CogSim modeling of COVID-19 spread

Combining epidemic data and simulation using AI

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Model-based simulations can inform government efforts to return to operations in the presence of COVID-19

- Providing operational assessments for the US Army and LLNL
 - What operating levels are tolerable?
 - Can testing and isolation enable more normal operations?
 - What confidence can you put in model predictions?
- Developing new models and methods for assessment
- Seeding long-term capabilities and interaction channels for improved public health and biosecurity





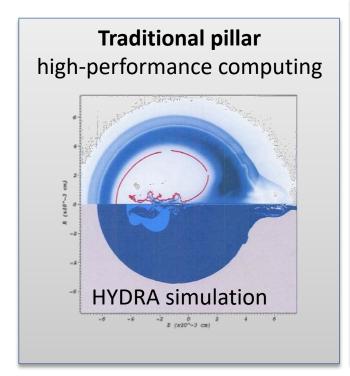


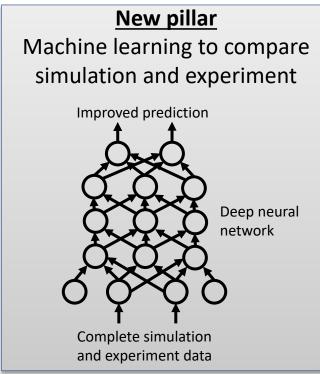


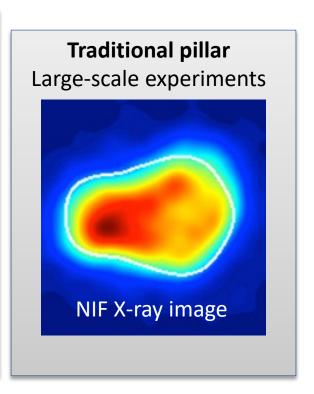


We've used CogSim methods to provide rapid solutions for the military and the Laboratory

Cognitive Simulation uses AI to combine experiment and simulation to produce more powerful modeling tools

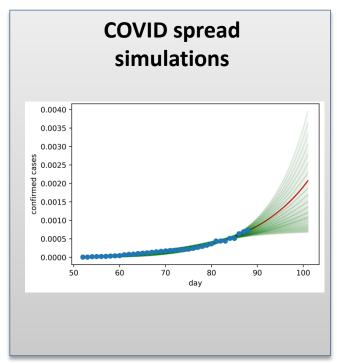


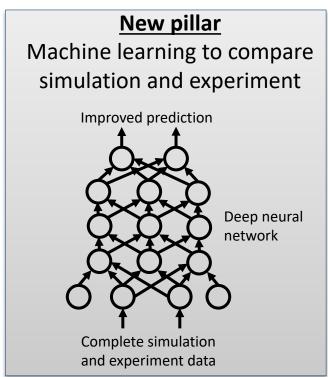


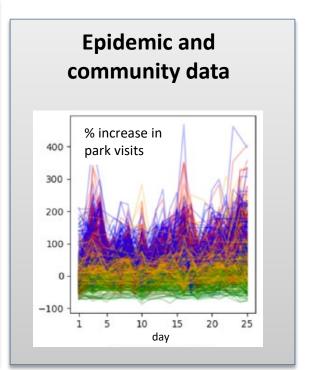


Machine learning allows us to use our full data sets to more rapidly advance our prediction capability

Cognitive Simulation uses AI to combine experiment and simulation to produce more powerful modeling tools



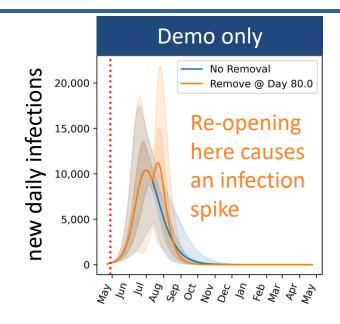




Machine learning allows us to use our full data sets to more rapidly advance our prediction capability

We have exploited our AI and HPC resources to advance COVID spread modeling

- Combine data and simulation using AI and UQ methods
- Infer and simulate the impact of non-pharmaceutical intervention (NPI) and testing/isolation
- Calibrate models using broad multimodal data sets
 - Epidemic data: cases, deaths
 - Community data:
 - business foot traffic
 - cell phone mobility
 - NPI application dates
 - NPI compliance data
 - Demographics
 - More

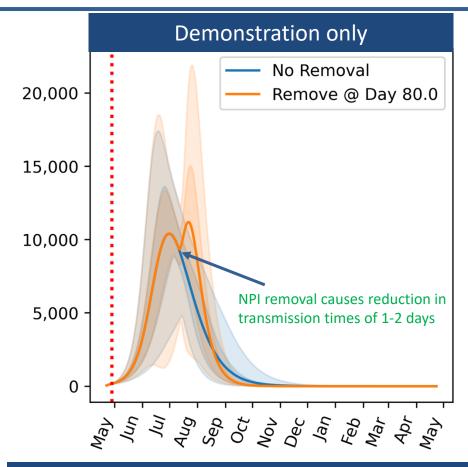




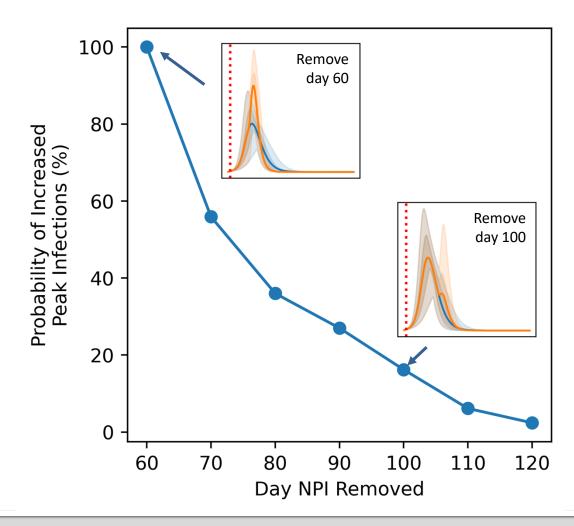
We've been able to deliver reliable predictions calibrated with real data packaged for senior decision makers



Given inference of the effect of removing NPI, we can put uncertainties on predicted change in resource burdens



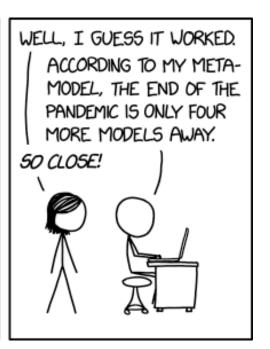
Real-world COVID-19 dynamics call for expanded modeling capabilities



We needed new simulation capabilities to interpret real-world data



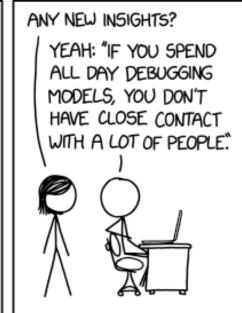


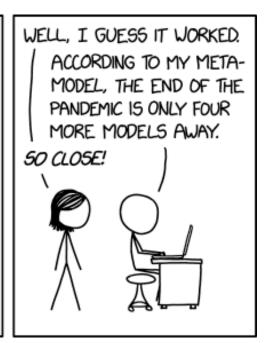


- Detailed dynamics and uncertainty quantification
- 2. Multi-fidelity testing
- 3. Tracing and isolation
- 4. Variable contact patterns
- Staged vaccination with variable efficacy
- 6. Al-driven analysis of realworld conditions

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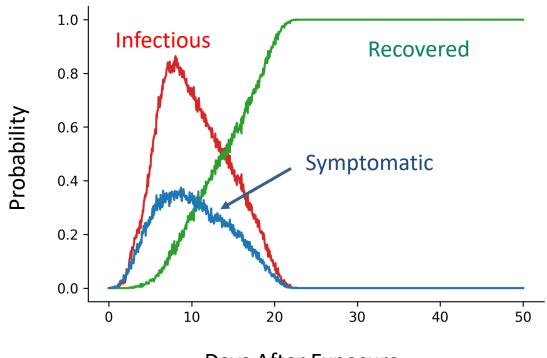






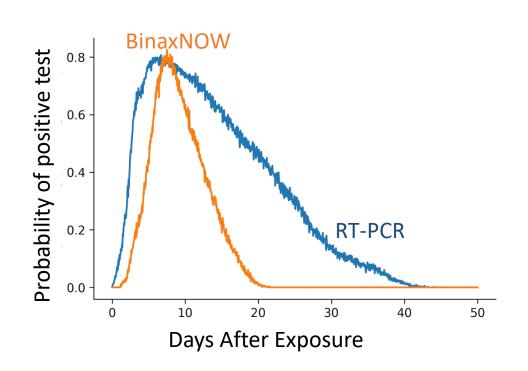
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Detailed COVID-19 dynamics extend beyond standard SEIR models and introduce key statistics



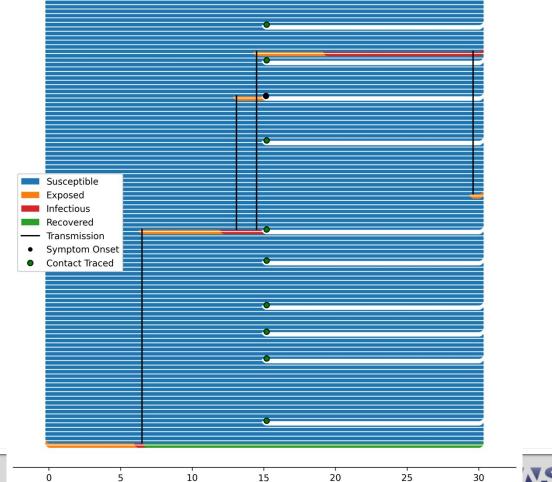
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Realistic testing response dynamics enable testing protocol optimization



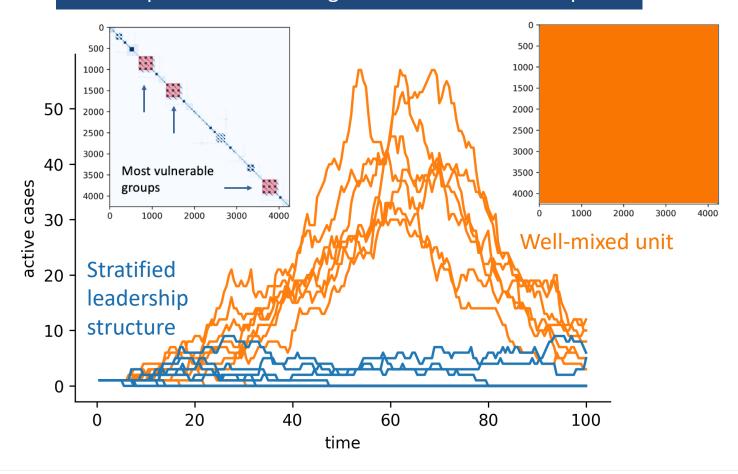
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Contact tracing allows us to evolve simulated outbreaks and track critical statistical outcomes



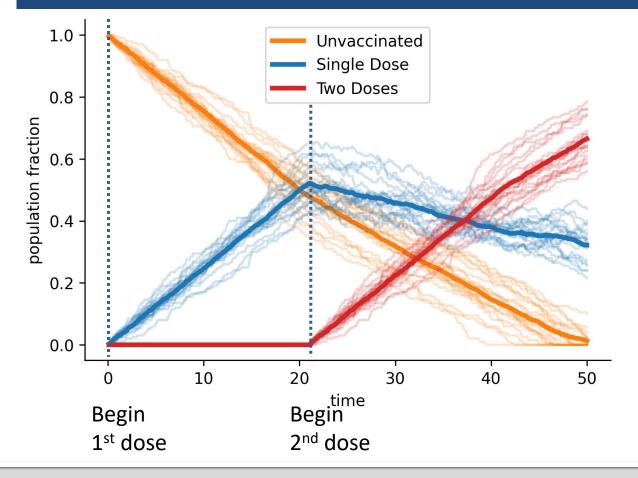
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Contact patterns have a large influence on disease spread



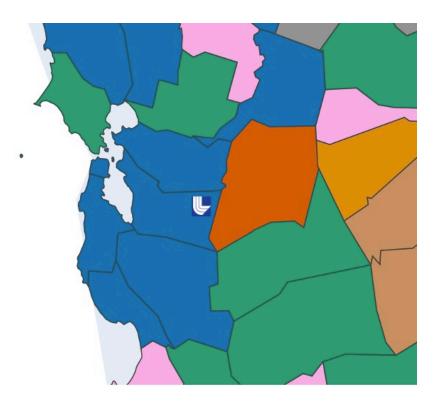
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Vaccination schedules can evolve dynamically to alter disease evolution



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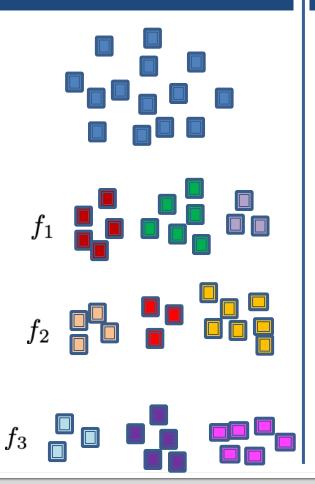
Intervention effectiveness varies strongly at the county level



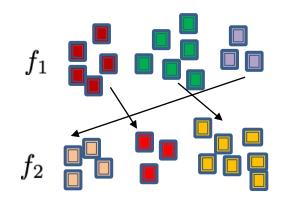
- Very short or very long trips
- 1 Time at Home
- 2 Age
- 3 Income & Mask Compliance
- 5 Trips & Population Density
- 6 Moderate trips
- 7 Unemployment

We can generate unique signatures of disease drivers for groups of US counties

1. Feature-level clustering of counties



2. Align clusterings for every feature pair



This is based on the amount of overlap in the cluster assignments

3. Identify semantic links for each county

For every cluster-pair find the intersection





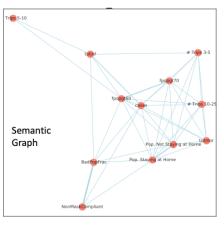
For each county in the intersection, create a semantic link between f1 and f2



Edge weight

$$\frac{C_1 \cap C_2}{|C_1|}$$

4. Identify semantic links for each county

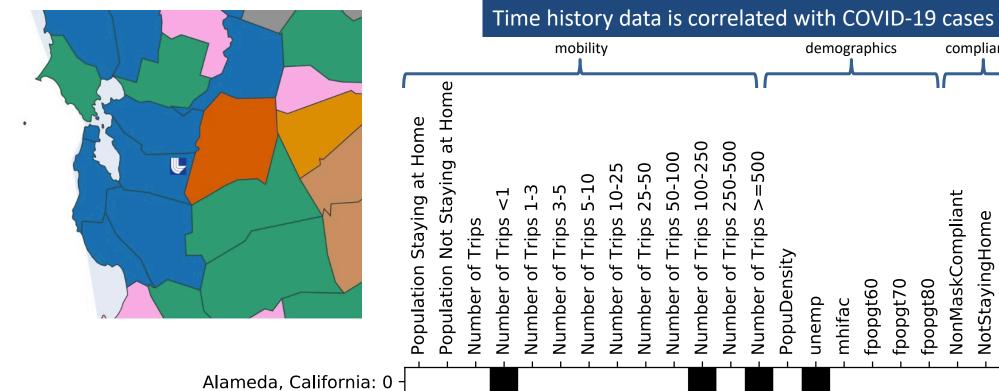


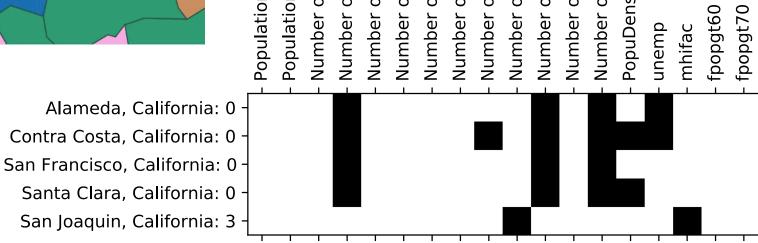




" the barcode"

Counties surrounding LLNL have unique signatures





Target Variable: Total Cases Per Day

compliance

NonMaskCompliant

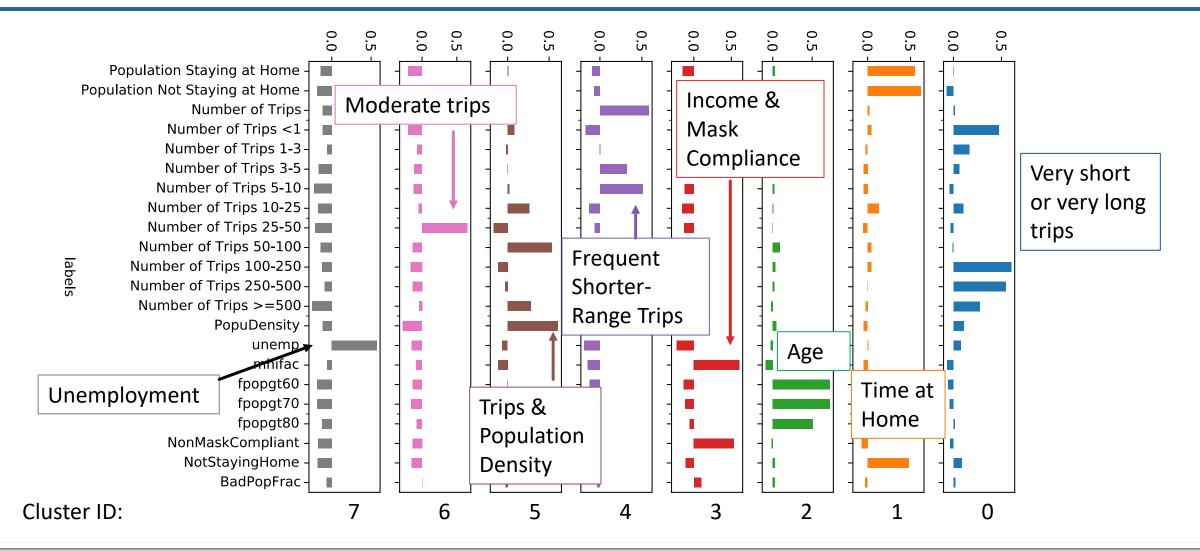
fpopgt80

NotStayingHome

BadPopFrac



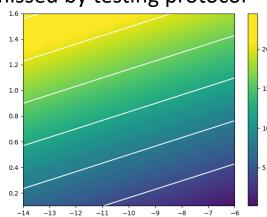
Relative frequency of features compared to average shows key aspects of different clusters



Our tools have informed operational decisions for the US Army and LLNL

Testing early can shorten movement restriction

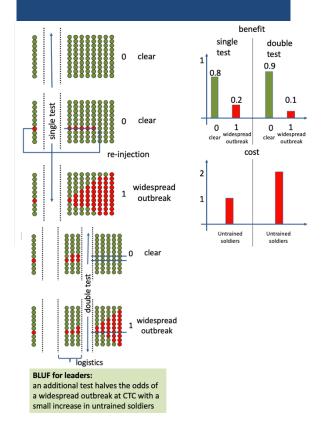
Number of infectious cases missed by testing protocol



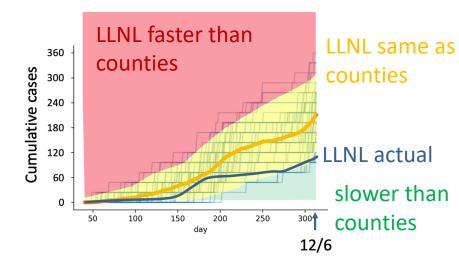
Test turnaround delay

Days in quarantine before movement

Optimal testing schedules

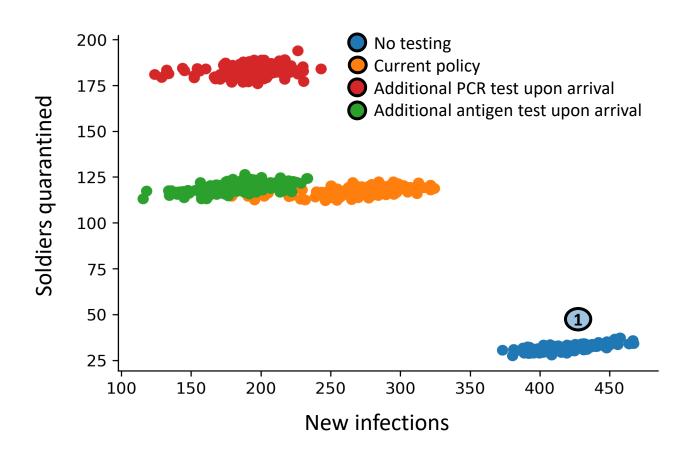


Assessments of operational mitigations on critical sub-populations



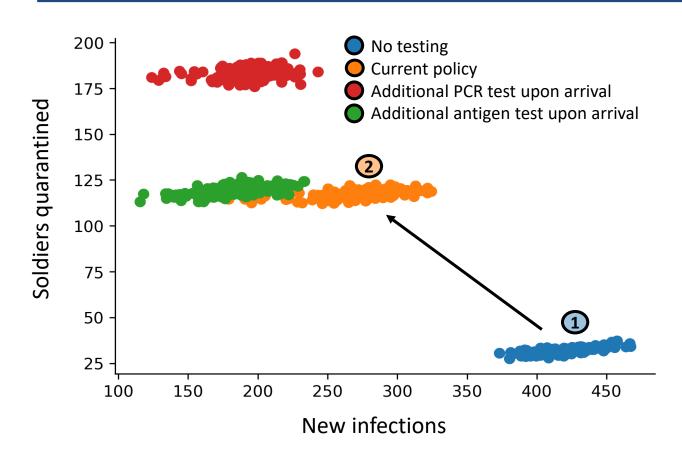
- Without testing, disease spreads readily
 - Many infections
 - Few quarantined
- Current ROM + pre-mov RT-PCR
 - fewer infections at cost of increased quarantines
- An additional RT-PCR test upon arrival at CTC
 - Small reduction of infections at large quarantine cost
 - Low-threshold test catches low-risk, recovering cases and their contacts
- A rapid antigen test is more suitable on arrival
 - Reduces infections without increasing quarantines
 - Higher detection threshold

Infections and quarantines during ROM and rotation



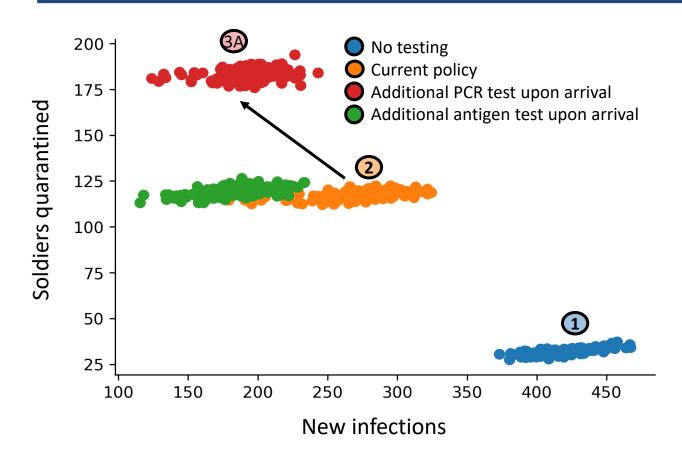
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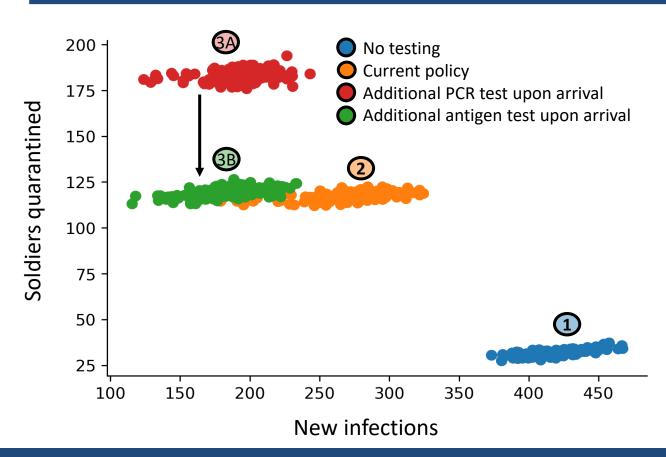
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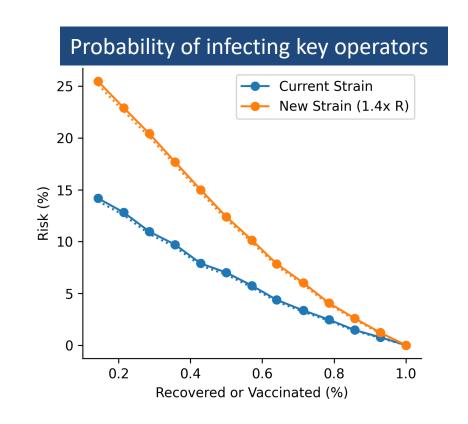


A second, low-fidelity test mitigates disease spread without the undue burden of lost training

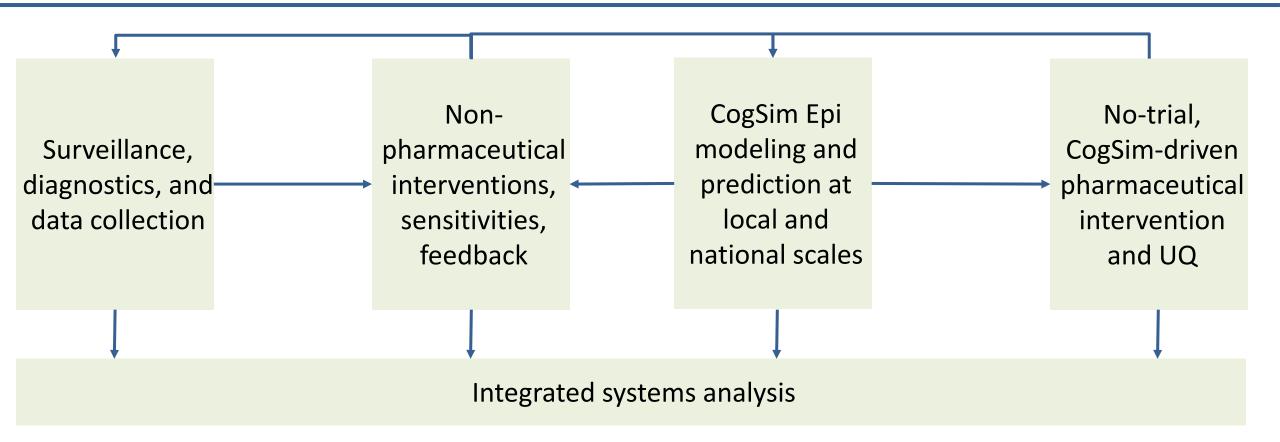


We are using our expanded capabilities to tackle current and emerging issues

- 1. Optimization of testing schedules and fidelities
- 2. Optimization of vaccination protocols: dose spacing, distribution rate, spectrum of efficacy
- 3. Assessments of new variants
- Coupling with LLNL counterparts to connect a comprehensive public health and biosecurity response



We are laying the foundation for a biosecurity response pipeline



We have the tools to develop a much more deliberate and organized response to the next bio threat



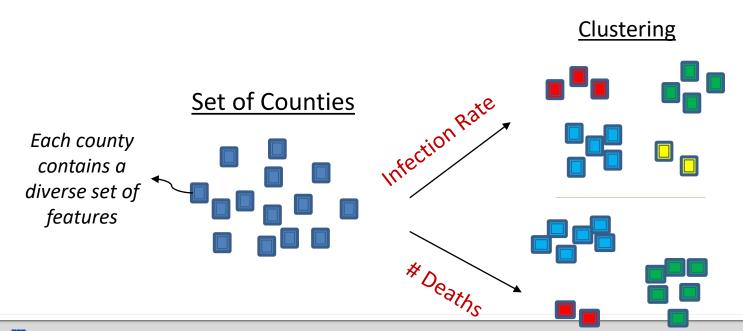
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Grouping Counties Requires the Design of a Complex Metric that Takes into Account Multiple Features

Each county contains multiple diverse features

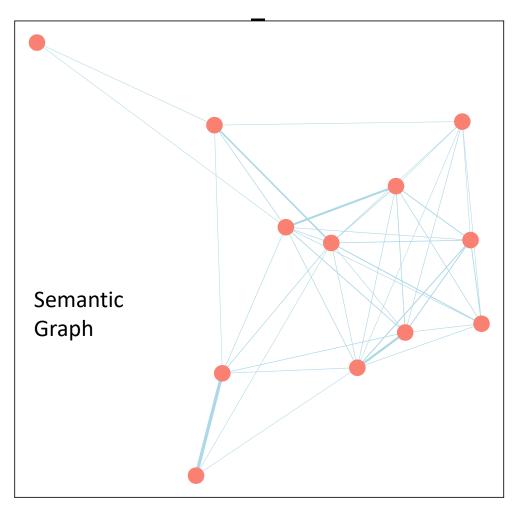
- Static (demography, income level etc. or aggregated statistics like total infections)
- Dynamic (time-histories of compliance, mobility etc.)

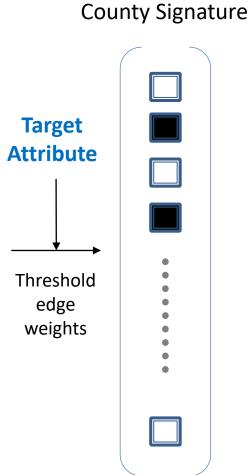


What metric can we use to "group" counties such that within each group a chosen "target attribute" exhibits similar trends?



Using the semantic graph, we generate county signatures that indicate influence on infection spread/mortality



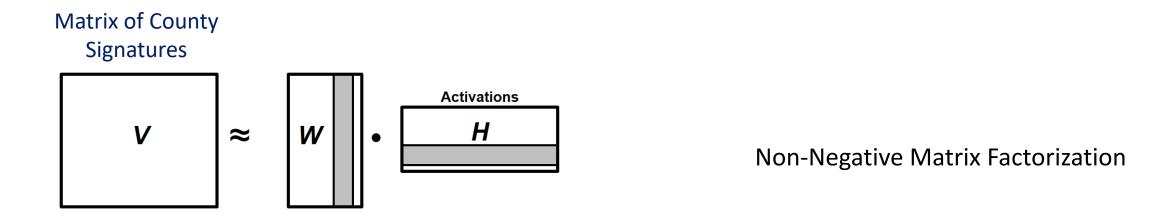


Each county is represented using a vector of K dimensions (number of features)

If there is an edge (> threshold) between a feature and the target we encode that with 1

This County Signature can be used for identifying county clusters

Topic Analysis of County Signatures to Identify Coherent Groups





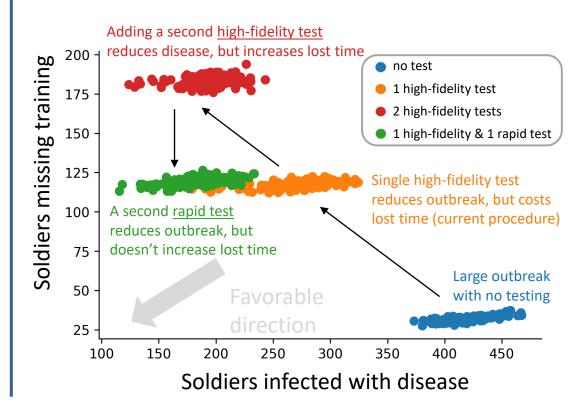
Our Method Can Automatically Identify Factors that Explain the Target

Attribute in Each County Group

Nuclear Security Administration

- Generic civilian disease models miss Army interaction patterns and realistic disease transmission
- New, Army-specific model captures key factors for Army disease transmission
 - Differences in person-to-person interactions due to chain of command
 - Availability of distributed surveillance testing
 - Detailed disease evolution in a military-age population
- Model allows investigation of a wide range of scenarios
 - Restriction of movement, testing, vaccination, contact tracing
 - Multiple populations: active duty, reserves, small forces, full brigades
- Supercomputing power executes model in hours
 - Rapid responses to leader questions
 - Quantified uncertainty to help decision making

Army-specific model offers COVID testing strategies that reduce lost training time while protecting against disease at CTC



This new Army-specialized model allows for optimal disease response while avoiding unnecessary mission detractors

LLNL-PRES-760736

Mational Nuclear Security Admini

Variants work

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