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“Mathematical tools for automated detection of antimicrobial peptides”.

This project is focused on developing a set of mathematical tools for performing systematic analysis of peptide sequence data that can be used, in particular, for automatic screening and anomaly detection based on various types of experimental data. In the Bishop lab that we collaborate with, functionalized hydrogel particles are used to harvest peptides from biological samples with the ultimate objective of identifying novel cationic antimicrobial peptides (CAMPs). There is a need to evaluate meaningful similarities and differences between sets of peptides captured by different particle types and between different harvests. We explore the role of different types of distance metrics and physical characteristics of the peptide sequences in the statistical analysis that includes dimension reduction, classification and clustering. Observations based on the phylogenetic and demographic information are used to guide experiments as well as algorithmic development. (Received September 17, 2019)