

S2-2

Hybrid Fungal Genome Annotation Pipeline Combining *ab initio*, Evidence-, and Homology-based gene model evaluation

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Fungal genome sequencing and assembly have been trivial in these days. Genome analysis relies on high quality of gene prediction and annotation. Automatic fungal genome annotation pipeline is essential for handling genomic sequence data accumulated exponentially. However, building an automatic annotation procedure for fungal genomes is not an easy task. FunGAP (*Fungal Genome Annotation Pipeline*) is developed for precise and accurate prediction of gene models from any fungal genome assembly. To make high-quality gene models, this pipeline employs multiple gene prediction programs encompassing *ab initio*, evidence-, and homology-based evaluation. FunGAP aims to evaluate all predicted genes by filtering gene models. To make a successful filtering guide for removal of false-positive genes, we used a scoring function that seeks for a consensus by estimating each gene model based on homology to the known proteins or domains. FunGAP is freely available for non-commercial users at the GitHub site (<https://github.com/CompSynBioLab-KoreaUniv/FunGAP>).