

Public Abstract

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Title:Alternative Applications of Whole Genome De Novo Assembly in Animal Genomics

Genome sequencing is the process by which the sequence of deoxyribonucleic acid (DNA) residues that comprise the genome, or complete set of genetic materials of an organism or individual, is determined. Down-stream analysis of genome sequencing data requires that short reads be compiled into contiguous sequences. These methods, called de novo assembly, are based in statistical methods and graph theory. In addition to genome assembly, the research presented in this dissertation demonstrates the alternative use of these methods. Using these novel approaches, de novo assembly algorithms can be utilized to gain insight into commensal and parasitic organisms of livestock, genes containing candidate mutations for genetic defects, and population-level and species-level variation in a poorly studied organisms.