I. Motivation

Background
- Based on case location, disease mapping estimates a risk of disease across a geographic region.
- Location at diagnosis does not necessarily correspond to location at exposure.
- Some disease have long latency periods (e.g., leukemia, mesothelioma).
- Time, duration, and location of exposure are unknown.
- Residential history has already been incorporated in tests for cluster detection [1,3].

Questions
- How can residential history be incorporated in disease mapping?
- Can location at exposure be identified more accurately?

II. Methods

a. Example of data (4 locations)

b. Creating Weights: \( W_k = G(D_k) \)

b. Evaluation of 1000 simulations

III. Results

a. Illustration with 1 simulation (q=50%)

- The higher risk circle is identified more accurately by mapping using duration or incubation weights, rather than by mapping using only location at diagnosis.
- The color cutoffs are determined by resampling from the reference population \( F_0 \).

b. Evaluation of 1000 simulations

IV. Conclusion

- Disease mapping can incorporate residential history of cases by using a weighting scheme.
- The accuracy at locating an increased risk improves by mapping with duration or incubation weights rather than mapping with location at diagnosis only.
- There are other choices for the function \( G \):
  - Step function
  - Weight all locations of a case equally
  - Include (time varying) covariates
- A similar method can be developed when cases are available with multiple daily locations (home/work/school) along with the proportion of the day spent at each location.
- In future work, we can relax some limitations in the methods (missing spatial information) and simulations (non-uniform population, atemporal dichotomized risk).

Thanks and acknowledgements

Thanks to JSM 2010, conference organizers and participants.
Research partially supported by:
- National Institutes of Health grant R01 EB006195
- Centers for Disease Control and Prevention grant R01 PH000021-01

References