

## INNOVATING CROSS-DOMAIN SOLUTIONS TO DETECT EMERGING BIOLOGICAL THREATS

# Statistical Relationships Across Epigenomes Using Large-scale Hierarchical Clustering

Anastasiia Kim LANL   Nicholas Lubbers LANL   Christina Steadman LANL   Karissa Sanbonmatsu LANL

Environmental toxins and pathogens can influence epigenetic modifications on chromosomes, thereby leaving trace evidence of exposures. However, the avalanche of epigenomic data is difficult to parse for biological interpretation given non-linear complex patterns and relationships. This attractive challenge in epigenomic data lends itself to machine learning for discerning infectivity and susceptibility. In this study, we explore over 3,000 epigenomes of uninfected individuals and provide a comprehensive characterization of the relationships among epigenetic modifiers, their modifiers, and specific immune cell types across all chromosomes using hierarchical clustering. We further validate our approach by applying it to data from samples collected from study participants diagnosed by DTRA collaborators as having been exposed to infections.

The study was supported by the Defense Threat Reduction Agency, Grant DTRA1308139949.