

NeoSemantic software environment

NeoSemantic™

overview

Neosemantic-Bio concept encapsulates a new computational cognitive model that is being developed for solving complex problems in bioinformatics. This cognitive model is dynamically elaborated based on observing biologists solving problems in their current environments.

The cognitive approach enables problem-solving within the postgenomic domain, characterized by the following attributes:

1. Mining and fusing massive heterogeneous data;
2. Growing and changing of information quantity on a monthly basis;
3. Challenging and changing of the knowledge base as biologists learn more on a very short schedule.

Neosemantic Framework

The Framework was established to implement the cognitive technologies for mining the postgenomic data. The framework adopted the efforts of bioinformatic freelancers, contributing their modules with the adjustable software development environment. The links between algorithmic modules involve both implicit and explicit knowledge, where knowledge is information the researchers find and new associations the scientists create while solving a problem.

Neosemantic Framework goes beyond the world of traditional Laboratory Information Management Suites by consolidating essentially different (orthogonal) research options into one cognitive architecture across the global enterprise:

Enterprise-wide knowledge management, identifying and tracking any piece of research activity, including the work with scientific papers, accessing the databases of biomolecules, chemicals and drugs, running the bioinformatic resources;

Intuitive knowledge processing virtually from any Internet access device to couple the ongoing research vector with the experimental information drifting from the 3rd party instruments and systems;

Collaborate interactively with researchers by sharing information, resources and experiences to organize your strategy of scientific development.

The Neosemantic Framework helps laboratories and research institutions to increase the efficiency of coordinated activities and to involve several groups of different expertise. The Framework automatically generates the statistical and probabilistic models fostering the hypothesis-driven research. The cross-scale knowledge representation is embedded into the Framework to integrate the distributed sources of biological data.

Key advantages

Technology Highlights

- Web Usage Mining (WUM) is utilized to create the knowledge domain of the research group
- Knowledge domain ascribes the semantic relationships between entities by elucidating the implicit WUM patterns
- Accelerating the data processing using GPU

Managing Research and Development on a Single Platform

- Simplify knowledge sharing with consolidated data and information
- Increase user acceptance with an intuitive user interface that is common across wide range of applications
- Access all the functionality through the Web browser, with no plug-ins or downloads

Built-in BiblioBase Content Management System

- Uploading and Web-publishing of knowledge domain through the easy-to-use content management system
- Calculation of the associations between informational entities according to the user-defined knowledge models
- Semantic search to capture the relation of the user's query with the knowledgebase

BiblioEngine™ solution

Neosemantic-Bio provides the pertinent laboratory information management features, which can be easily extended combining different software modules. The Neosemantic Framework follows the open-source strategy, creating a junction between user-developed software and the semantic core of the framework. The flexible configuration is allowing the same solution to be tailored to the unique requirements of each laboratory as well as across organization.

The BiblioEngine (side) comprises the core of knowledge management system embracing the wide range of applications in genomics, transcriptomics, proteomics etc. delivered with a flagship product, Neosemantic Framework.

The Neosemantic Framework involves the software development kit, the BiblioEngine and BiblioBase Content Management System, Name Entity Recognition Modules. These components are used to assemble the Semantic Enterprise Platform, capable to integrate the 3rd party instruments and applications.

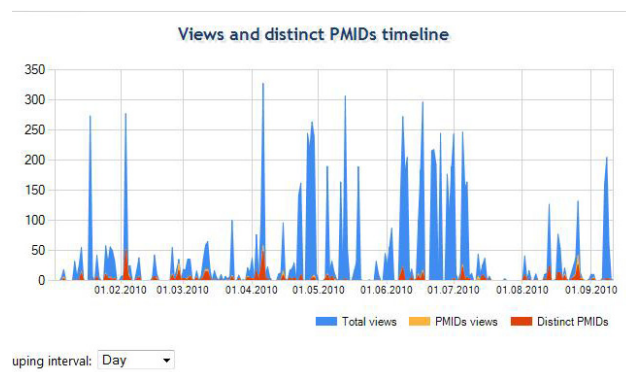
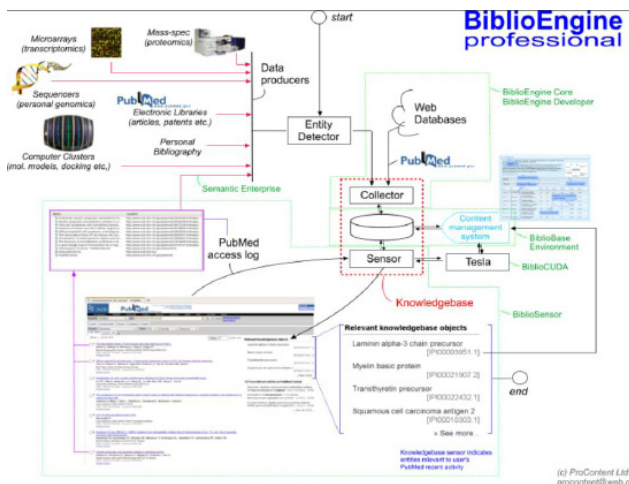
gaining the information on the Bio-Internet surfing habits of employees. This information is processed on a regular basis to report the following:

- overall and daily activity;
- general research trends for the time frame, visualized as gene-centric and MeSH-centric semantic networks;
- cross-period comparison of research trends
- more frequently accessed resources and papers
- implicit, statistically reliable novel research trends
- matching the research interests between laboratories and groups

Semantic Enterprise offers a perfect way to provide clients and putative collaborators with the informative and useful Web-site search tool for clients and putative collaborators. Using the SE Search feature the user's query is matched to the statistical data on the major research trends, that resemble the personal activity of the team.

Semantic Enterprise Platform

Semantic Enterprise (SE) was developed as an integrated solution using the Neosemantic software environment to create the in-house centralized knowledge warehouse. The SE assignee obtains the middle-ware for



uping interval: Day

Modules

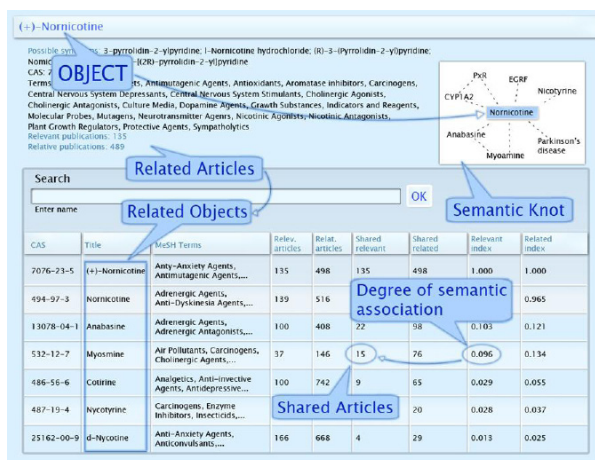
Neosemantic Modules

The Neosemantic Framework meets the challenges unique to up-to-date laboratories and offers specific IT and end-user driven modules to address these different needs. The table below shows the key features of most frequently used modules.

Module	BiblioBase	Content Management System	BiblioEngine
Description	Utilizing the information, which originates from the data-intensive strategies in genome, transcriptome and proteome research	Graphical representation of the BiblioBase content in a form of the network, connecting genes, proteins, chemicals, keywords etc.	Automating the assembly of BiblioBase within a user-defined knowledge domain.
Module	Name Entity Recognition	BiblioSensor	Software Development Kit
Features	Accurately tracking the data formats, linking other Framework modules to the global repositories (UniProt, GenBank etc.)	Toolbar for the Web-browser for collecting the personal information about Bio-Internet surfing.	The programming library and API to embed the user-developed modules to the Neosemantic platform

Web Usage Mining with BiblioSensor

The WUM technology is utilized for several purposes: (1) to accumulate the user-biased view on the relationships between knowledgebase informational entities, (2) to extract the summary of the knowledgebase content, which is most closely related to the individual research preferences, (3) to offer the latest information and bioinformatic services, which appear on Bio-Internet, and (4) to preserve the history of Bio-Internet surfing for presenting a user's activity in statistical relationship to what others do, and what he/she has previously done.



Integration of Instruments & Applications

The Neosemantic technology naturally integrates essentially different laboratory systems and pipelines, including full-genome sequencing and genotyping, shotgun proteomics, genome-scale transcriptomics. Besides, a traditional molecular biology research implemented with cell cultures, in vitro and in vivo models, etc., can significantly contribute to the understanding of large-scale results being intrinsically interlinked within the unified knowledge sharing framework.

Articles, relevant to (+) Nicotinic and Cotinine

Jump to relative articles list (65).

PMID	Article	Author
10027825	(S)-(-)-Cotinine, the major brain metabolite of nicotine, stimulates nicotinic receptors to evoke [3H]dopamine release from rat striatal slices in a calcium-dependent manner.	Dwojski LP et al., 1999
19004590	Determination of nicotine, cotinine, and related alkaloids in human urine and saliva by automated in-tube solid-phase micro-extraction coupled with liquid chromatography-mass spectrometry.	Ikemura S et al., 2001
14757175	Nicotine-related alkaloids and metabolites as inhibitors of human cyclooxygenase P-450 2A6.	Daston TT et al., 2004
19004590	Determination of nicotine, cotinine, and related alkaloids in human urine and saliva by automated in-tube solid-phase micro-extraction coupled with liquid chromatography-mass spectrometry.	Kazuo H et al., 2009
19123193	Enantioseparation of nicotine alkaloids in cigarettes by CE using sulfated beta-CD as a chiral selector and a capillary coated with amino groups.	Kudama S et al., 2009
19366487	The addition of five minor tobacco alkaloids increases nicotine-induced hyperactivity, sensitization and intravenous self-administration in rats.	Clemens KJ et al., 2009
18686186	Nicotine metabolism in pregnant and nonpregnant rabbits.	Turka P et al., 2006
1845770	Meclofenolol nicotine and metabolites by liquid chromatography-tandem mass spectrometry: differentiation of passive and nonexposed and correlation with neonatal outcome measures.	Gray TR et al., 2008
19013262	Smoking and Parkinson's disease: does nicotine affect alpha-synuclein fibrillation?	Hong DP et al., 2009

Services overview

Servicing the solution, not the software

Neosemantic-Bio team combines global research and technical resources to analyze each customer's specific requirements and to implement the Neosemantic Framework solution best tailored to their specifications. The servicing strategy goes beyond software delivery to facilitate deployment and knowledge transfer solutions within your organization.

Subscription

The BiblioBase products can be subscribed on the annual basics. Subscriptions ensures the access to the pre-compiled deliverables of data-intensive research strategies, such as:

- high-throughput experiments in personal genomics, haplotype mapping, transcriptomics, proteomics and other «-omics»;
- establishing coherence between genetic polymorphisms and diseases, individual susceptibility to pharmaceuticals, mechanisms of side effects;
- quest for potential drug targets and for widening the indications of already approved drugs.

SaaS

The BiblioEngine is offered as a service on our Neosemantic GRID. Compiling and publishing the knowledgebase of your excellence in expertise goes in the background mode, with no programming and no manual consumptions. The resulting product can be used internally, as well as licensed to the commercial distribution through the Neosemantic Framework.Summary

Remote installation

The Neosemantic Framework can be installed remotely via Internet. The configuration of the system according to the customer's specific requirements is performed as a remote service. In addition any module can be bound/deactivated in the remote mode. Remote installation services enhance performance, reliability and scalability of the solutions.

Customer support

- Comprehensive support program offered includes:
- our 24/7 Customer Support website
- Skype support during regular business hours
- Emergency response time within 1 working hour
- Software installation support

Training

We offer the Webinar Training Program to teach how to manage Neosemantic Framework and to develop new applications. Customers are able to ask questions in real time mode. Attendees may also ask follow-up questions at the end of the event and receive the answers via email or through the posted webinar notes.

Collaboration

Neosemantic community is open for collaboration with research institutions and companies. The ultimate goal of collaboration is widening the applications of the knowledge-based cognitive approaches in life science. The collaborator enters the coalition to share the proprietary knowledge and obtain necessary tools to implement such sharing.

Knowledgebase
Knowledge discovery
Data mining
Text mining
Semantic analysis

Semantic resonance
Postgenomic repository
Proteomic technology

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