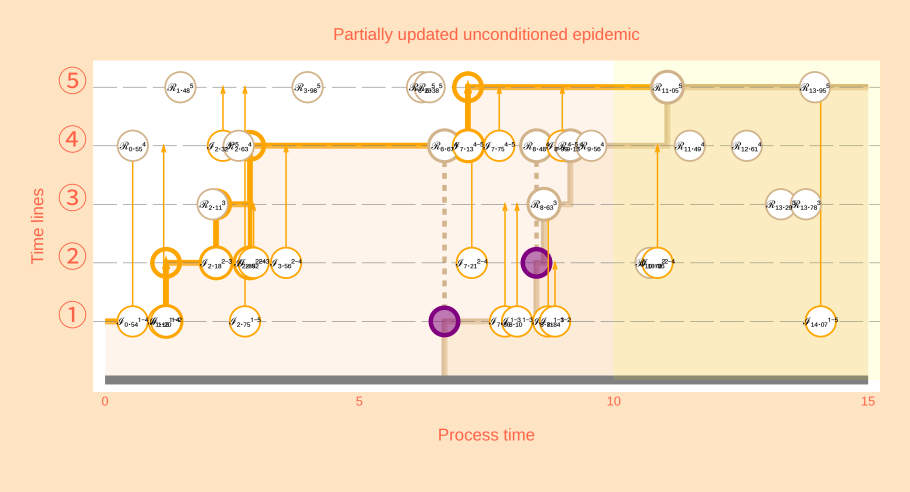

Figure 9: Re-sample last third of infections;

Illustration of technical point (7/8)

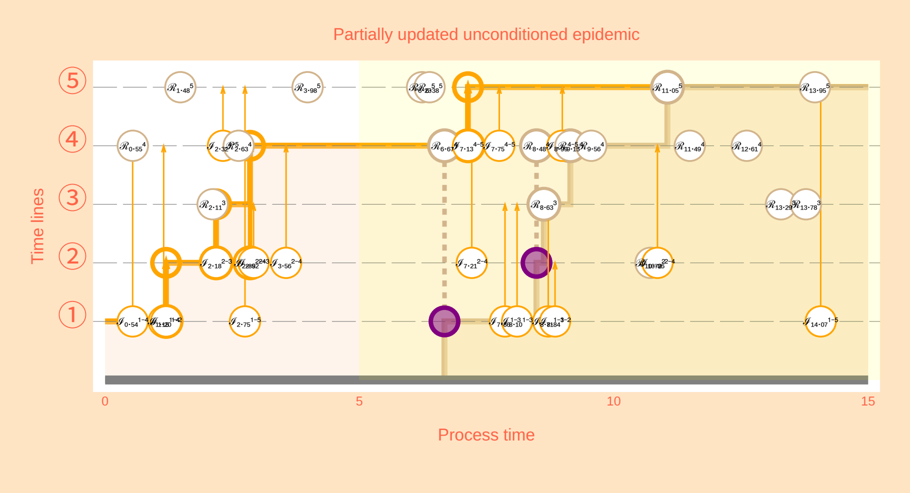

Figure 10: Re-sample last two-thirds of infections;

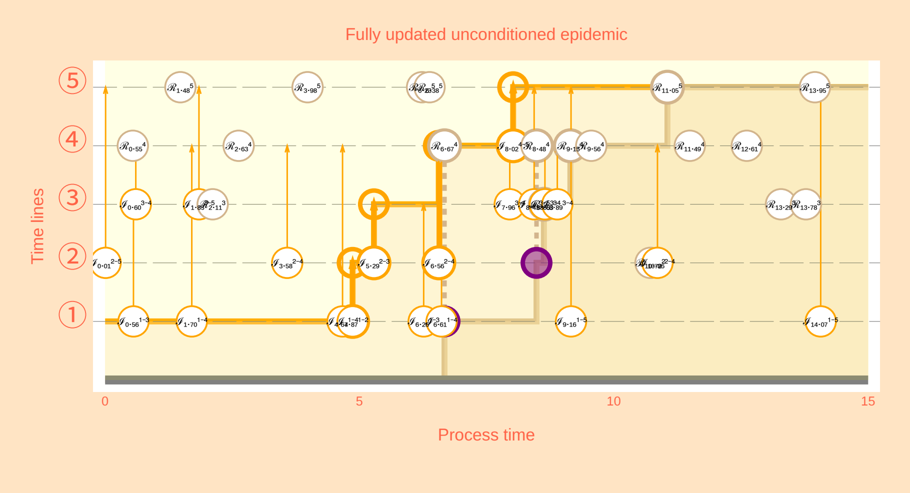

Figure 11: All infections now re-sampled.

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

Initial conditional epidemic

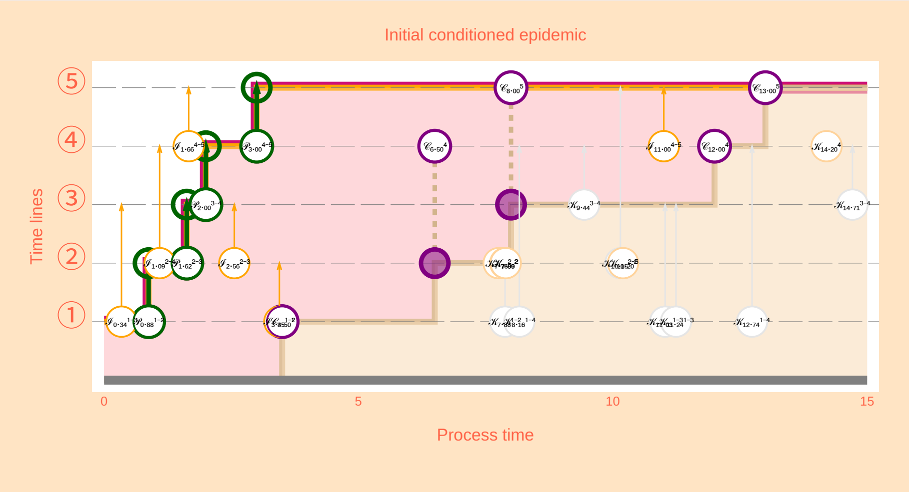

Figure 12: Initial epidemic with conditioned removals indicated using purple circles (and purple disks when different timelines are infected).

Conditional epidemic update

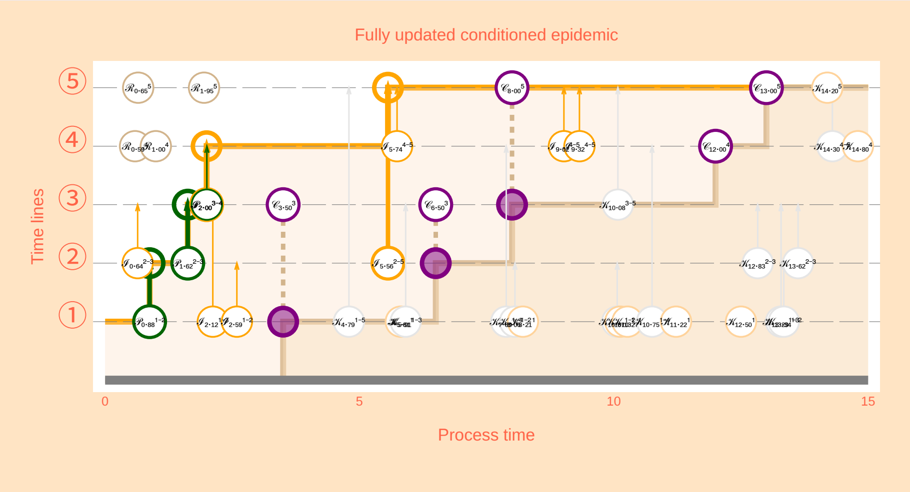

Figure 13: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

Last feasible epidemic (LFE)

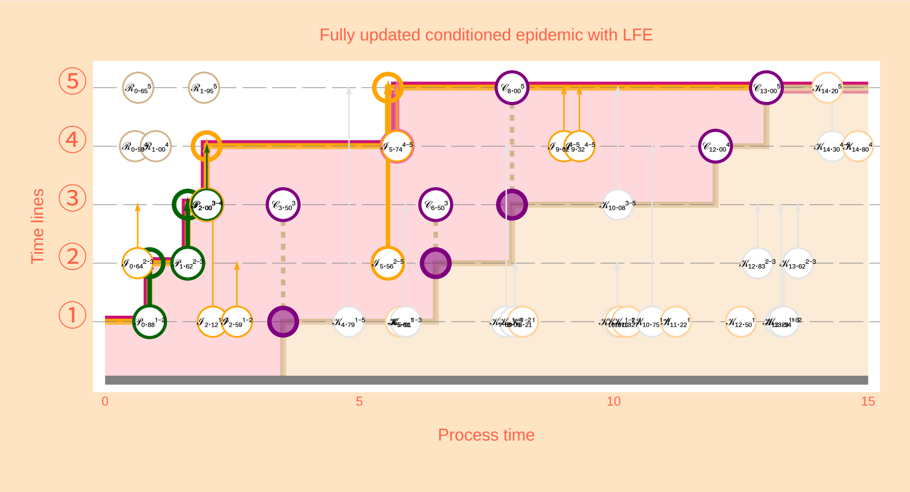

Figure 14: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

No-fly zone (NFZ)

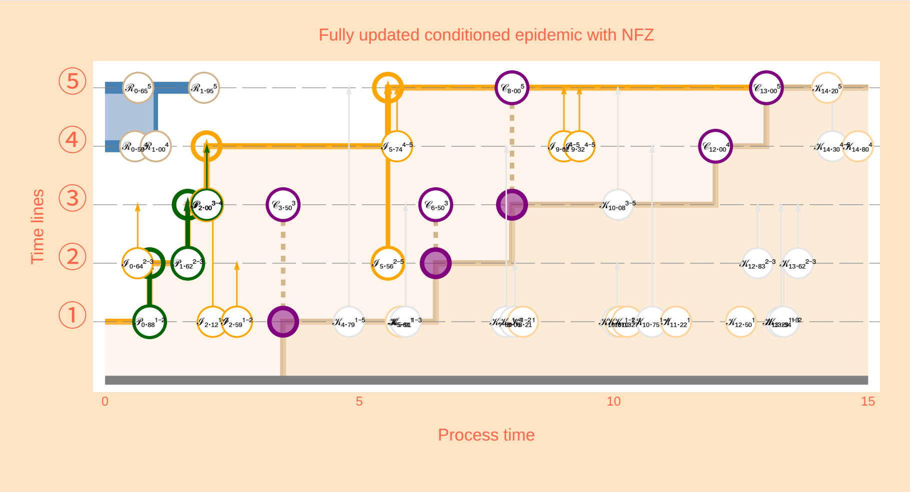

Figure 15: NFZ computed recursively working right-to-left: it traces the region of timelines that must not be infected if one is not to activate unobserved removals.

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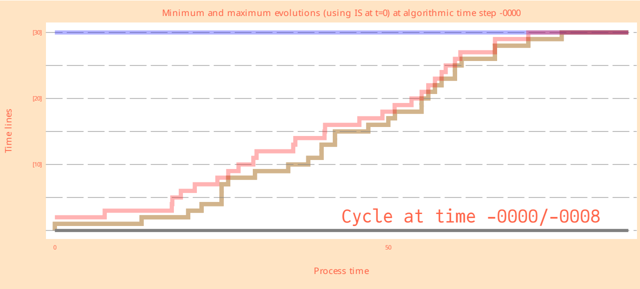

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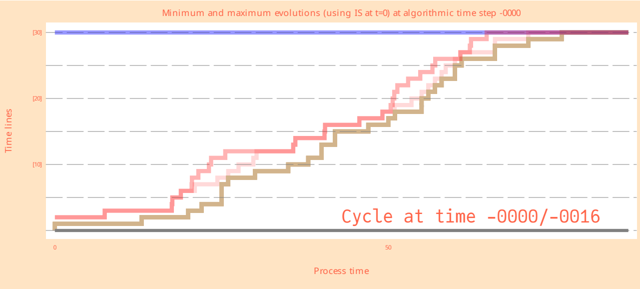

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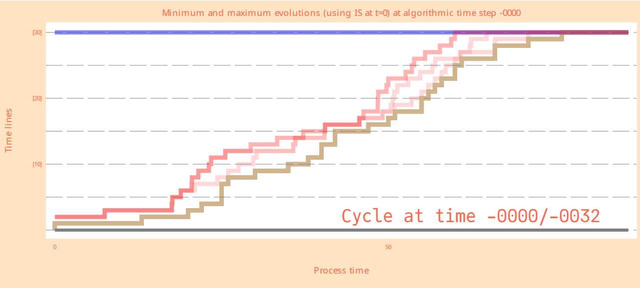

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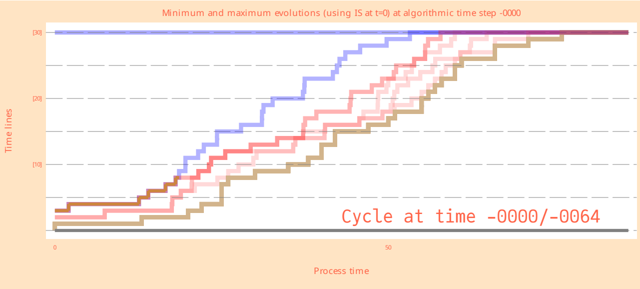

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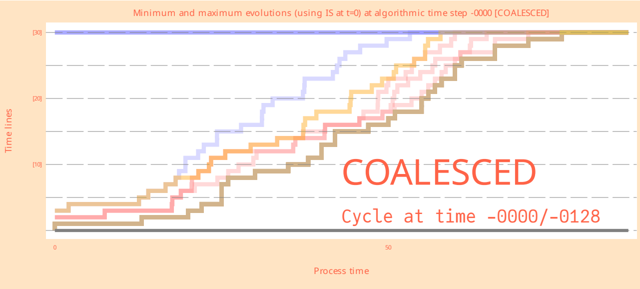

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- Finally: generalize to other suitable compartment models?

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- Thank you for your attention! **QUESTIONS?**

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References I

Bailey, N.T.J. (1975) *The mathematical theory of infectious diseases and its applications*, 2nd Ed. ed. Griffin.

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.

Huber, M.L. (2015) *Perfect Simulation*. Boca Raton: Chapman; Hall/CRC.

References II

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.

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.

SBC & WSK (2024) Perfect Epidemics.

Whittle, P. (1955) The outcome of a stochastic epidemic—a note on Bailey's paper. *Biometrika*, **42**, 116–122.

References III

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

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 (12min)	Warwick
15/05/24	McMC and Perfect Simulation	Graduate Seminar, Aristotle Univ. (50min)	Thessaloniki
17/01/25	Perfect Epidemics	Applied Probability Seminar (50min)	Warwick

Appendix A: A “near-maximal” configuration

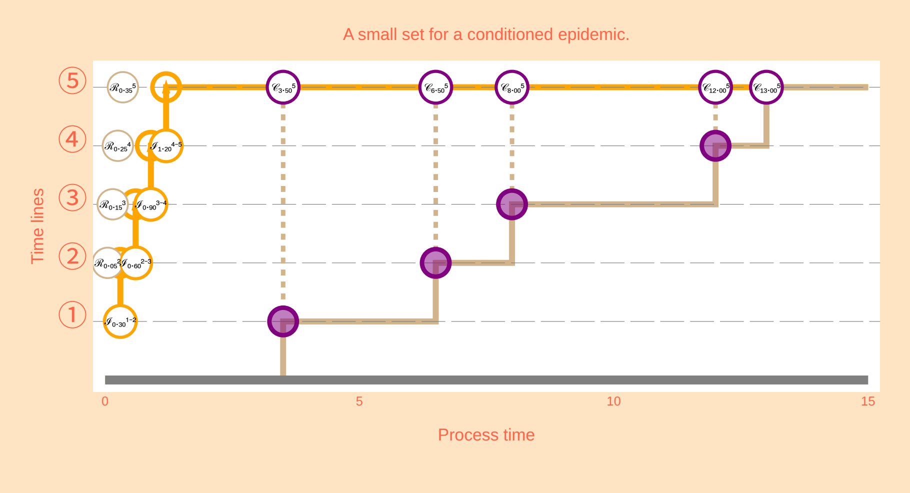

Figure 16: A conditional epidemic in which all activated infections occur before time 3.0, also before smallest observed removal time.

Appendix B: Updating a conditional epidemic INCOMPLETE

We now work through the update of the conditional epidemic in stages.

Warwick Statistics

Initial conditional epidemic (1/8)

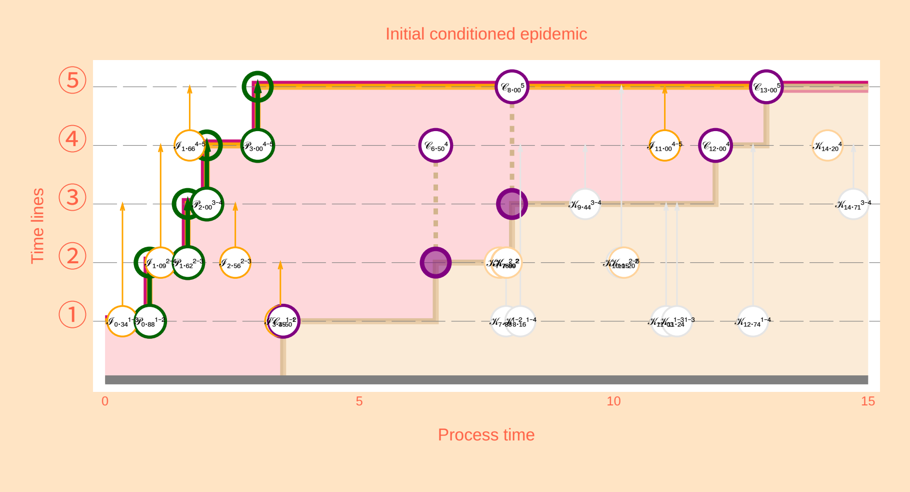

Figure 17: Initial epidemic with conditioned removals indicated by purple circles.

Conditional epidemic (2/8)

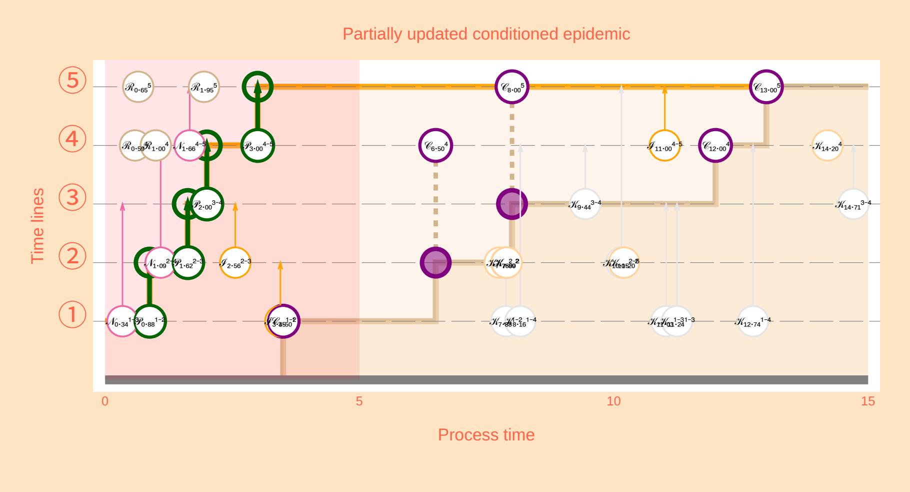

Figure 18: Replace first third of removals, infections unchanged;

Conditional epidemic (3/8)

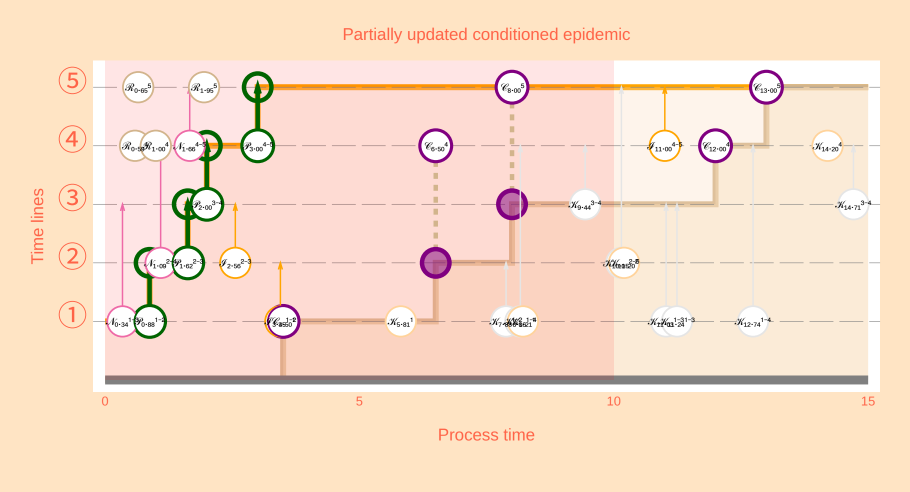

Figure 19: Replace second third of removals, infections unchanged;

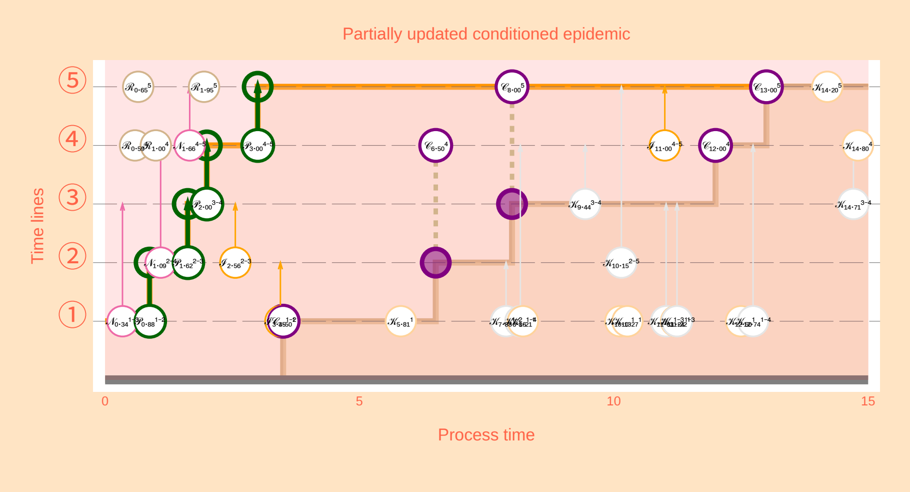

Figure 20: Replace remaining removals, infections unchanged;

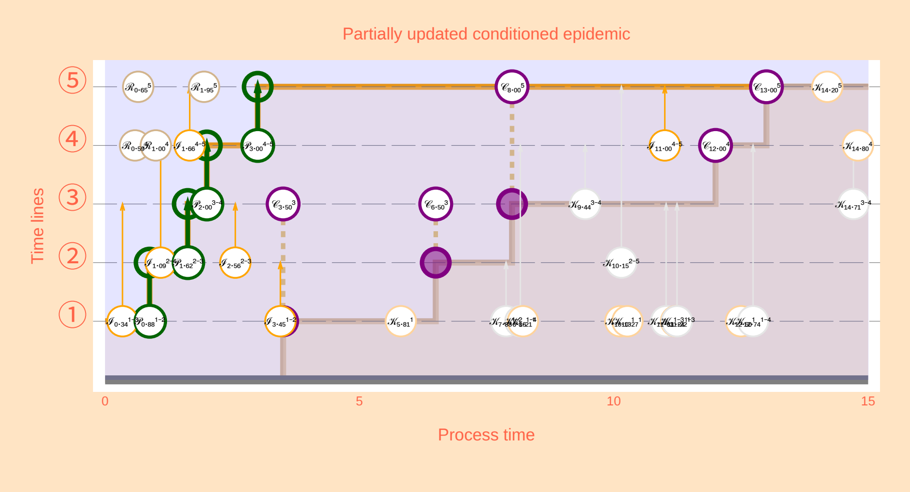

Figure 21: Re-sample all removal timelines, infections as yet unchanged;

Eventual conditional epidemic after use of an innovation (6/8)

Still to be done: 1/3 of way through new infections, display current LFE and NFZ.

Eventual conditional epidemic after use of an innovation (7/8)

Still to be done: 2/3 of way through new infections, display current LFE and NFZ.

Eventual conditional epidemic after use of an innovation (8/8)

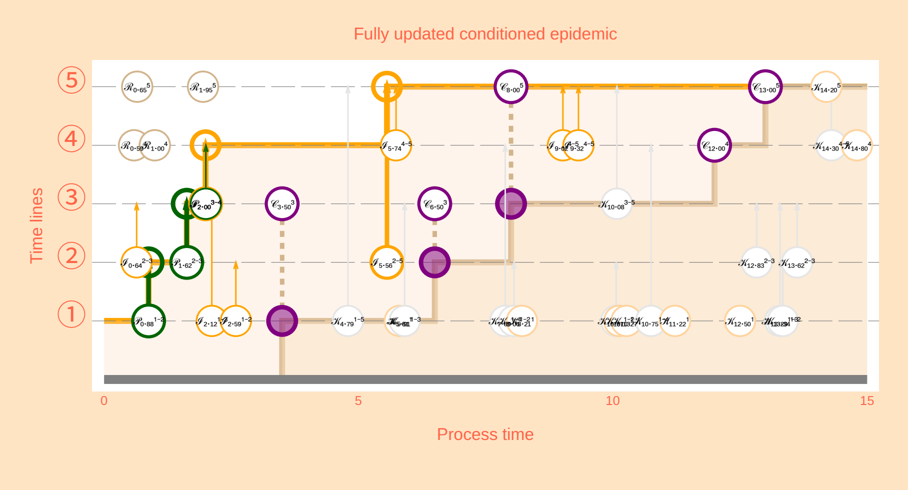

Figure 22: All infections now re-sampled. Green infections are “perpetuated”.

Appendix C: Naive approach to compartment models fails

- Consider a modification of this approach to the case of compartmentalized populations.

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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.

Timelines and incidents for the compartmental generalization

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Process dynamics

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

1. initially infected timelines i possess no $\mathcal{R}_i$ and contribute $(i, [0, t))$ to the epidemic if possessing a (single) $\mathcal{C}_i(t)$, otherwise $(i, [0, T)$;

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3. the inactivated removal $\mathcal{R}_i(t)$ lies on a timeline i that is not initially infected only if $t < s$, where s is the time of first infection.

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Dynamics in algorithmic time

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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 detailed lemmas

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;

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.

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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.

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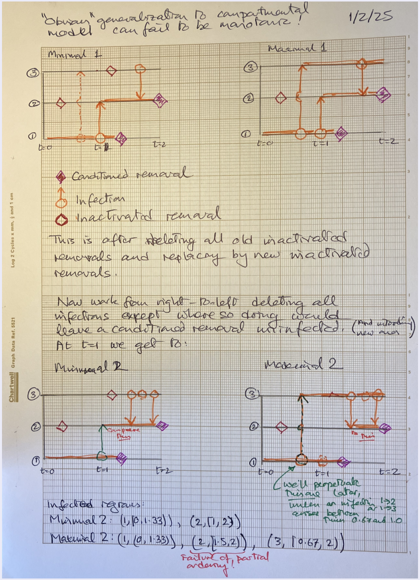
Counterexample to monotonicity



Other technical information

Software versions

Software used in computations:

Software	*Version*	*Branch*	*Date of last commit*
`quarto`	`1.6.39`	—	
Running under `julia`	`1.11.3`	—	
Module `EpidemicsCFTP`	`2.2.492`	`main`	`Thu Jan 23 20:50:07 2025`
Module `EpidemicsUtilities`	`0.1.2.156`	`main`	`Thu Jan 23 12:06:14 2025`
This `quarto` script	`2.2.612`	`Wilfrid-2025-01-30-compartment`	`Fri Jan 31 17:40:24 2025`

Revision notes

These notes were produced from `PerfectEpidemics.qmd`:

Version:	`2.2.613, origin/Wilfrid-2025-01-30-compartment` [`Wilfrid-2025-01-30-compartment`]
Author:	Wilfrid Kendall <`W.S.Kendall@warwick.ac.uk`>
Date:	Sat Feb 1 14:26:43 2025 +0000
Summary:	Counterexample to naive compartent model generalization.