

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)



Introduction

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



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.

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.

Gregory: The dog did nothing in the night-time.

Holmes: That was the curious incident.

("The Adventure of Silver Blaze", Sir Arthur Conan Doyle, 1892)

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.

Gregory: The dog did nothing in the night-time.

Holmes: That was the curious incident.

("The Adventure of Silver Blaze", Sir Arthur Conan Doyle, 1892)

① Introduction to perfect simulation:

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.

Gregory: The dog did nothing in the night-time.

Holmes: That was the curious incident.

("The Adventure of Silver Blaze", Sir Arthur Conan Doyle, 1892)

- ① Introduction to perfect simulation:
- ② A little theory about CFTP;

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.

Gregory: The dog did nothing in the night-time.

Holmes: That was the curious incident.

("The Adventure of Silver Blaze", Sir Arthur Conan Doyle, 1892)

- Ⓐ Introduction to perfect simulation;
- Ⓑ A little theory about CFTP;
- Ⓒ Epidemics and the R -number;

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.

Gregory: The dog did nothing in the night-time.

Holmes: That was the curious incident.

("The Adventure of Silver Blaze", Sir Arthur Conan Doyle, 1892)

- ① Introduction to perfect simulation;
- ② A little theory about CFTP;
- ③ Epidemics and the R -number;
- ④ "Contact tracing": inferring infection pattern if removals observed;

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.

Gregory: The dog did nothing in the night-time.

Holmes: That was the curious incident.

("The Adventure of Silver Blaze", Sir Arthur Conan Doyle, 1892)

- Ⓐ Introduction to perfect simulation;
- Ⓑ A little theory about CFTP;
- Ⓒ Epidemics and the R -number;
- Ⓓ “Contact tracing”: inferring infection pattern if removals observed;
- Ⓔ Example with real data.

1. Introduction to Perfect Simulation

- ① Propp & Wilson (1996) invented exact simulation / Coupling from the Past (CFTP) / perfect simulation;

1. Introduction to Perfect Simulation

- ① Propp & Wilson (1996) invented exact simulation / Coupling from the Past (CFTP) / perfect simulation;
- ② The term “perfect simulation” (WSK, 1998) was chosen to encourage you to be suspicious: perfection is never achieved!

1. Introduction to Perfect Simulation

- ① Propp & Wilson (1996) invented exact simulation / Coupling from the Past (*CFTP*) / perfect simulation;
- ② The term “perfect simulation” (WSK, 1998) was chosen to encourage you to be suspicious: perfection is never achieved!
- ③ Key ideas of “classic *CFTP*”:

1. Introduction to Perfect Simulation

- ➊ Propp & Wilson (1996) invented exact simulation / Coupling from the Past (*CFTP*) / perfect simulation;
- ➋ The term “perfect simulation” (WSK, 1998) was chosen to encourage you to be suspicious: perfection is never achieved!
- ➌ Key ideas of “classic *CFTP*”:
 - ▶ extend simulation *backwards* through time not forwards;

1. Introduction to Perfect Simulation

- ① Propp & Wilson (1996) invented exact simulation / Coupling from the Past (*CFTP*) / perfect simulation;
- ② The term “perfect simulation” (WSK, 1998) was chosen to encourage you to be suspicious: perfection is never achieved!
- ③ Key ideas of “classic *CFTP*”:
 - ▶ extend simulation *backwards* through time not forwards;
 - ▶ exploit monotonicity (*couple* maximal and minimal processes);

1. Introduction to Perfect Simulation

- ➊ Propp & Wilson (1996) invented exact simulation / Coupling from the Past (*CFTP*) / perfect simulation;
- ➋ The term “perfect simulation” (WSK, 1998) was chosen to encourage you to be suspicious: perfection is never achieved!
- ➌ Key ideas of “classic *CFTP*”:
 - ▶ extend simulation *backwards* through time not forwards;
 - ▶ exploit monotonicity (*couple* maximal and minimal processes);
 - ▶ seek coalescence.

1. Introduction to Perfect Simulation

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

Classic CFTP for a simple random walk (I)

- ① Consider a simple random walk on $0:9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.

Classic CFTP for a simple random walk (I)

- ① Consider a simple random walk on $0:9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.
 - ▶ $\mathbb{P} [+1 \text{ jump}] = p \in (0, 1)$, while $\mathbb{P} [-1 \text{ jump}] = 1-p$, **except that**

Classic CFTP for a simple random walk (I)

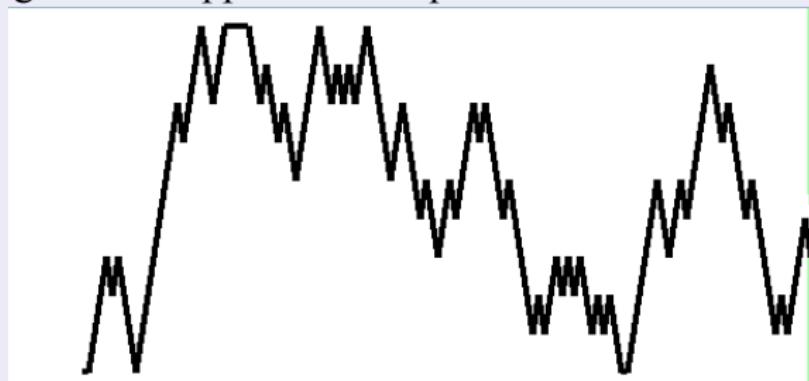
- ① Consider a simple random walk on $0:9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.
 - ▶ $\mathbb{P} [+1 \text{ jump}] = p \in (0, 1)$, while $\mathbb{P} [-1 \text{ jump}] = 1-p$, **except that**
 - ▶ at state 9 replace the +1 jump by “staying still”, **and**

Classic CFTP for a simple random walk (I)

- ① Consider a simple random walk on $0:9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.
- ▶ $\mathbb{P} [+1 \text{ jump}] = p \in (0, 1)$, while $\mathbb{P} [-1 \text{ jump}] = 1-p$, **except that**
 - ▶ at state 9 replace the +1 jump by “staying still”, **and**
 - ▶ at state 0 replace the -1 jump by “staying still”.

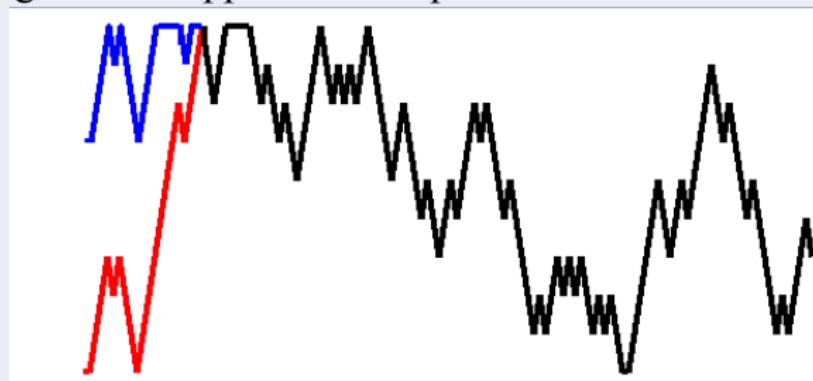
Classic CFTP for a simple random walk (I)

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



Classic CFTP for a simple random walk (I)

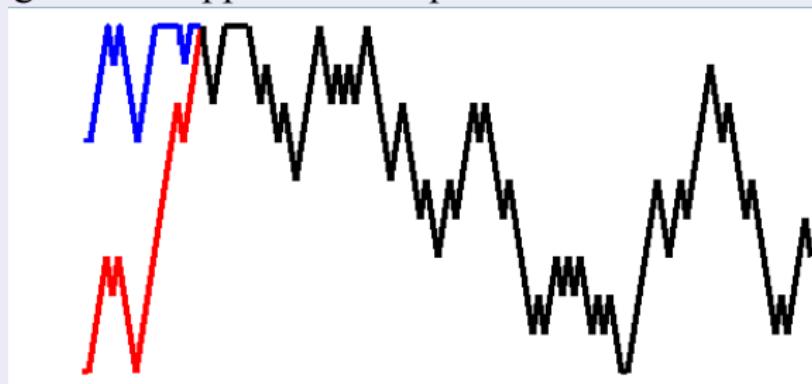
- ① Consider a simple random walk on $0:9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.
 - ▶ $\mathbb{P} [+1 \text{ jump}] = p \in (0, 1)$, while $\mathbb{P} [-1 \text{ jump}] = 1-p$, **except that**
 - ▶ at state 9 replace the $+1$ jump by “staying still”, **and**
 - ▶ at state 0 replace the -1 jump by “staying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



- ③ How long? One way to *estimate* this is to run two (or several?) coupled copies till they meet. If probability of meeting by time T is high, then deviation of X_T from equilibrium is statistically small;

Classic CFTP for a simple random walk (I)

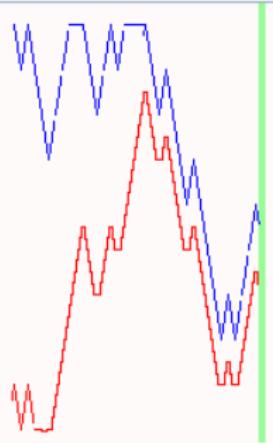
- ① Consider a simple random walk on $0:9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.
 - ▶ $\mathbb{P} [+1 \text{ jump}] = p \in (0, 1)$, while $\mathbb{P} [-1 \text{ jump}] = 1-p$, **except that**
 - ▶ at state 9 replace the $+1$ jump by “staying still”, **and**
 - ▶ at state 0 replace the -1 jump by “staying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



- ③ How long? One way to *estimate* this is to run two (or several?) coupled copies till they meet. If probability of meeting by time T is high, then deviation of X_T from equilibrium is statistically small;
- ④ Generally **not true** that location *at coupling* is a draw from equilibrium.

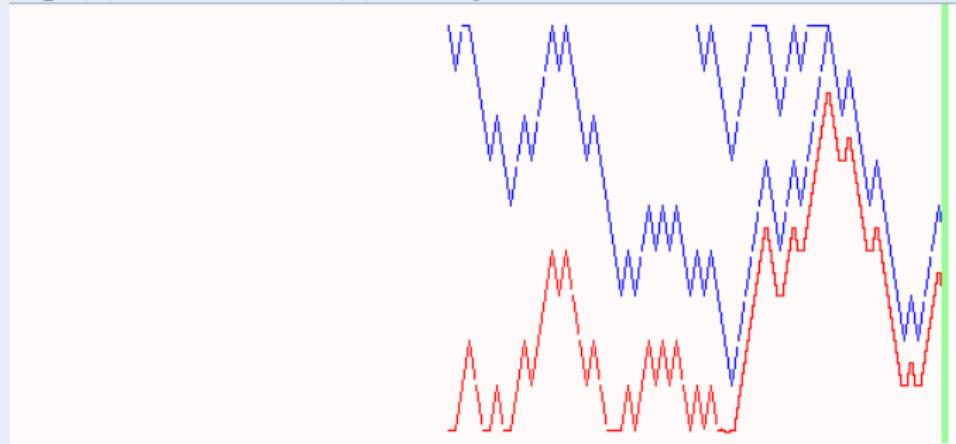
Classic CFTP for a simple random walk (I)

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



Classic CFTP for a simple random walk (I)

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

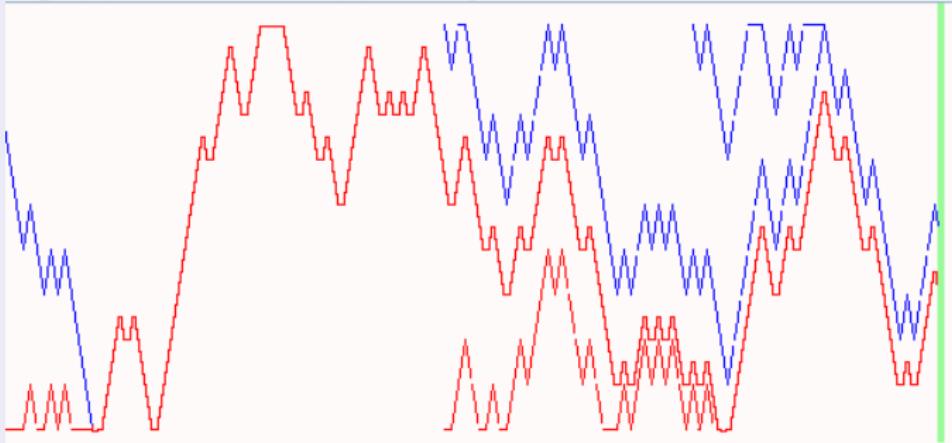


- ② If not coupled by time 0, than back-off to time $-2T$ and repeat.

NB: re-use randomness!

Classic CFTP for a simple random walk (I)

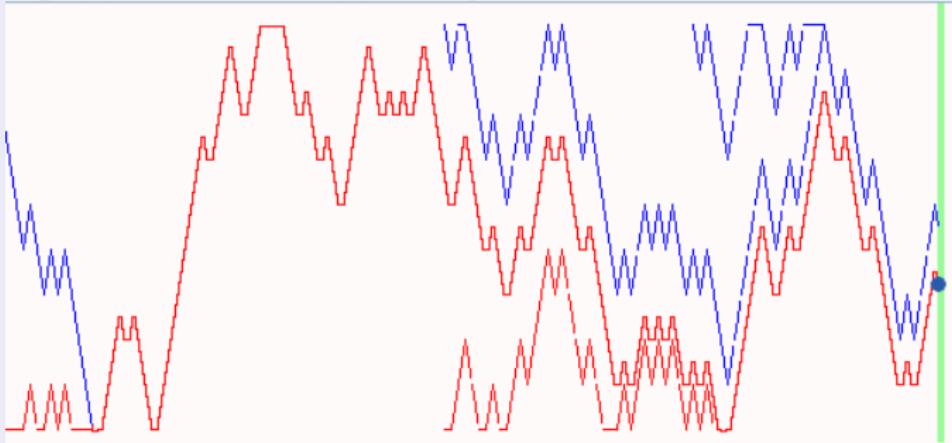
- ① Start at top (9) and bottom (0) at negative time $-T$, run to time 0.



- ② If not coupled by time 0, then back-off to time $-2T$ and repeat.
NB: re-use randomness!
- ③ May need to iterate back-off doubling several times.

Classic CFTP for a simple random walk (I)

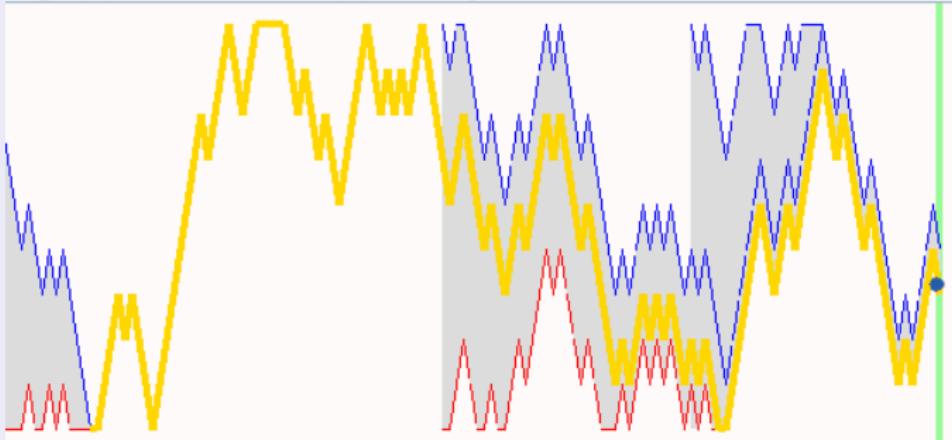
- ① Start at top (9) and bottom (0) at negative time $-T$, run to time 0.



- ② If not coupled by time 0, then back-off to time $-2T$ and repeat.
NB: re-use randomness!
- ③ May need to iterate back-off doubling several times.
- ④ When coupled, top and bottom yield a common value at time 0.

Classic CFTP for a simple random walk (I)

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



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

A little CFTP theory

- ① What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):

A little CFTP theory

- ➊ What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):
 - ▶ cross-couple upper and lower envelope processes;

A little CFTP theory

- ➊ What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):

- ▶ cross-couple upper and lower envelope processes;
- ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process).

A little CFTP theory

- ➊ What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):
 - ▶ cross-couple upper and lower envelope processes;
 - ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process).
- ➋ Theoretical limits: *in principle*

A little CFTP theory

- ① What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):

- ▶ cross-couple upper and lower envelope processes;
- ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process).

- ② Theoretical limits: *in principle*

- ▶ *Classical CFTP* equivalent to uniform ergodicity (Foss & Tweedie, 1998);

A little CFTP theory

- ① What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):

- ▶ cross-couple upper and lower envelope processes;
- ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process).

- ② Theoretical limits: *in principle*

- ▶ *Classical CFTP* equivalent to uniform ergodicity (Foss & Tweedie, 1998);
- ▶ *Dominated CFTP* achievable under geometric ergodicity (WSK, 2004);

A little CFTP theory

- ➊ What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):

- ▶ cross-couple upper and lower envelope processes;
- ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process).

- ➋ Theoretical limits: *in principle*

- ▶ *Classical CFTP* equivalent to uniform ergodicity (Foss & Tweedie, 1998);
- ▶ *Dominated CFTP* achievable under geometric ergodicity (WSK, 2004);
- ▶ Dominated CFTP can work in some **non**-geometrically ergodicity cases (SBC & WSK, 2007a; *nb* corrigendum SBC & WSK, 2007b).

A little CFTP theory

- ① What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):
 - ▶ cross-couple upper and lower envelope processes;
 - ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process).
- ② Theoretical limits: *in principle*
 - ▶ Classical CFTP equivalent to uniform ergodicity (Foss & Tweedie, 1998);
 - ▶ Dominated CFTP achievable under geometric ergodicity (WSK, 2004);
 - ▶ Dominated CFTP can work in some non-geometrically ergodicity cases (SBC & WSK, 2007a; *nb* corrigendum SBC & WSK, 2007b).
- ③ Dominated CFTP delivers perfect simulation for stable point processes (WSK & Møller, 2000);

A little CFTP theory

- ➊ What if monotonicity fails? or there isn't a sensible “maximal” process?
Ideas (WSK, 1998):
 - ▶ cross-couple upper and lower envelope processes;
 - ▶ dominate by amenable “dominating process” (time-reversible, can draw from equilibrium, can couple target processes below dominating process).
- ➋ Theoretical limits: *in principle*
 - ▶ Classical CFTP equivalent to uniform ergodicity (Foss & Tweedie, 1998);
 - ▶ Dominated CFTP achievable under geometric ergodicity (WSK, 2004);
 - ▶ Dominated CFTP can work in some non-geometrically ergodicity cases (SBC & WSK, 2007a; *nb* corrigendum SBC & WSK, 2007b).
- ➌ Dominated CFTP delivers perfect simulation for stable point processes (WSK & Møller, 2000);
- ➍ 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 :

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

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

2. Perfect Epidemics: a challenge problem for CFTP

S-I-R deterministic epidemic:

based on susceptibles s , infectives i , removals r :

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

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

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

Infection: $S \rightarrow S - 1$, $I \rightarrow I + 1$ at rate $\alpha S I$,

Removal: $I \rightarrow I - 1$, $R \rightarrow R + 1$ at rate βI .

2. Perfect Epidemics: a challenge problem for CFTP

S-I-R deterministic epidemic:

based on susceptibles s , infectives i , removals r :

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

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

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

Infection: $S \rightarrow S - 1$, $I \rightarrow I + 1$ at rate $\alpha S I$,

Removal: $I \rightarrow I - 1$, $R \rightarrow R + 1$ at rate βI .

Both make an unrealistic assumption: homogeneous mixing.

In contrast, Fraser *et al* (2021) use a UK model with 10^6 agents!

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



The first question asked about a new epidemic

“What is the R-number?”

The first question asked about a new epidemic

“What is the R-number?”

The R-number is $\alpha s_0 / \beta$: mean number of new infectives produced per infective at *start* of epidemic with initially s_0 susceptibles.

Whittle (1955)’s threshold theorem: R-number $\gg 1$ means strongly positive chance of epidemic infecting significant proportion of the population.

The first question asked about a new epidemic

“What is the R-number?”

The R-number is $\alpha s_0 / \beta$: mean number of new infectives produced per infective at *start* of epidemic with initially s_0 susceptibles.

Whittle (1955)’s threshold theorem: R-number $\gg 1$ means strongly positive chance of epidemic infecting significant proportion of the population.

Wikipedia: “The British-registered *Diamond Princess* was the first cruise ship to have a major [COVID-19] outbreak on board, with the ship quarantined at Yokohama from 4 February 2020 for about a month. Of 3711 passengers and crew, around 700 people became infected and 9 people died.”

Evidently $\alpha s_0 / \beta \gg 1$ – as was sadly later confirmed, a sorrow for us all.



Inference on the R-number

Important, because the R-number controls severity of epidemic. However:

- ➊ Modelling is **tough**. *Either* massive assumptions (homogeneous mixing) *or* very many parameters;

Inference on the R-number

Important, because the R-number controls severity of epidemic. However:

- ① Modelling is **tough**. *Either* massive assumptions (homogeneous mixing) *or* very many parameters;
- ② Inference is **really tough**: hard to get information about infection times;

Inference on the R-number

Important, because the R-number controls severity of epidemic. However:

- ➊ Modelling is **tough**. *Either* massive assumptions (homogeneous mixing) *or* very many parameters;
- ➋ Inference is **really tough**: hard to get information about infection times;
- ➌ It is all **especially tough** in early stages. Answers are most needed when hardly any information is available (a simplified example for a Warwick UG second-year statistics module shows how tough this can be);

Inference on the R-number

Important, because the R-number controls severity of epidemic. However:

- ① Modelling is **tough**. *Either* massive assumptions (homogeneous mixing) *or* very many parameters;
- ② Inference is **really tough**: hard to get information about infection times;
- ③ It is all **especially tough** in early stages. Answers are most needed when hardly any information is available (a simplified example for a Warwick UG second-year statistics module shows how tough this can be);
- ④ Markov chain Monte Carlo (MCMC) can be used (see next slide) but what about burn-in?

Inference on the R-number

Important, because the R-number controls severity of epidemic. However:

- ➊ Modelling is **tough**. *Either* massive assumptions (homogeneous mixing) *or* very many parameters;
- ➋ Inference is **really tough**: hard to get information about infection times;
- ➌ It is all **especially tough** in early stages. Answers are most needed when hardly any information is available (a simplified example for a Warwick UG second-year statistics module shows how tough this can be);
- ➍ Markov chain Monte Carlo (MCMC) can be used (see next slide) but what about burn-in?
- ➎ Can we use **perfect simulation**?

An easier question

The simplest possible variant of contact tracing:

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

(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

An easier question

The simplest possible variant of contact tracing:

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

(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

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

- ➊ Suppose n, α, β are known. Eventually removal times are observed, but unobserved infection times **must be inferred**.

An easier question

The simplest possible variant of contact tracing:

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

(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

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

- ① Suppose n, α, β are known. Eventually removal times are observed, but unobserved infection times **must be inferred**.
- ② Visualize n timelines, along which incidents are scattered:

An easier question

The simplest possible variant of contact tracing:

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

(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

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

- ① Suppose n, α, β are known. Eventually removal times are observed, but unobserved infection times **must be inferred**.
- ② Visualize n timelines, along which incidents are scattered:
 - ▶ potential removals, activated if timeline is infected;

An easier question

The simplest possible variant of contact tracing:

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

(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

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

- ① Suppose n, α, β are known. Eventually removal times are observed, but unobserved infection times **must be inferred**.
- ② Visualize n timelines, along which incidents are scattered:
 - ▶ potential removals, activated if timeline is infected;
 - ▶ potential infections, activated if timeline is infected *and* if designated target timeline is lowest uninfected timeline.

An easier question

The simplest possible variant of contact tracing:

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

(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

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

- ① Suppose n, α, β are known. Eventually removal times are observed, but unobserved infection times **must be inferred**.
- ② Visualize n timelines, along which incidents are scattered:
 - ▶ potential removals, activated if timeline is infected;
 - ▶ potential infections, activated if timeline is infected *and* if designated target timeline is lowest uninfected timeline.
- ③ Poisson point processes *of appropriate rates* yield an S-I-R epidemic.

An easier question

The simplest possible variant of contact tracing:

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

(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

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

- ① Suppose n, α, β are known. Eventually removal times are observed, but unobserved infection times **must be inferred**.
- ② Visualize n timelines, along which incidents are scattered:
 - ▶ potential removals, activated if timeline is infected;
 - ▶ potential infections, activated if timeline is infected *and* if designated target timeline is lowest uninfected timeline.
- ③ Poisson point processes *of appropriate rates* yield an S-I-R epidemic.
- ④ First step: evolve whole S-I-R trajectory in *algorithmic time* (alter potential infections and removals using immigration-death in discrete algorithmic time).

An easier question

The simplest possible variant of contact tracing:
“When did the infections occur, supposing we only observe removals?”
(Gibson & Renshaw, 1998; O’Neill & Roberts, 1999; Gibson & Renshaw, 2001)

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

- ① Suppose n, α, β are known. Eventually removal times are observed, but unobserved infection times **must be inferred**.
- ② Visualize n timelines, along which incidents are scattered:
 - ▶ potential removals, activated if timeline is infected;
 - ▶ potential infections, activated if timeline is infected *and* if designated target timeline is lowest uninfected timeline.
- ③ Poisson point processes *of appropriate rates* yield an S-I-R epidemic.
- ④ First step: evolve whole S-I-R trajectory in *algorithmic time* (alter potential infections and removals using immigration-death in discrete algorithmic time).
- ⑤ Result: *trajectory-valued chain*, unconditioned S-I-R as equilibrium.

From incidents to unconditioned epidemic trajectories (1/3)



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

From incidents to unconditioned epidemic trajectories (2/3)

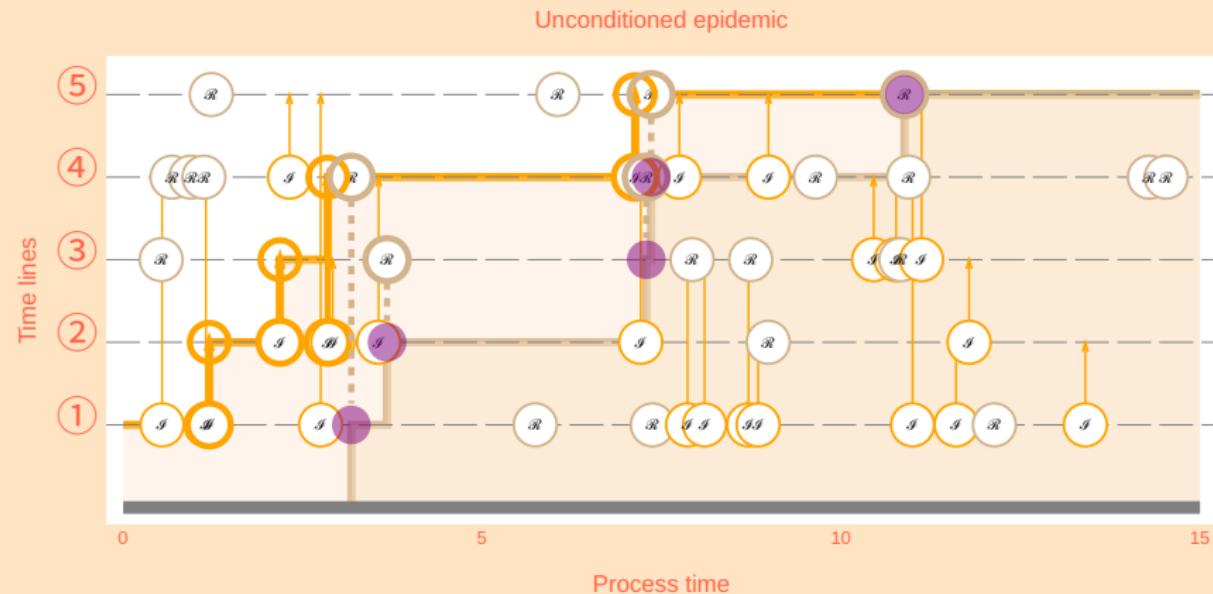


Figure 2: (a) *Infection* activates if target lies on the lowest uninfected timeline; and (b) *removal* activates if on infected timeline; remove lowest infected (purple disk).

From incidents to unconditioned epidemic trajectories (3/3)

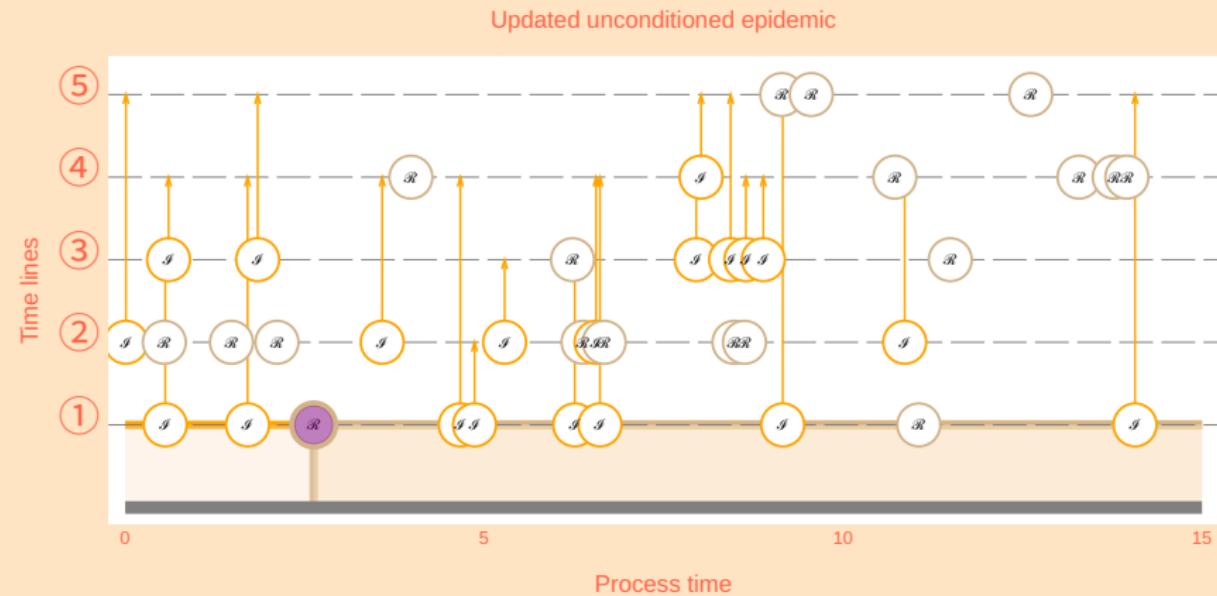


Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing all original incidents by an entirely new set of incidents.

Crucial technical point

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

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ➊ Replace removals (\mathcal{R}_S);

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ➊ Replace removals (\mathcal{R}_S);
 - ➋ Re-sample timelines (though not times) of \mathcal{R}_S ;

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R}_s);
 - ② Re-sample timelines (though not times) of \mathcal{R}_s ;
 - ③ Replace infections (\mathcal{I}_s).

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R}_s);
 - ② Re-sample timelines (though not times) of \mathcal{R}_s ;
 - ③ Replace infections (\mathcal{I}_s).
- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R} s);
 - ② Re-sample timelines (though not times) of \mathcal{R} s;
 - ③ Replace infections (\mathcal{I} s).
- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.
 - ① For $2nT < \tau < (2n+1)T$, update old \mathcal{R} s with times in $(0, \tau - 2nT)$;

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R} s);
 - ② Re-sample timelines (though not times) of \mathcal{R} s;
 - ③ Replace infections (\mathcal{I} s).
- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.
 - ① For $2nT < \tau < (2n+1)T$, update old \mathcal{R} s with times in $(0, \tau - 2nT)$;
 - ② For $\tau = (2n+1)T$, resample timelines (not times) of \mathcal{R} s;

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R} s);
 - ② Re-sample timelines (though not times) of \mathcal{R} s;
 - ③ Replace infections (\mathcal{I} s).
- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.
 - ① For $2nT < \tau < (2n+1)T$, update old \mathcal{R} s with times in $(0, \tau - 2nT)$;
 - ② For $\tau = (2n+1)T$, resample timelines (not times) of \mathcal{R} s;
 - ③ For $(2n+1)T < \tau < (2n+2)T$, update old \mathcal{I} s in $((2n+2)T - \tau, T)$.

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-) *time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R} s);
 - ② Re-sample timelines (though not times) of \mathcal{R} s;
 - ③ Replace infections (\mathcal{I} s).
- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.
 - ① For $2nT < \tau < (2n+1)T$, update old \mathcal{R} s with times in $(0, \tau - 2nT)$;
 - ② For $\tau = (2n+1)T$, resample timelines (not times) of \mathcal{R} s;
 - ③ For $(2n+1)T < \tau < (2n+2)T$, update old \mathcal{I} s in $((2n+2)T - \tau, T)$.
- Thus the original update is expressible as a (continuous) composition of updates, each of which satisfies detailed balance in equilibrium.

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-) *time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R} s);
 - ② Re-sample timelines (though not times) of \mathcal{R} s;
 - ③ Replace infections (\mathcal{I} s).
- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.
 - ① For $2nT < \tau < (2n+1)T$, update old \mathcal{R} s with times in $(0, \tau - 2nT)$;
 - ② For $\tau = (2n+1)T$, resample timelines (not times) of \mathcal{R} s;
 - ③ For $(2n+1)T < \tau < (2n+2)T$, update old \mathcal{I} s in $((2n+2)T - \tau, T)$.
- Thus the original update is expressible as a (continuous) composition of updates, each of which satisfies detailed balance in equilibrium.
- The connection “restriction=conditioning” still holds.

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-) *time-reversible*: so restriction to a subset S of state-space (the *activated / conditioned* removals to occur precisely at the specified set of times) implies a new equilibrium which is the old equilibrium conditioned to lie in S .
- For later purposes it is convenient to stage the replacement as follows:
 - ① Replace removals (\mathcal{R} s);
 - ② Re-sample timelines (though not times) of \mathcal{R} s;
 - ③ Replace infections (\mathcal{I} s).
- Re-express using *continuously varying* τ . Process time runs over $[0, T]$.
 - ① For $2nT < \tau < (2n+1)T$, update old \mathcal{R} s with times in $(0, \tau - 2nT)$;
 - ② For $\tau = (2n+1)T$, resample timelines (not times) of \mathcal{R} s;
 - ③ For $(2n+1)T < \tau < (2n+2)T$, update old \mathcal{I} s in $((2n+2)T - \tau, T)$.
- Thus the original update is expressible as a (continuous) composition of updates, each of which satisfies detailed balance in equilibrium.
- The connection “restriction=conditioning” 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

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

Implications:

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

Implications:

- ▶ a removal can be introduced only if it doesn't activate;

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

Implications:

- ▶ a removal can be introduced only if it doesn't activate;
- ▶ a conditioned removal timeline can be altered only if it doesn't de-activate;

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

Implications:

- ▶ a removal can be introduced only if it doesn't activate;
- ▶ a conditioned removal timeline can be altered only if it doesn't de-activate;
- ▶ an infection cannot be removed if that action loses a conditioned removal;

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

Implications:

- ▶ a removal can be introduced only if it doesn't activate;
- ▶ a conditioned removal timeline can be altered only if it doesn't de-activate;
- ▶ an infection cannot be removed if that action loses a conditioned removal;
- ▶ an infection can be introduced only if no new observed removals result.

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

Implications:

- ▶ a removal can be introduced only if it doesn't activate;
 - ▶ a conditioned removal timeline can be altered only if it doesn't de-activate;
 - ▶ an infection cannot be removed if that action loses a conditioned removal;
 - ▶ an infection can be introduced only if no new observed removals result.
- Does this produce a *feasible* and suitably *monotonic* algorithm?

3. Conditioning on observed removals

- The trajectory-valued chain is *dynamically reversible*, in *continuous algorithmic time*.
- Irreducibility is *vital* (otherwise equilibrium depends on starting point). Consequently:
 - ▶ conditioned removals must be able to change timeline (but not time of occurrence);
- Forbidding removal of observed removals, and forbidding creation of new activated removals, yields a modified chain whose invariant probability measure conditions on observed pattern of removals.

Implications:

- ▶ a removal can be introduced only if it doesn't activate;
- ▶ a conditioned removal timeline can be altered only if it doesn't de-activate;
- ▶ an infection cannot be removed if that action loses a conditioned removal;
- ▶ an infection can be introduced only if no new observed removals result.
- Does this produce a *feasible* and suitably *monotonic* algorithm?
- **Housekeeping details** used to establish that monotonicity still works: *laziest feasible epidemic (LFE)* and *no-fly zone (NFZ)*.

Initial conditioned epidemic

The initial conditioned epidemic

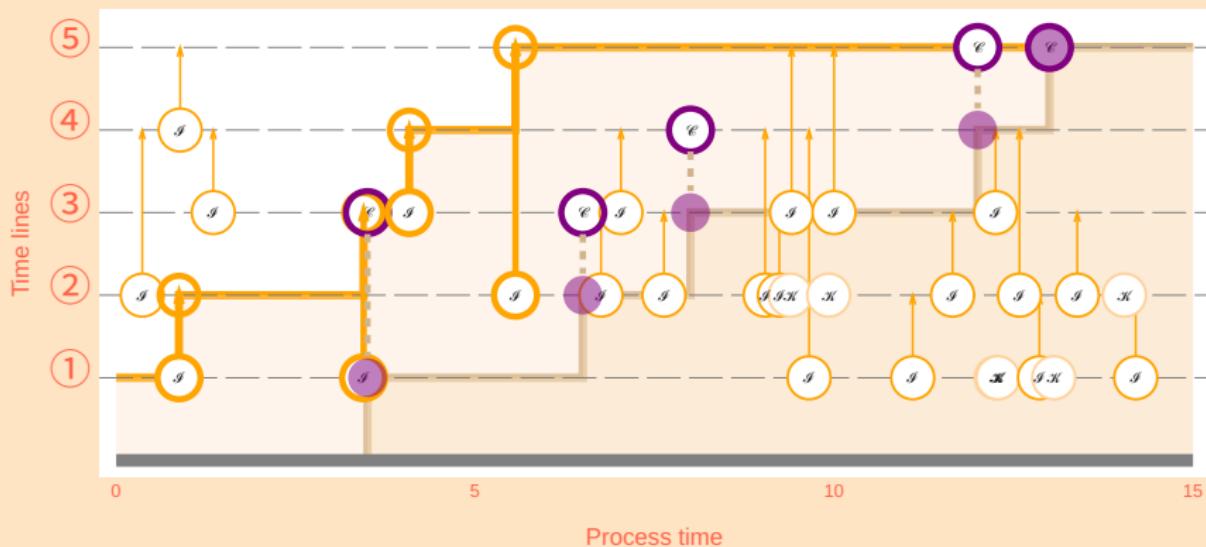


Figure 4: Initial conditioned epidemic, with conditioned removals indicated using purple circles (and purple disks when non-target timelines are infected).

Conditional epidemic update

Fully updated conditioned epidemic

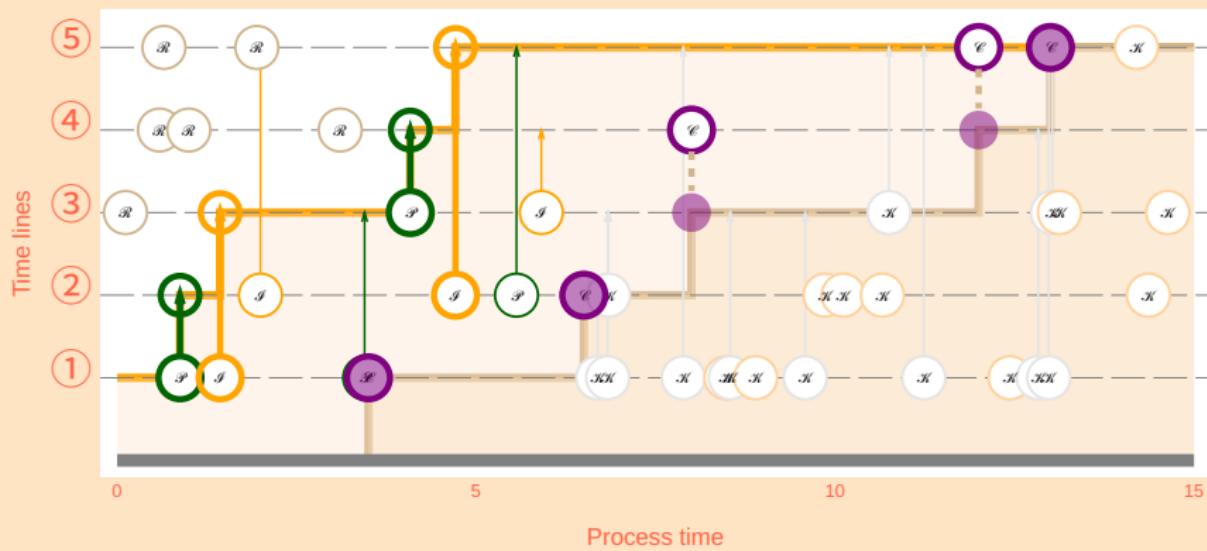


Figure 5: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been “perpetuated”.

Laziest feasible epidemic (LFE)

Fully updated conditioned epidemic with LFE

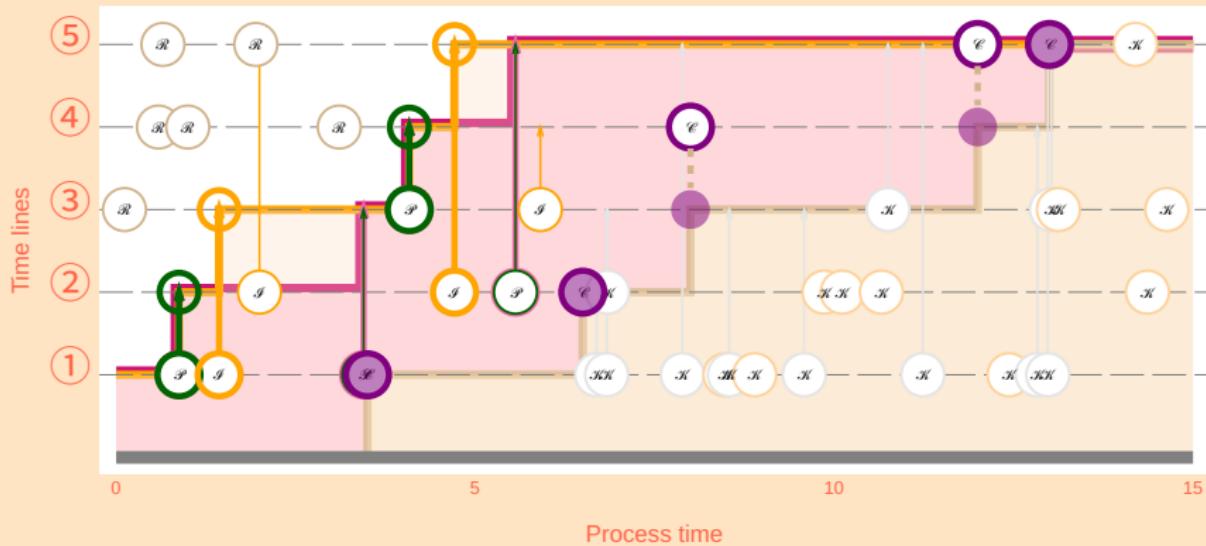


Figure 6: LFE computed recursively working right-to-left: slowest sequence of infections (including perpetuated infections) generating all observed removals in order.

Fully updated conditioned epidemic with NFZ

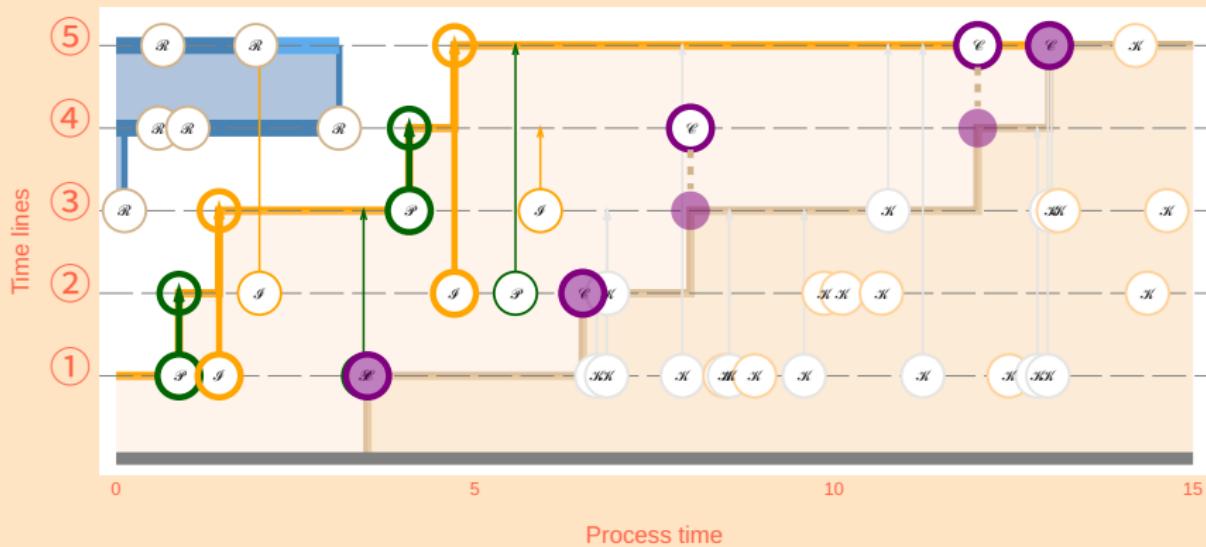


Figure 7: NFZ computed recursively working right-to-left: it traces the region of timelines that must not be infected if one is not to activate unobserved removals.

Conditioned evolution evolving in continuous algorithmic time

GIF MP4

4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).

4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**

4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;

4. Example

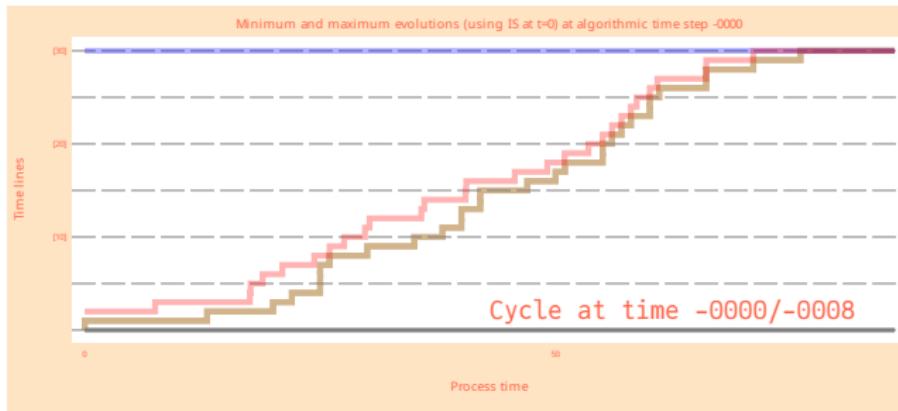
- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;
 - ▶ *all* removals are recorded;

4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;
 - ▶ *all* removals are recorded;
 - ▶ no further removals after last observed removal (makes life easier).

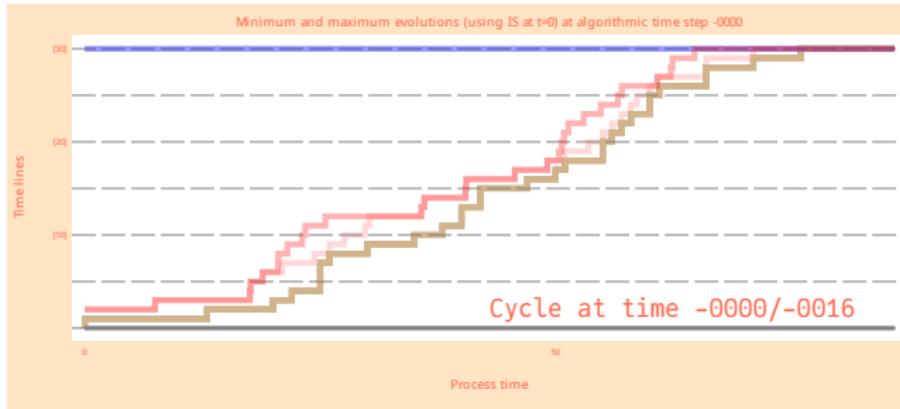
4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;
 - ▶ *all* removals are recorded;
 - ▶ no further removals after last observed removal (makes life easier).
- Coding in **julia** (**Bezanson et al., 2017**), animates (**GIF** or **MP4**) a perfect simulation of a draw from unobserved pattern of infections.



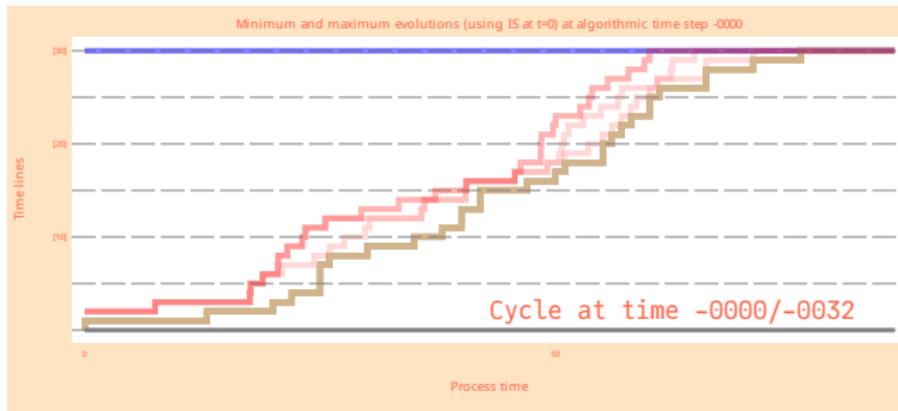
4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;
 - ▶ *all* removals are recorded;
 - ▶ no further removals after last observed removal (makes life easier).
- Coding in **julia** (**Bezanson et al., 2017**), animates (**GIF** or **MP4**) a perfect simulation of a draw from unobserved pattern of infections.



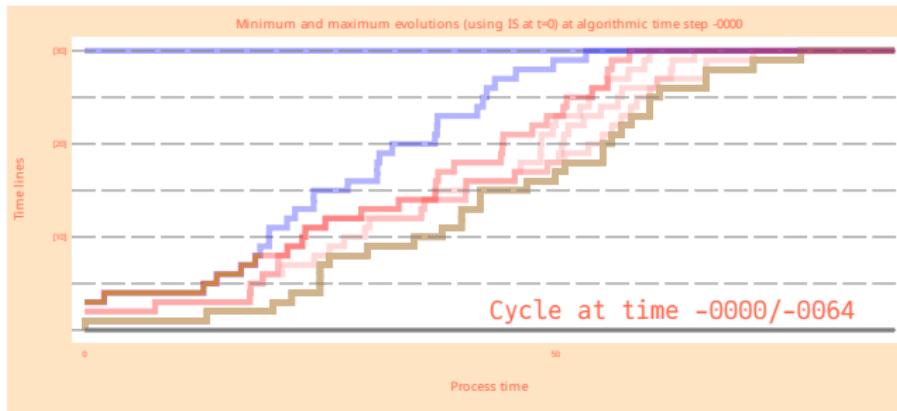
4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;
 - ▶ *all* removals are recorded;
 - ▶ no further removals after last observed removal (makes life easier).
- Coding in **julia** (**Bezanson et al., 2017**), animates (**GIF** or **MP4**) a perfect simulation of a draw from unobserved pattern of infections.



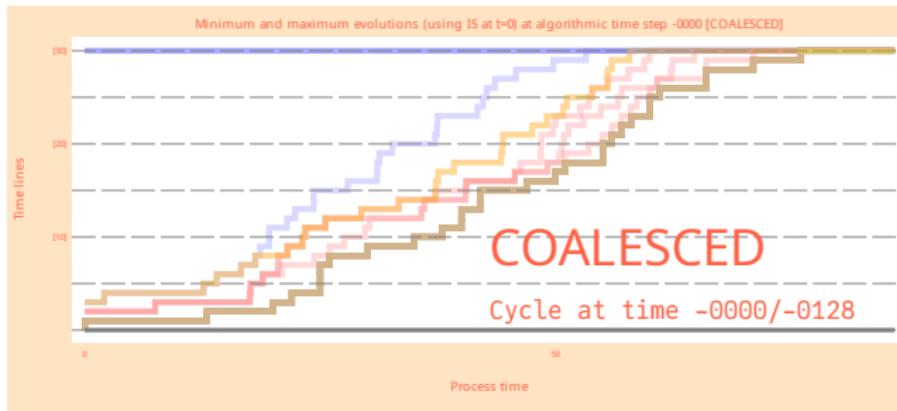
4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;
 - ▶ *all* removals are recorded;
 - ▶ no further removals after last observed removal (makes life easier).
- Coding in **julia** (**Bezanson et al., 2017**), animates (**GIF** or **MP4**) a perfect simulation of a draw from unobserved pattern of infections.



4. Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see page 125 of **Bailey, 1975**).
- **Assume**
 - ▶ first observed removal is also the first removal: under a plausible improper prior we can then deduce what is the distribution of infectives I_0 at time 0;
 - ▶ *all* removals are recorded;
 - ▶ no further removals after last observed removal (makes life easier).
- Coding in **julia** (**Bezanson et al., 2017**), animates (**GIF** or **MP4**) a perfect simulation of a draw from unobserved pattern of infections.



So what?

- What about accept-reject methods?

So what?

- What about accept-reject methods?
- Why this emphasis on unobserved infections given fixed α and β , when we need inference on R-number $\alpha n / \beta$ for *unknown* α and β ?

So what?

- What about accept-reject methods?
- Why this emphasis on unobserved infections given fixed α and β , when we need inference on R-number n/β for *unknown* α and β ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different* α and β . The perfect simulation provides exact simulation-based computation to integrate out pattern of unobserved infections.

So what?

- What about accept-reject methods?
- Why this emphasis on unobserved infections given fixed α and β , when we need inference on R-number n/β for *unknown* α and β ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different* α and β . The perfect simulation provides exact simulation-based computation to integrate out pattern of unobserved infections.
- So (**next steps after SBC & WSK, 2024**)

So what?

- What about accept-reject methods?
- Why this emphasis on unobserved infections given fixed α and β , when we need inference on R-number n/β for *unknown* α and β ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different* α and β . The perfect simulation provides exact simulation-based computation to integrate out pattern of unobserved infections.
- So (**next steps after SBC & WSK, 2024**)
 - ▶ estimate likelihood test statistic for specified α and β ;

So what?

- What about accept-reject methods?
- Why this emphasis on unobserved infections given fixed α and β , when we need inference on R-number n/β for *unknown* α and β ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different* α and β . The perfect simulation provides exact simulation-based computation to integrate out pattern of unobserved infections.
- So (**next steps after SBC & WSK, 2024**)
 - ▶ estimate likelihood test statistic for specified α and β ;
 - ▶ construct steepest ascent algorithm (in effect, variant of Robbins-Monro stochastic optimization) to find *maximum a posterior* estimates of α and β ;

So what?

- What about accept-reject methods?
- Why this emphasis on unobserved infections given fixed α and β , when we need inference on R-number n/β for *unknown* α and β ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different* α and β . The perfect simulation provides exact simulation-based computation to integrate out pattern of unobserved infections.
- So (**next steps after SBC & WSK, 2024**)
 - ▶ estimate likelihood test statistic for specified α and β ;
 - ▶ construct steepest ascent algorithm (in effect, variant of Robbins-Monro stochastic optimization) to find *maximum a posterior* estimates of α and β ;
 - ▶ or even, with some computational effort, compute the entire posterior joint density for α and β !

So what?

- What about accept-reject methods?
- Why this emphasis on unobserved infections given fixed α and β , when we need inference on R-number n/β for *unknown* α and β ?
- Good question. But a re-weighting argument allows us to get (unbiased) estimates based on *different* α and β . The perfect simulation provides exact simulation-based computation to integrate out pattern of unobserved infections.
- So (**next steps after SBC & WSK, 2024**)
 - ▶ estimate likelihood test statistic for specified α and β ;
 - ▶ construct steepest ascent algorithm (in effect, variant of Robbins-Monro stochastic optimization) to find *maximum a posterior* estimates of α and β ;
 - ▶ or even, with some computational effort, compute the entire posterior joint density for α and β !
- Finally: can we generalize to other suitable compartment models?

Conclusion

- If MCMC burn-in is a concern, try to build a perfect simulation!

Conclusion

- If MCMC burn-in is a concern, try to build a perfect simulation!
- CFTP works even for significantly complex and relevant models of real-life phenomena.

Conclusion

- If MCMC burn-in is a concern, try to build a perfect simulation!
- CFTP works even for significantly complex and relevant models of real-life phenomena.
- *Of course* detailed models resist perfect simulation (but it will be helpful to compare with a simpler model using fewer parameters).

Conclusion

- If MCMC burn-in is a concern, try to build a perfect simulation!
- CFTP works even for significantly complex and relevant models of real-life phenomena.
- *Of course* detailed models resist perfect simulation (but it will be helpful to compare with a simpler model using fewer parameters).
- Experiments suggest CFTP out-competes non-naïve accept-reject.

Conclusion

- If MCMC burn-in is a concern, try to build a perfect simulation!
- CFTP works even for significantly complex and relevant models of real-life phenomena.
- *Of course* detailed models resist perfect simulation (but it will be helpful to compare with a simpler model using fewer parameters).
- Experiments suggest CFTP out-competes non-naïve accept-reject.
- Still to be done: seek faster CFTP; statistical estimation of parameters, generalization to other compartment models.

Conclusion

- If MCMC burn-in is a concern, try to build a perfect simulation!
- CFTP works even for significantly complex and relevant models of real-life phenomena.
- *Of course* detailed models resist perfect simulation (but it will be helpful to compare with a simpler model using fewer parameters).
- Experiments suggest CFTP out-competes non-naïve accept-reject.
- 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. (2021) 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*. 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 (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.

References III

- 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

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	2.2.532	develop	Tue Jul 8 17:13:42 2025 +0100
EpidemicsUtilities	0.1.2.176	main	Fri Sep 26 15:11:24 2025 +0100
This quarto script	0.2.2.719	2025-10-09-Dublin-preparation	Thu Oct 9 10:38:07 2025 +0100

Project information

Version:	0.2.2.721 (2025-10-09-Dublin-preparation)
Author:	Wilfrid Kendall <W.S.Kendall@warwick.ac.uk>
Date:	Thu Oct 9 13:04:22 2025 +0100

Comment:

Fixed Fraser et al reference