

Genedata Phylosopher®

NutriLead Edition



The enterprise system for integrated nutrigenomics research

Many diseases and disorders are related to deficits of essential nutrients, imbalance of macronutrients or even toxic concentrations of certain food components. It is well known that common diseases such as obesity, diabetes type II or cancer are critically dependent on nutrition and genetic predisposition of individuals. The relationship between nutrition and health is solidly anchored in molecular interactions on the levels of DNA, mRNA, proteins and metabolites. As our diet consists of a mixture of many potentially bioactive chemical compounds, which are

Genedata Phylosopher® NutriLead Edition Overview

typically chronically administered in different compositions, a complex biological response arises. The newly developed so called '-omics' technologies enable for the first time a direct and unbiased monitoring of the effect of nutrients on the genomic, transcriptomic, proteomic and metabolomic level. The data produced by these '-omics' technologies form the basis of a comprehensive "nutrigenomics" approach. Currently, the challenge in nutrigenomics is to systematically structure, integrate, analyze and ultimately interpret the data in its biological and nutritional context.

Genedata



The Genedata Phylosopher[®] NutriLead edition represents a unique computational system that specifically focuses on applications in nutrigenomics research. The system represents the most comprehensive encyclopedia of the latest knowledge on nutrient catabolism and biosynthesis. Phylosopher NutriLead comes with a comprehensive library of metabolic, signaling and regulatory pathway maps that facilitates an in-depth understanding of nutrients on biochemical networks. Moreover, the system comes with

Disentangling the Complex Effects of Nutrients

The various '-omics' technologies are increasingly used to monitor the molecular mechanisms of nutrients. Analyzing transcriptomics, proteomics and metabolomics data in the context of the most recent information of human metabolism and genome structure leads to an in-depth understanding of the complex effects of nutrition. Together with comprehensive information on all encoded genes, polymorphisms, transcripts, splicing variants, proteins, protein interactions, as well as detailed metabolic and signaling pathway maps, Phylosopher NutriLead represents the ideal framework to identify and interpret dietary signals in mRNA, protein and metabolite expression profiles. specialized tools for testing hypotheses, identifying and validating markers, developing assays and performing nutrient mechanismof-action and efficacy studies. Transcriptomics, proteomics and metabolomics data can be directly utilized to investigate the often subtle dietary effects and to disentangle combined multicompound, multi-target effects. Tools for a thorough investigation of the molecular mechanisms of nutrients and their constituents help to examine their influence on onset, frequency, development and severity of nutrition-related diseases.



Characterizing Gene-Nutrient Interactions .

Phylosopher NutriLead provides modules for characterizing the molecular mechanism-of-action of bioactive nutrient constituents. They systematically investigate the effect of compounds on metabolism, signaling and regulatory pathways to reconstruct the multifaceted picture of the effect of food on the molecular level. The analysis of experimental mRNA, protein and metabolite expression data in the context of high quality biological information provided by Phylosopher NutriLead's database assists in a better understanding of disease-induced metabolic changes.

Assessing Compound Efficacy and Safety 斗

Identifying the optimal intake of bioactive food components is critical for balancing the maximum benefit with minimal risk. Phylosopher NutriLead provides algorithms for parallel safety-efficacy studies of food constituents. Specialized modules evaluate compounds by identifying dietary signatures indicative for beneficial effects and for a possible toxicity potential. Compounds are ranked according to their underlying efficacy mechanisms, while taking into account potential negative side effects. Phylosopher NutriLead's modules are particularly helpful for evaluating libraries of natural products and complex food mixtures.

Identifying and Validating Biomarkers

Robust biomarkers that can reflect subtle changes in homeostasis are urgently needed for assessing the individual risk and tailoring an optimal personalized diet. Phylosopher NutriLead comes with an extensive library of potential biomarkers and specialized statistical tools to detect markers that go beyond the classical "singlegene" (-protein, -metabolite) approach. Additionally, the system comes with tools that pinpoint novel biomarkers by linking single nucleotide polymorphisms (SNPs) to changed transcript, protein and metabolite levels, as well as affected metabolic, signaling and regulatory pathways.

Towards Individualized Dietary Interventions

The possibility to rapidly identify genotype differences for the first time ever helps to systematically correlate polymorphisms with positive or adverse health effects. Phylosopher NutriLead permits an evaluation of persons' predisposition to diseases based on their genetic make up. This in turn can help in tailoring a personalized diet which avoids the consumption of risk associated nutrients and increases the intake of beneficial dietary components. Comprehensive polymorphism maps, tightly linked with phenotypes, nutrition-induced whole-genome mRNA, protein and metabolite profiles represent the coordinate system for tools that bridge from disease diagnosis and predisposition to a persons response to nutrition, thereby helping to pave the way for a personalized approach to nutrition.









For further information about Phylosopher NutriLead and other focused Phylosopher editions, please visit our website at www.genedata.com or contact us at phylosopher@genedata.com © 2004 Genedata. All rights reserved. Genedata Phylosopher® is a registered trademark of Genedata.