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LYNX – a systems biology platform for integrative medicine

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Abstract

Progress in understanding of molecular mechanisms underlying complex heritable disorders (*e.g.,* autism, schizophrenia, diabetes) depends on availability of bioinformatics resources for systems-level analysis and identification of disease-specific patterns of inheritance. Efficient mining of vast and complex data sets for the needs of biomedical research critically depends on seamless integration of clinical, genomic and experimental information with prior knowledge about genotype-phenotype relationships accumulated in a plethora of publicly available databases. Furthermore, such experimental data should be accessible to a variety of algorithms and analytical pipelines that drive computational analysis and data mining.

We present an integrated web-based computational database LYNX (http://lynx.ci.uchicago.edu:8080/) to support translational medicine studies from the systems biology perspective. Our approach is based on a large-scale integration of various classes of biological information from over 35 public and private databases into LYNX knowledge base. This data is used for analysis of genomic data using LYNX tools.

LYNX analytical workbench includes tools for annotation and enrichment analysis of genomic data. It also provides algorithms for networks-based gene prioritization and prediction of high-confidence genetic factors and molecular mechanisms contributing to the phenotypes of interest. Annotation and analytical services in Lynx are available via the Web-based user interface and web services.

We will illustrate the utility of our approach using analysis of brain connectivity disorders (e.g. agenesis of corpus callosum, autism, schizophrenia) as an example. Our analysis allowed uncovering some of the common molecular mechanisms that underlie these disorders. This knowledge will eventually lead to the development of efficient diagnostic and therapeutic strategies.

Biography

Natalia Maltsev, M.D (Pediatrics and Internal Medicine), Ph.D. (Immunology and Microbiology) from the Russian State Medical University (Moscow, Russia). She played an active role in the development of the WIT bioinformatics platforms for metabolic reconstructions from sequence data developed at Argonne National Laboratory and led the development of the first Grid-based computational platform PUMA2 for evolutionary analysis of genomes and metabolic networks. Her group at Prof. Gilliam's lab at the University of Chicago is developing LYNX for analysis of multigene disorders. Dr. Maltsev has authored over 40 publications in peer-reviewed journals and gave numerous presentations at the international conferences.