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How to Use FAANGMine to Perform Functional Analysis of a Gene List

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FAANGMine (http://faangmine.org), developed by the Elsik lab at the University of Missouri, is a genomic data mining warehouse for domesticated animal species. FAANGMine provides simple and sophisticated search tools to allow researchers to gather and analyze information about genes and genomes. FAANGMine contains genomes and genes of cat, chicken, cow, dog, goat, horse, pig, sheep, and water buffalo. Genes of humans, mice, and rats are also included to facilitate comparison to model organisms.

My role in the FAANGMine project is beta-testing FAANGMine and assisting in the development of usage examples. In this poster, I will show how to use the FAANGMine List Tool to analyze gene functions, using a published dataset of genes that are differentially expressed between two chicken breeds that differ in their tolerance to harsh temperature environments [1]. With the List Tool, users can upload lists of gene identifiers to access information about gene function. The example will demonstrate the application of three data sources that provide information about gene function. The Gene Ontology (GO) [2] is a set of vocabulary terms used to describe biological and molecular functions of genes, as well as locations of gene products (e.g. proteins) within cells. KEGG [3] and Reactome [4] are biological pathway datasets that describe how gene products interact with each other to carry out biological functions. The FAANGMine List Analysis Tools will be used with GO, KEGG and Reactome to perform gene enrichment analyses to determine whether the set of differentially expressed genes has an overabundance of certain gene functions, which will provide insight into mechanisms of tolerance to harsh environments.

References

- 1. Xie S, Yang X, Wang D, Zhu F, Yang N, Hou Z, Ning Z. Thyroid transcriptome analysis reveals different adaptive responses to cold environmental conditions between two chicken breeds. PLoS One. 2018 Jan 10;13(1):e0191096. doi: 10.1371/journal.pone.0191096.
- 2. The Gene Ontology Consortium. The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Res. 2019 Jan 8;47(D1):D330-D338. doi: 10.1093/nar/gky1055.
- 3. Kanehisa M, Furumichi M, Sato Y, Ishiguro-Watanabe M, Tanabe M. KEGG: integrating viruses and cellular organisms. Nucleic Acids Res. 2021 Jan 8;49(D1):D545-D551. doi: 10.1093/nar/gkaa970.
- 4. Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. Nucleic Acids Res. 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031.