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A Supervised Strain Classifier

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science with a major in Computer Science.

by

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Abstract: Several bacterial and viral species are human pathogens and contain strains exhibiting different degrees of virulence. Nucleic acid sequencing enables strain fingerprinting, which is a term used for identifying bacterial and viral strain species and subtypes based on their DNA. Strain fingerprinting methods are becoming increasingly important in the threat of epidemic outbreaks and the possibility of biothreat agents. This thesis examines the use of oligonucleotide word signatures for strain fingerprinting and related classifications. An investigation into word signature differences exhibited by different strains of the same subtype reveals that words not expressed by individual genomes offer the most potential as differentiating features. Thus, a supervised classifier is built with feature sets derived from absent words. Resulting accuracies are high and are listed for five classifications at different levels of phylogenetic resolution: Mixed Pathogens: 100%, Influenza A virus/Influenza B virus:100%, Influenza A virus subtypes (human host):92%, Avian Influenza A virus H5N1 lineages: 94%, Avian to Human Transmission H5N1 lineages:100%. While the data set used does not allow complete confirmation of reported accuracies, it is suggested that this method could be a valuable tool in comparative genomics and enable geographic origination determination of Influenza A virus and other pathogenic isolates.

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