

AN INTEGRATED GENE AND PROTEIN ID MAPPING TOOL WITH BATCH ORTHOLOG PREDICTION

M. Fleisch, U. Evani, S. D. Mooney

*Mooney Laboratory, The Buck Institute for Age Research, 8001 Redwood Blvd
Novato, CA 94947, USA*

**Email: mfleisch@buckinstitute.or*

The Bioinformatics core at the Buck Institute for Age Research was created to develop tools for enabling new science. Our goal is to create programs and web tools to take current databases and make them accessible to our local scientists in an efficient way. To this end we have developed two tools. The first tool is called the Gene identifier Network (GiN) which is used for mapping identifiers between various publicly available biological databases. The databases we currently support are NCBI, UniProt, Flybase, WormBase, Saccharomyces Genome Database (SGD) and the Mouse Genome Informatics (MGI). The second tool called the ortholog portal is for mapping between orthologous proteins in different species. Orthology is an evolutionary concept wherein two protein sequences are derived by a speciation event from a single ancestral sequence from a common ancestral species. These two proteins generally perform similar functions. We use annotations from NCBI Homologene database for mapping orthologs. Both these tool can be accessed through a web service and support batch submissions. All queries are securely saved on the server and the user has the option of either accessing it online or exporting it in a CSV (Comma Separated Version) format. In our poster we will be discussing in detail the schema and the performance of these tools along with plans for incorporating other data and annotation datasets.