

2024 Update on GeneNetwork.org

by Pjotr Prins, Rob W. Williams & the broader GeneNetwork team

Our GeneNetwork web-service (GN – formerly WebQTL) was developed for the needs of the mouse community, and represents over 25 years of research, data and software. Running and expanding such a web service is no mean feat and requires continues updates to code, algorithms and data.

In this talk, if time allows, we will discuss reorganization of the informatics of biomedical research and how that can go a long way towards addressing two problematic areas common to both human and model organism analysis: access to massive and complex `omics' data, and the need for robust but accessible systems for analysis of joint statistical/causal models that produce useful predictions. We greatly improved search facilities and we are adding flexible data end-points exposing data and metadata. We have expanded search and GNQA, a question-answer service that adds large language model (LLM) support for mining thousands of publications — with a focus on the topics of aging and diabetes — in conjunction with the GeneNetwork database. I will give a demonstration of these powerful facilities.

Combining and integrating datasets from old and new research will lead to novel connections and ideas followed by insight. That also means we actively invite new communities to contribute their data to GeneNetwork and we can organize workshops to introduce data submission and analysis options. We are adding 'apps' such as Dr. Chen's GeneCup.org flask app, that mines PubMed for Gene Relationships using Custom Ontologies and Dr. Ashbrook's R/shiny longevity app. These services and apps can be adapted to your research questions and we can host your app too. Today we are also adding support for other species, including rat and human. We have an ongoing effort adding new datasets, such as *C. elegans*, *A. thaliana*, Kilifish and Medaka fish.