



Category: Bioinformatics

Pipeline to upgrade the genome annotations

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Abstract

Current era of functional genomics is enriched with good quality draft genomes and annotations for many thousands of species and varieties with the support of the advancements in the next generation sequencing technologies (NGS). Around 25,250 genomes, of the organisms from various kingdoms, are submitted in the NCBI genome resource till date. Each of these genomes was annotated using various tools and knowledge-bases that were available during the period of the annotation. It is obvious that these annotations will be improved if the same genome is annotated using improved tools and knowledge-bases. Here we present a new genome annotation pipeline, strengthened with various tools and knowledge-bases that are capable of producing better quality annotations from the consensus of the predictions from different tools. This resource also perform various additional annotations, apart from the usual gene predictions and functional annotations, which involve SSRs, novel repeats, paralogs, proteins with transmembrane helices, signal peptides etc. This new annotation resource is trained to evaluate and integrate all the predictions together to resolve the overlaps and ambiguities of the boundaries. One of the important highlights of this resource is the capability of predicting the phylogenetic relations of the repeats using the evolutionary trace analysis and orthologous gene clusters. We also present a case study, of the pipeline, in which we upgrade the genome annotation of *Nelumbo nucifera* (sacred lotus). It is demonstrated that this resource is capable of producing an improved annotation for a better understanding of the biology of various organisms.

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