Objective

- Investigate the effectiveness of CDR for prioritising partner services/contact tracing
- Quantify the effectiveness of CDR-based allocation of partner services relative to other strategies

Approach

- Develop a network-based stochastic branching process model to describe the spread of HIV transmission clusters in MSM
- Simulate HIV evolution and genetic distances in clusters
- Identify how quickly clusters can be detected
- Simulate variable rates of sampling, variable time to diagnosis, variable time to sequencing, and variable time to intervention
- Simultaneously consider alternative ways of prioritising patients for intervention:
  - Random allocation amongst new diagnoses
  - RITA based methods (prioritising recent infections)
  - Network-based interventions (prioritise new diagnoses with more self-reported recent partners)

Model

Population structure

- Dynamic network model with three modes of contact:
  - Long-term partnerships (mean duration 7 mo's)
  - Casual partnerships (mean duration 2 mo's)
  - One-off contacts
- Joint distribution of contact types calibrated to US MSM ARTNet survey data (Weiss et al, Epidemics 2020)

Model

Dynamics

- Continuous time stochastic branching process
- Simulation progresses using Gillespie exact simulation with competing rates for the following events:
  - Changing partnerships
  - One-off contacts
  - Transmission
  - Diagnosis
  - Treatment
  - Sequencing
  - Progression to AIDS and death
- Transmissibility per contact follows viral loads resulting in time-dependent rate of transmission per partnership
- Diagnosis & treatment further modify transmission rate

Model

Interventions

- Intervention effectiveness is measured in terms of how quickly diagnosis is accerlated by partner services/contact tracing.
- Developed a metric for the cumulative undiagnosed time averted (UTA) per patient
- Cluster-based prioritisation studied with genetic distance thresholds from 0.5% to 2% and cluster size thresholds from 2-5
  - Not currently considering cluster growth. Should we?
- Network-based prioritisation uses a threshold self-reported cumulative partners over 7 months
- Intervention is modelled with exponential (90 day) delays
- Sequencing turnaround times are based on San Diego cohort data and are relatively short

Model

Calibration

- All model parameters are based when possible on R Goyal et al's individual-based model: https://github.com/mathematica-pub/abm_hiv
- Contact rates per partnership were calibrated to yeild stable incidence ($R_0 = 1$)