



Title: Synteny-based Pipeline for the Annotation of Gene Orthologs (SPAGO)

Andrea Falcón-Cortés

Abstract: Comparative genomics has been traditionally focused on sequence analysis. Because of mutations, genetic sequences gradually change over time; the more closely related two organisms are, the less their genetic sequences have diverged. Sequence similarity allows inferring homologous genes and following the organism's evolutionary history. Yet, obtaining a unique path following a gene across different species' is still difficult. Synteny -- the conservation of gene order -- can provide valuable information to uncover how genes flow across species. Here, we combine sequence similarity and syntenic information to relate genes across different species and we encode these relationships into a network. In this network each connected component represent a set of orthologous genes, i.e., the same coding DNA in different genomes. Preliminary results indicate that our approach significantly improves the quality of orthologous genes annotations.