Perfect Epidemics

Applied Probability Seminar
Department of Statistics, University of Warwick

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Warwick, York

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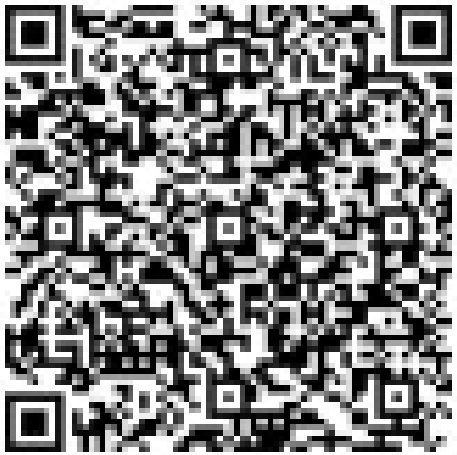
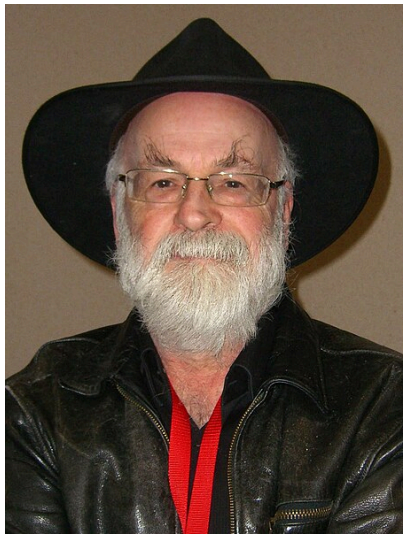


Introduction

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



Handout available on the web: use the `QR-code`

or visit https://wilfridskendall.github.io/talks/PerfectEpidemics/.

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1: Introduction to Perfect Simulation

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

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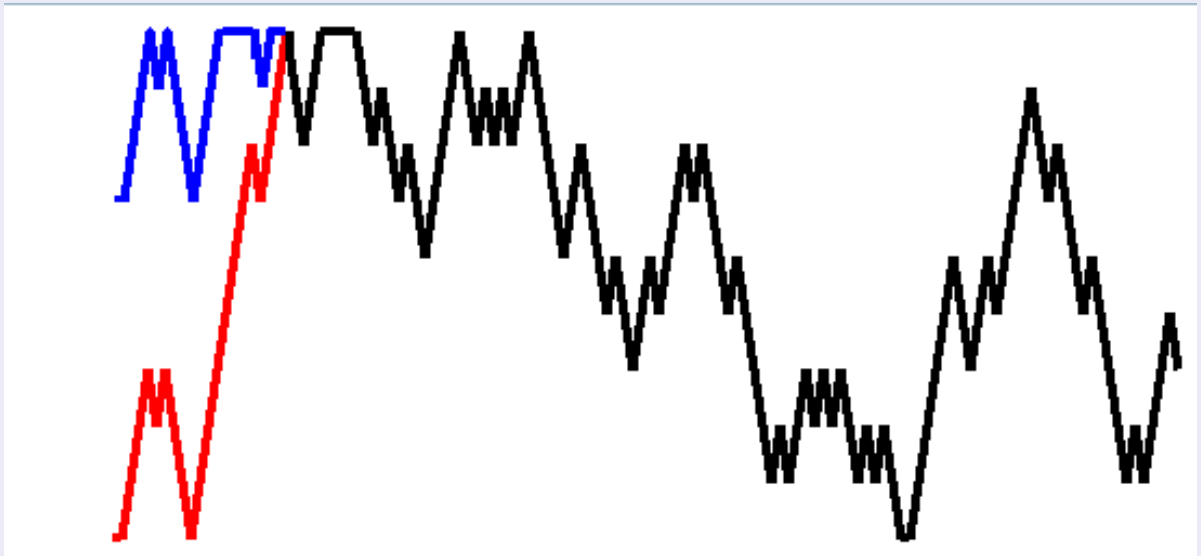
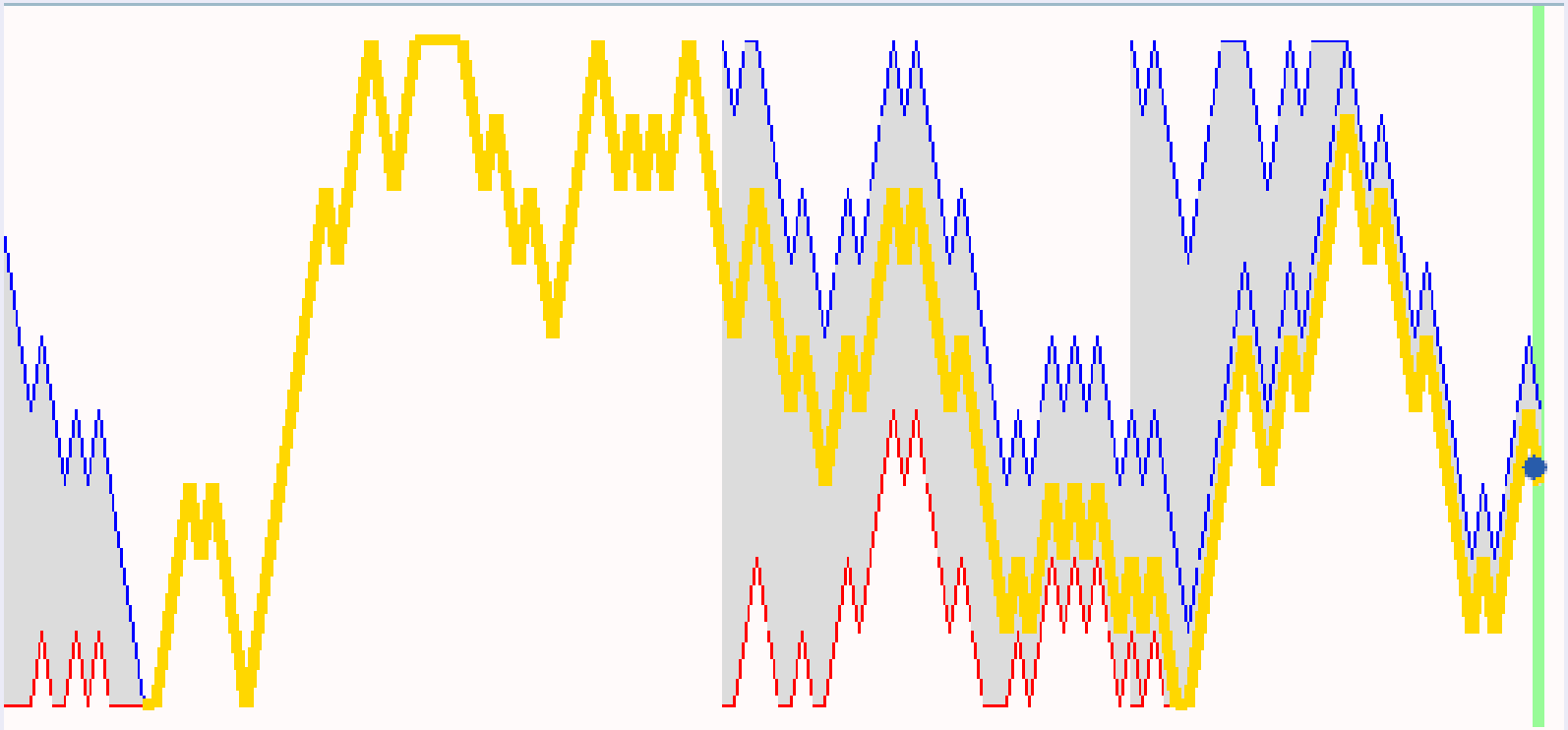
Classic CFTP for a simple random walk (I)

- Consider a simple random walk on $\{0, 1, 2, 3, 4, 5, 6, 7, 8, 9\}$.
  - $\mathbb{P}[+1 \text{ jump}] = p \in (0, 1)$, while $\mathbb{P}[-1 \text{ jump}] = 1-p$, **except that**
  - at state 9 replace $+1$ jump by staying still, **and**
  - at state 0 replace -1 jump by staying still.
- Conventional MCMC picks a starting point, then runs the simple random walk for long time till approximate equilibrium.
- How long? One way to *estimate* this is to run two (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,
- Generally not true that location at coupling is a draw from equilibrium.



Classic CFTP for a simple random walk (I)

- So now start at top (9) and bottom (0) at negative time $-T$, run to time 0.
- If not coupled, than back-off to time $-2T$ and repeat.
- May need to iterate back-off doubling several times.
- When coupled, top and bottom yield a common value at time 0.
- The common value is an exact draw from equilibrium!



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2: A short section on some theory about CFTP

- What about cases where 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);
- 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 (Connor & WSK, 2007a, *nb* corrigendum);
- *Dominated CFTP* can be used to carry out perfect simulation for stable point processes (WSK & Møller, 2000);
- Detailed expositions: WSK (2005), Huber (2015).
  (Want to implement CFTP in R? see WSK, 2015.)

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3: Perfect Epidemics: a challenge problem for CFTP

Many important inferential questions (Cori & Kucharski, 2024).

Simplest models (versus UK model with 10^6 agents!, Fraser & Others, 2023):

S-I-R deterministic epidemic: susceptibles s, infectives i, removals r (constant total population $s + i + r = n$):

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

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

Infection:	$S \to S - 1\,,$	$I \to I + 1$	at rate	$\alpha\, S\, I\,,$
Removal:	$I \to I - 1\,,$	$R \to R + 1$	at rate	$\beta\, I\,.$

Massive assumption for these simple models: **homogeneous mixing**.

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 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.

4: 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?
5. Can we use perfect simulation?

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5: An easier question

An absurdly simple variant on contact tracing:
"When did the infections occur. if we only observe removals?"
(Gibson & Renshaw, 1998; O'Neill & Roberts, 1999; Gibson & Renshaw, 2001)

1. Thus n, α, β known, removal times 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. 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.

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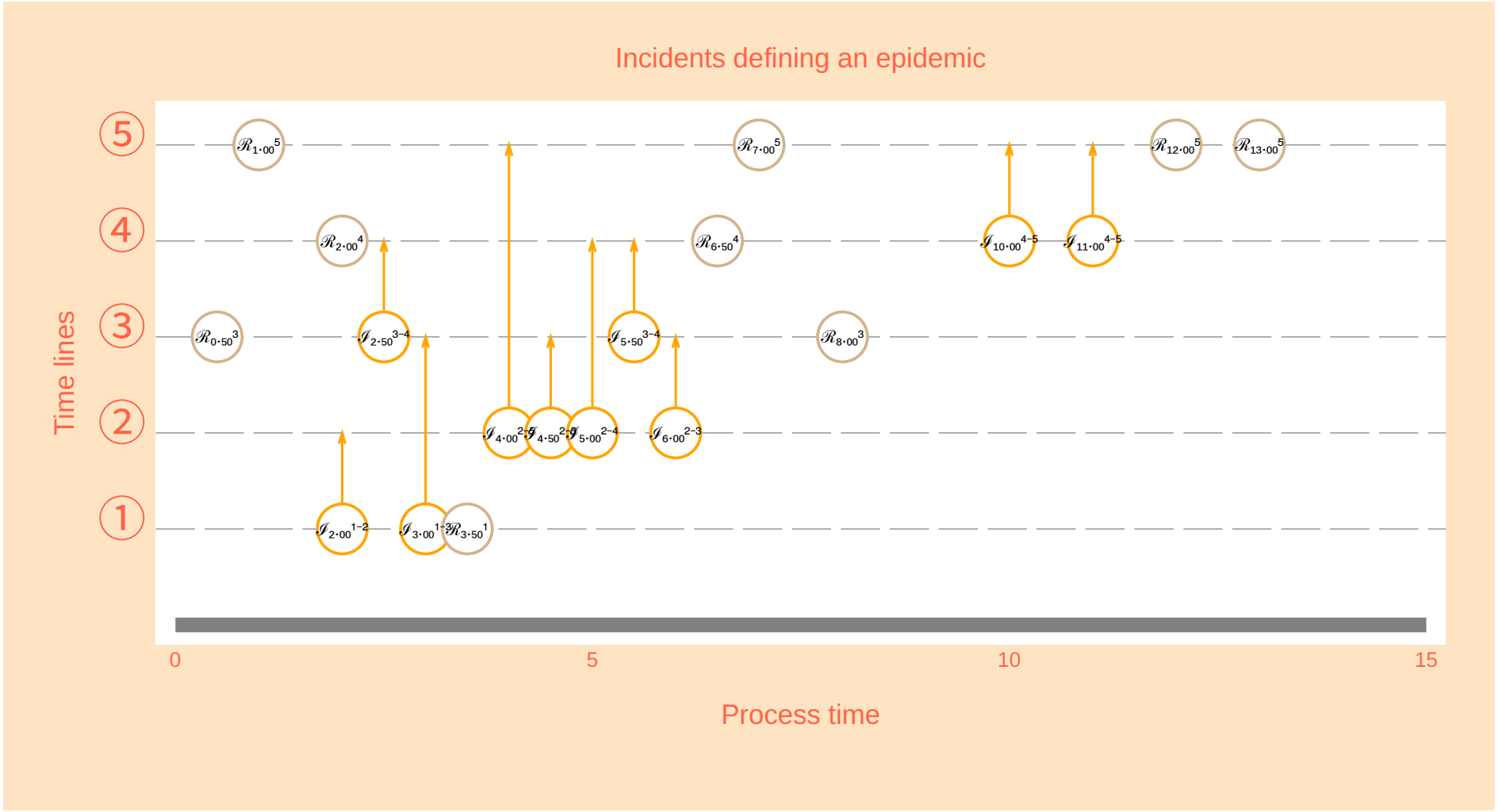

Figure 1: Light-orange circles denote potential infections (arrows point upwards to targets); light-brown circles denote potential removals.

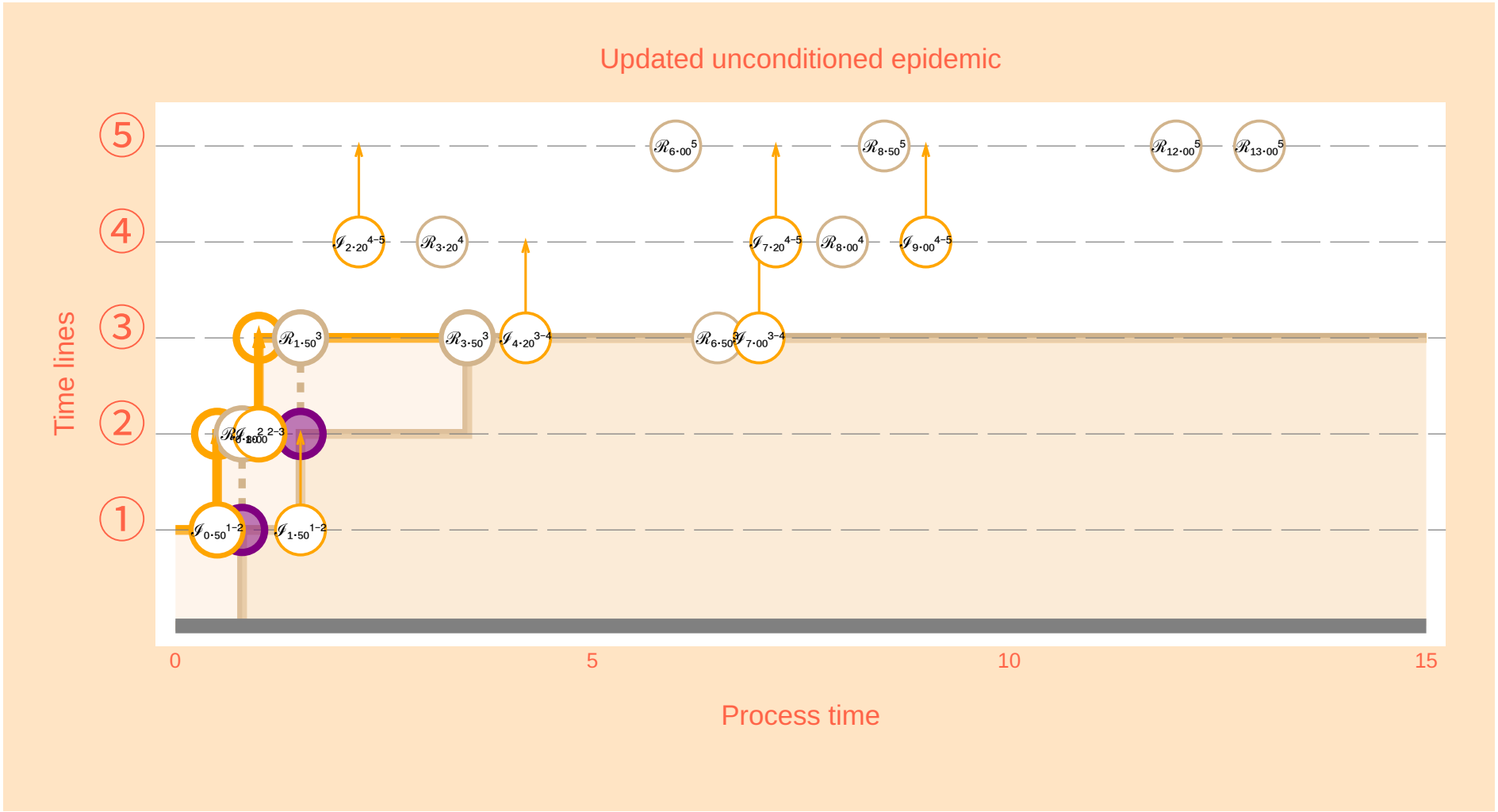

Figure 3: A step in algorithmic time for the unconditioned epidemic simply involves replacing all incidents by a new set of incidents.

Crucial technical point

- Updates in algorithmic time τ are then (algorithmic-)*time-reversible*: so restriction to subset S of state-space (in our case, *activated* removals occurring precisely at 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 (Rs);
  2. Re-sample timelines (though not times) of Rs;
  3. Replace infections (Is).
- It is convenient to re-express this for continuously varying τ:
  1. For $2nT < \tau < (2n+1)T$, update old Rs with times in $(0, \tau - 2nT)$;
  2. For $\tau = (2n+1)T$, resample timelines (not times) of Rs;
  3. For $(2n+1)T < \tau < (2n+2)T$, update old Is 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" is thereby preserved.
- Crucially, step 2 ensures composition action is irreducible over S! (So equilibrium under conditioning is unique.)

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Illustration of technical point (1/8)

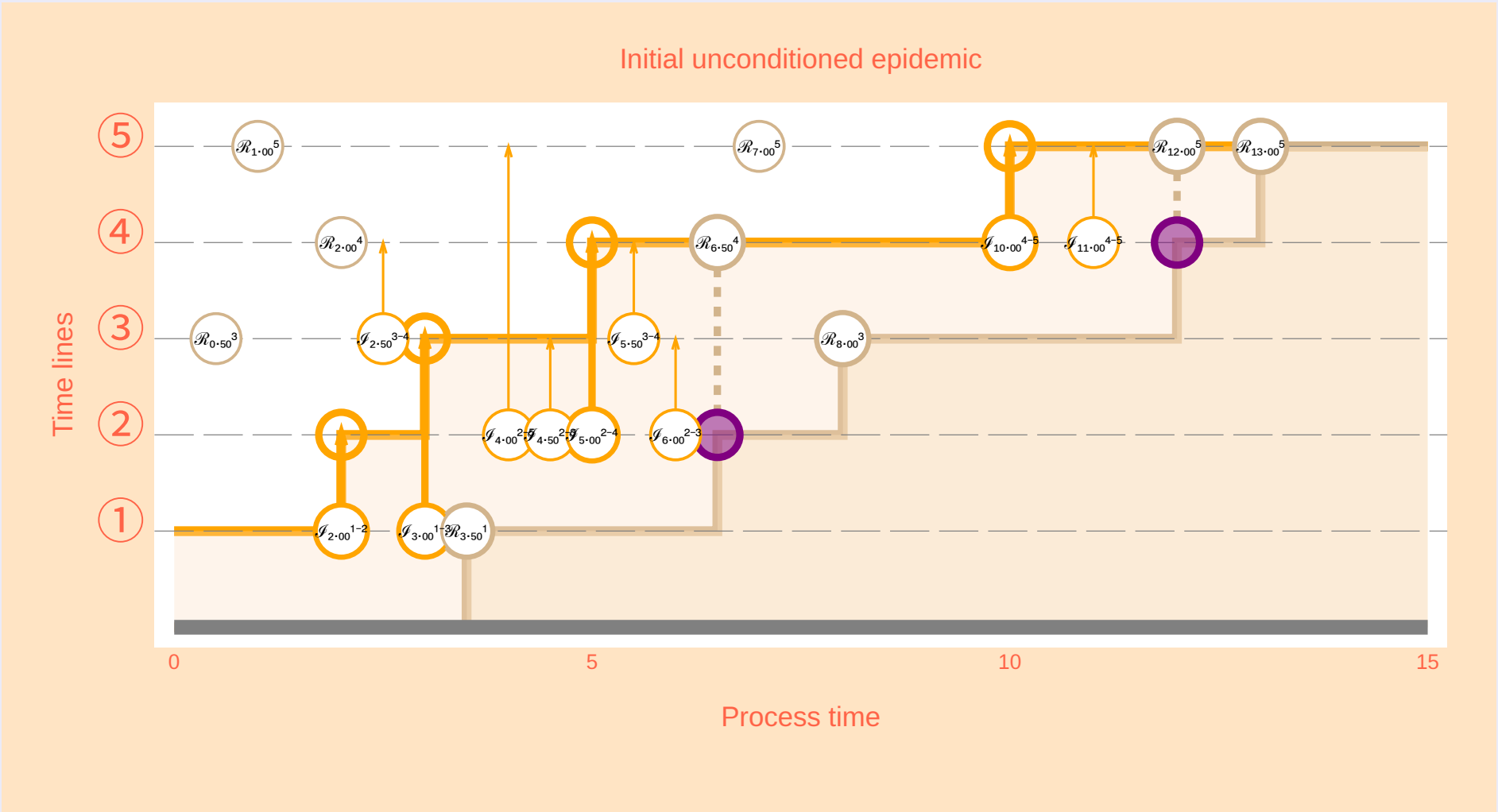

Figure 4: No change to removals or infections

Illustration of technical point (2/8)

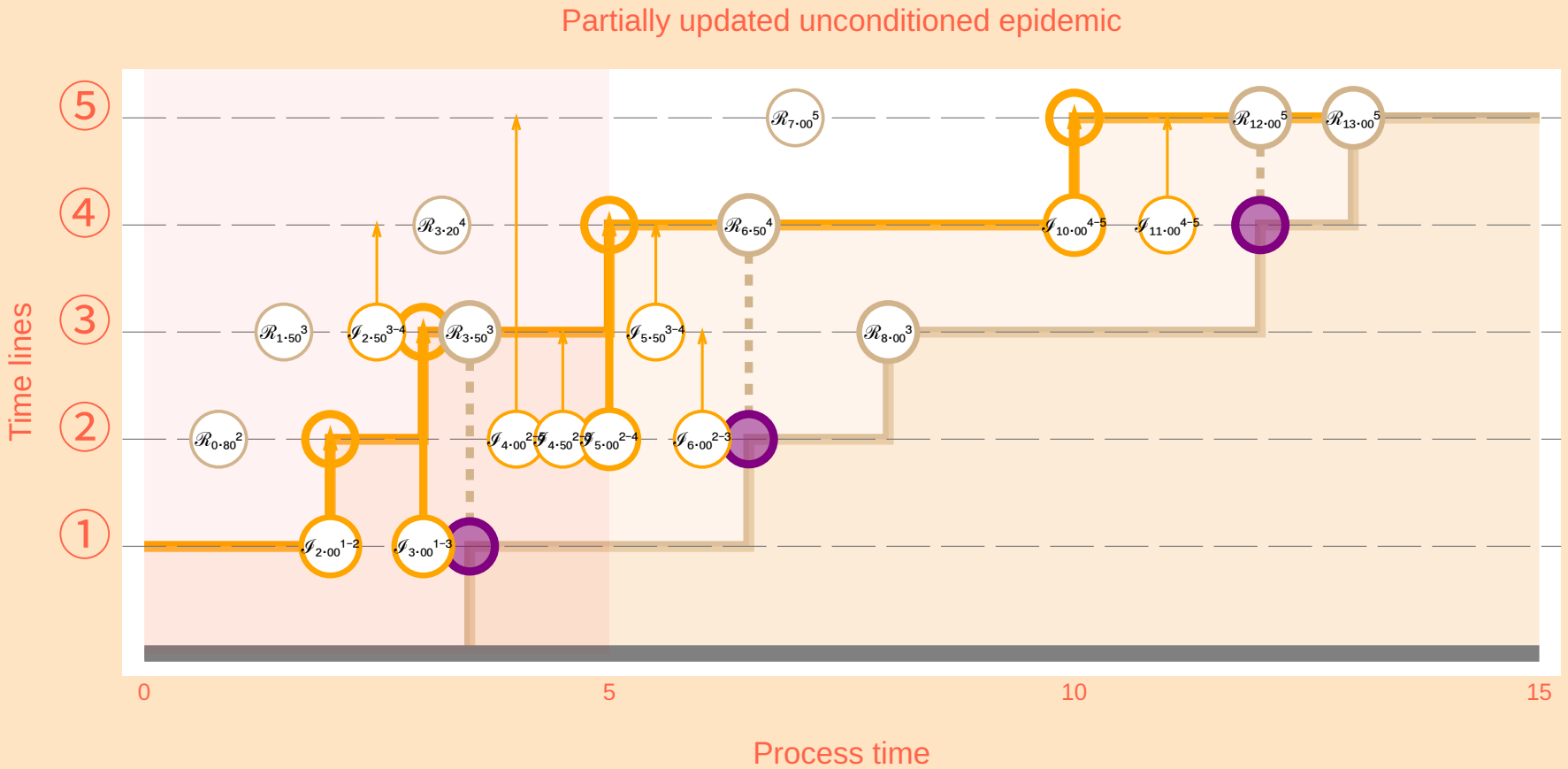

Figure 5: Replace first third of removals, infections unchanged

Illustration of technical point (3/8)

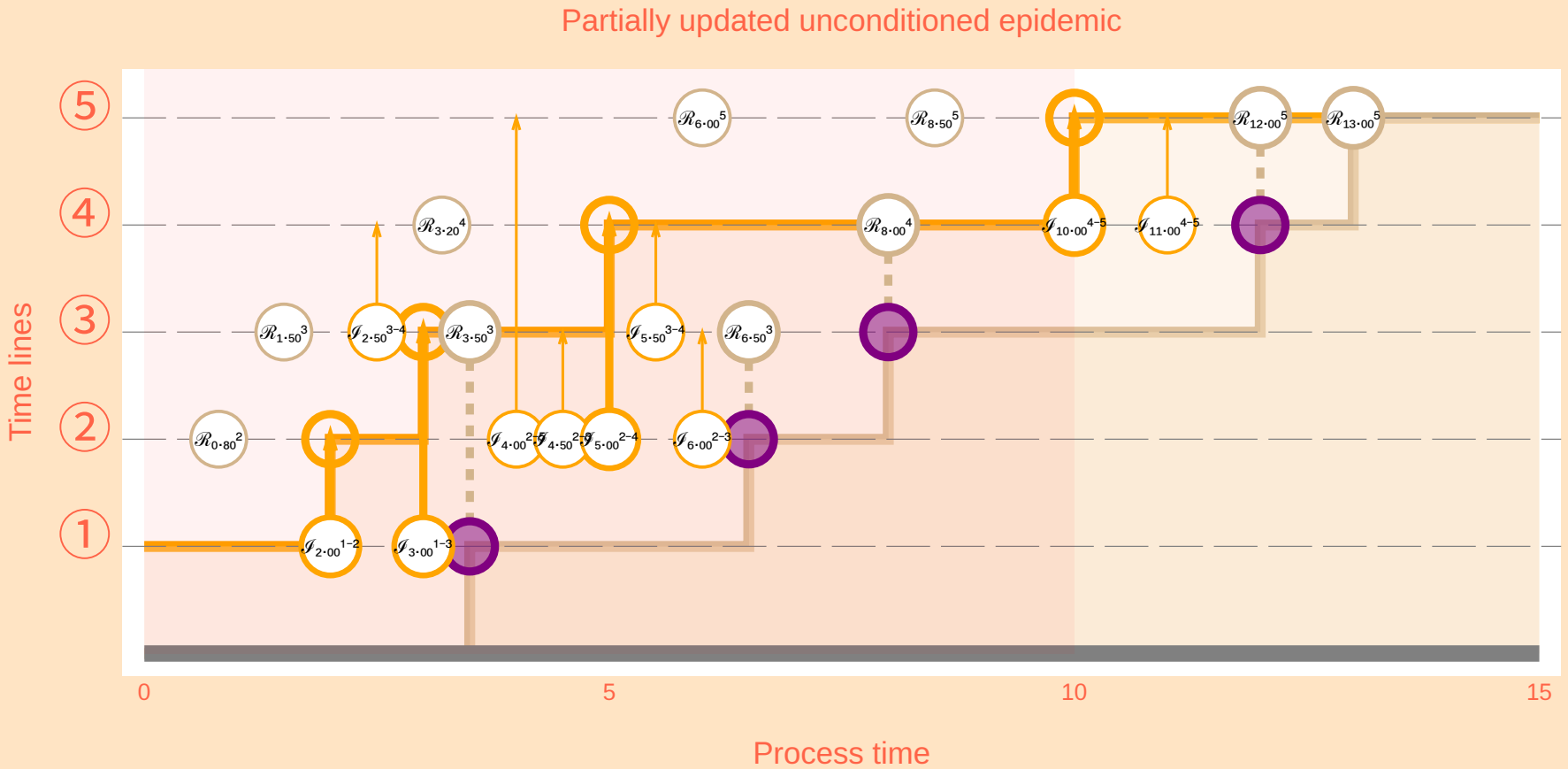

Figure 6: Replace first two-thirds of removals, infections unchanged

Illustration of technical point (4/8)

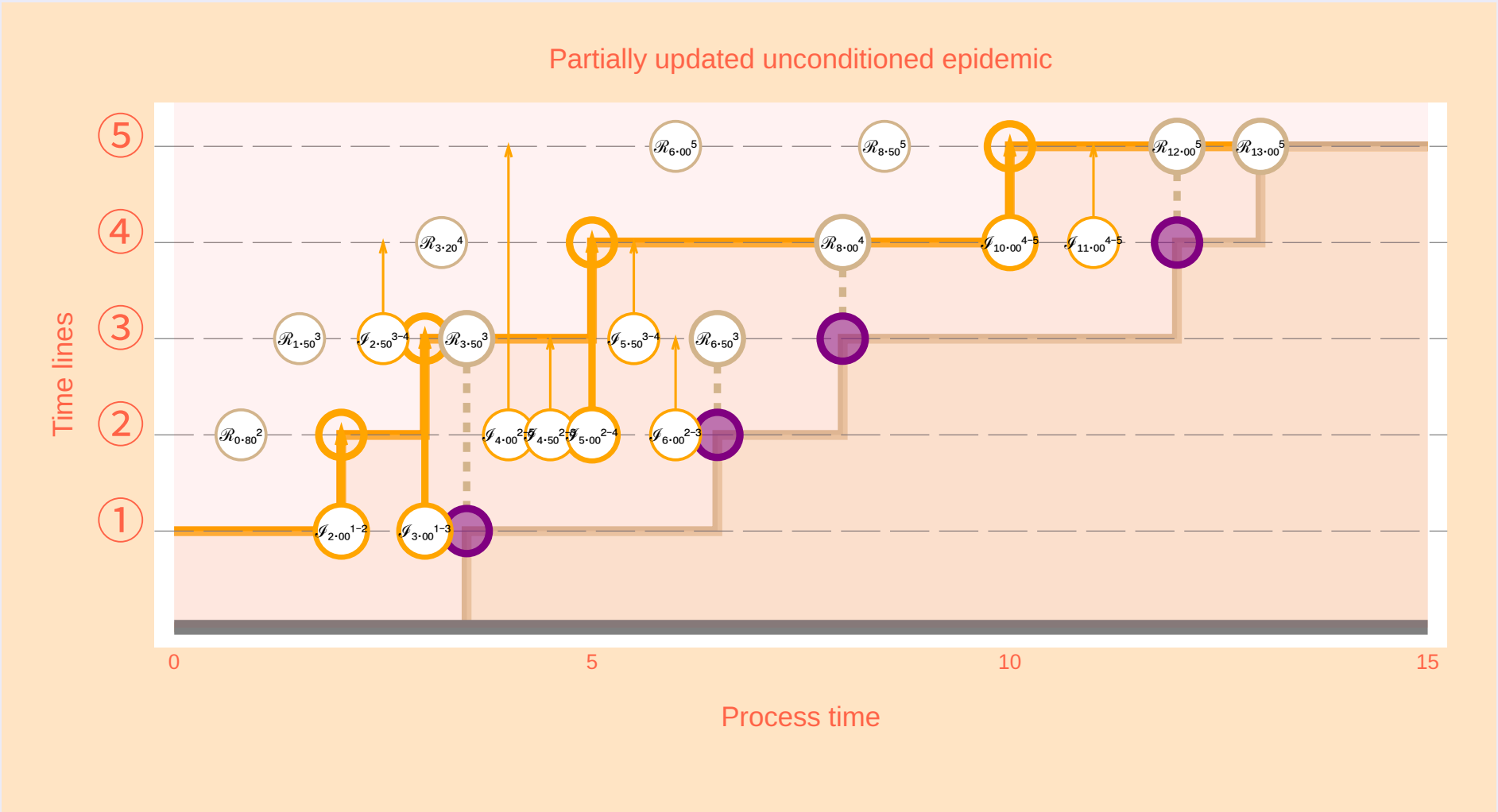

Figure 7: Replace all removals, infections unchanged

Illustration of technical point (5/8)

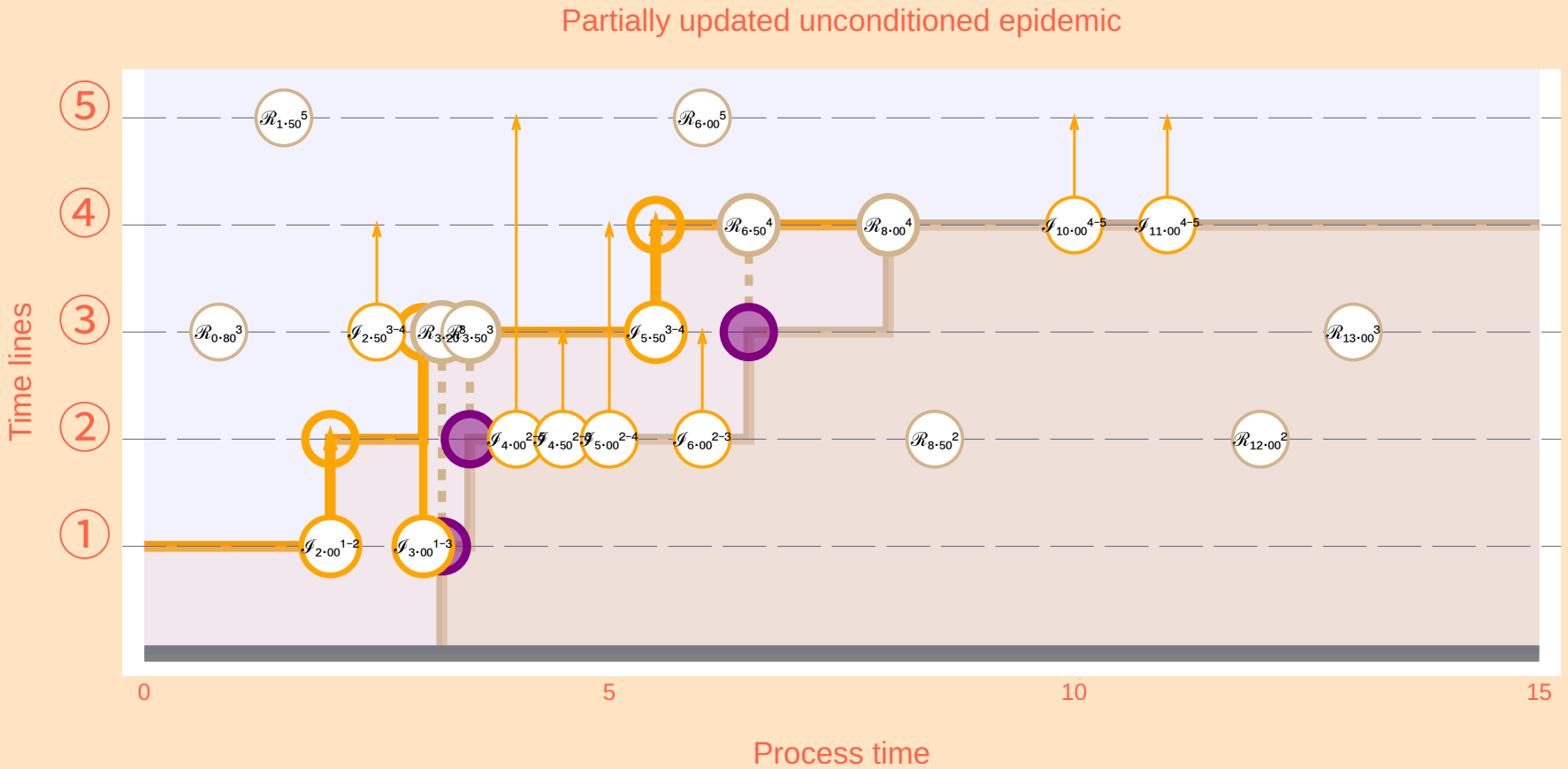

Figure 8: Re-sample all removal timelines, infections unchanged

Illustration of technical point (6/8)

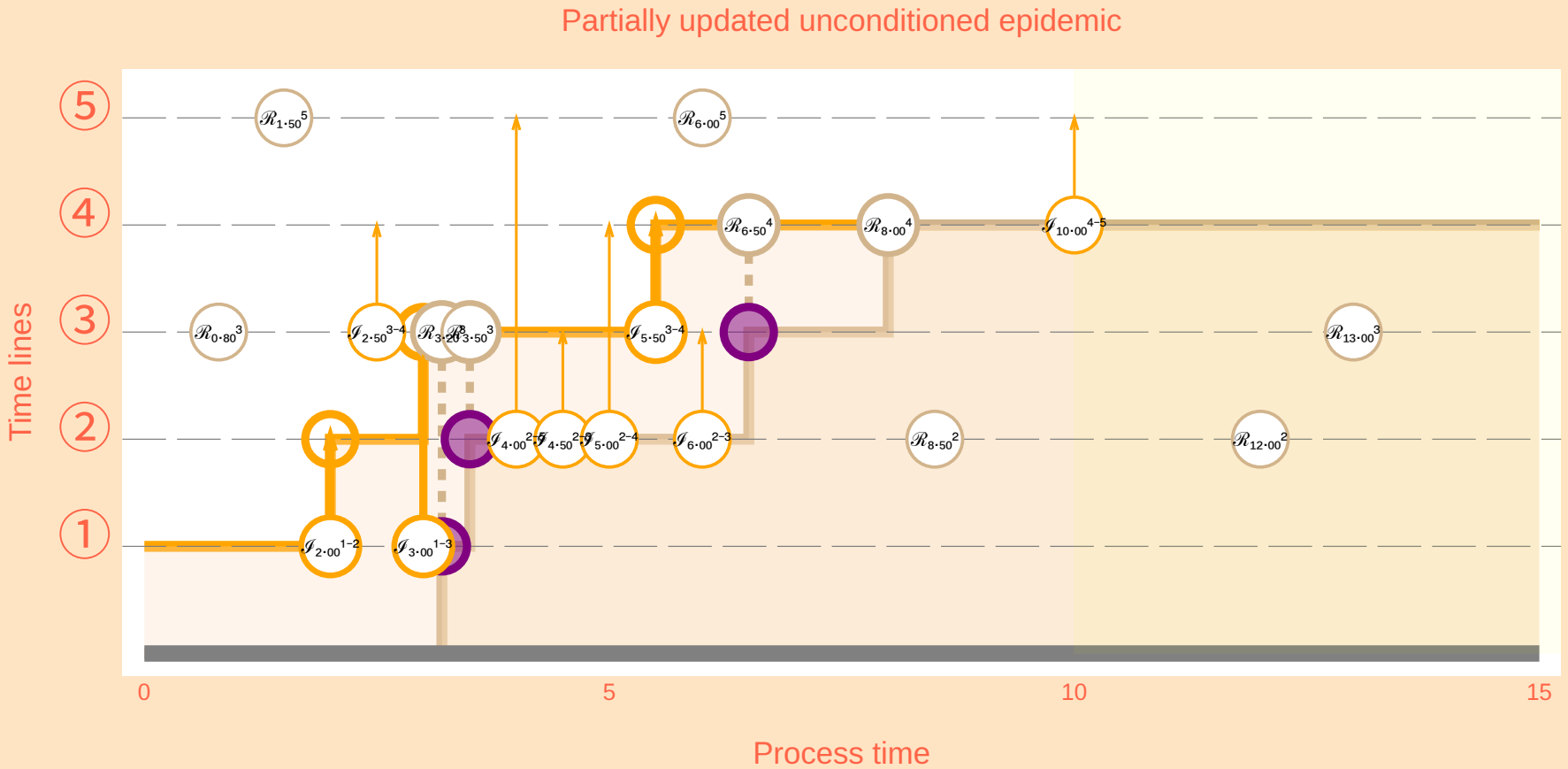

Figure 9: Re-sample last third of infections

Illustration of technical point (7/8)

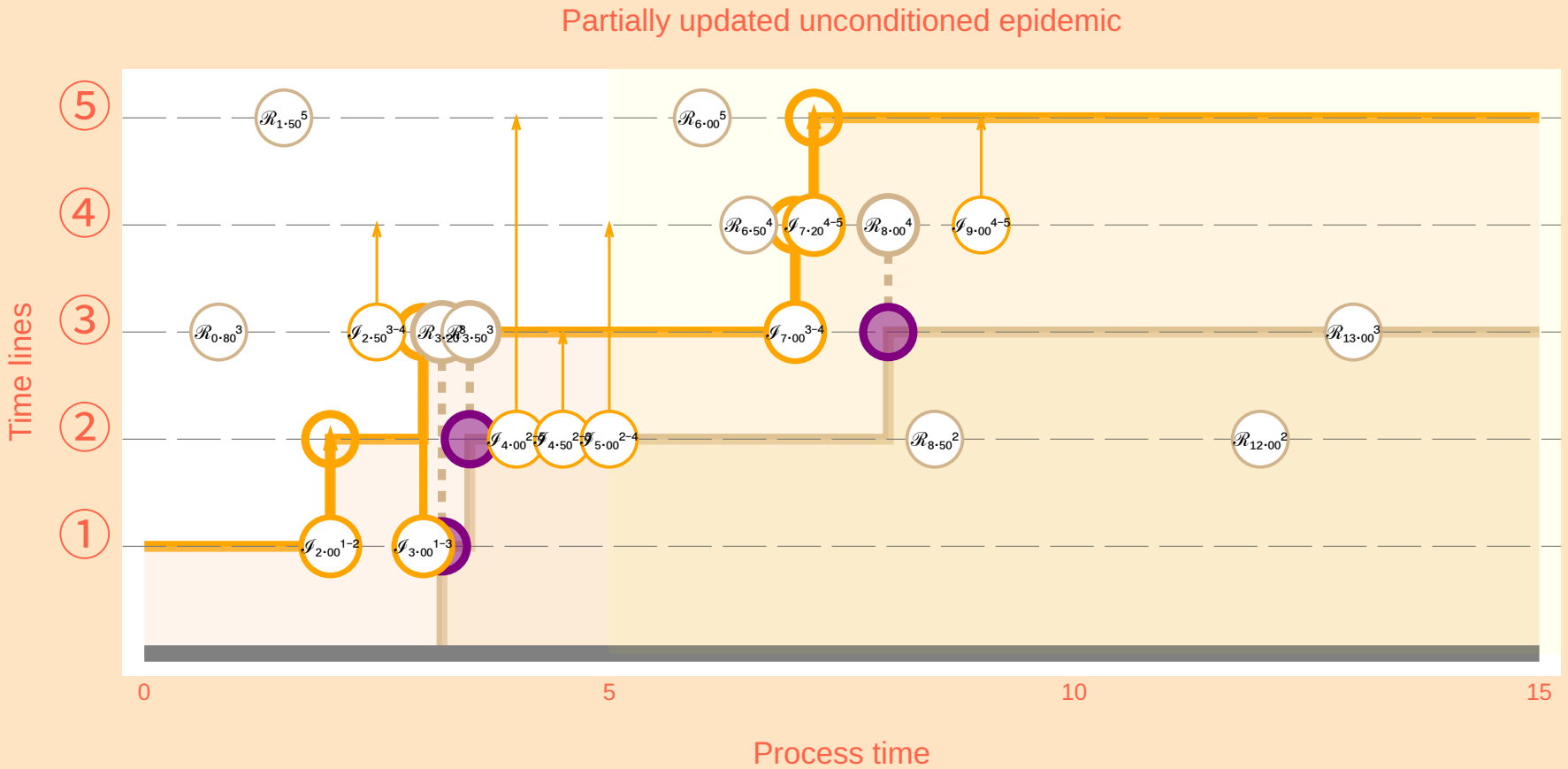

Figure 10: Re-sample last two-thirds of infections

Illustration of technical point (8/8)

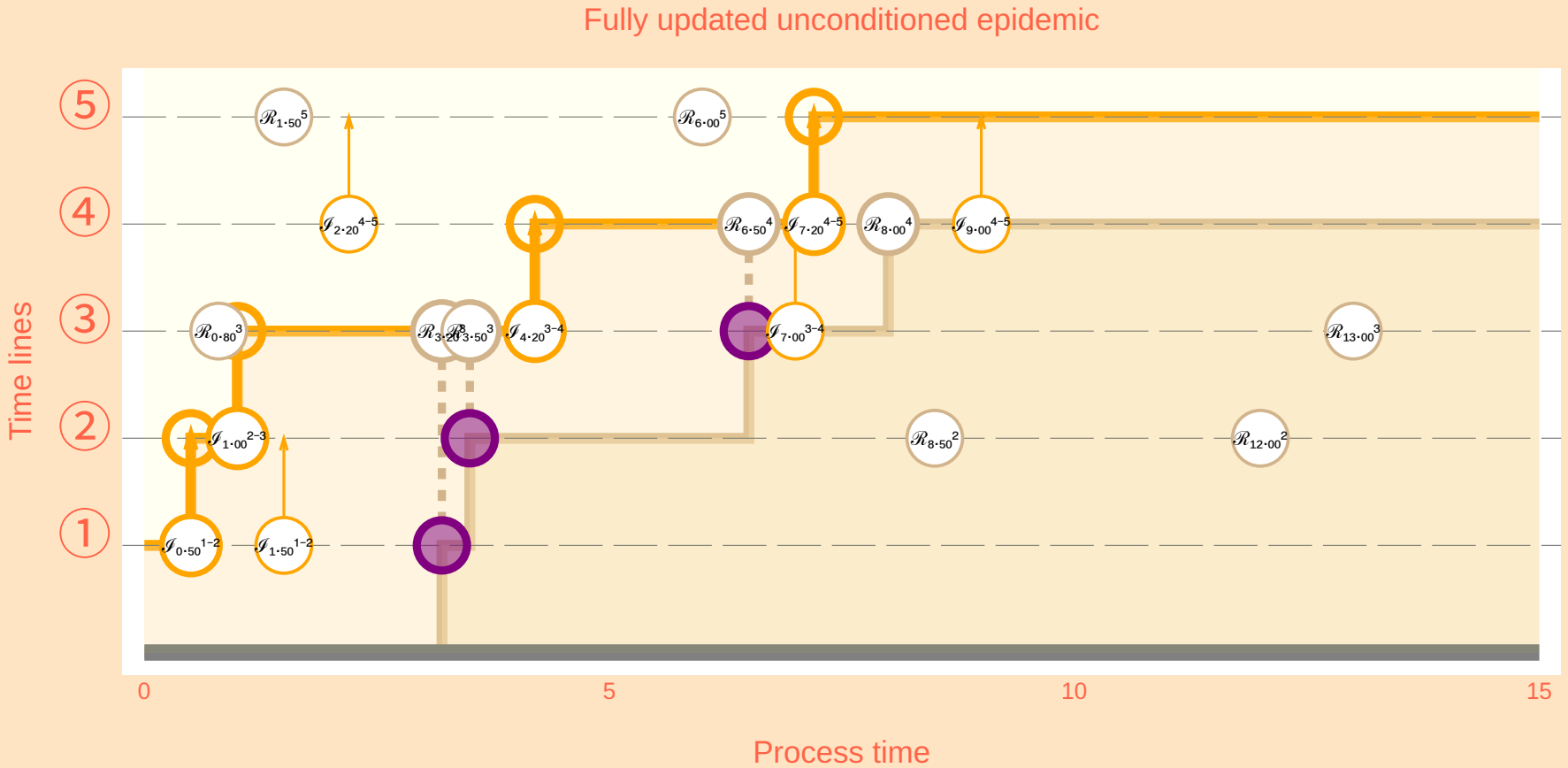

Figure 11: Re-sample all infections

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 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 required to establish that monotonicity still works. Key notions: *last feasible epidemic* (LFE) and *no-fly zone* (NFZ).

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Initial conditional epidemic

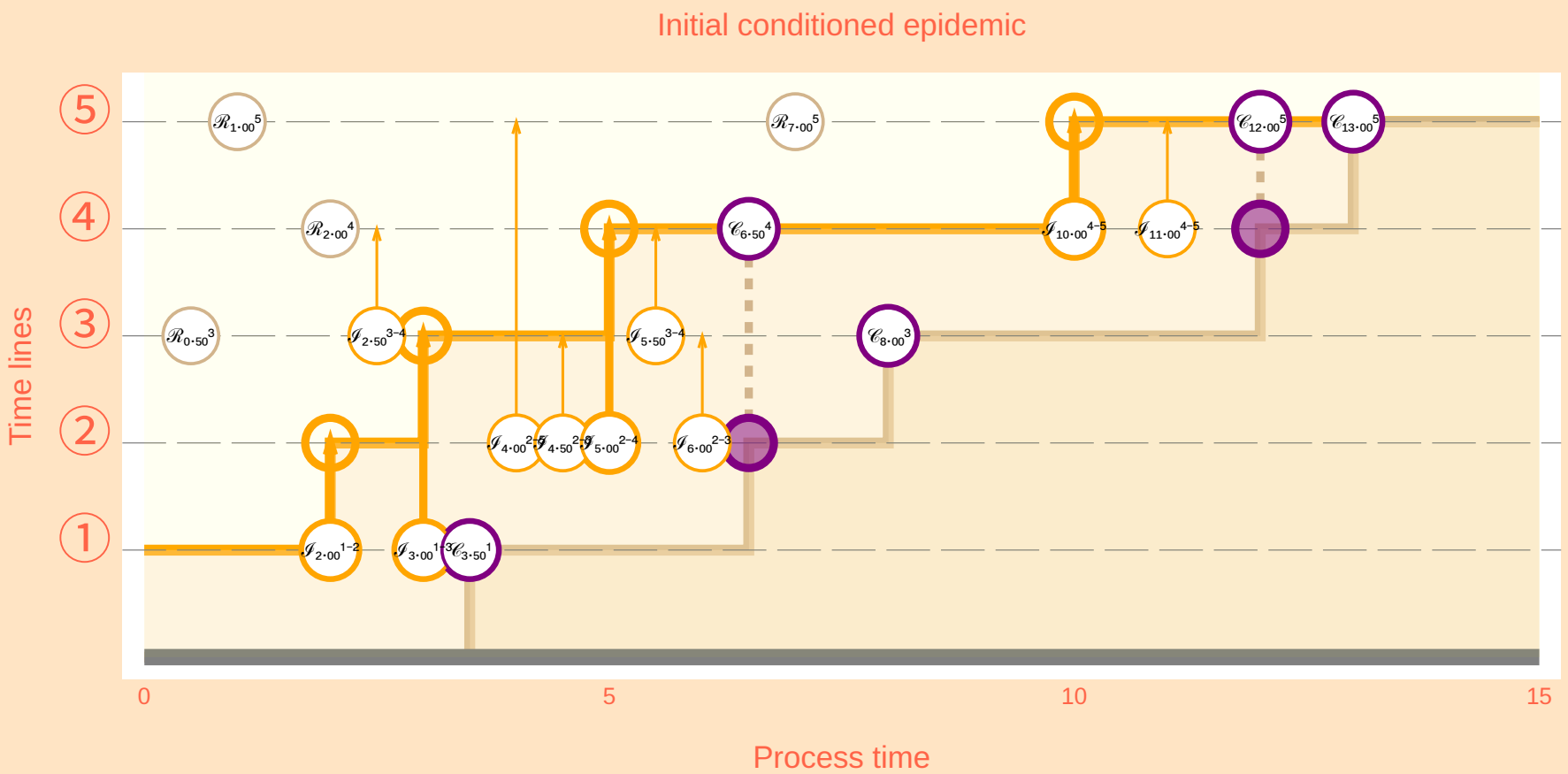


Figure 12: Initial epidemic with conditioned removals indicated using purple circles (and purple disks when different timelines are infected).

Conditional epidemic update

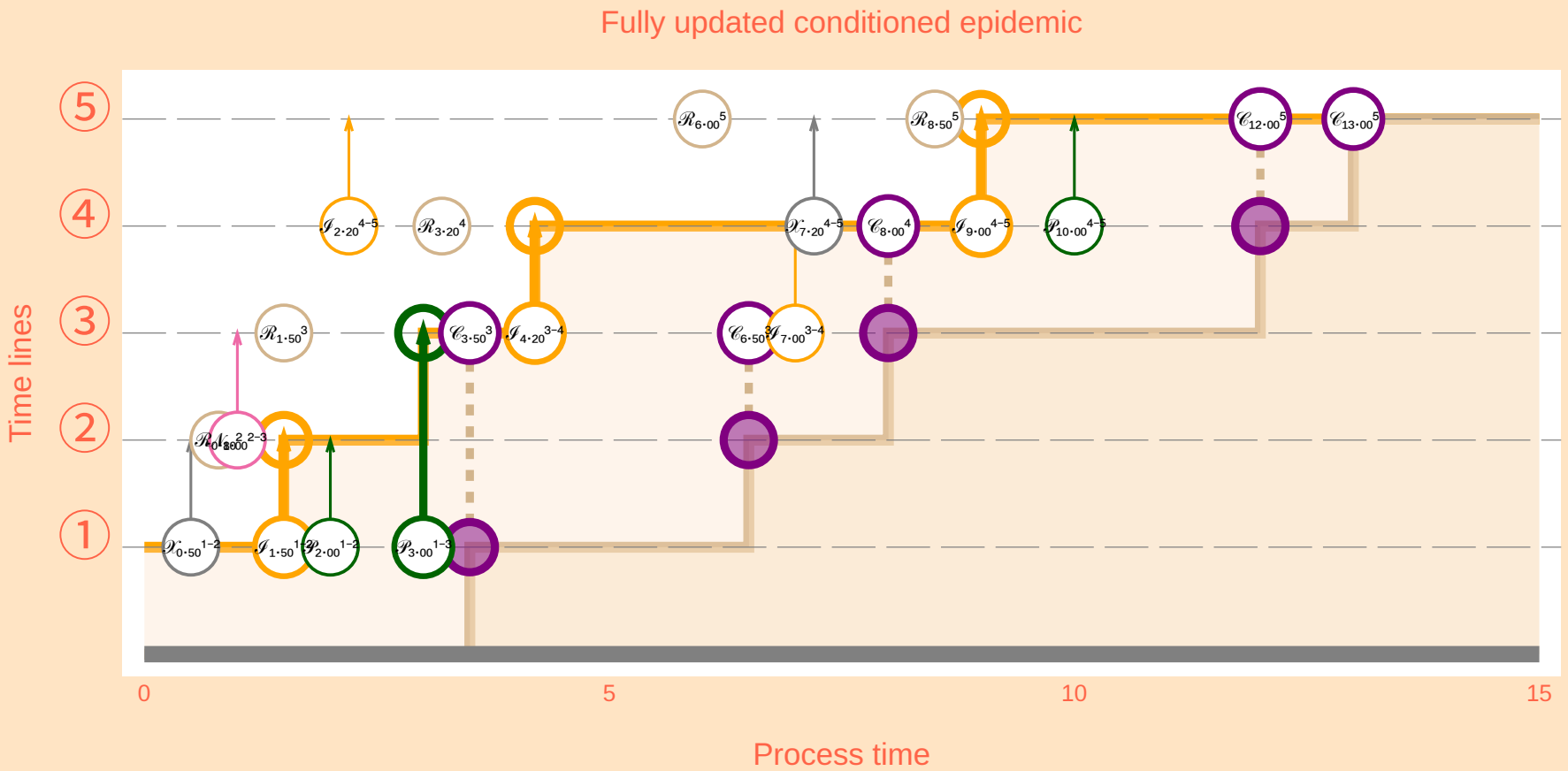


Figure 13: Epidemic updated under restriction: all conditioned removals remain activated, no new removals are activated. Green infections have been "perpetuated".

Last feasible epidemic (LFE)

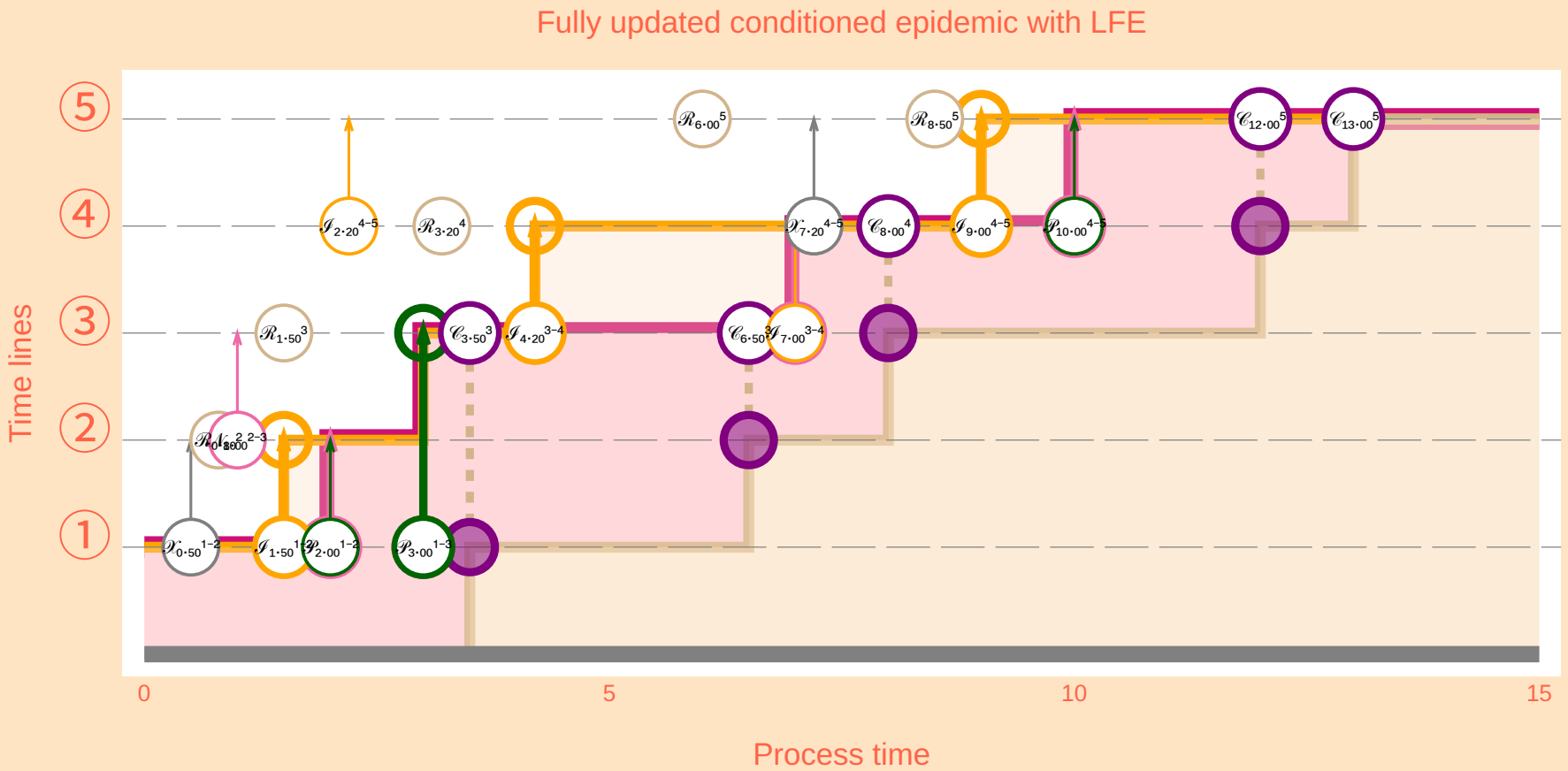


Figure 14: LFE computed recursively working right-to-left: the slowest sequence of infections deals with all infected timelines in order (includes perpetuated infections).

No-fly zone (NFZ)

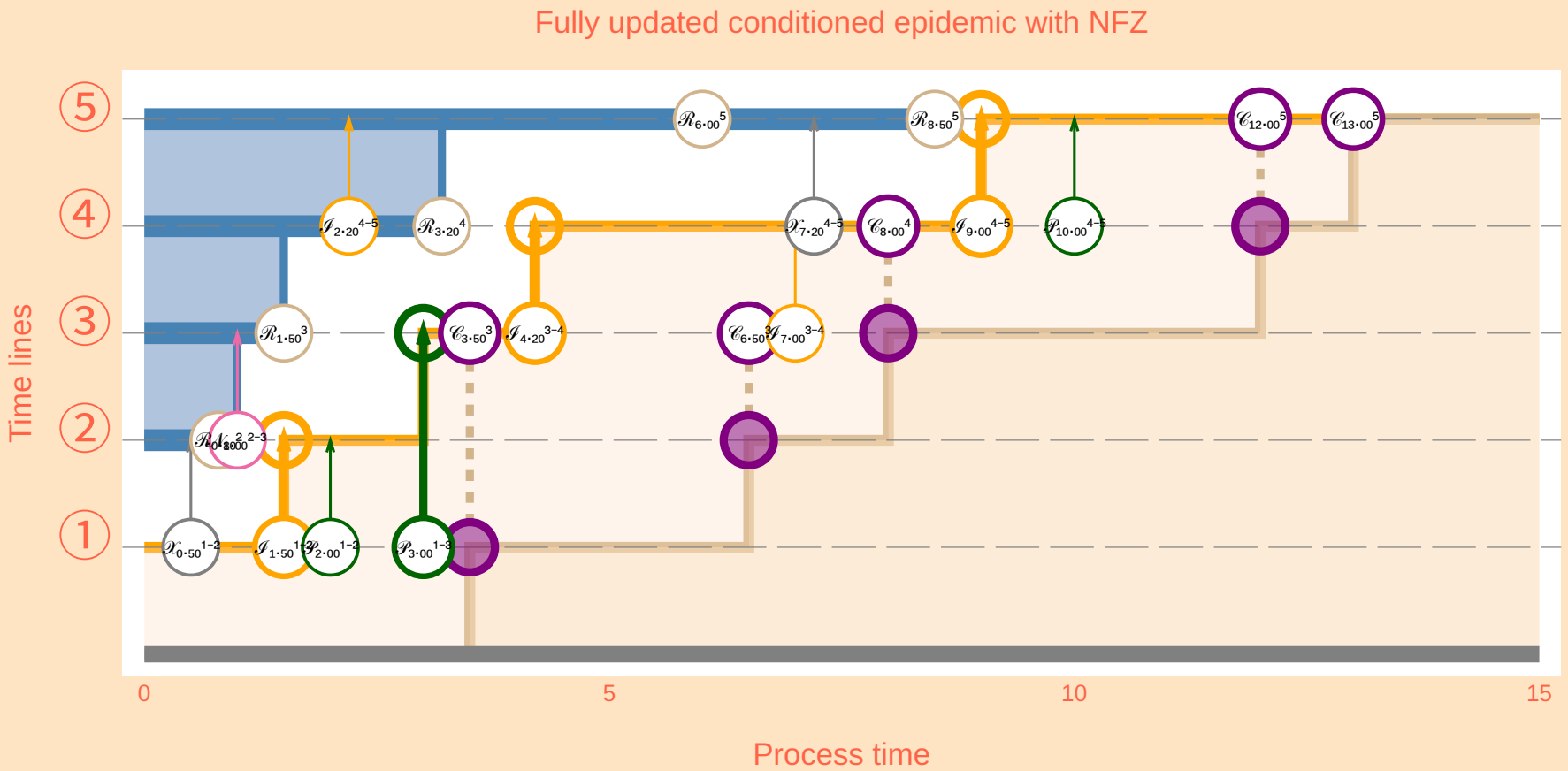
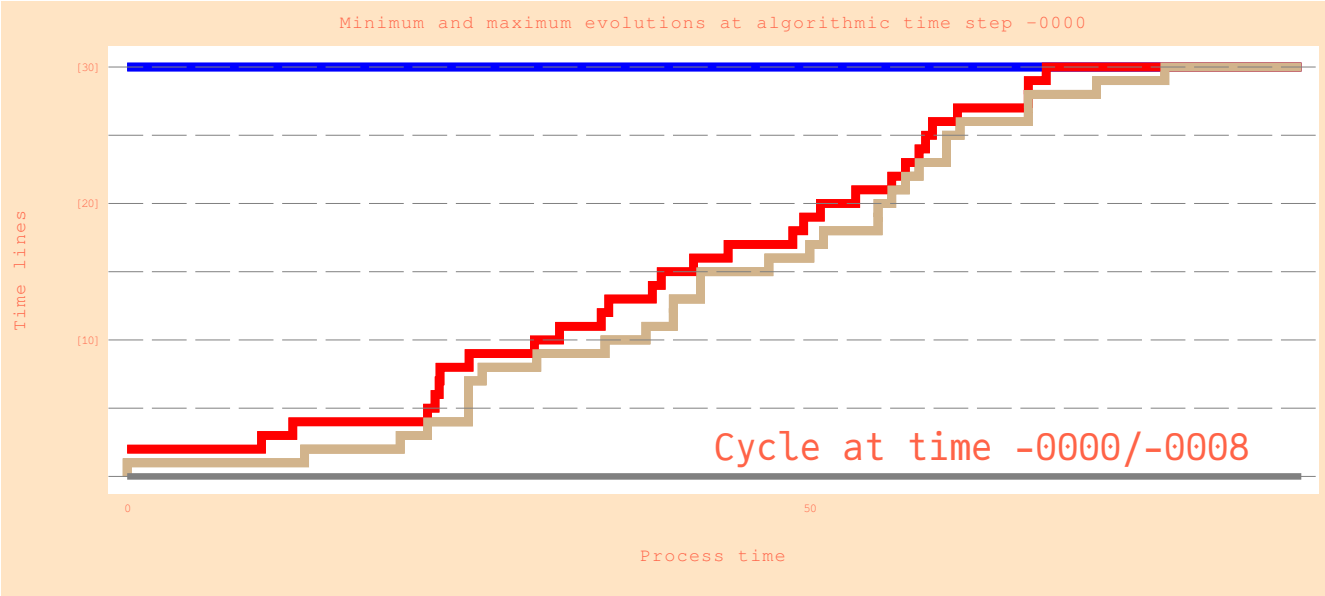


Figure 15: NFZ computed recursively working right-to-left: trace region of timelines that must not be infected if one is not to activate unobserved removals.

Example

- Smallpox outbreak in a closed community of 120 individuals in Abakaliki, Nigeria (much studied! see p. 125, 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), we can construct a perfect simulation GIF yielding a draw from unobserved pattern of infections.



So what?

- 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?
- 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** Connor & 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: generalize to other suitable compartment models?

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

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Classic CFTP for a simple random walk	Result of code written by WSK	
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Epidemic CFTP images and animation	Result of code written by WSK	

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Summary:	Added quote and picture.
	Checked URL links for handout and simulation.