

No time to waste: practical statistical contact tracing with few low-bit messages

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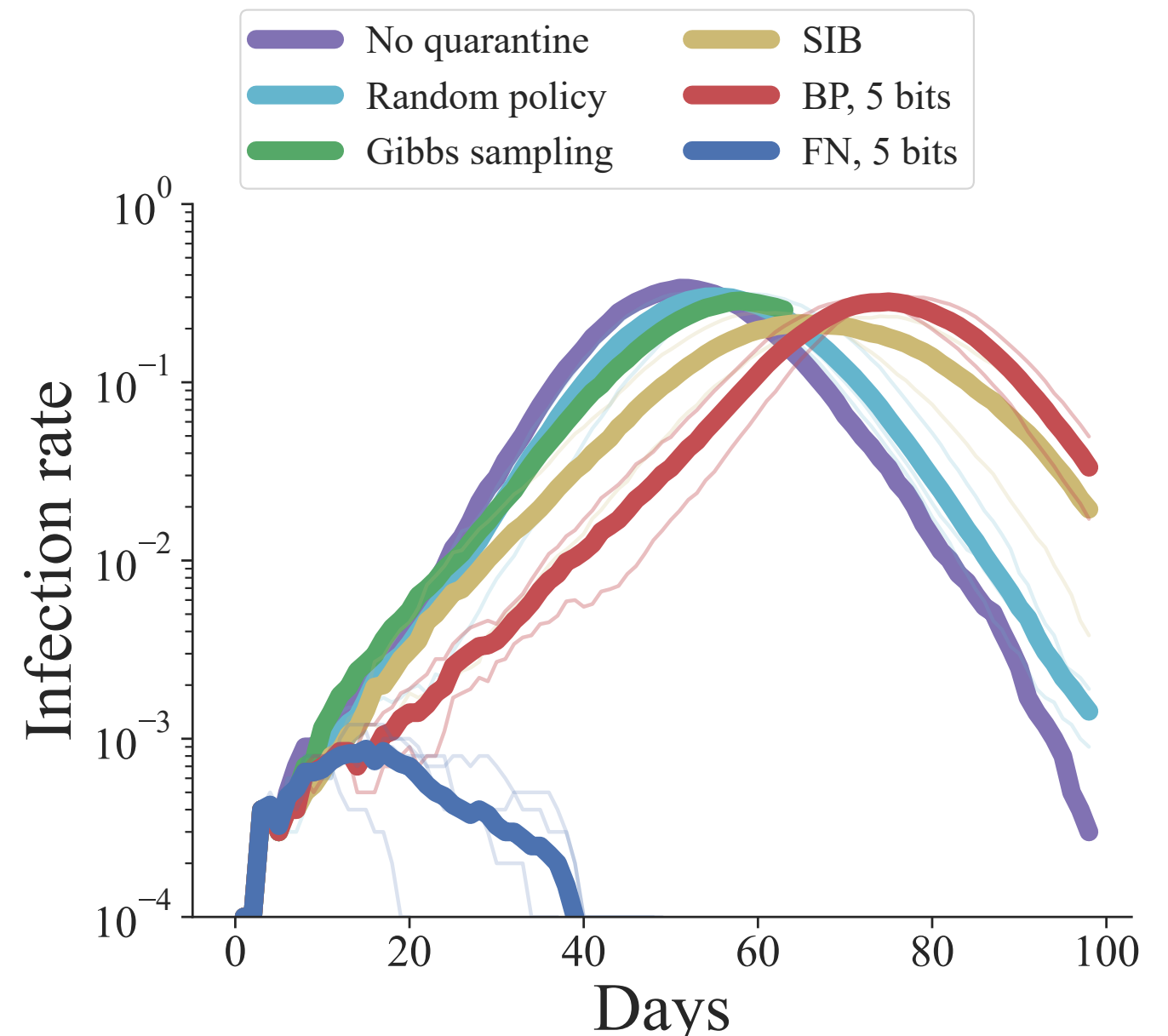
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- Problem: a virus pandemic like COVID19 had enormous consequences. Previous work established that statistical contact tracing can inform testing and quarantine policies and thus prevent a peak infection rate in the pandemic [1][2].

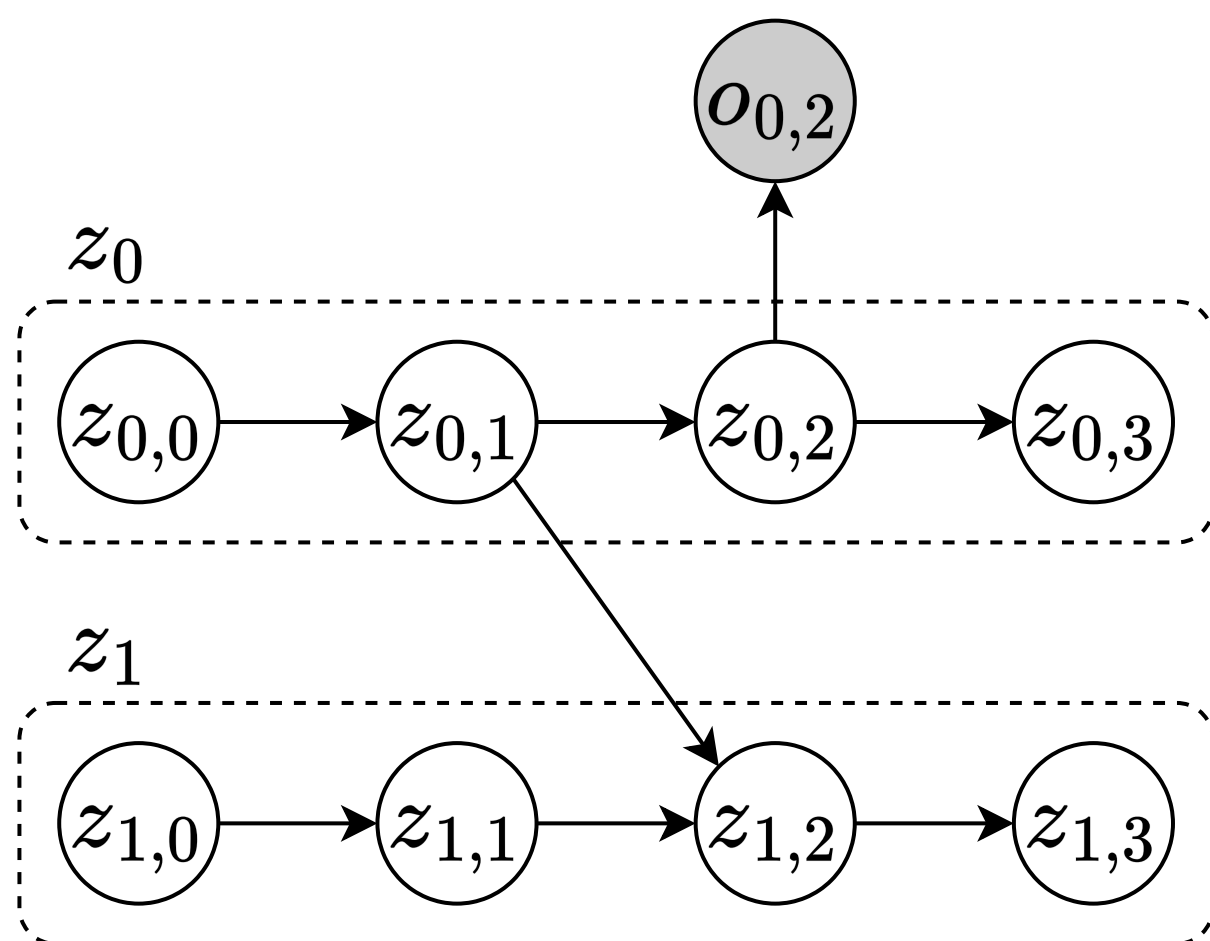
- Existing algorithms, however, require tens to hundreds of updates per day per contact to reach converge. Such an amount of messages is practically infeasible [1][2].

- We run experiments on two simulators, and in two challenging scenarios. The realistic OpenABM simulator is based on six household and nine age categories and its more than 150 parameters are based on population surveys. The paper has two robustness studies where we simulate very noise tests, and stale updates from phones.

- Our algorithm is able to monitor and suppress a peak infection (see Figure), with as few as five update rounds, where each message uses only four bits.

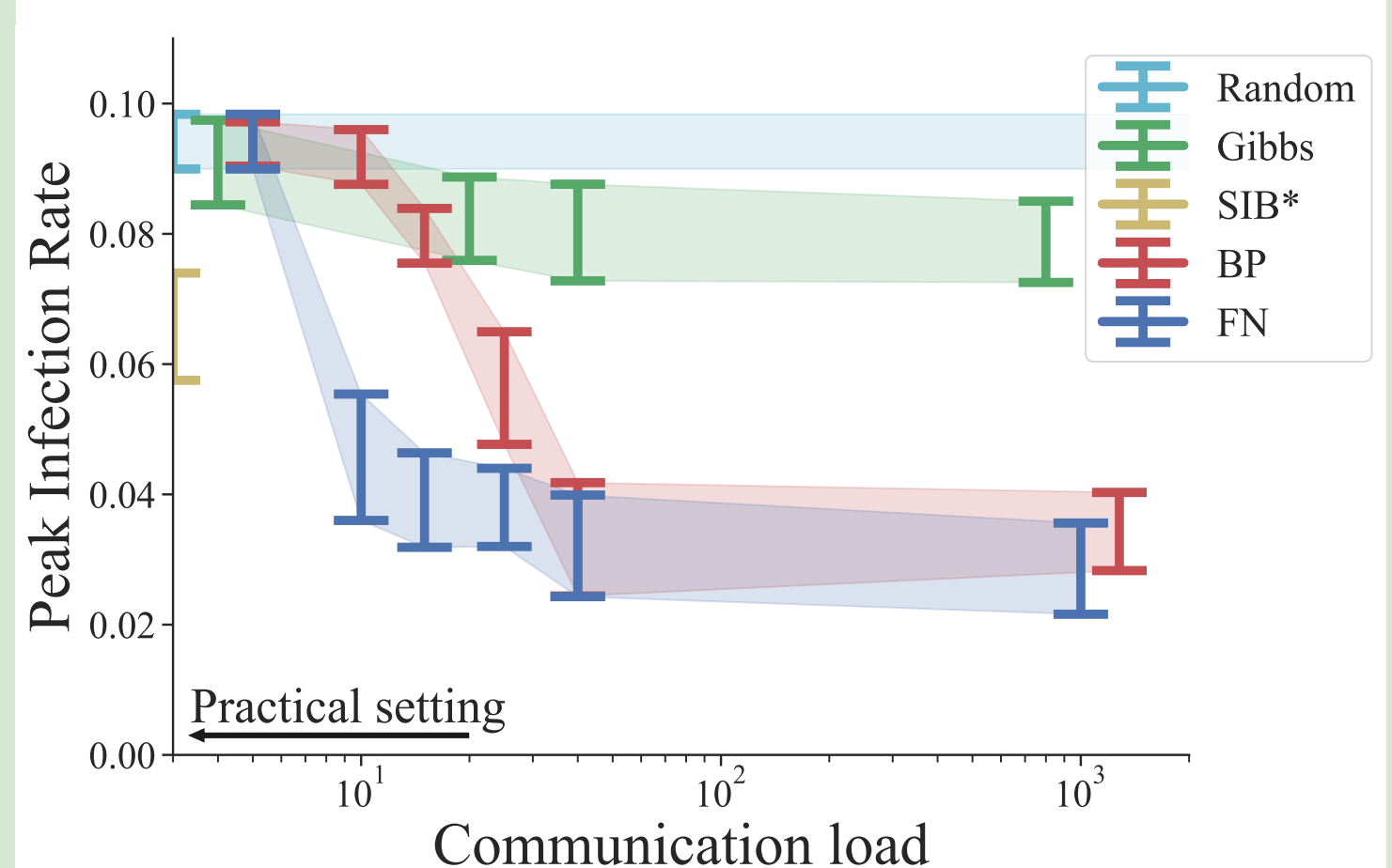


Infection rates on the OpenABM simulator [4]. Parameters for the simulator follow population surveys in the United Kingdom and other academic research. Compared to BP or Gibbs sampling, FN results in lower infection rate. Thin lines indicate single realizations, thick lines correspond to population averages.



Example of a Probabilistic Graphical Model with two users and one observation. User 0 has a directed contact with user 1 on day 1. This contact could potentially transmit the virus, causing user 1 to switch from S state to E state on day 2. Each node is in one of four states: Susceptible (S), Exposed (E), Infected (I), Recovered (R).

We show that computation for our algorithm, FN [3], scales linearly in the number of contacts per user per day, which is better than variational inference, which scales exponentially.



Comparing epidemic mitigation at increasing communication budget. Both BP and FN send five daily messages per contact, which we deem practically feasible. Communication load on the x-axis indicates multiples of an algorithm that sends 1 message of 1 bit per day per contact. * the SIB algorithm is unquantized and thus plotted on the y-axis for reference. Error bars are calculated over four random seeds and shown as the population mean, plus-minus one standard deviation.

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Code available at: github.com/QUVA-Lab/nttw

[1] "Epidemic mitigation by statistical inference from contact tracing data", Baker et al. 2020
[2] "CRISP: A Probabilistic Model for Individual-Level COVID-19 Infection Risk Estimation Based on Contact Data", Herbrich et al. 2020
[3] "The dir hierarchy of approximate inference", Rosen-Zvi et al. 2012
[4] "OpenABM-Covid19—An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing", Hinch et al. 2021
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