

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.

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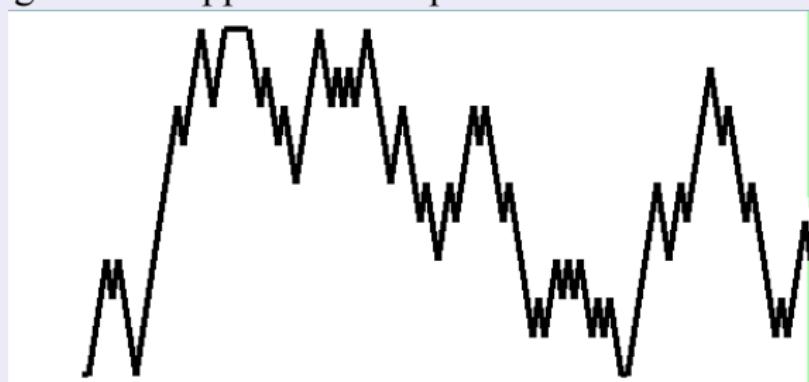
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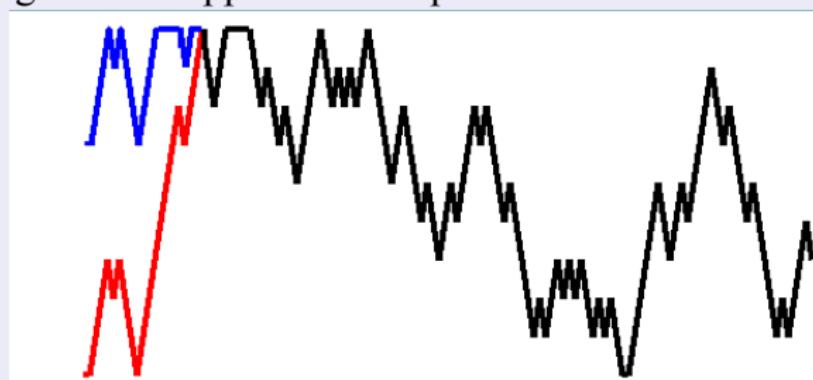
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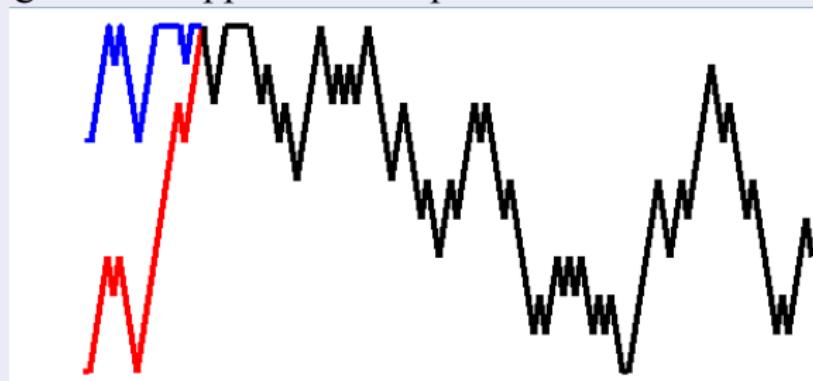
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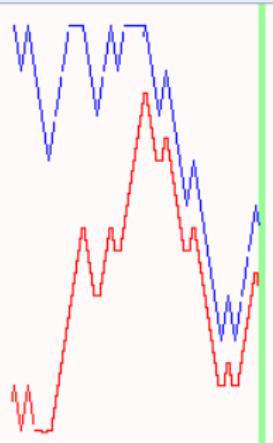
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- Generally **not true** that location *at coupling* is a draw from equilibrium.

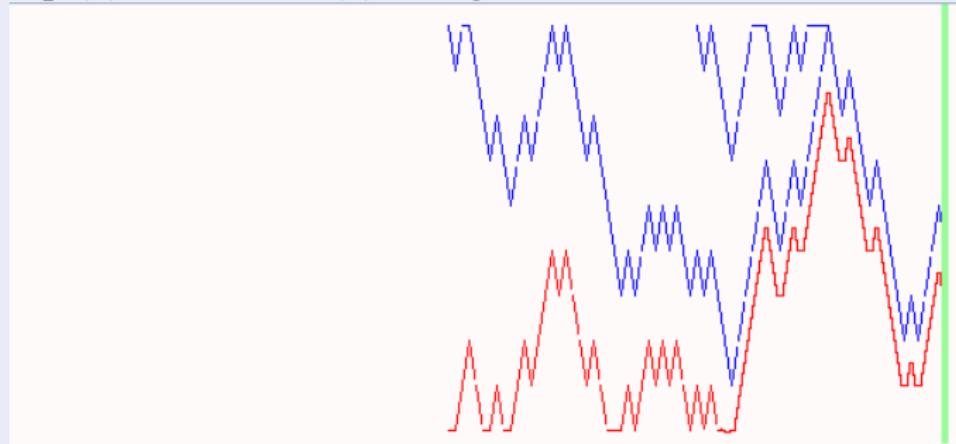
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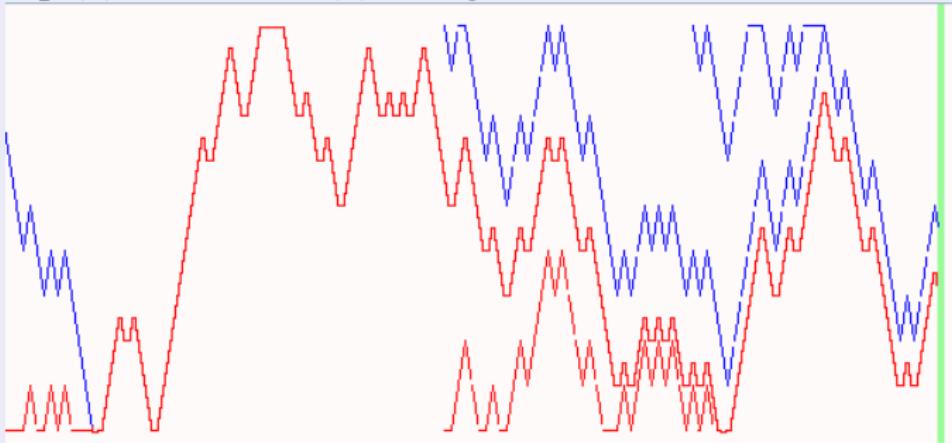
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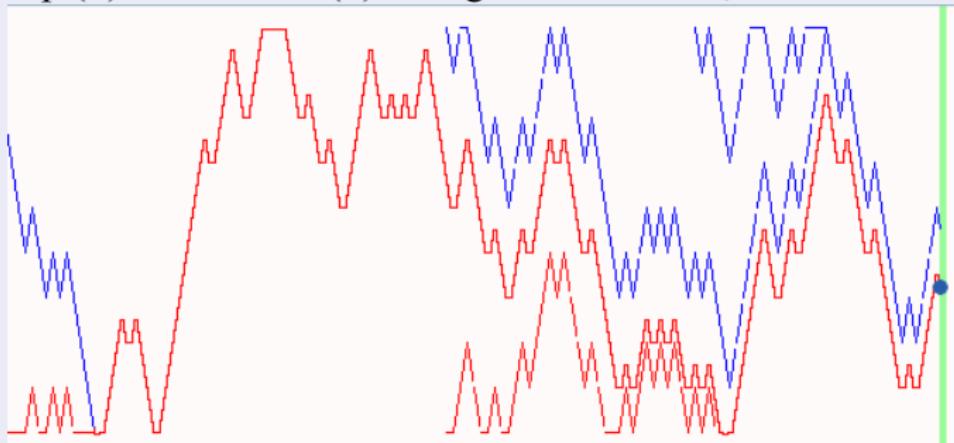
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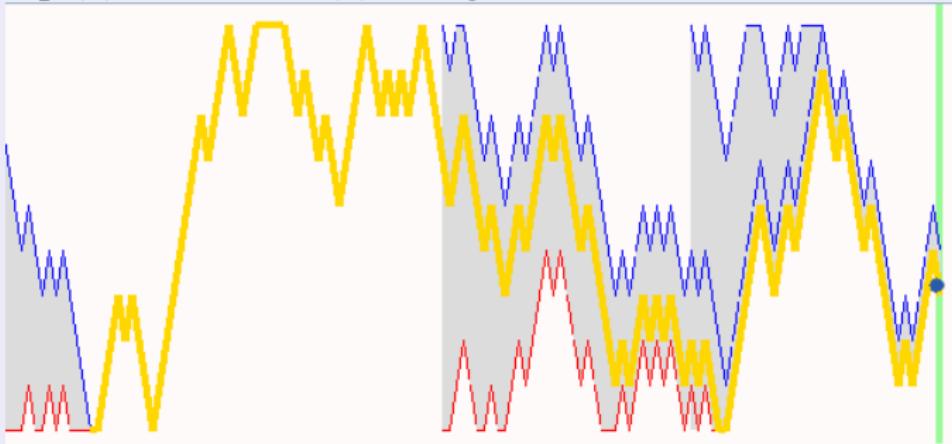
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- When coupled, top and bottom yield a common value at time 0.
- The common value (golden thread) is an exact draw from equilibrium!

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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 $s + i + r = n$):

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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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- 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

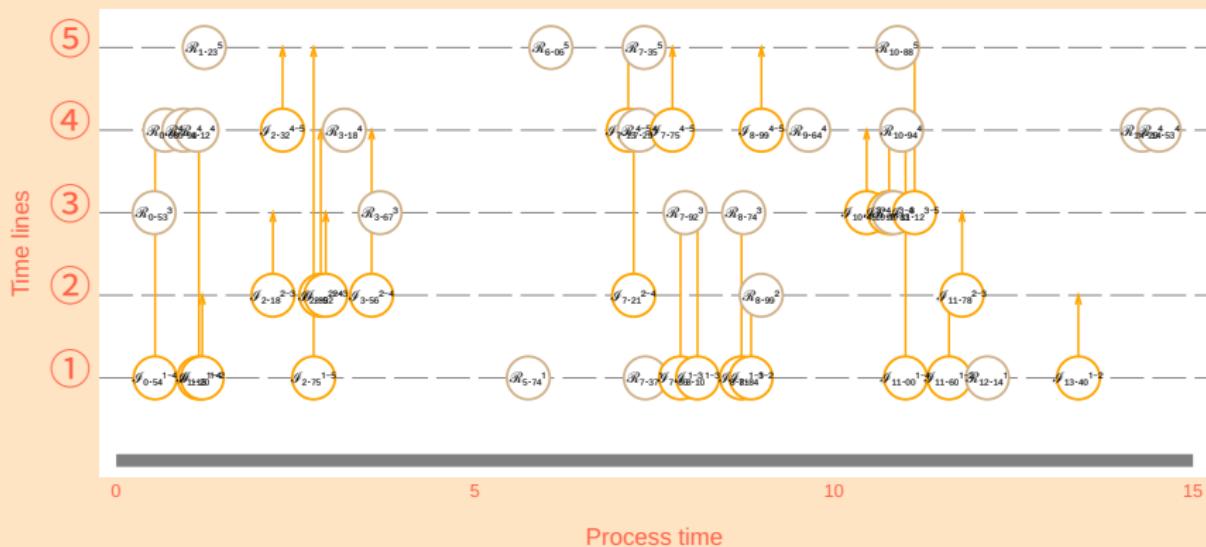


Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

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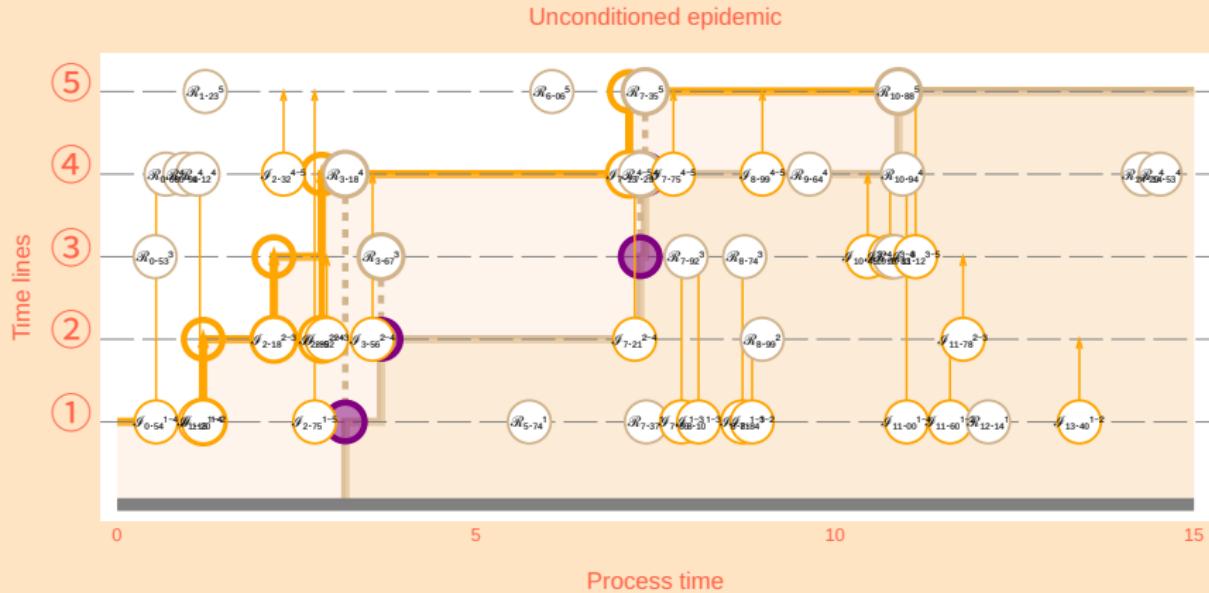


Figure 2: (a) *Infection* activates if target lies on the lowest uninfected timeline; and (b) *removal* activates if on infected timeline; remove lowest infected (purple disk).

From incidents to unconditioned epidemic trajectories (3/3)

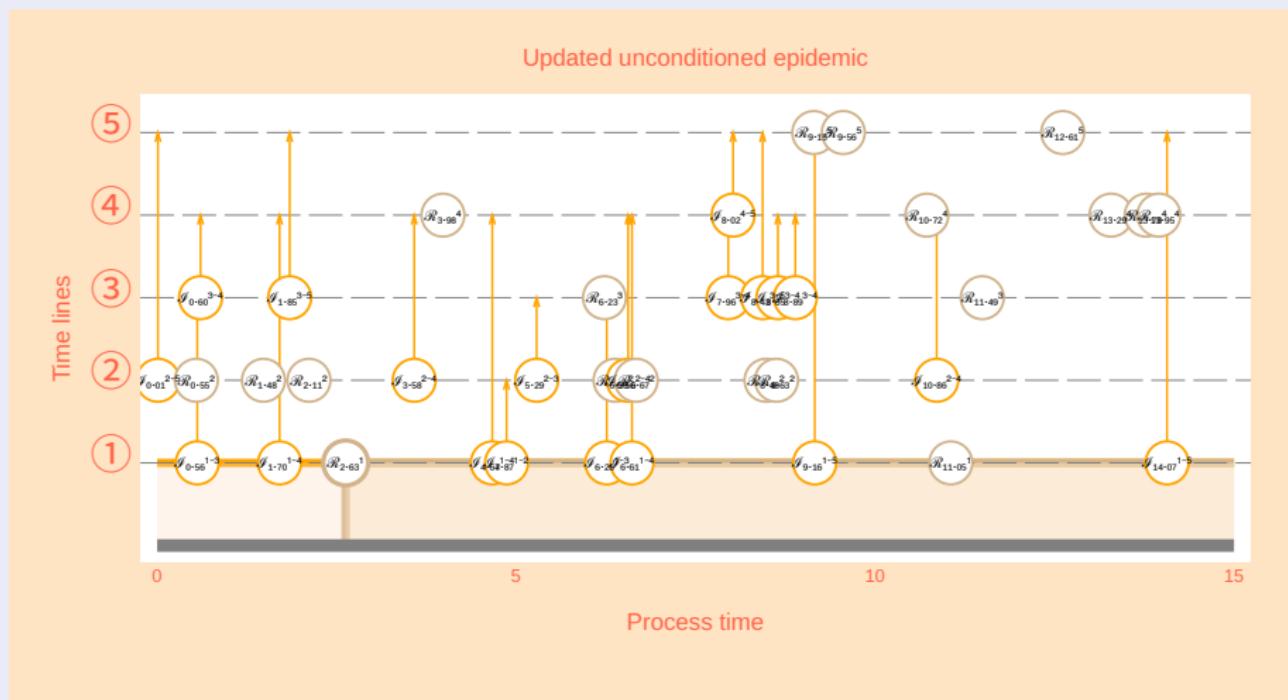


Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing all original incidents by an entirely new set of incidents.

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

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- Thus the original update is expressible as a (continuous) composition of updates, each of which satisfies detailed balance in equilibrium.
- The connection “restriction=conditioning” still holds.
- Crucially, step 2 ensures composition action is irreducible over S !
(So equilibrium under conditioning is unique.)

Illustration of technical point (1/8)

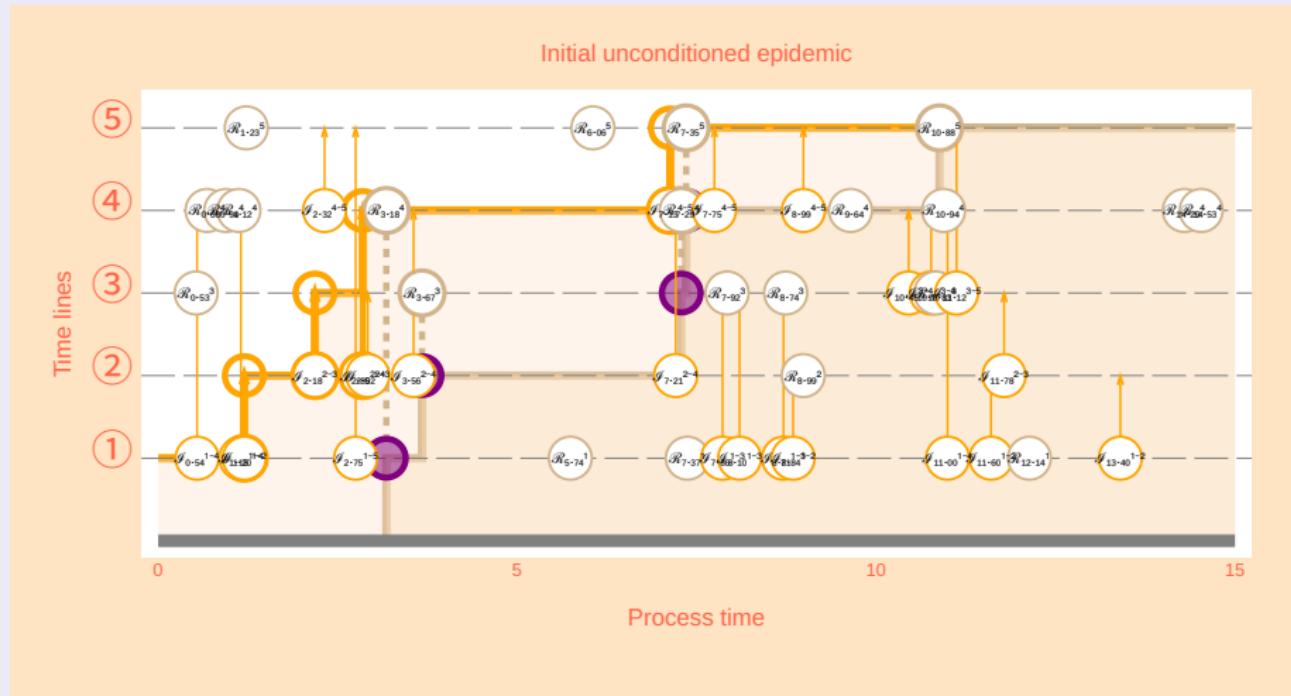


Figure 4: No change yet to removals or infections;

Illustration of technical point (2/8)

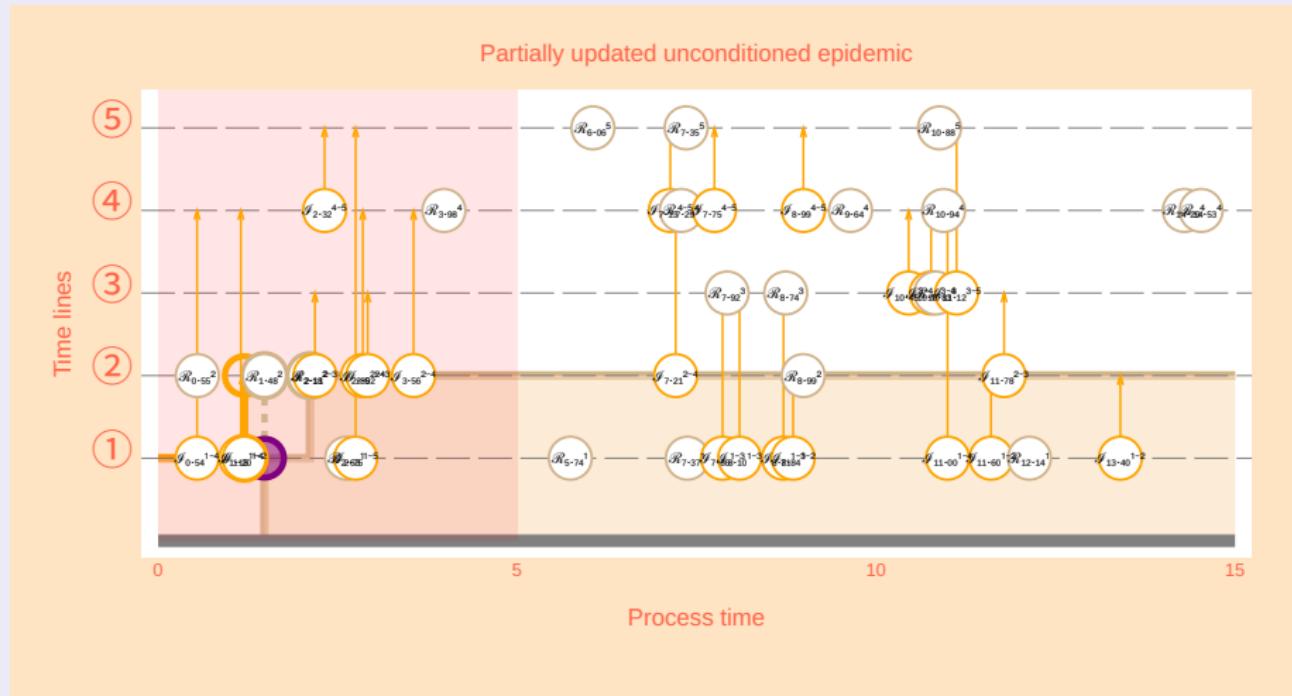


Figure 5: Replace first third of removals, infections unchanged;

Illustration of technical point (3/8)

Partially updated unconditioned epidemic

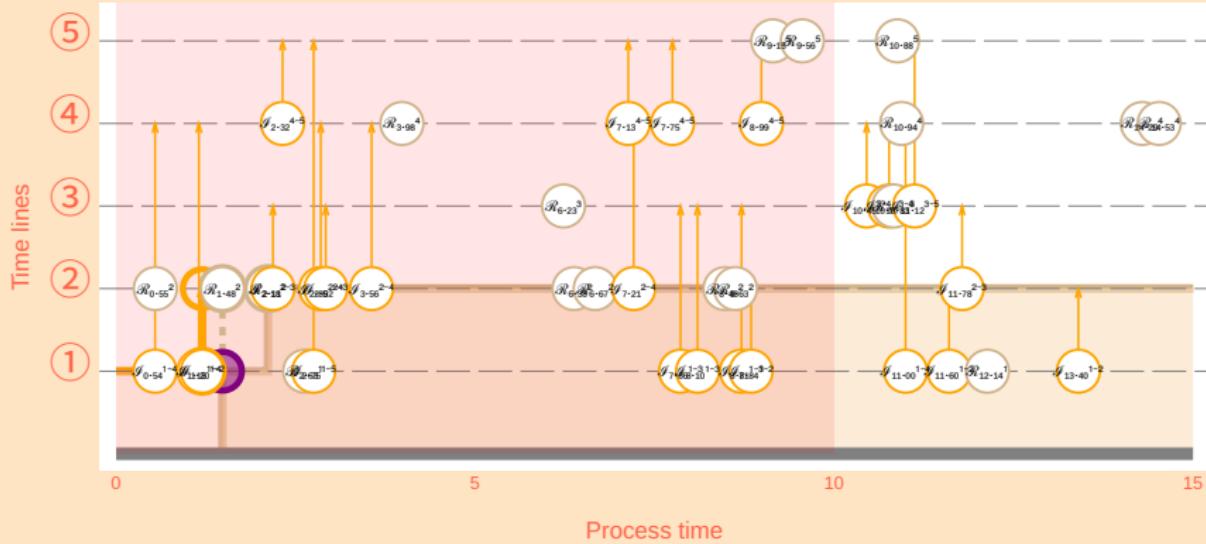


Figure 6: Replace first two-thirds of removals, infections unchanged;

Illustration of technical point (4/8)

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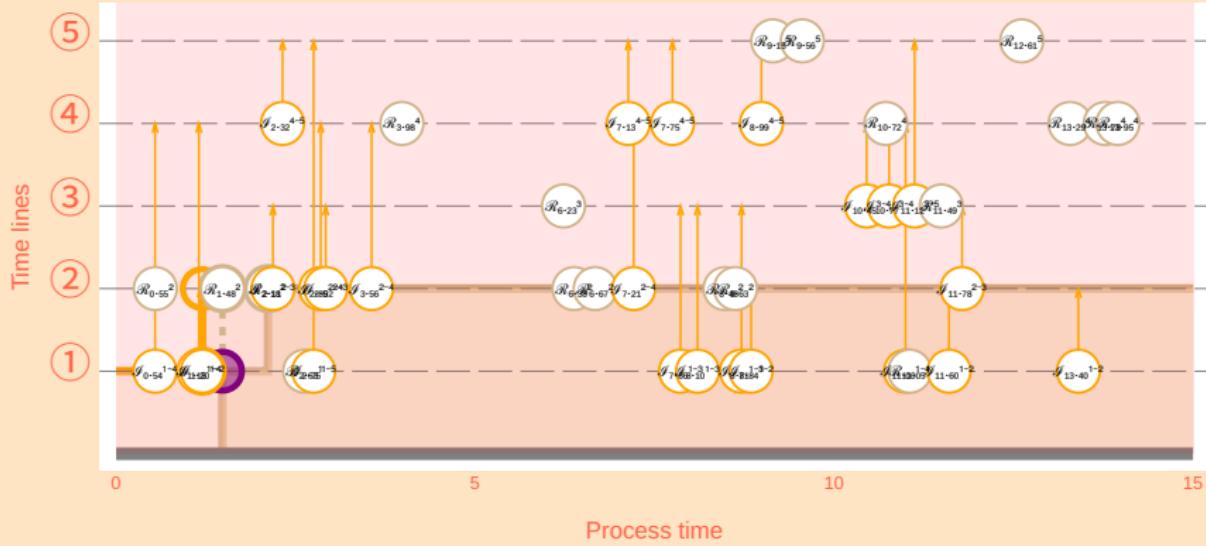


Figure 7: All removals resampled, infections as yet unchanged;

Illustration of technical point (5/8)

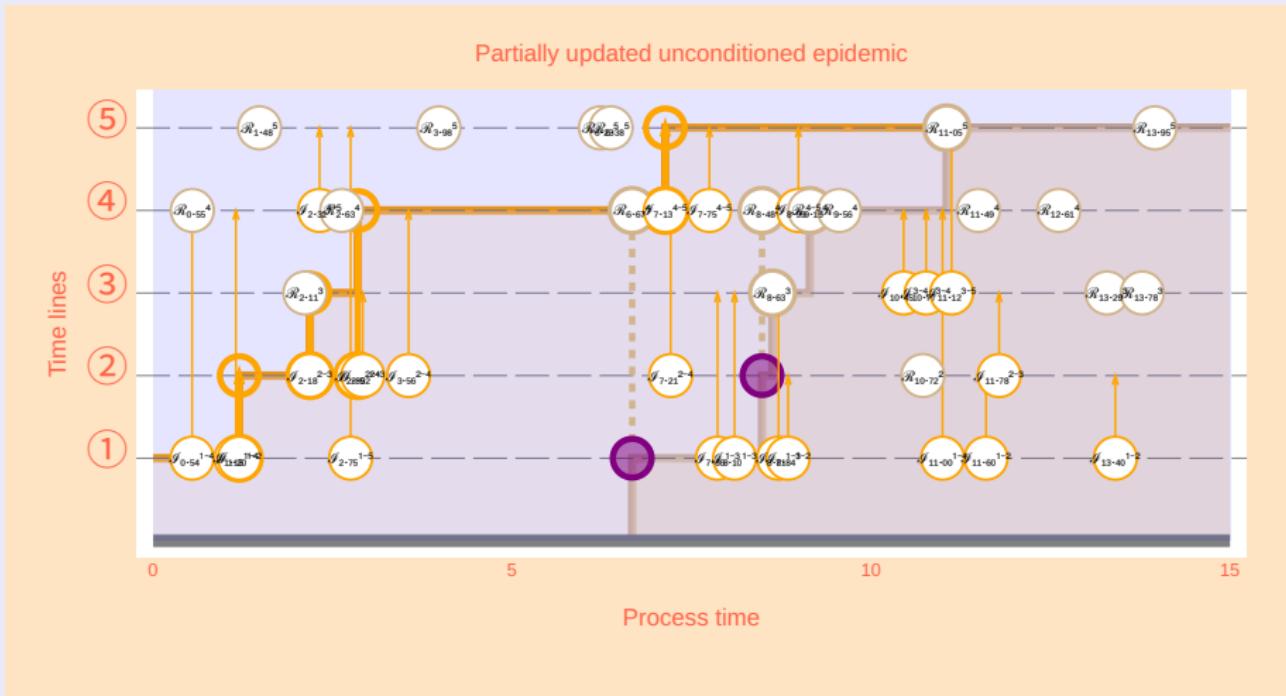


Figure 8: Re-sample all removal timelines, infections as yet unchanged;

Illustration of technical point (6/8)

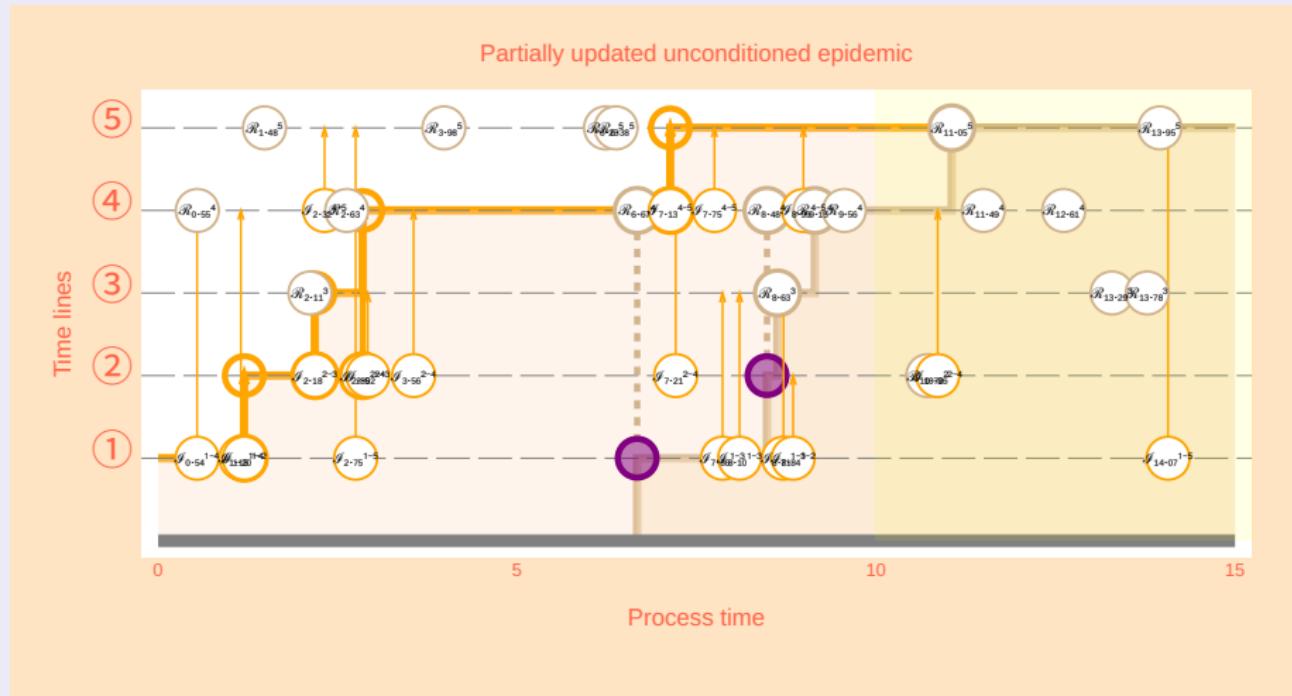


Figure 9: Re-sample last third of infections;

Illustration of technical point (7/8)

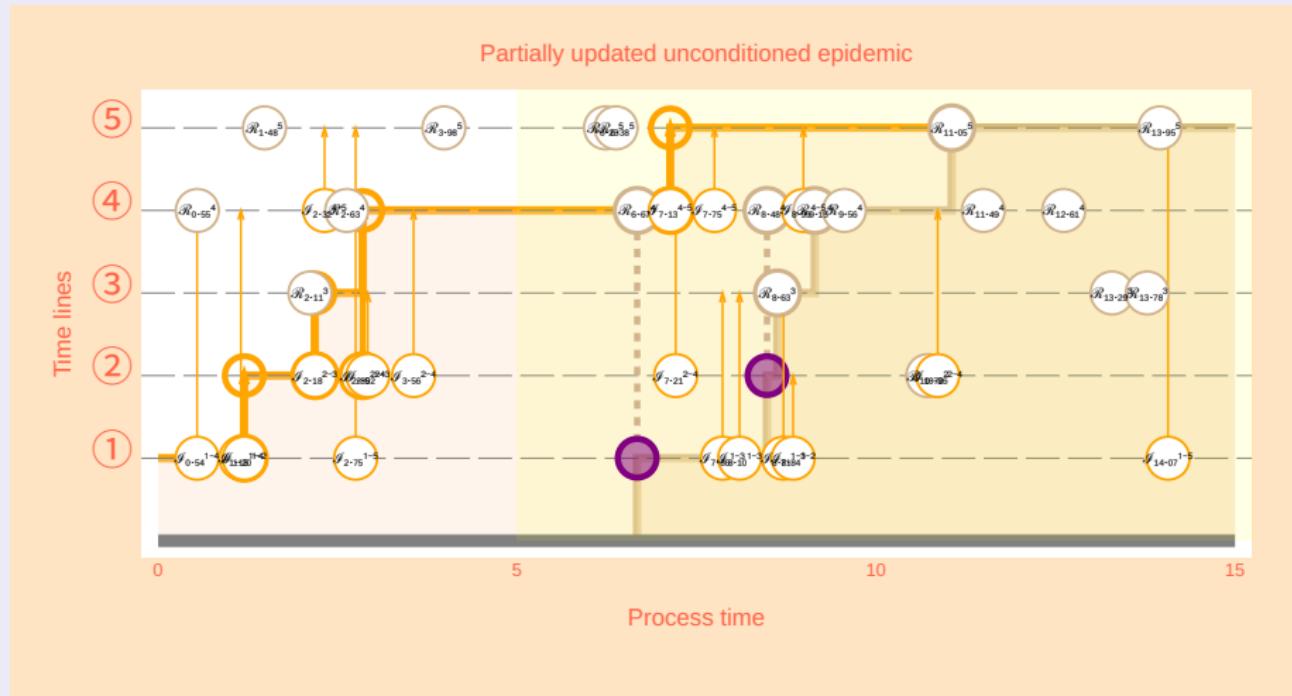


Figure 10: Re-sample last two-thirds of infections;

Illustration of technical point (8/8)

Fully updated unconditioned epidemic

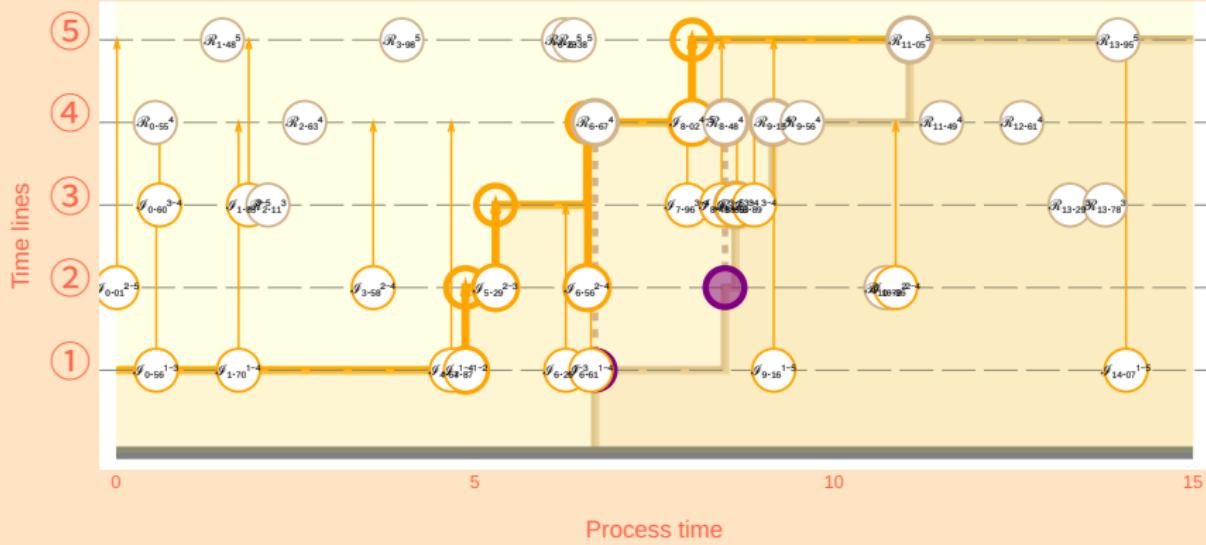


Figure 11: All infections now re-sampled.

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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

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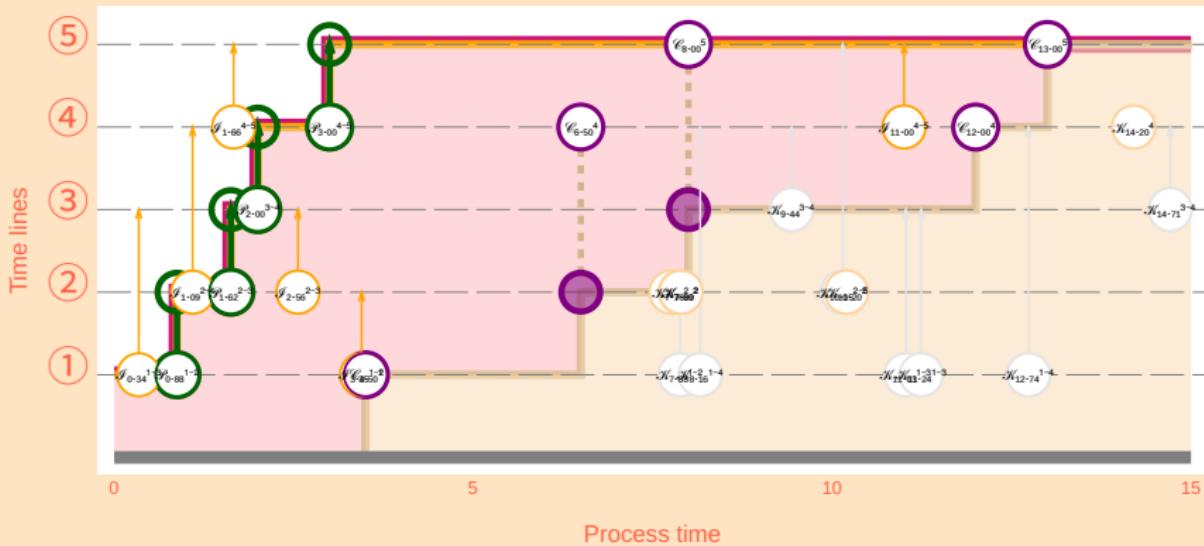


Figure 12: Initial epidemic with conditioned removals indicated using purple circles (and purple disks when different timelines are infected).

Conditional epidemic update

Fully updated conditioned epidemic

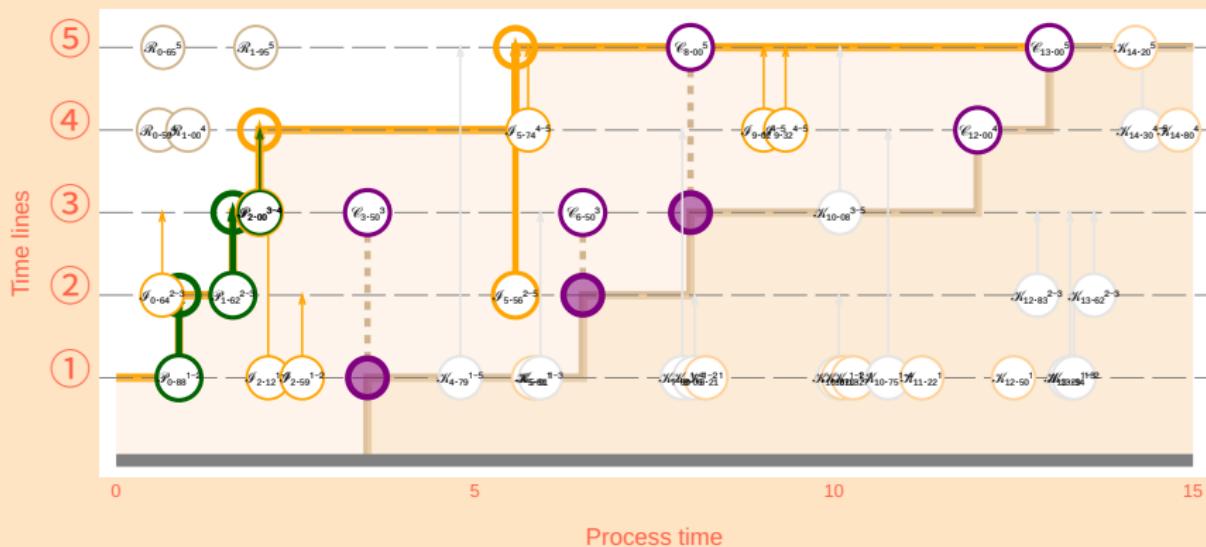


Figure 13: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

Last feasible epidemic (LFE)

Fully updated conditioned epidemic with LFE

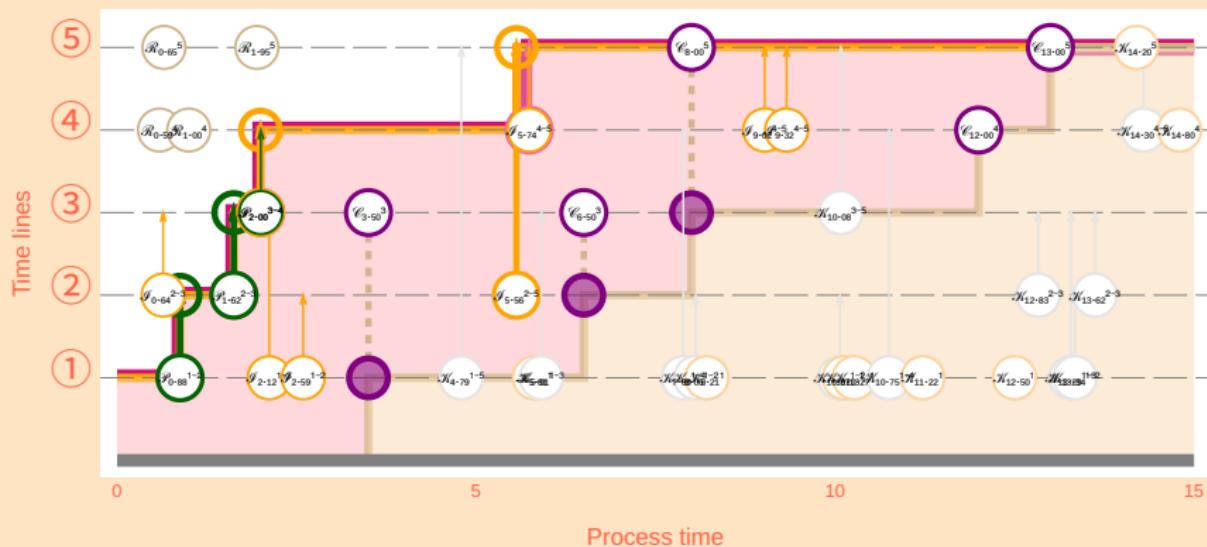


Figure 14: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

No-fly zone (NFZ)

Fully updated conditioned epidemic with NFZ

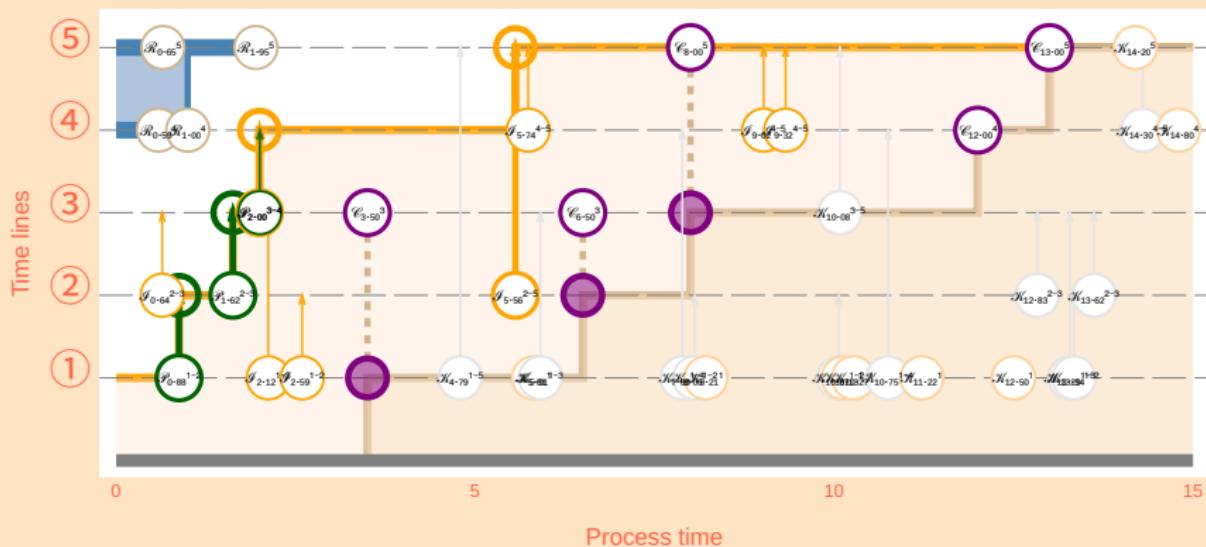


Figure 15: NFZ computed recursively working right-to-left: it traces the region of timelines that must not be infected if one is not to activate unobserved removals.

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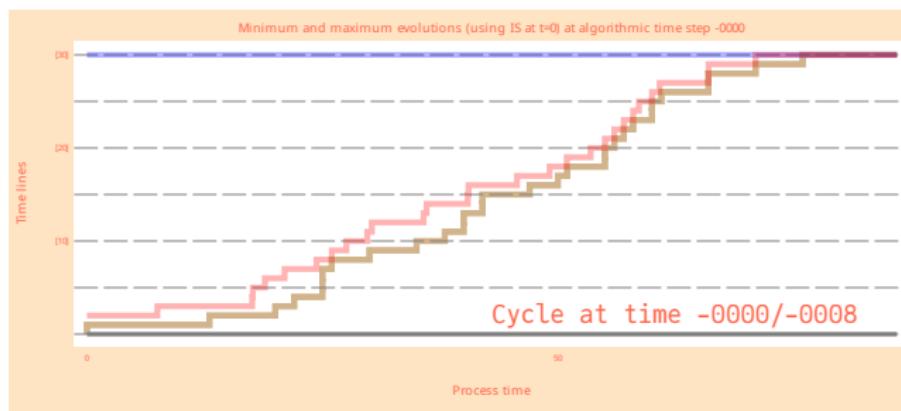
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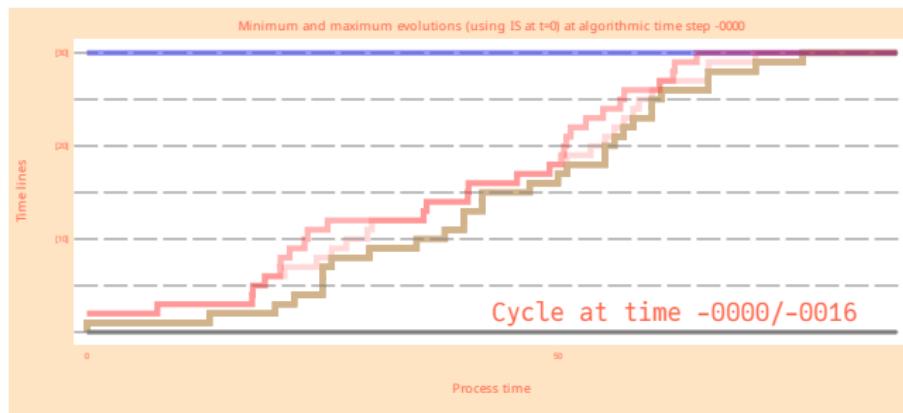
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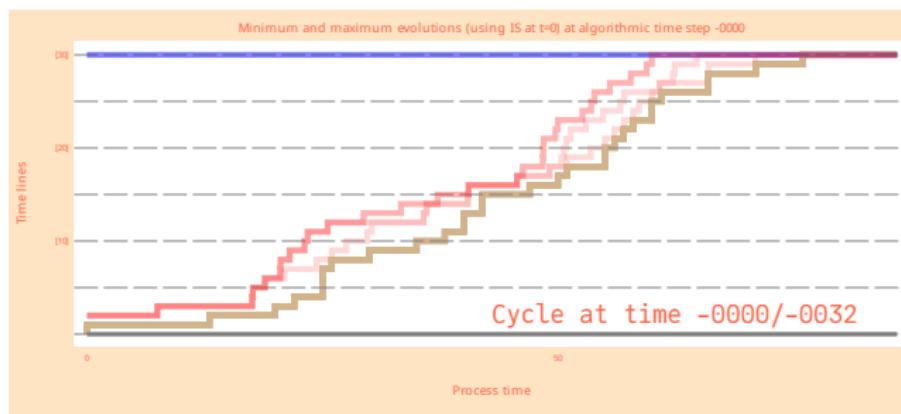
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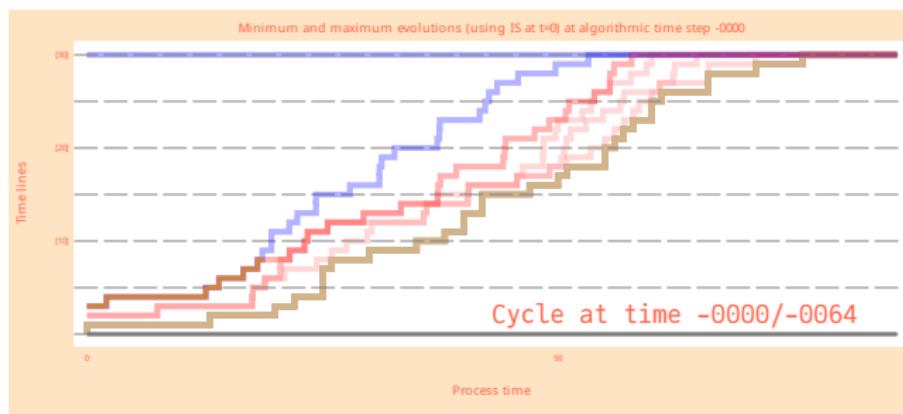
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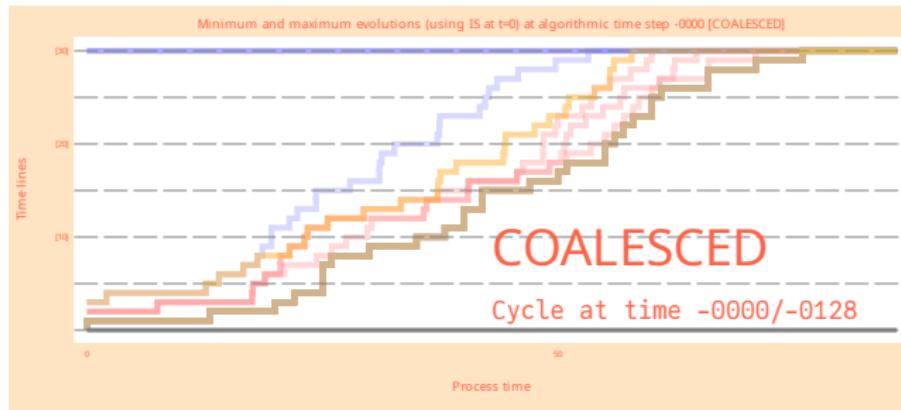
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- Finally: can we generalize to other suitable compartment models?

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- 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.
- 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.
- Liggett, T.M. (1985) *Interacting particle systems*. Springer Verlag.

References II

- 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) Omniperturbational 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.
- WSK (1998) Perfect Simulation for the Area-Interaction Point Process. *Probability towards 2000* (Accardi, L. & Heyde, C.C. eds). Springer-Verlag, pp. 218–234.

References III

- 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> | Luigi Novi | <i>CC BY 3.0</i> |
| Classic CFTP for a simple random walk | Result of code written by WSK | |
| <i>Diamond Princess</i> | Alpsdake | <i>CC BY-SA 4.0</i> |
| Epidemic CFTP images and animation | Result of code written by WSK | |

Previous instances of this talk

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

Appendix A: A “near-maximal” configuration

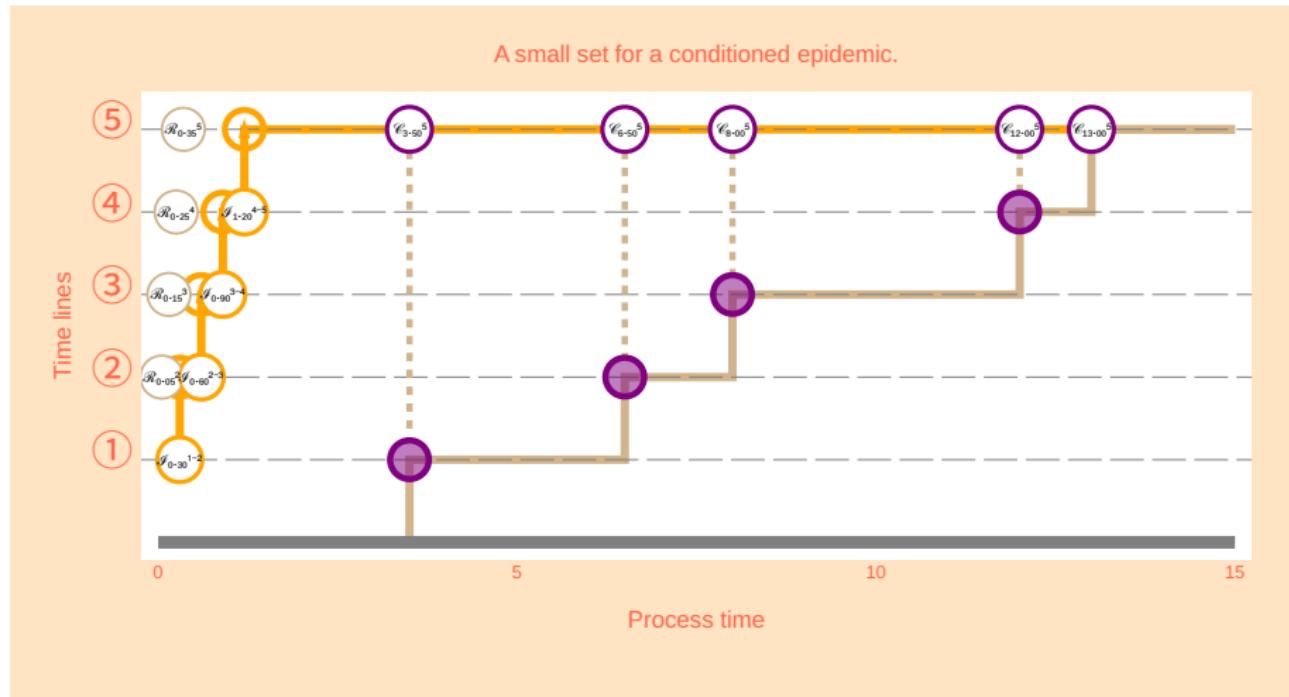


Figure 16: A conditioned epidemic in which all activated infections occur before time 3.0, also before smallest observed removal time.

Appendix B: Updating a conditioned epidemic

INCOMPLETE

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

Initial conditioned epidemic (1/8)

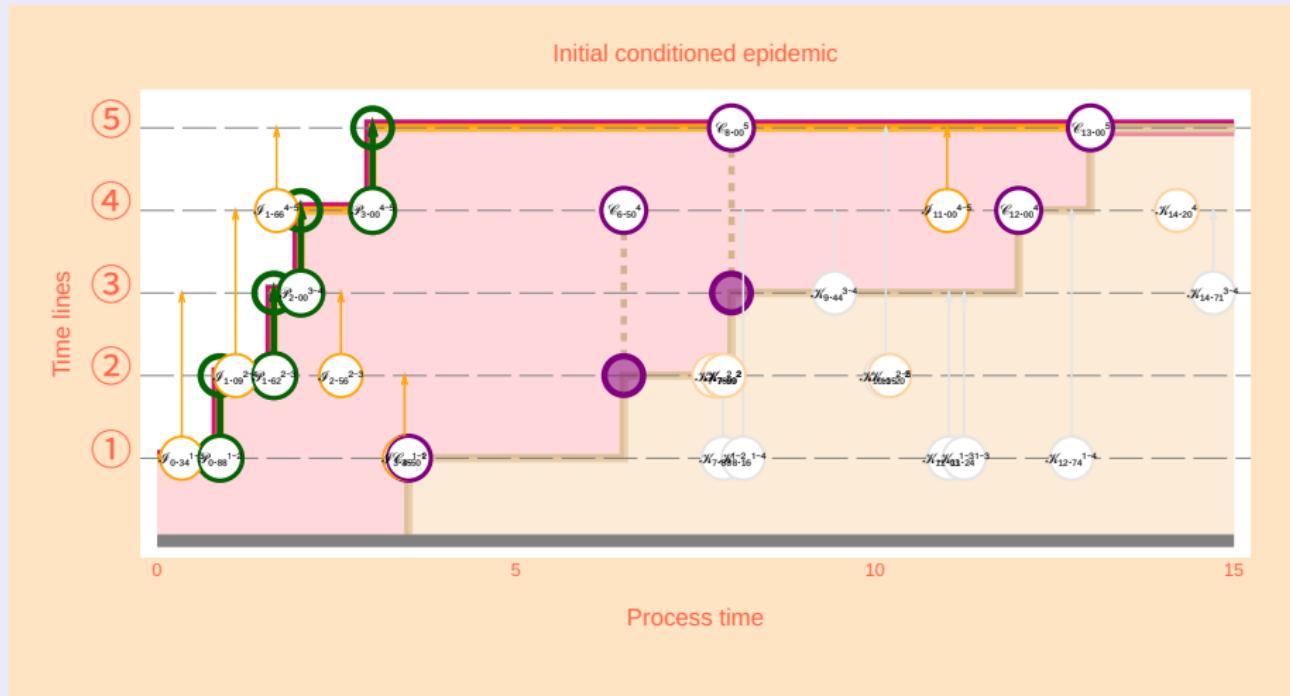


Figure 17: Initial epidemic with conditioned removals indicated by purple circles.

Conditional epidemic (2/8)

Partially updated conditioned epidemic

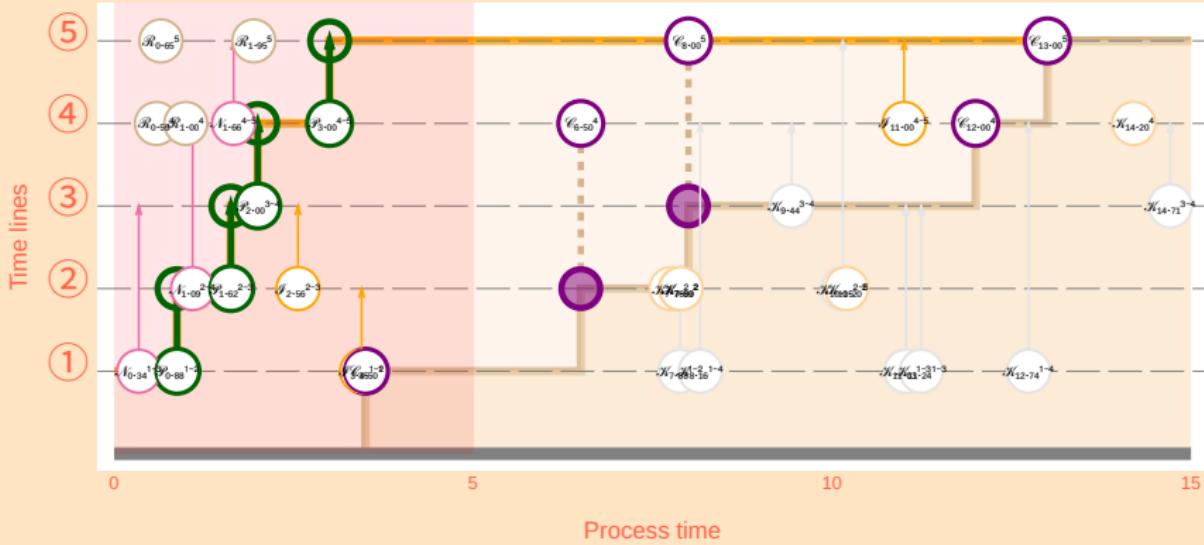


Figure 18: Replace first third of removals, infections unchanged;

Conditional epidemic (3/8)

Partially updated conditioned epidemic

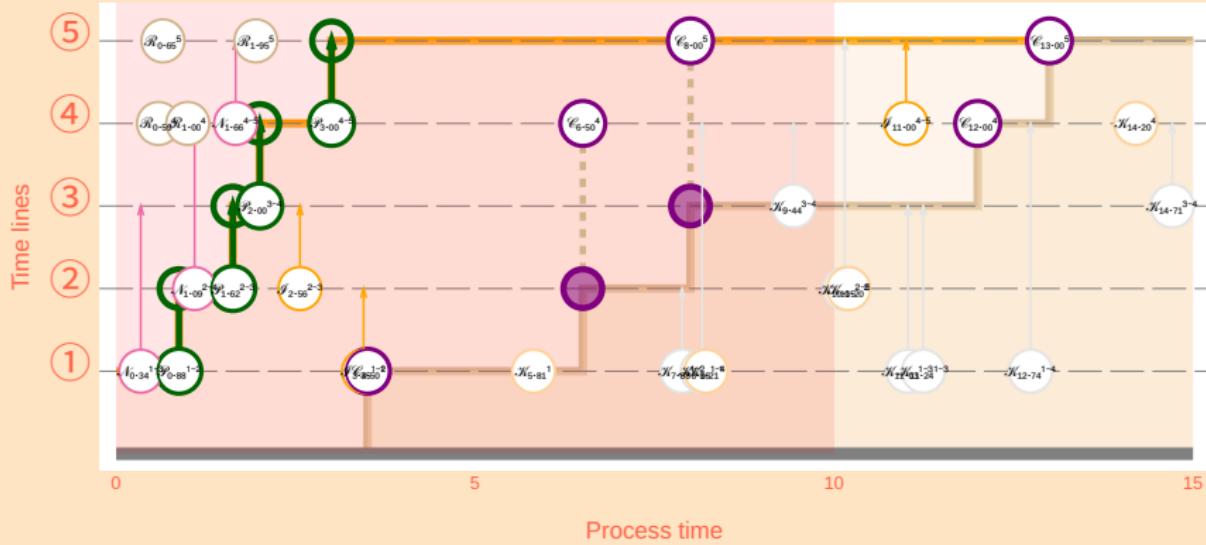
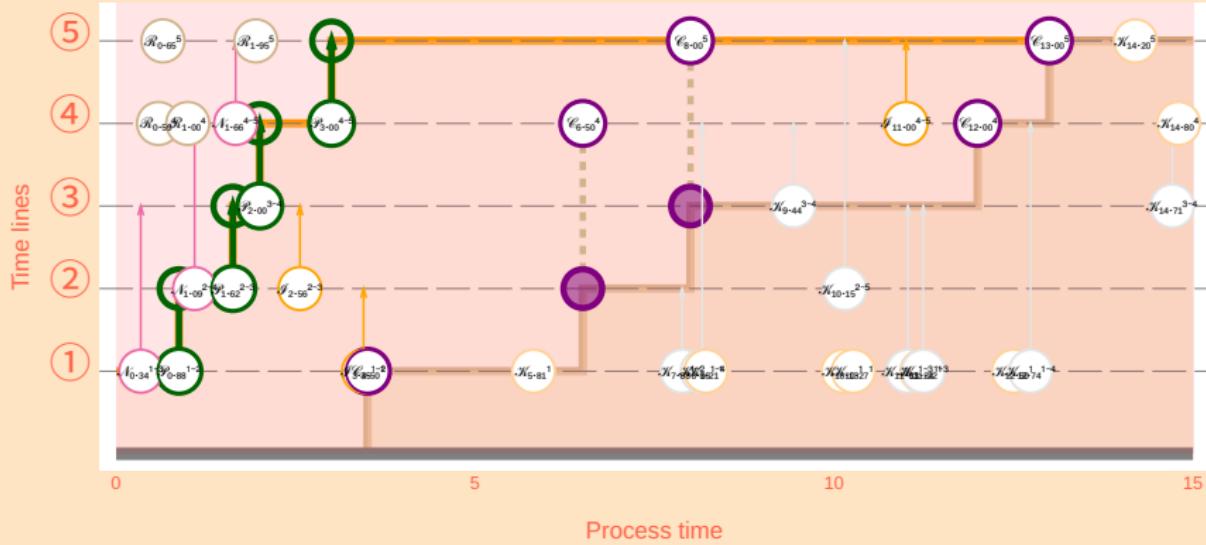


Figure 19: Replace second third of removals, infections unchanged;

Conditional epidemic (4/8)

Partially updated conditioned epidemic



Conditional epidemic (5/8)

Partially updated conditioned epidemic



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

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

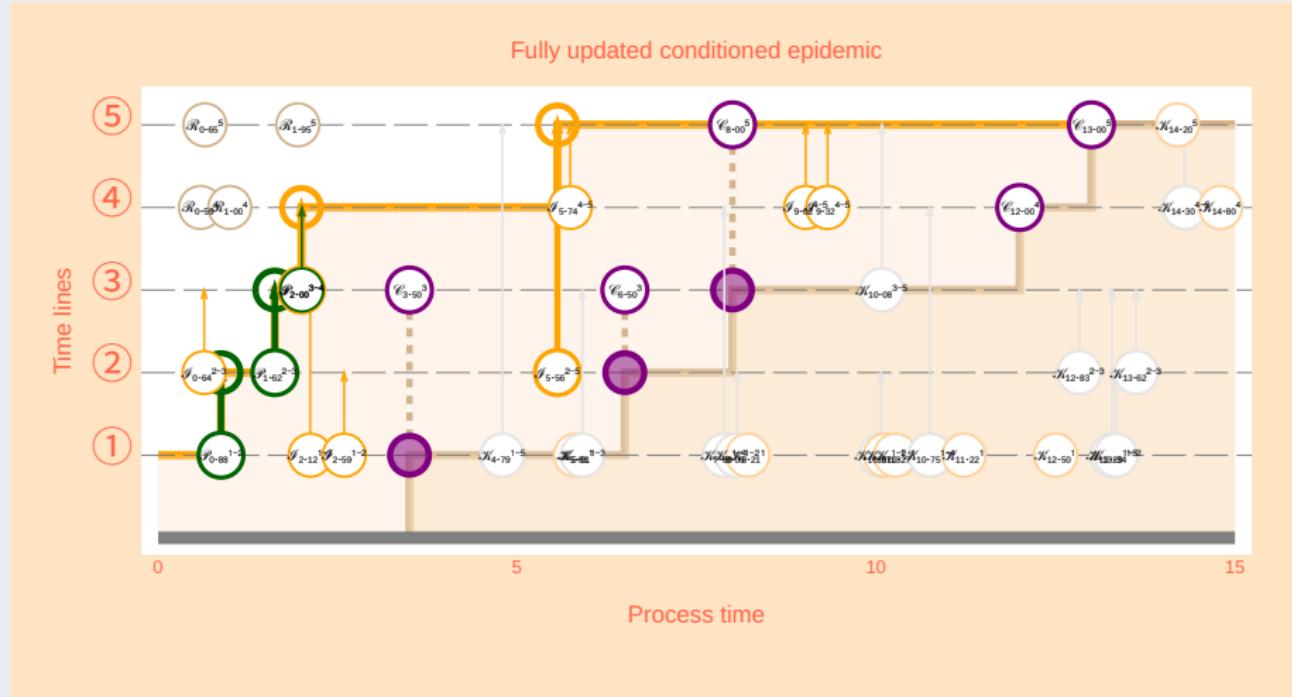


Figure 22: All infections now re-sampled. Green infections are “perpetuated”.

Appendix C: Naive approach to compartment models fails

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- 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).

Dynamics in algorithmic time

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 - ▶ 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.

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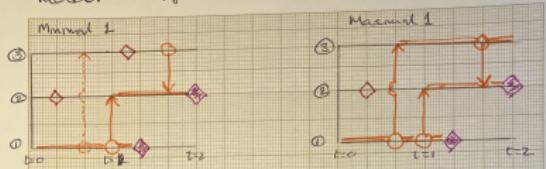
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Then CFTP would make sense, and it would only be necessary to show that accessibility of a set of near-maximal configurations guarantees eventual coalescence.

Counterexample to monotonicity

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

1/2/25



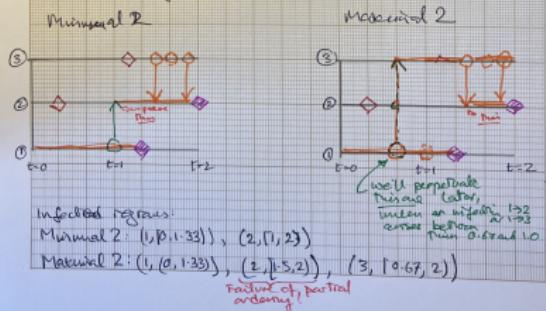
◆ Conditioned removal

◆ 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 | 1.11.3 | — | |
| EpidemicsCFTP | 2.2.492 | main | Thu Jan 23 20:50:07 2025 |
| EpidemicsUtilities | 0.1.2.156 | main | Thu Jan 23 12:06:14 2025 |
| This quarto script | 2.2.621 | Wilfrid-2025-01-30-compartment | Mon Feb 3 18:33:41 2025 |

Revision notes

These notes were produced from `PerfectEpidemics.qmd`:

Version: 2.2.623 [Wilfrid-2025-01-30-compartment]
Author: Wilfrid Kendall <W.S.Kendall@warwick.ac.uk>
Date: Tue Feb 4 18:19:36 2025 +0000
Summary: See what this does!
