

# Perfect Epidemics

## Seminar at University College Dublin

W S Kendall    S B Connor

Warwick, York

20 October 2025



# Introduction

Homage to Dublin  
(Book of Kells, 9th century)



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



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

# Plan of talk

*Gregory*: Is there any other point to which you would wish to draw my attention?

*Holmes*: To the curious incident of the dog in the night-time.

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- ⑤ Example with real data.

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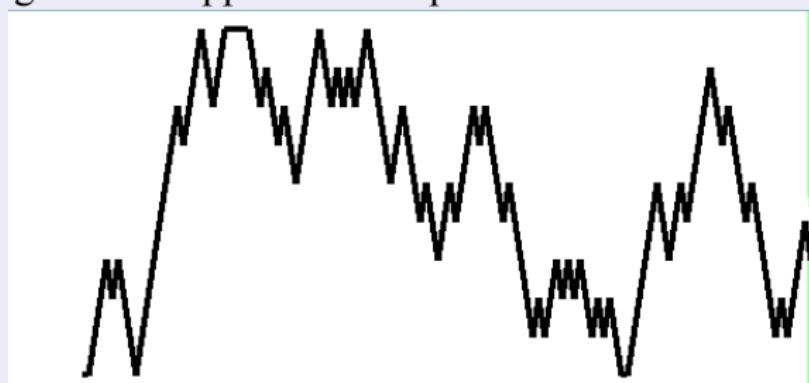
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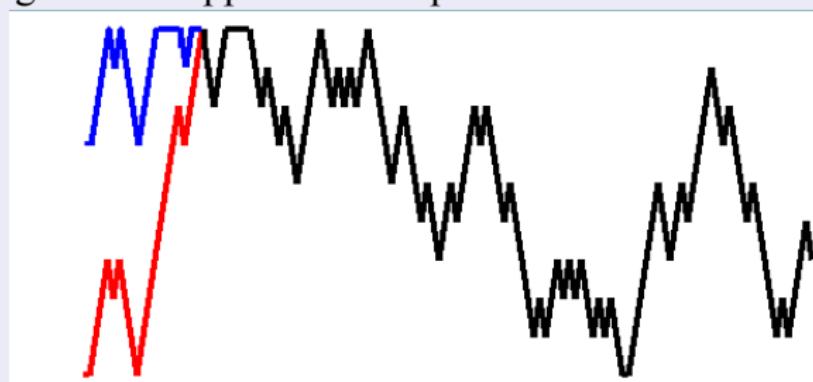
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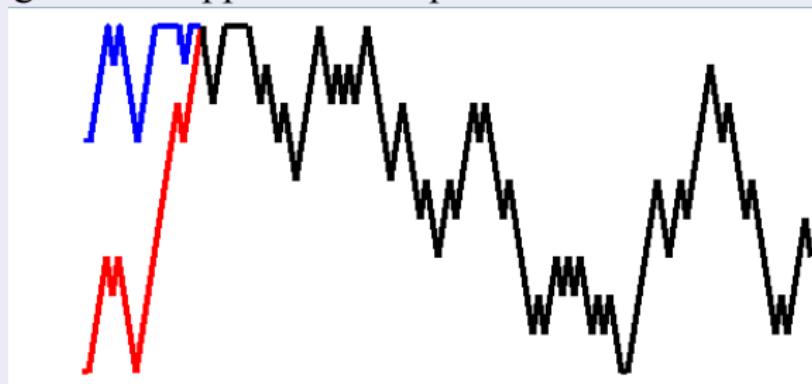
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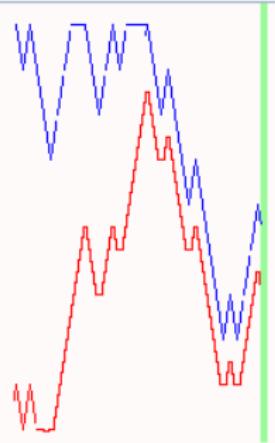
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- ④ Generally **not true** that location *at coupling* is a draw from equilibrium.

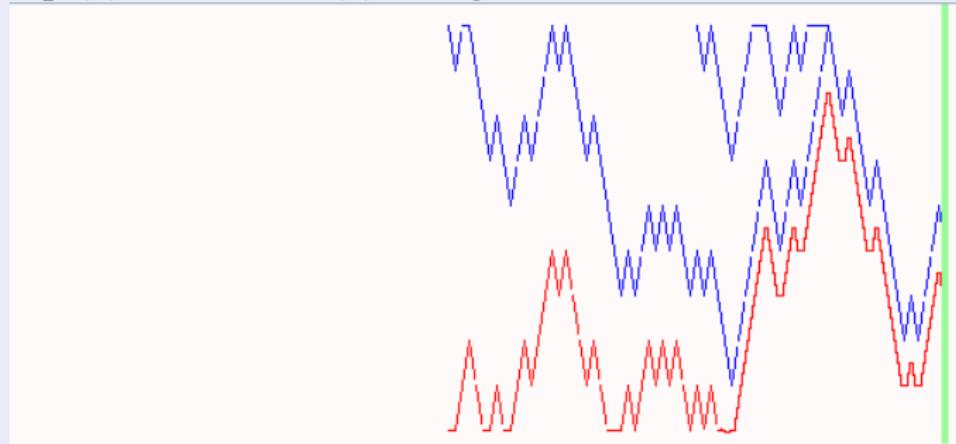
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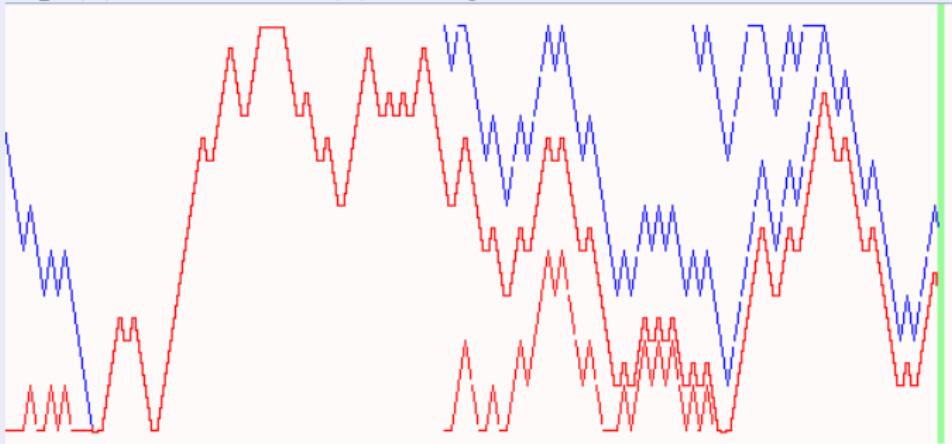


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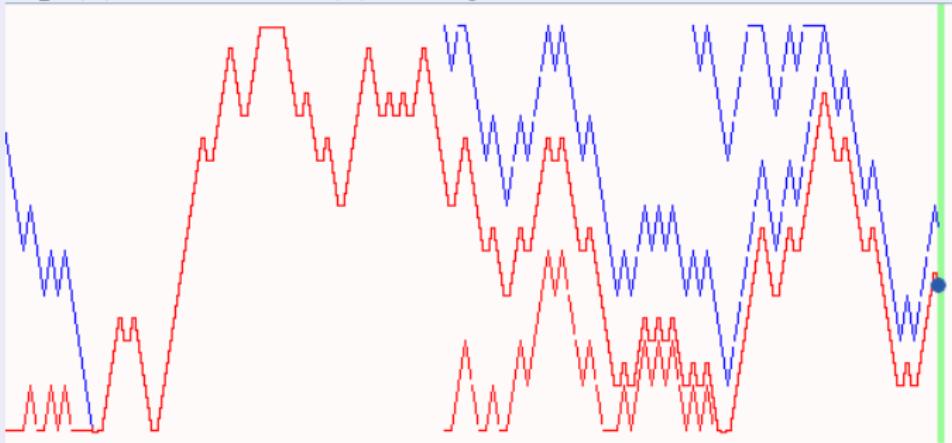
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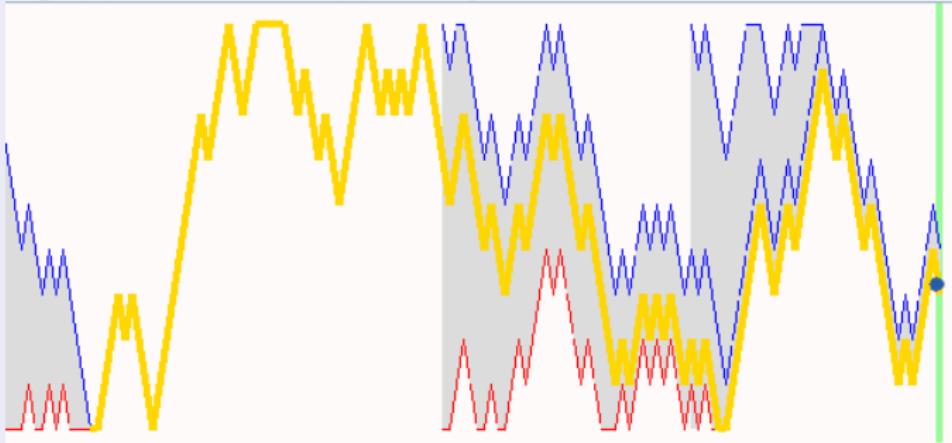
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- ⑤ The common value (golden thread) is an exact draw from equilibrium!

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

## 2. 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 *et al* (2023) use a UK model with  $N=10^6$  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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The simplest possible variant of contact tracing:

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

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- ④ First step: evolve whole S-I-R trajectory in *algorithmic time* (alter potential infections and removals using immigration-death in discrete algorithmic time).

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- 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.

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

Incidents defining an epidemic

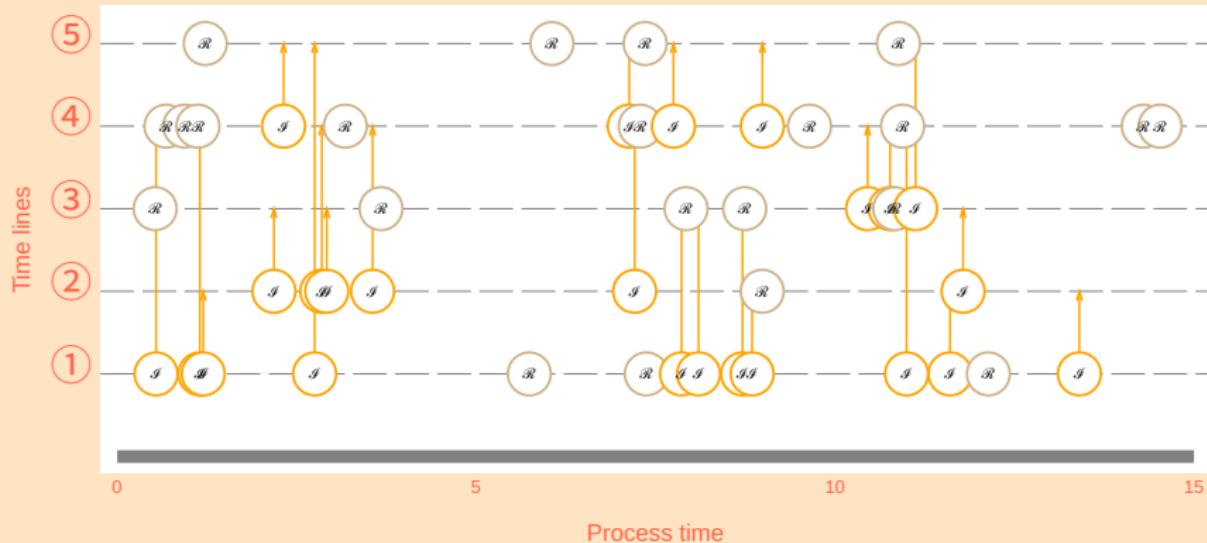


Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

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

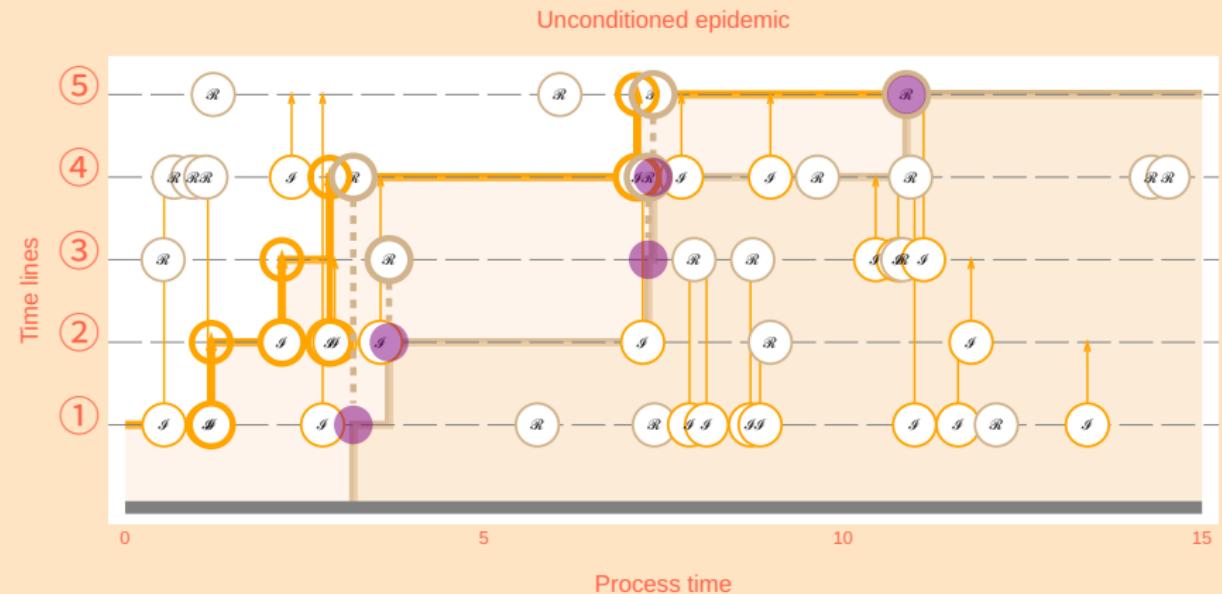


Figure 2: (a) *Infection* activates if target lies on the lowest uninfected timeline; and (b) *removal* activates if on infected timeline; remove lowest infected (purple disk).

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

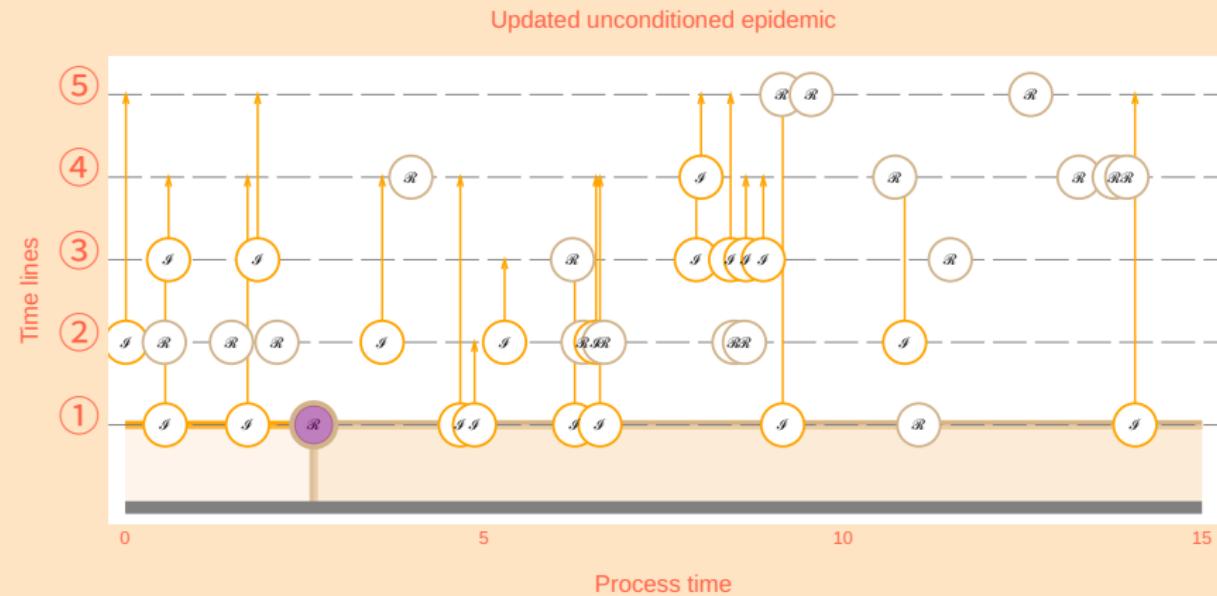


Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing all original incidents by an entirely new set of incidents.

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- Updates in algorithmic time  $\tau$  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  $S$ .

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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, re-sampling step 2 ensures composite evolution is irreducible over  $S$ ! (So equilibrium under conditioning is unique.)

# Free evolution evolving in continuous algorithmic time

GIF MP4



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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

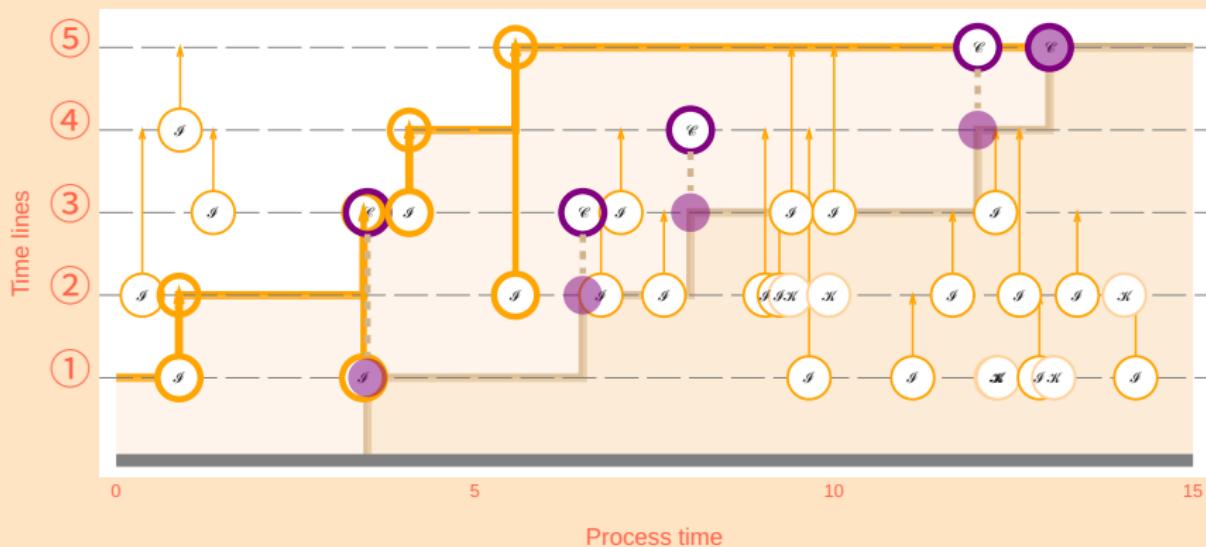


Figure 4: Initial conditioned epidemic, with conditioned removals indicated using purple circles (and purple disks when non-target timelines are infected).

# Conditional epidemic update

Fully updated conditioned epidemic

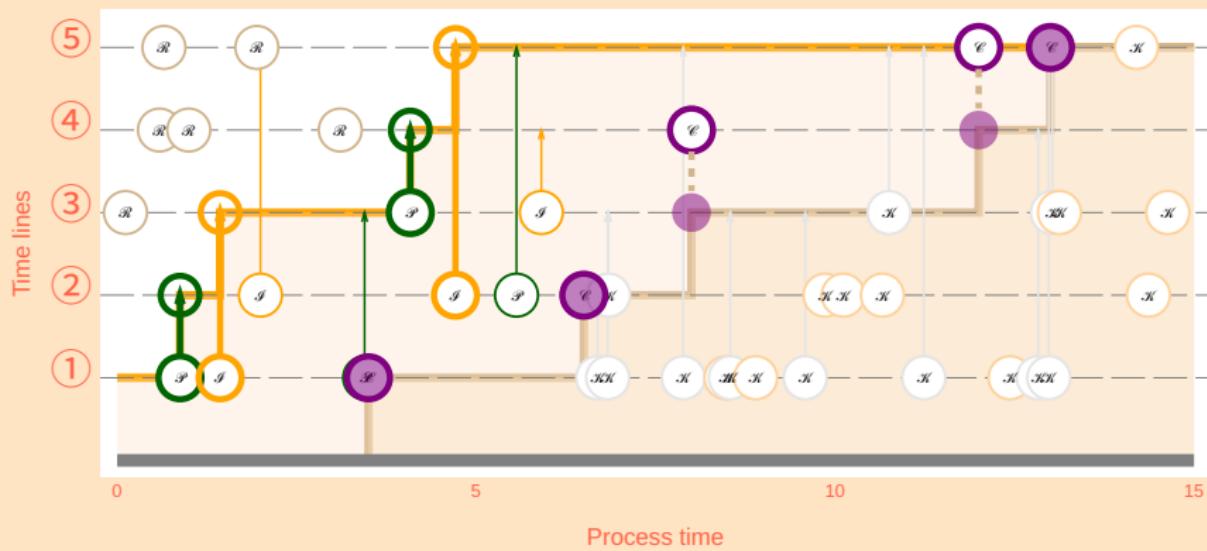


Figure 5: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

# Laziest feasible epidemic (LFE)

Fully updated conditioned epidemic with LFE

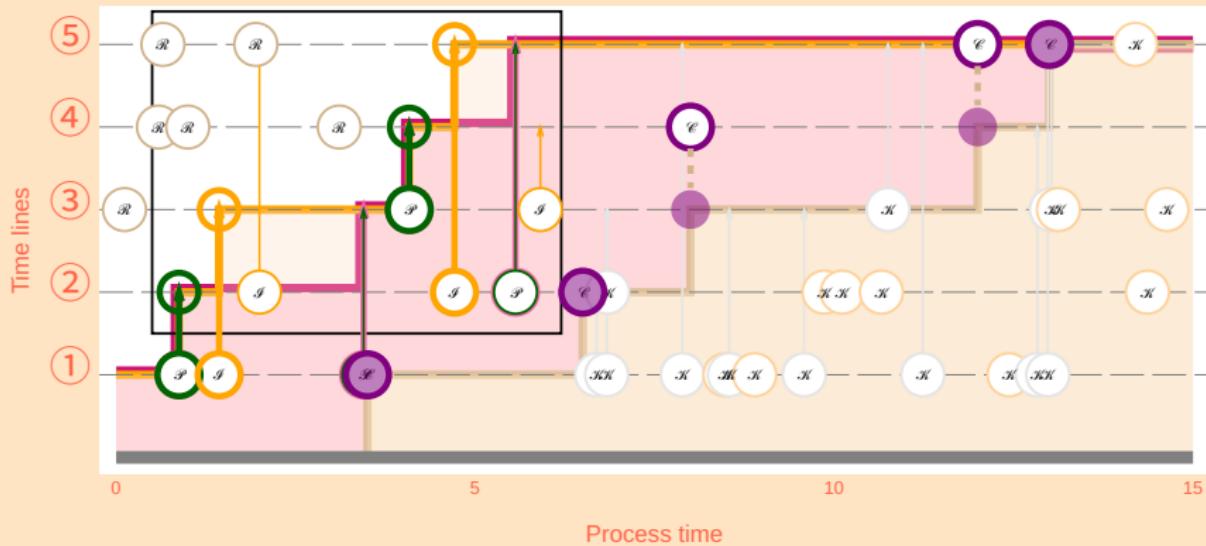
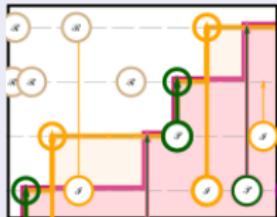


Figure 6: LFE computed recursively working right-to-left: slowest sequence of infections (and perpetuated infections) generating all conditioned removals. Can be used to identify perpetuated infections.

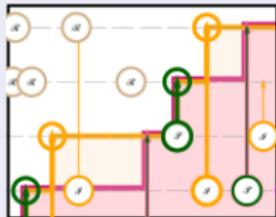
## LFE: construction details



- ① Recursive definition of LFE: working over  $[0, T)$ ,

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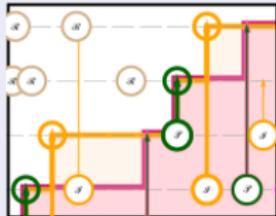
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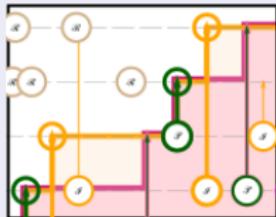
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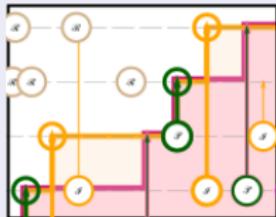
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- ③ Comparisons based on intrinsic definition show monotonic dependence of LFE on previous epidemic history.

## Fully updated conditioned epidemic with NFZ

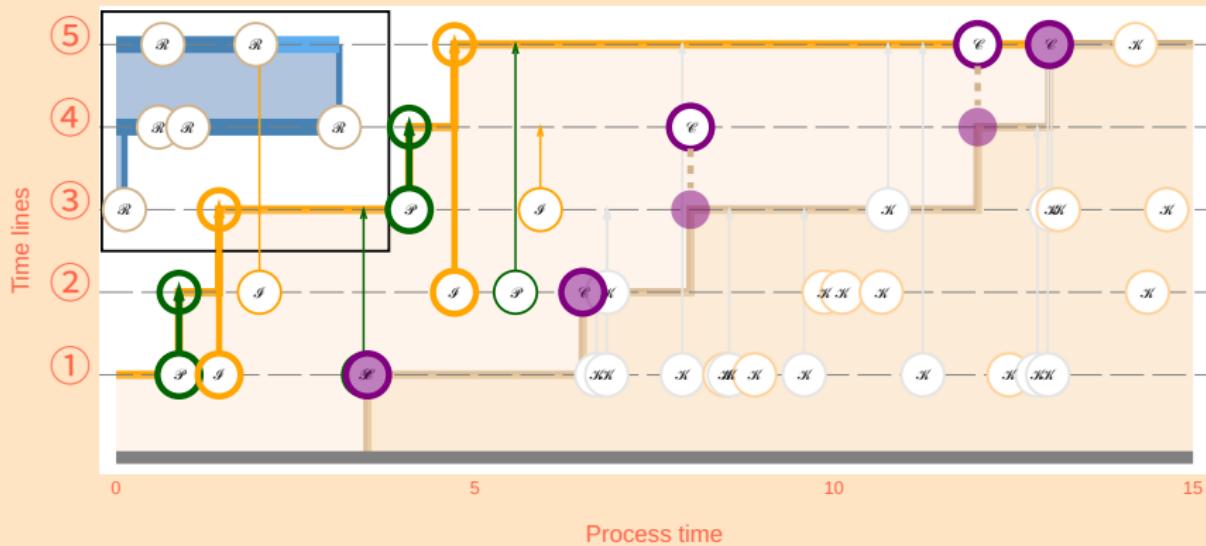
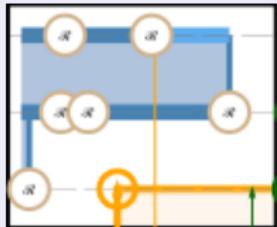


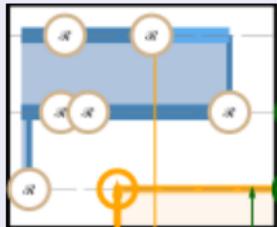
Figure 7: NFZ computed recursively working right-to-left: it traces a region of timelines such that unobserved removals are not activated if region not infected.

## NFZ: construction details



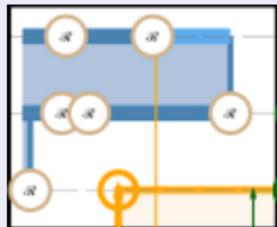
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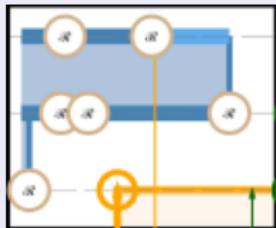
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- ➋ Can then show monotonic dependence of NFZ on previous epidemic history.

GIF MP4

If a new  $\mathcal{J}_t^{i < j}$  has  $i, j$  in infectious zone then **LFE** is relevant;  
if  $i$  in infectious zone and  $j$  in susceptible zone then **NFZ** is relevant.

*New epidemic is monotonic in LFE, NFZ!*

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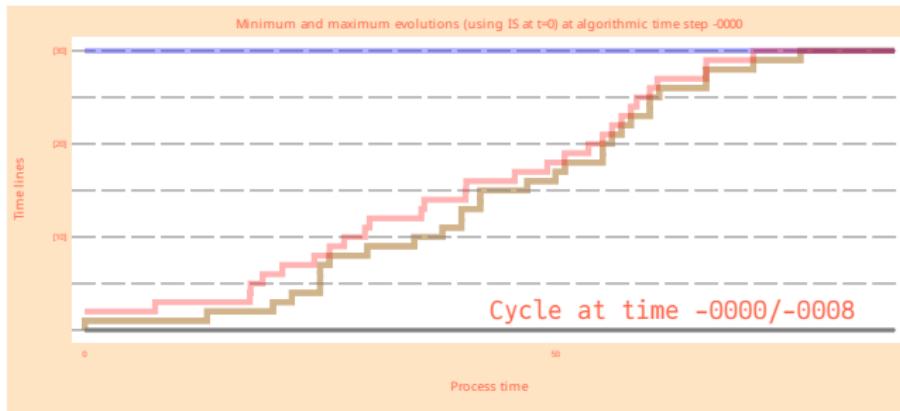
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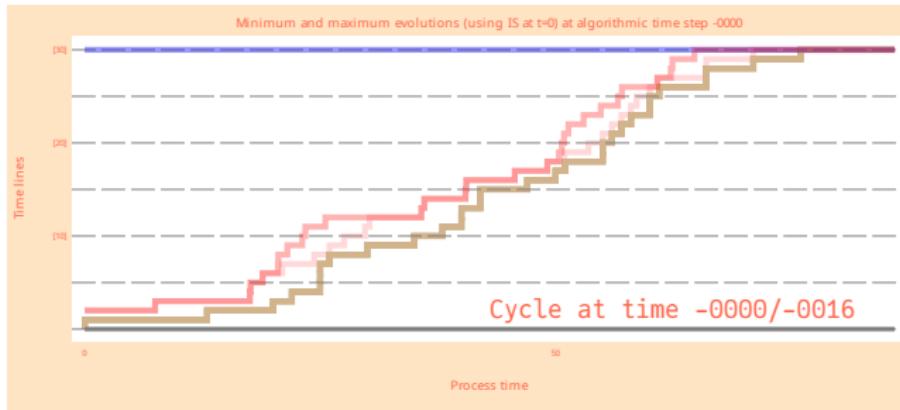
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- Coding in **julia** (**Bezanson et al., 2017**), animates (**GIF** or **MP4**) a perfect simulation of a draw from unobserved pattern of infections.



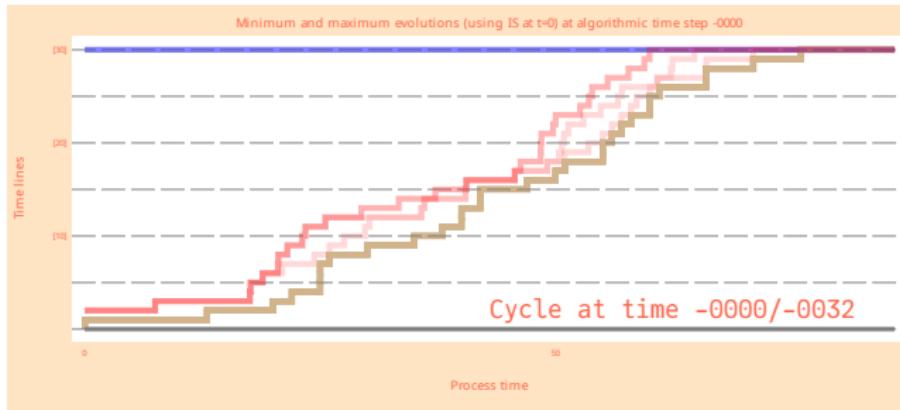
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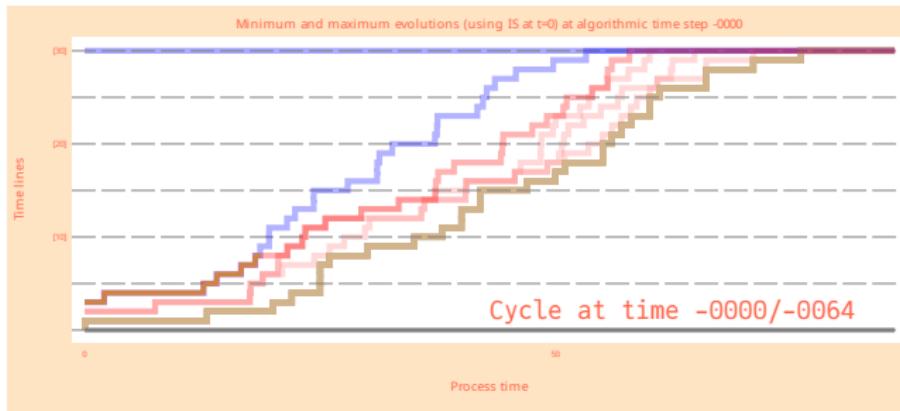
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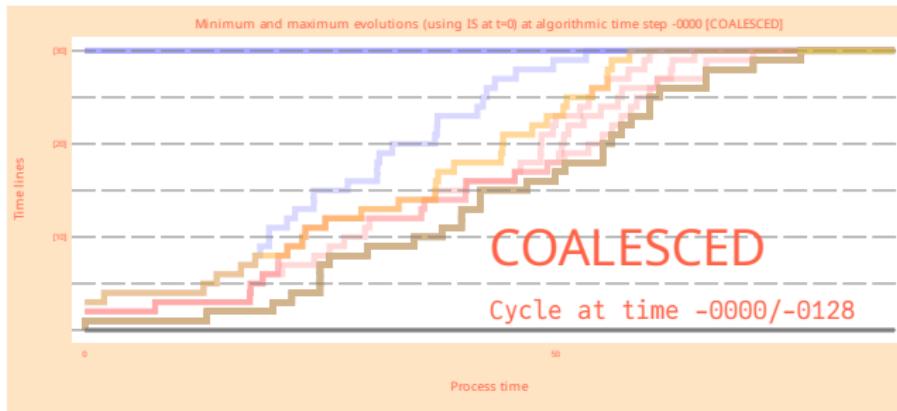
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- **Finally:** generalize to other suitable compartment models?

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



# 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.
- Diaconis, P. (2009) The Markov Chain Monte Carlo Revolution. *Bulletin of the American Mathematical Society*, **46**, 179–205.
- 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.

## References II

- 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.
- 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.
- 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 (2007a) Perfect simulation for a class of positive recurrent Markov chains. *Annals of Applied Probability*, **17**, 781–808.
- SBC & WSK (2007b) Perfect simulation for a class of positive recurrent Markov chains (corrigendum). *Annals of Applied Probability*, **17**, 1808–1810.
- SBC & WSK (2015) Perfect simulation of M/G/c queues. *Advances in Applied Probability*, **47**, 1039–1063.

# References III

- SBC & WSK (2025) Perfect Epidemics.
- Sigman, K. (2011) Exact simulation of the stationary distribution of the FIFO M/G/c queue. *Journal of Applied Probability*, **48**, 209–213.
- 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>Book of Kells</i>	Huber Gerhard	<i>CC BY 4.0</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	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
20/10/25	Perfect Epidemics	Seminar	Dublin

# 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	1.12.0	—	
EpidemicsCFTP	2.2.532	develop	Tue Jul 8 17:13:42 2025 +0100
EpidemicsUtilities	0.1.2.177	main	Fri Sep 26 15:35:26 2025 +0100
This quarto script	0.2.2.725	2025-10-09-Dublin-preparation	Tue Oct 14 18:01:39 2025 +0100

## Project information

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**Version:** 0.2.2.725 (2025-10-09-Dublin-preparation)

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**Author:** Wilfrid Kendall <W.S.Kendall@warwick.ac.uk>

**Date:** Tue Oct 14 18:01:39 2025 +0100

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### Comment:

Near-final preparation for Dublin October 2025 talk. Added material on LFE and NFZ including some sketches of monotonicity arguments. Added note on Rao-Blackwell-ization.