

Knowledge Management in Neuroscience

using

Informatics

METHODS IN MOLECULAR BIOLOGY™ 401

Neuroinformatics

Edited by

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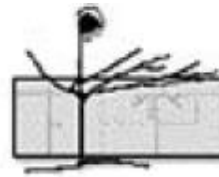
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Information-extraction from Neuroscience-specific Databases



NeuronDB

[Back](#)

Thalamic reticular neuron

Mode: [Overview](#) [Data/Search](#) [plus Connectivity](#) [Models](#)

Region: [Ded](#) [Dem](#) [Dep](#) [Soma](#) [AH](#) [A](#) [T](#)

Properties: [Receptors](#) [Channels](#) [Transmitters](#)

Interoperation: [Gene and Chromosome](#) [Experimental Data \(neurodatabase.org\)](#) [Microscopy Data \(CCDB\)](#)

Are: [Present](#) [Absent](#)

Neuron type: interneuron

Organism: Vertebrates

Input Receptors

Intrinsic Currents

Output Transmitters

Ded

Axon collateral terminals of thalamocortical relay neurons	Glutamate
	AMPA
Combining preembedding and postembedding immunostaining at the EM level, GluR2/3 and NMDAR1 immunoreactivity was located in somata and in proximal and distal dendrites (Liu XB, 1997 [rat cat] ²⁵¹).	
	NMDA
Combining preembedding and postembedding immunostaining at the EM level, GluR2/3 and NMDAR1 immunoreactivity was located in somata and in proximal and distal dendrites (Liu XB, 1997 [rat cat] ²⁵¹).	

Gaba	Dem and Dep of other TRN neurons
----------------------	----------------------------------

NeuroText

(<http://senselab.med.yale.edu/textmine/neurotext.pl>), designed specifically to extract information relevant to neuroscience-specific databases, [NeuronDB](#) and [CellPropDB](#) (<http://senselab.med.yale.edu/senselab/>), housed at the Yale University School of Medicine.

NeuroText and Information Extraction

“NLP (Natural Language Processing) Tools”

N_{eu}roT_{ext}

has been developed to identify articles as relevant citations in the SenseLab databases CellPropDB and NeuronDB by scanning the Natural Language text of neuroscience articles. The program uses a knowledgebase consistent with the SenseLab architecture, contextual and lexical scanners, and two independent evolution methods to score articles based on relevance of deposition. NeuroText uses a two step approach. The first step is aimed at specificity; the second at sensitivity. The Journal of Neuroscience was used in this pilot study. Users can choose demonstration files of NeuroText results for any issues analyzed.

Choose the volume and issue number

Volume Number	Issue
14 ^	1 ^
17	2
20 v	3
	4
	5 v

Reset

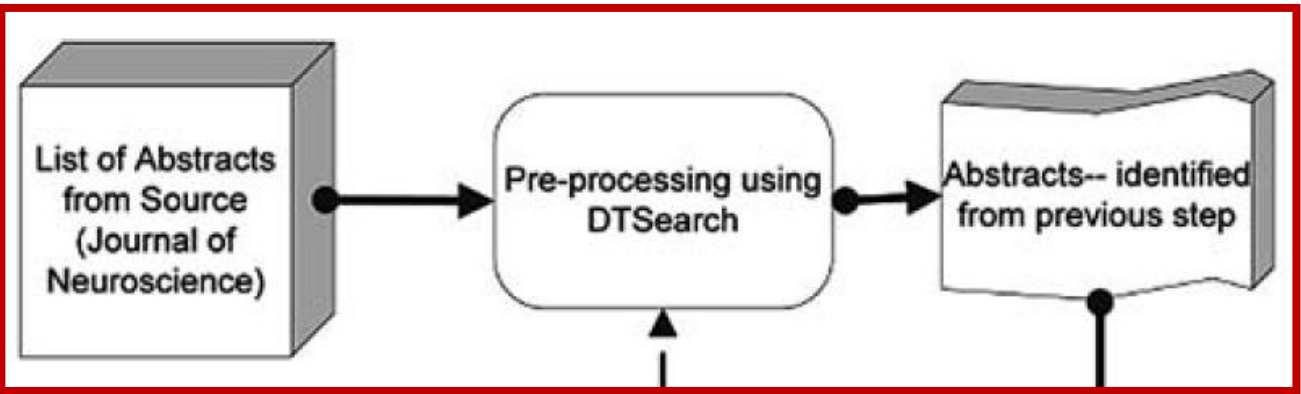
SUBMIT

<http://senselab.med.yale.edu/senselab>

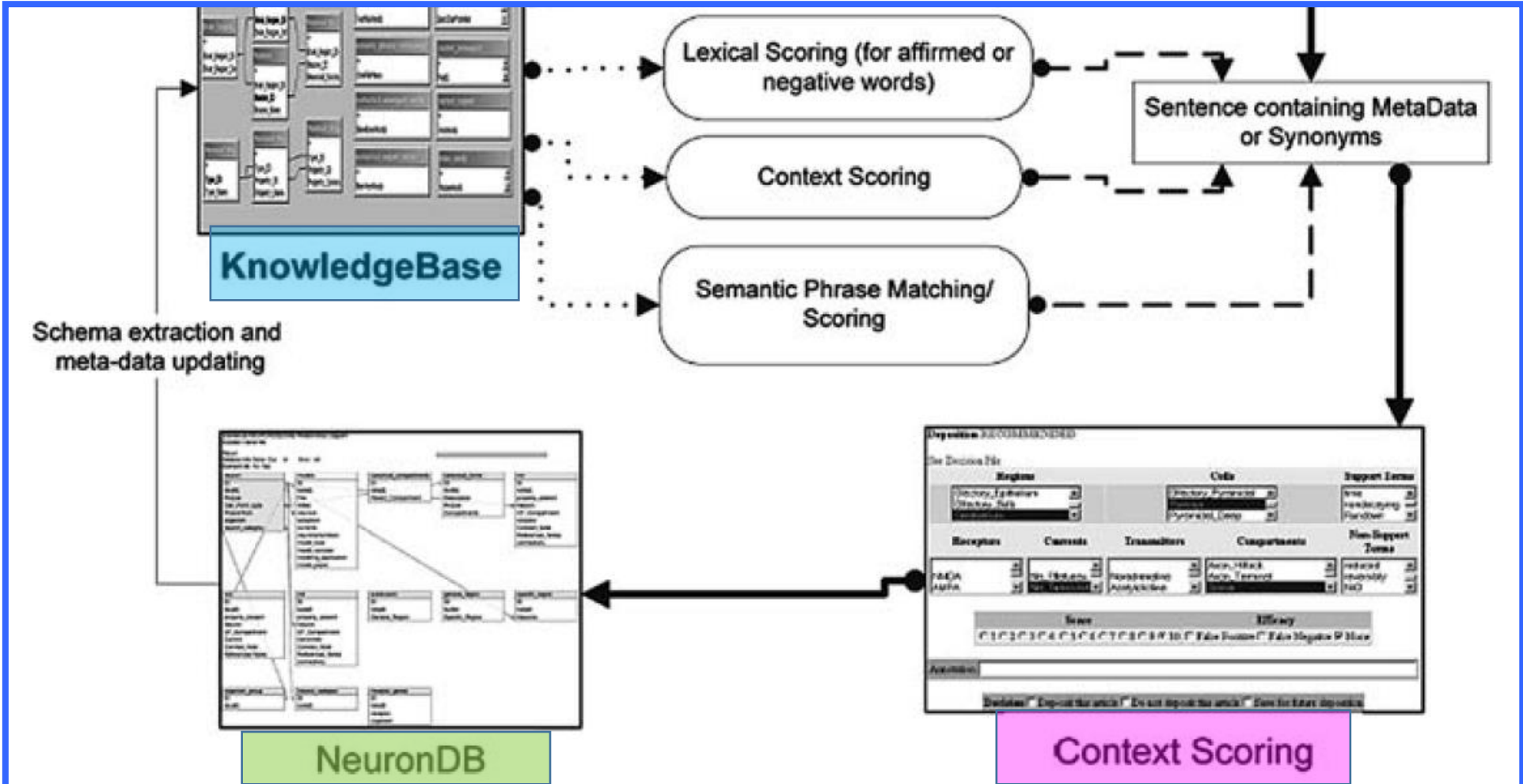
NeuroText's approach

NeuroText's approach included the following:

- Keyword counting for potential relevance.
- Using contextual constraints to refine potential relevance.
- Recognizing relevance of keywords to primary subject in the publication.
- Identifying important relationships between keywords.
- Easy automated updating of the knowledgebase.
- The domain expert needs to make the final decision.
- Presenting the results of NeuroText's analysis to the expert for validation and automatic deposition.




NeuroText Operation



NeuroText Result: Deposition Recommended

A result of “**Deposition Recommended**” for a sample abstract. NeuroText found occurrences of keyword “**medium spiny neuron**” in the neostriatum, which expressed **alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA)** and glutamate receptors.



819.pdf-Link to Full-Text of Article 819.xml XML-Link

Volume 17, Number 2, Issue of January 15, 1997 pp. 819-833

Cellular, Subcellular, and Subsynaptic Distribution of **AMPA-Type Glutamate** Receptor Subunits in the **Neostriatum** of the Rat

Received Sept. 4, 1996; revised Oct. 29, 1996; accepted Nov. 4, 1996.

Véronique Bernard, Peter Somogyi, and J. Paul Bolam

Medical Research Council, Anatomical Neuropharmacology Unit, University Department of Pharmacology, Oxford University, Oxford OX1 3TH, United Kingdom

Glutamate released in the basal ganglia is involved in the expression of clinical symptoms of neurodegenerative diseases like Parkinson's or Huntington's. **Neostriatal** neurons are the targets of glutamatergic inputs derived from the cortex

the **thalamus** acting via **AMPA-type** as well as other **glutamate** receptors. To **determine** the location of subunits of the **AMPA** subclass of **glutamate** receptors (GluR) in the rat **neostriatum**, we applied multiple immunocytochemical techniques

NeuroText Result: Deposition Not Recommended



A result of “**Deposition Not Recommended**” for a sample abstract. NeuroText found several instances of “**brain region**” keywords but did not find any discernible relationships with neurons. The “Ca²⁺ ion channel” was not associated with a specific neuron. The metadata elements from the databases are in boldface and large.

1226.pdf-Link to Full-Text of Article 1226.xml XML-Link

Volume 17, Number 4, Issue of February 15, 1997 pp. 1226-1242

N -arachidonoyl PE in adult brain tissue and the enzyme pathways that underlie its biosynthesis are, however, still undetermined. We report here that rat brain tissue contains both anandamide (11 ± 7 pmol/gm wet tissue) and N -arachidonoyl

PE (22 ± 16 pmol/gm), as assessed by gas chromatography/mass spectrometry. We describe a N -acyltransferase activity in brain that **catalyzes** the biosynthesis of N -arachidonoyl PE by transferring an arachidonate group from the sn -1

of phospholipids to the ~~amino~~-group of PE. We also show that sn -1 arachidonoyl phospholipids are present in brain, where they constitute ~0.5% of total phospholipids. N -acyltransferase activity is **Ca²⁺ dependent** and is enriched in brain

and testis. Within the brain, N -acyltransferase activity is highest in brainstem; intermediate in cortex, **striatum, hippocampus, medulla, and cerebellum;** and lowest in **thalamus,** hypothalamus, and **olfactory** bulb. Pharmacological inhibition

of N -acyltransferase activity in primary cultures of **cortical** neurons prevents **Ca²⁺** -stimulated N -arachidonoyl PE biosynthesis. Our results demonstrate, therefore, that rat brain tissue contains the complement of enzymatic activity and

Domain-Expert Validation and Depositing NeuroText Results

The form shows that [NeuroText](#) has identified a sodium transient current in the Purkinje cell of the cerebellum. The form is provided so that the domain expert can override any erroneous findings during validation.



See Decision File

Regions		Cells		Support Terms	
Olfactory_Bulb		Olfactory_Pyramidal		Volume	
Cerebellum		Purkinje		Number	
Neocortex		Pyramidal_Deep		Issue	

Receptors	Currents	Transmitters	Compartments	Non-Support Terms
NMDA	Na_Plateau	Noradrenaline	Soma	Volume
AMPA	Na_Transient	Acetylcholine	Dendrite	Number
			Apical_Dendrite	Issue

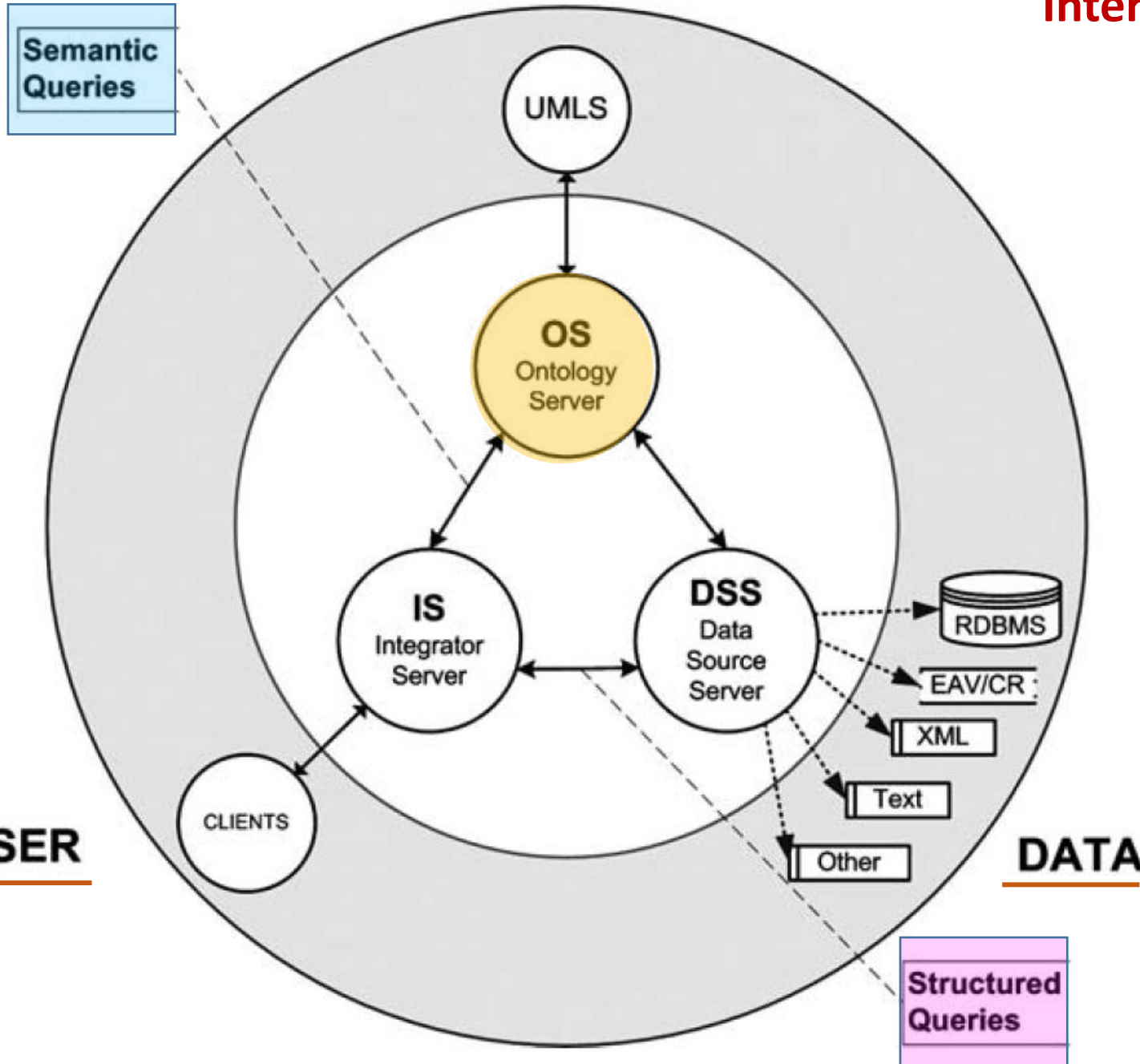
Score	Efficacy
<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6 <input type="radio"/> 7 <input type="radio"/> 8 <input type="radio"/> 9 <input checked="" type="radio"/> 10	<input type="checkbox"/> False Positive <input type="checkbox"/> False Negative <input checked="" type="checkbox"/> None

Annotation

Decision ☐ Deposit this article ☐ Do not deposit this article ☐ Save for future deposition

Interoperability Across NeuroSc. Databases

Query Integration System—architectural overview



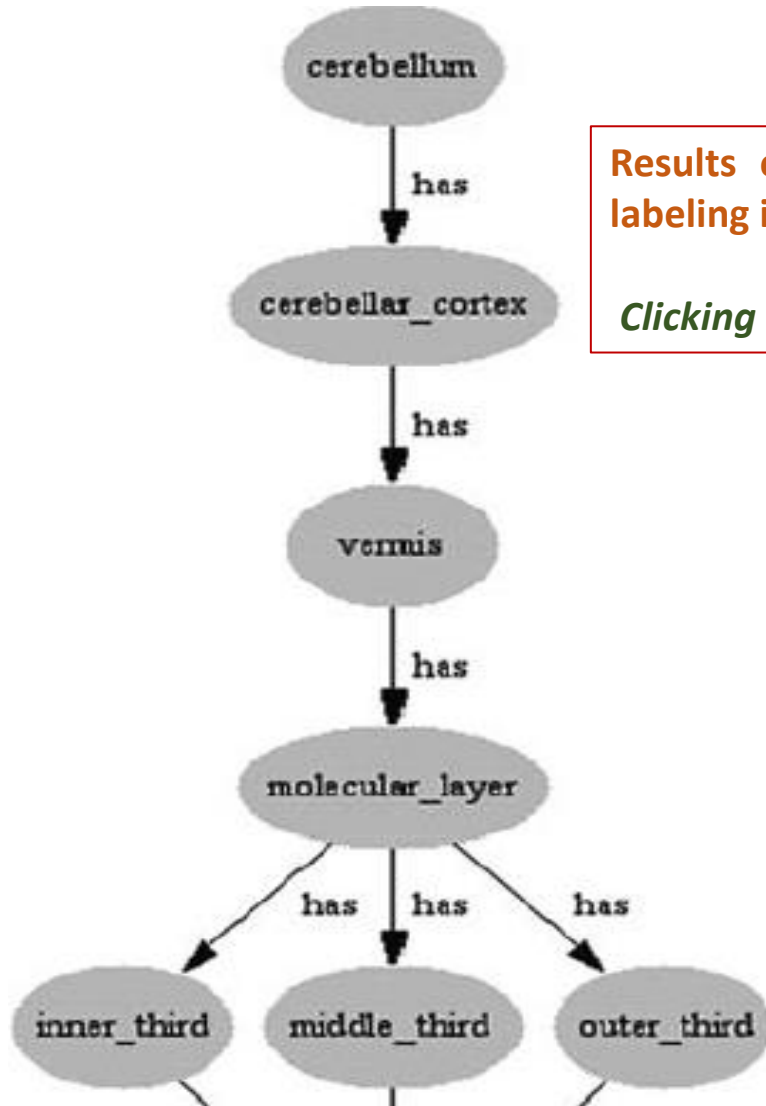
Based on three middle-tier servers:

1. Data Source Server (DSS): Connects to disparate supported data sources.
2. Integrator Server (IS): Stores, coordinates query execution, and returns query results to Web applications.
3. Ontology Server (OS): Maps data sources' metadata and data elements to concepts in standard vocabularies.

➤ UMLS: Unified Medical Language System

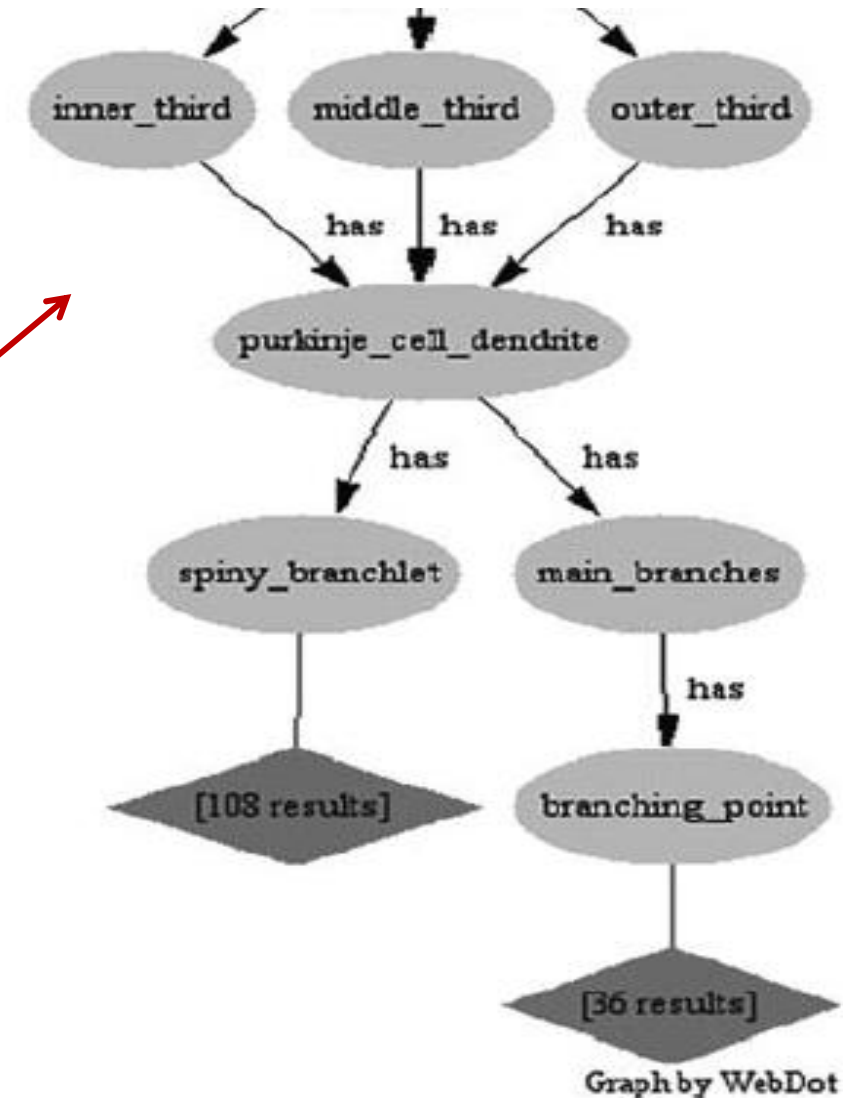
Bioinformatics Research Network (BIRN): *Mediator and Tools*

- BIRN-CC's data integration system, referred to as the “Mediator”,
- enable researchers to perform unified conceptual queries.



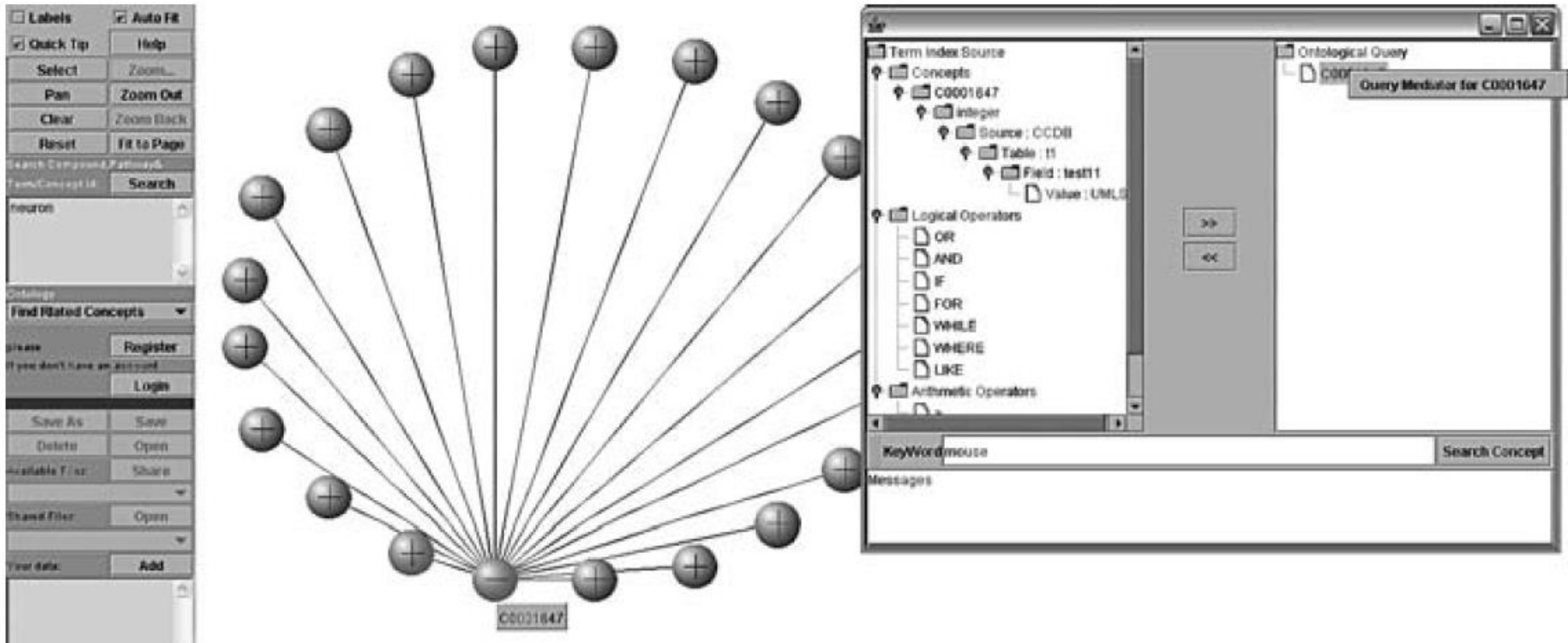
Results of a query asking for images of protein labeling in cerebellar cortex.

Clicking on the diamonds returns the raw data.



Query results for the Mediator

- Results are in context of the UMLS.
- Nodes that are referenced directly to data contained in one of the BIRN databases are highlighted.



A graphical environment allowing users to query, browse, and edit ontologies.

