

Have you ever wanted to learn about the cladistics origin of operons? Take our TAXI (Taxonomic Innovations)

Ferreira, L. M.¹, Ortega, J.M.²

²*Laboratório de Biodados, Departamento de Bioquímica e de Imunologia, ICB, Universidade Federal de Minas Gerais (UFMG)*

Comparative studies amongst prokaryotic genomes shows genes being shared between them. These genes are not shared only with phylogenetically sister organisms, but are also shared along higher phylogenetic distances. These genes can be translated alone, or grouped into structures denominated operons. Alone or comprising operons, genes can be transferred from one organism to another via horizontal genes transfer. Moreover, genes do not exist in a synthenic orientation within operons in all prokaryotes; there is a clade of origin. In this study were developed a database called TAXI - Taxonomy Innovations, which addresses the innovations along the cladogenesis of bacteria and archaea genomes. This database was built with information from 1752 bacteria and 94 archaea collected from Microbes Online data warehouse. From this data warehouse is was also collected the information of gene clusters, and with the taxonomic distribution we determined the clade of origin of all comprised operons and their genes. For presenting this database we developed a user friendly web interface where the researcher can perform searches for genes or operons and inspect the innovations gained in desired clade. Therefore, knowing the orthologues, their taxonomic/synthenic distribution, ancient *versus* recent genes and operons can be studied. In conclusion, whenever one wants to inspect the epoch of evolution (phylum, class, family, species) in with a gene of operon has first appeared, take our TAXI (Taxonomic Innovations database) available at biodados.icb.ufmg.br/taxi.