Computational Epidemiology Research Laboratory (CERL)

UNT

CERL has been established in 2004 to conduct and promote research in computational epidemiology. As opposed to mathematical and statistical epidemiology, computational epidemiology is in its infancy. It does by no means replace but rather complement methodologies in epidemiology that have been developed during the last century. Its primary purpose is to apply computer and computational science paradigms to the domain of Public Health, thereby providing novel tools for epidemiologists and scientists. These tools will aid in the prediction and analysis of disease manifestation and spread in a given population through modeling, simulation, and visualization, thereby enabling epidemiologists to conduct focused what-if-analyses that facilitates the allocation of public health resources.

From Modeling to Visualization

Demographics
Public Health Actions
Disease Parameters
Health Risk Behavior
Geography
Data Sets → Visualization

At CERL, faculty and students from different domains are working together to develop new scientific methods that will enhance the understanding of the intricate interplay of disease and population.

CERL Core Faculty

Armin R. Mikler (CERL Director), UNT Department of Computer Science and Engineering, mikler@cs.unt.edu

Joseph Oppong, UNT Department of Geography, oppong@unt.edu

Samuel F. Atkinson, UNT Department of Biological Sciences, atkinson@unt.edu

Karan Singh, Department of Biostatistics, UNT Health Science Center School of Public Health, ksingh@hsc.unt.edu

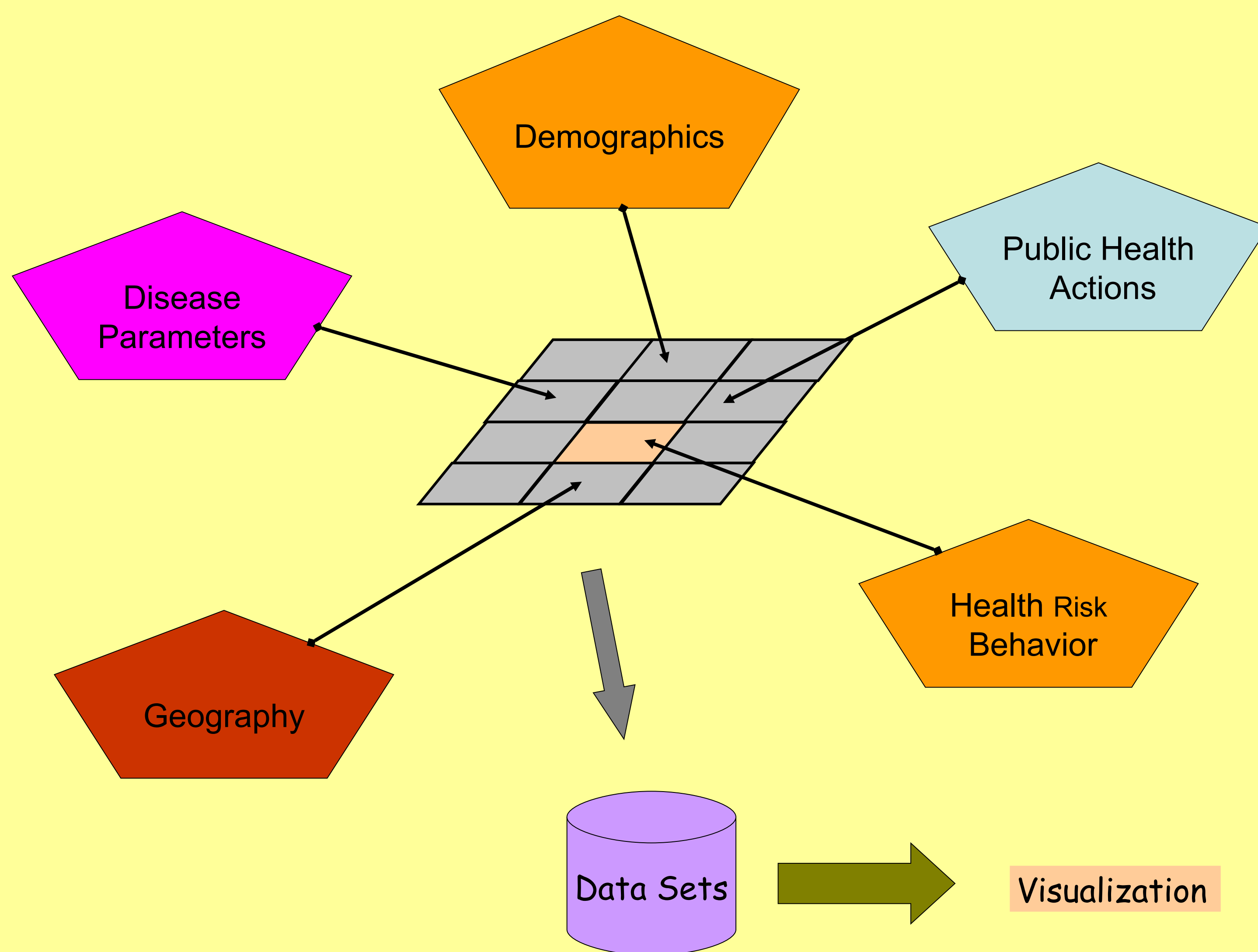## Computational Epidemiology is ..

Addressing broader aspects of Epidemiology
Disease Tracking, Analysis, and Surveillance through:
–High Performance Computing (HPC)
–Simulation
–Data visualization.

Tools that facilitate:
–Disease Outbreak Analysis
–Disaster Preparedness
–Risk Assessment
–Vaccination Strategies
–Modeling Spread of Disease over Distances

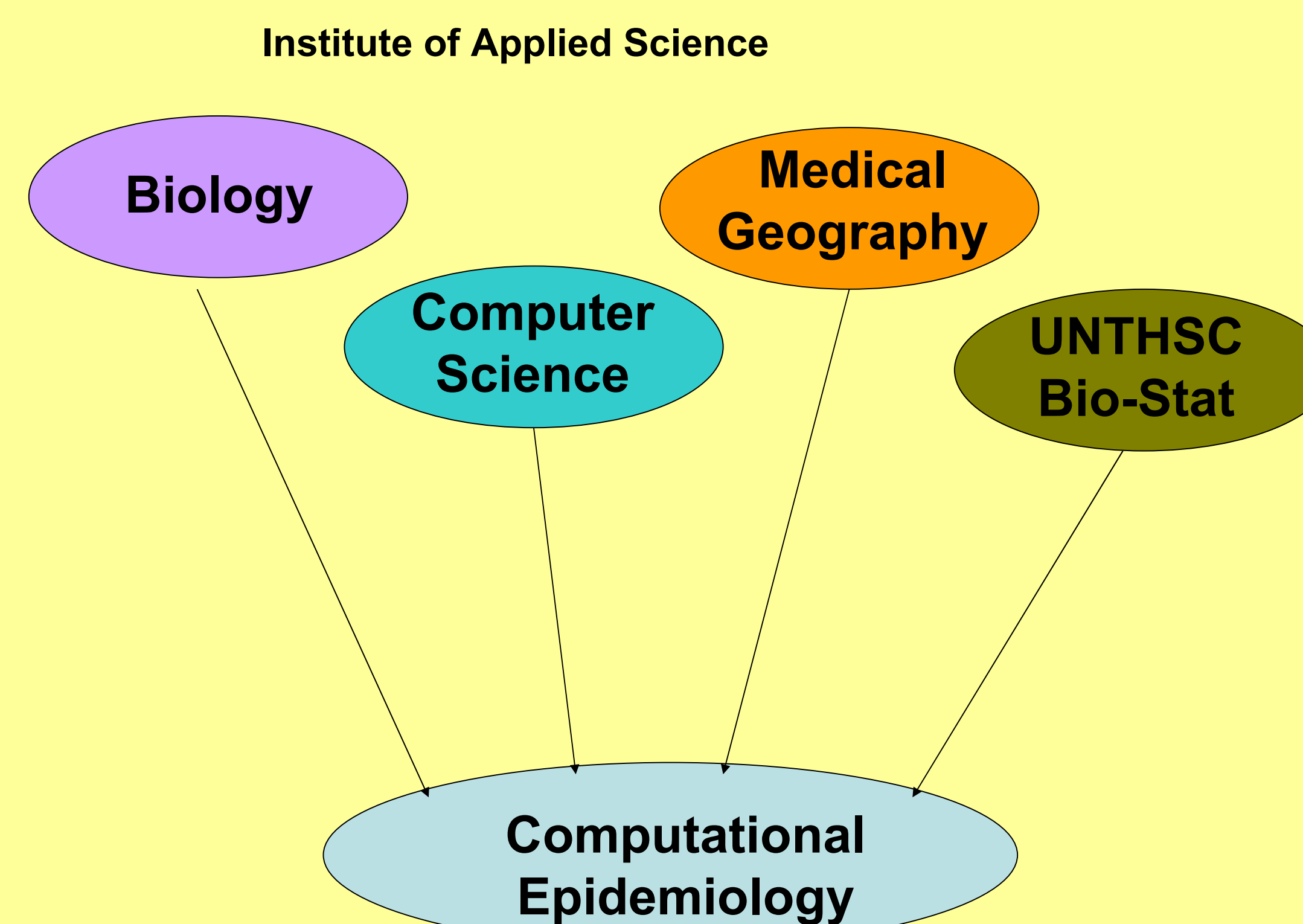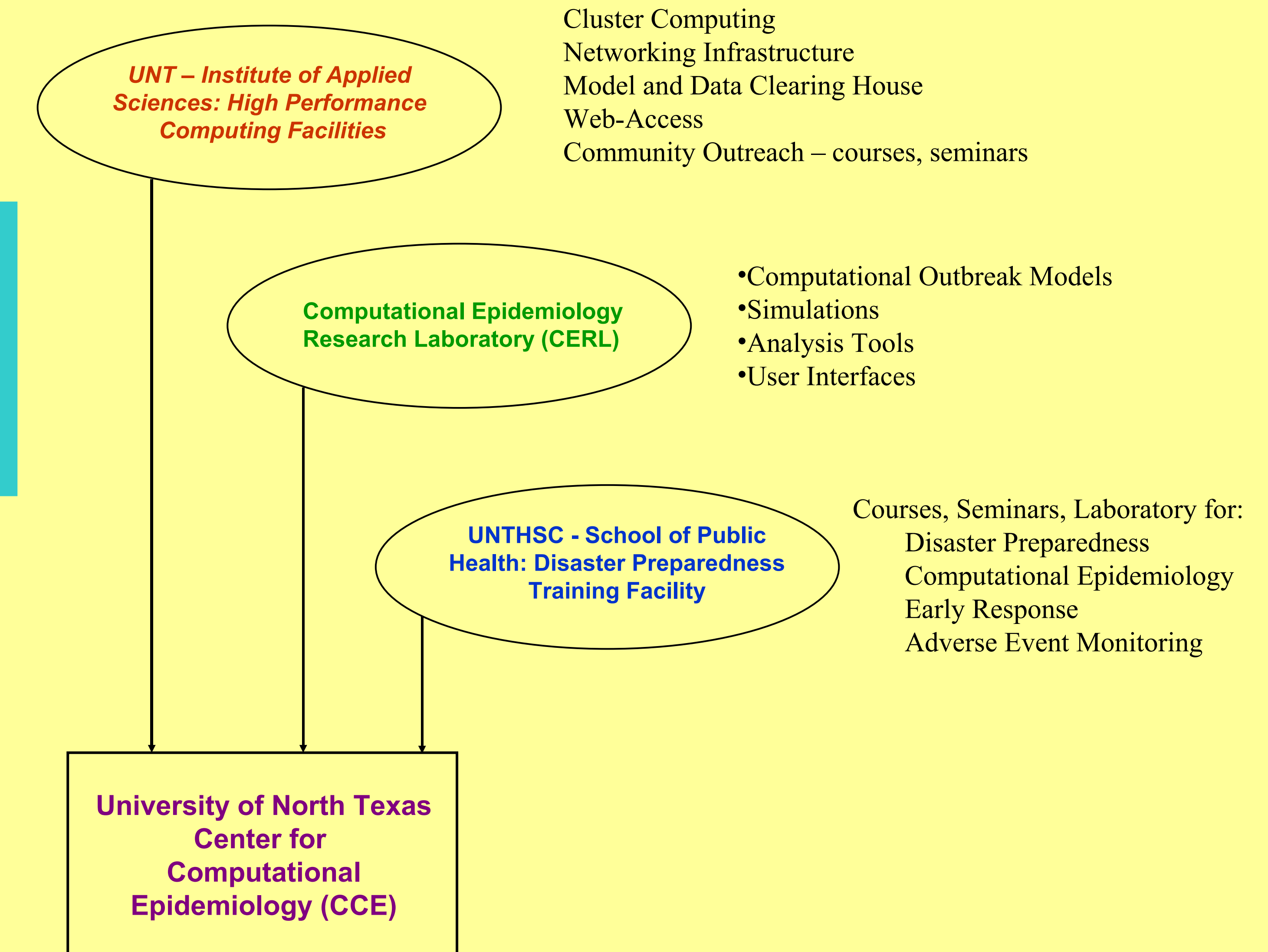The ability to predict how a disease might manifest itself in the population at large is essential for identifying disease monitoring and control strategies. Epidemiologists are traditionally relying on data that have been collected during previous outbreaks. However, for newly emerging or re-emerging infectious diseases, such data are often unavailable or outdated. Changes in population composition and dynamics require the design of models that bring together knowledge of the specific infectious diseases with the demographics and geography of the region under investigation.

Collaboration at UNT

Institute of Applied Science

Biology
Medical Geography
Computer Science
UNTHSC Bio-Stat
Computational Epidemiology

Towards a Center for Computational Epidemiology

UNT – Institute of Applied Sciences: High Performance Computing Facilities

Cluster Computing
Networking Infrastructure
Model and Data Clearing House
Web-Access
Community Outreach – courses, seminars

Computational Epidemiology Research Laboratory (CERL)

•Computational Outbreak Models
•Simulations
•Analysis Tools
•User Interfaces

UNTHSC - School of Public Health: Disaster Preparedness Training Facility

Courses, Seminars, Laboratory for:
Disaster Preparedness
Computational Epidemiology
Early Response
Adverse Event Monitoring

University of North Texas Center for Computational Epidemiology (CCE)

Recent CERL Publications

ii. Abbas, K., Mikler, A.R., and Gatti, R., 2005, "Temporal Analysis of Infectious Diseases: Influenza." Proceedings of the ACM Symposium on Applied Computing (SAC '05), Sante Fe, NM, March.
iii. Abbas, K., Mikler, A.R., Ramezani. A.R. and Menezes, S., 2004, "Computational Epidemiology: Bayesian Disease Surveillance." Proceedings of the International Conference on Bioinformatics and its Applications (ICBA'04), Fort Lauderdale, FL, December.
iv. Corley, C., and Mikler, A.R., 2005 "Predicting Human Papilloma Virus Prevalence and Vaccine Policy Effectiveness in Demographic Strata" Proceedings of IEEE Fifth Symposium on Bioinformatics and Bioengineering (BIBE '05), pgs 73-80. Minneapolis, MN October.
v. Mikler A.R., Venkatachalam S., and Abbas K. " Modeling Infectious Diseases using Global Stochastic Automata". The Journal of Biological Systems, Vol. 13, No. 4 (2005) 421-439.
vi. Mikler, A.R., Jacob, R., Gunupudi, V. and Patolla, P., 2006, "Agent-based Simulation Tools in Computational Epidemiology". Proceedings of the International Conference on Innovative Internet Community Systems (I2CS '04), Guadalajara,Mexio, June 2004, Springer LNCS 3473, pp 212 - 223.
vii.Moonan, P. K, Oppong, J., Sahbazian, B., Singh, K.P., Sandhu, R., Drewyer, G.,LaFon, T., Marruffo, M., Quitugua, T.N., Wallace, C. and Weis, S.E., 2006, "What is the Outcome of Location-based Targeted Tuberculosis Screening Based on Universal Genotyping?" American Journal of Respiratory Critical Care Medicine. published 25 May 2006,
viii.Oppong J.R., Mikler A.R., Moonan P., and Weis S., 2006, "From Medical Geography to Computational Epidemiology – Dynamics of Tuberculosis Transmission in Enclosed Spaces". Proceedings of the International Conference on Innovative Internet Community Systems (I2CS '04), Guadalajara,Mexio, June 2004 Springer LNCS 3473, pp. 189 – 197.
ix. Venkatachalam, S. and Mikler, A.R., 2005, "Towards Computational Epidemiology: Using Stochastic Cellular Automata in Modeling Spread of Diseases." Proceedings of the 4th Annual International Conference on Statistics, Mathematics and Related Fields, Honolulu, HI, January.
x. Venkatachalam, S. and Mikler, A.R., 2006, "An Infectious Disease Outbreak Simulator Based on the Cellular Automata Paradigm". to appear in the Proceedings of the International Conference on Innovative Internet Community Systems (I2CS '04), Guadalajara, Mexico, June 2004, Springer LNCS 3473, 2006, 198 - 211.