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# CS4980: Computational Epidemiology

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<https://homepage.cs.uiowa.edu/~sriram/4980/spring20/>

# CDI Transmission

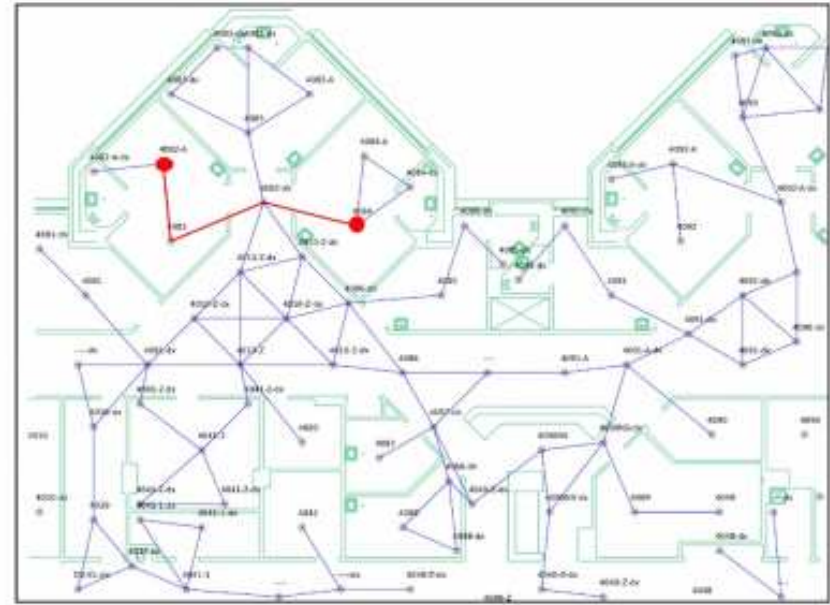
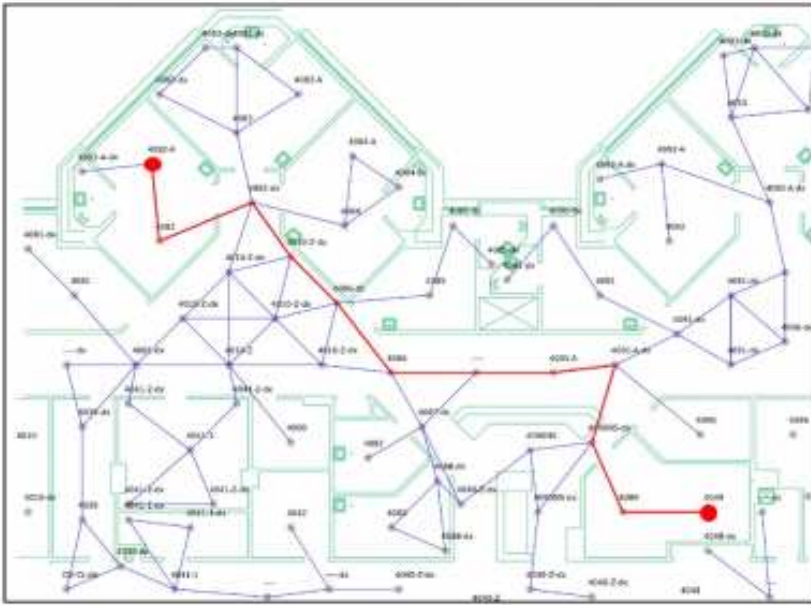
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Samore (1999) lists 3 mechanisms for CDI transmission: **direct** (*e.g.*, from HCW hands), **environmental** (*e.g.*, from spores left in the environment) and **endogenous** (*i.e.*, self colonized).

Each of these pathways can be addressed by a different intervention (*e.g.*, better hand hygiene, deep cleaning at discharge, or improved ABX Rx and patient transfer practices).

Effective intervention rely on understanding which of these pathways is in play.

# Consider Space and Time for CDI

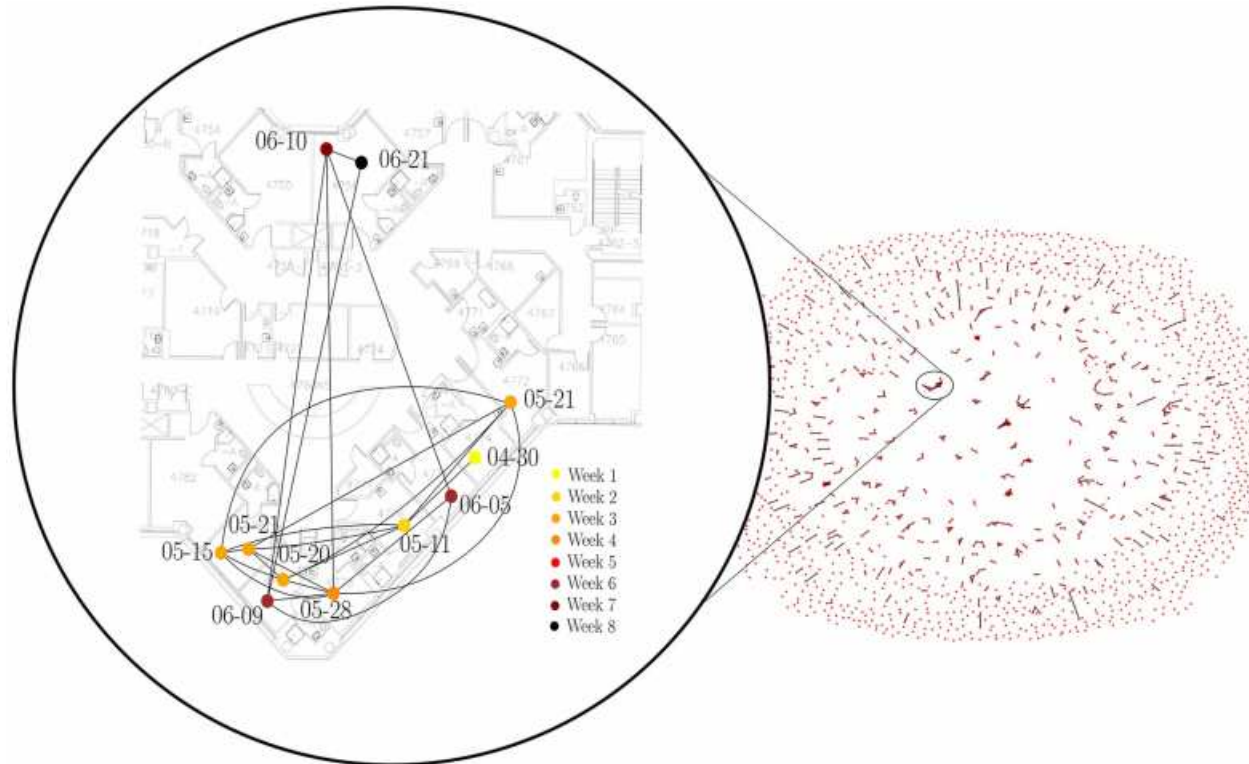


Recall our goal is to see if the observed “clustering” of CDI is accidental or the result of some underlying pathway.

Construct a *case proximity graph* for CDI using various  $t$  and  $d$  values based on timestamp and UIHC location of positive CDI test result.

# The Case Proximity Graph (t=14, d=5)

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How can we use such case proximity graphs to “measure” the spatiotemporal relationship between CDI cases?

# Deriving a Metric of Spatiotemporal Correlation

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The Knox test uses two  $C \times C$  matrices,  $s$  and  $t$ , where  $C$  is the number of CDI cases, where  $s_{ij}$  is 1 iff cases  $i$  and  $j$  are within threshold  $D$  of each other. Similarly,  $t_{ij}$  is 1 iff cases  $i$  and  $j$  are within threshold  $T$  of each other.

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Summing  $s_{ij} \times t_{ij}$  for  $i < j$  yields a test statistic that counts how many cases are close enough in space and time.

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This process produces a distribution of Knox metrics where there is no expectation of space/time correlation.

We then compare the observed metric with the distribution.

# The Mantel Test

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Here, we calculate not the number of co-located indicator variables but the sum of the correlations of the two distances at corresponding matrix locations.

The Monte Carlo estimation process is the same as for the Knox test.

# The Mantel Test: Details

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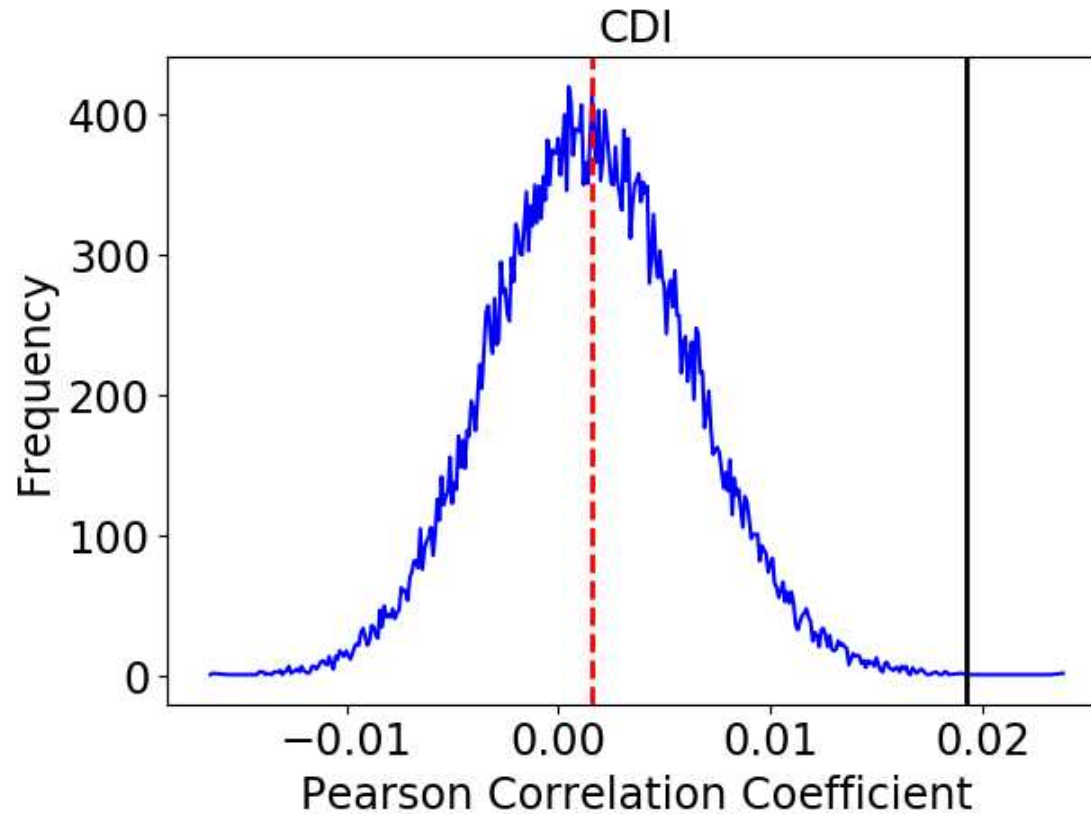
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The permutation test (a form of bootstrapping, where we randomize the correspondance of matrix elements) can be used to derive a p-statistic (count number of times  $r_{bootstrap}$  exceeds  $r_{observed}$ ). Confidence intervals can also be derived in a similar fashion.

## Result: CDI Clustering

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Result of the Mantel test on 20,000 permutations of space/time for CDI clusters; black line is the observed value, dotted red line the experimental mean.

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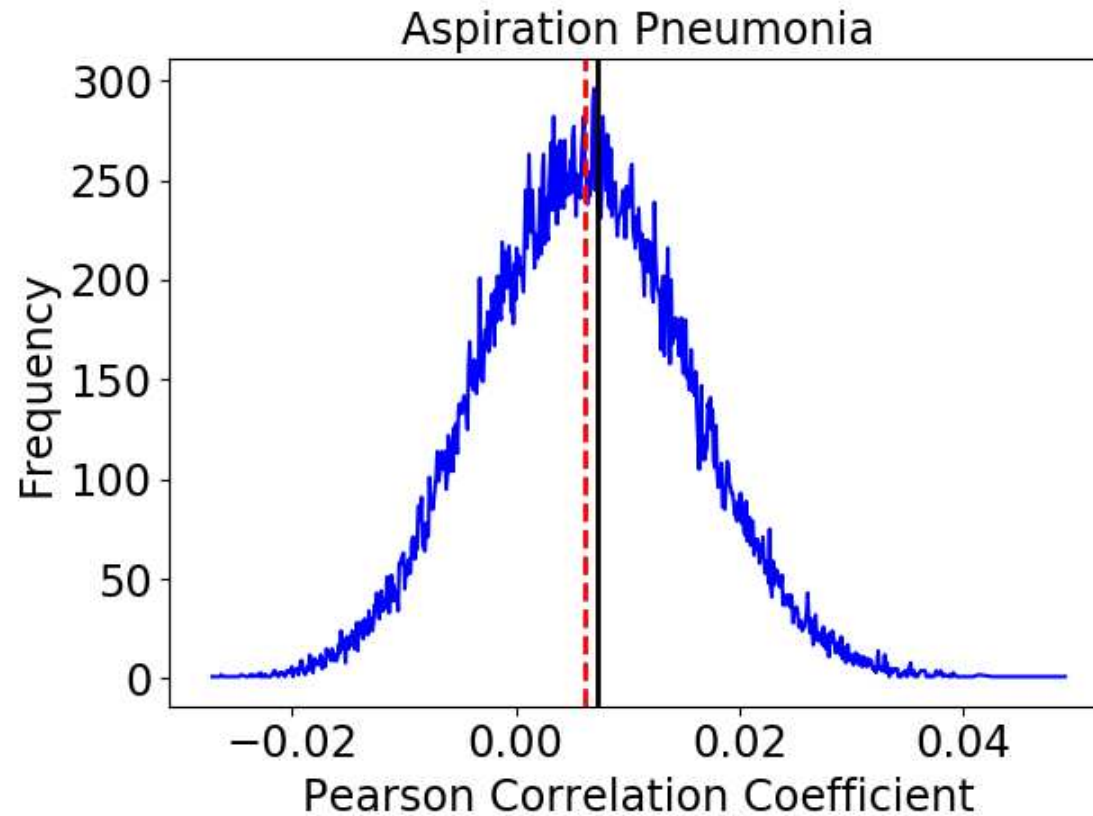
Consider *aspiration pneumonia*, an infection of the lungs that is mechanically induced by aspirating saliva or other substances.

We built a case proximity graph for 790 cases of AP from the UIHC data; because AP is not contagious, we do not expect to observe any spatiotemporal correlation between them.



## Result: AP clustering

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Result of the Mantel test on 20,000 permutations of space/time for AP clusters; black line is the observed value, dotted red line the experimental mean.

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The results argue against endogenous (asymptomatic, self-colonized) transmission of CDI, contradicting Walker (2010), although it does not entirely rule out this pathway.

It does confirm hand hygiene and deep cleaning of patient rooms are critical defenses against nosocomial CDI.