

Calcolo Distribuito e Coordinazione

Università di Camerino

Corso di Laurea Specialistica in Informatica

12 CFU

I periodo didattico

Emanuela Merelli

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Struttura del Corso

Il corso consiste in

48 ore di lezioni e seminari

24 di laboratorio

2 ore settimanali di ricevimento studenti

Collaboratori didattici

Francesca Piersigilli

Ezio Bartocci

Il corso viene valutato in

12 CFU (Crediti Formativi Universitari)

Sono previsti seminari su
argomenti specifici

Orario Lezioni

dal 10 ottobre al 9 dicembre 2005

Lunedì dalle 17:00 alle 19:00

Martedì dalle 15:00 alle 18:00*

Mercoledì e Giovedì dalle 15:00 alle 17:00**

*** Progettazione**

**** In caso di impegni istituzionali, la lezione subirà un
cambiamento di orario**

Orario Ricevimento

Martedì
dalle 17:00 alle 19:00

2° Piano stanza no.9
Polo d'Informatica

Materiale del corso

Pagina Web

<http://dmi.unicam.it/merelli/calcolo05>

Obiettivi Formativi

- Analizzare le principali caratteristiche dei sistemi distribuiti
- Progettare applicazioni software complesse in moderni ambienti distribuiti
- Utilizzare i concetti fondamentali che caratterizzano i vari modelli di calcolo distribuito e di coordinazione
- Classificare, valutare e applicare alcuni linguaggi per la coordinazione
- Affrontare in modo autonomo la progettazione di applicazioni distribuiti

Testi di Riferimento

1: Andrew Tanenbaum, *Distributed Systems*, Prentice Hall, 2002

2: Andrea Omicini, F. Zambonelli, M. Klisch, R. Tolksdorf, *Coordination of Internet Agents* Springer, 2001

Note: *Articoli e appunti distribuiti durante le lezioni –
E' disponibile una bibliografia annotata*

Programma del Corso - Teoria

Introduzione ai sistemi distribuiti

Modello client-server

Paradigmi di comunicazione

Tipi di processi

Sistemi distribuiti basati sulla coordinazione

Calcolo distribuito e modelli formali

Algebre di processo e process behaviours

Cenni CCS, CSP, Petri Nets

UML Activity diagrams

Modelli di coordinazione

Linda e derivati

Linguaggi di coordinazione

Linda e derivati

Middleware per la coordinazione

Object-based

Agent-based

Agenti software e coordinazione

KLAIM, Lime, TUCSON

Modalità d'esame

L'esame consiste nello sviluppo di un progetto e in un seminario per la presentazione dei risultati ottenuti

Per sostenere l'esame è necessario iscriversi all'esame tramite pagina web:
web.unicam.it/matinf

Appelli d'esame

I periodo

lunedì 12 dicembre 2005
lunedì 19 dicembre 2005
lunedì 9 gennaio 2006

II Periodo

lunedì 27 marzo 2006

III Periodo

lunedì 19 giugno 2006

Sessione Recupero

Concordata con gli studenti

Coordination

Coordination is a key concept for studying the **activities** of complex **dynamic systems**

Coordination is managing **dependencies** between **activities**

Such a definition implies that all instances of coordination include **agents** performing **activities** that are **interdependent** [Malone and Crowston 94]

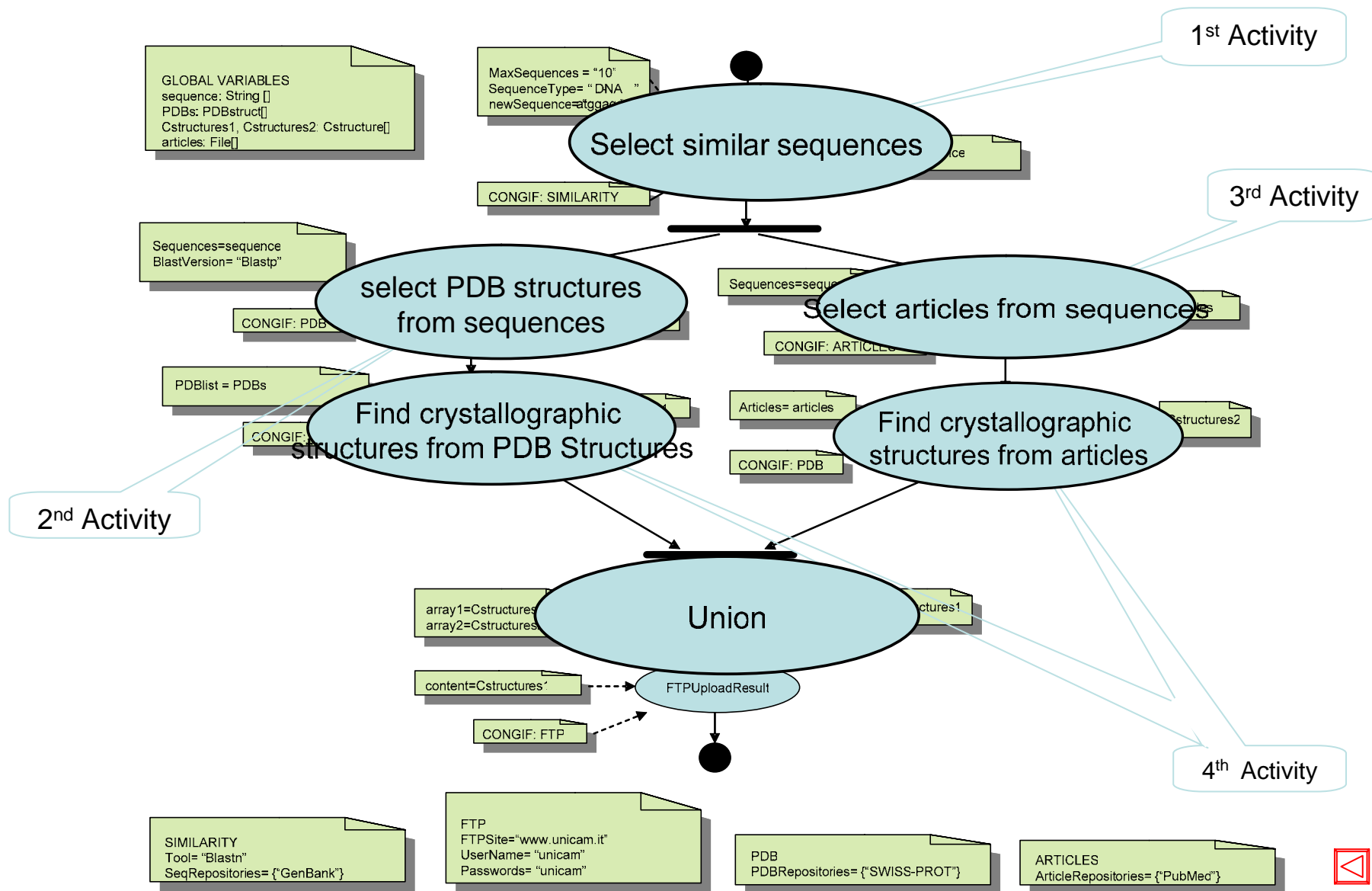
Due to its fundamentality, this notion covers a lot of facets, for instance in distributed artificial intelligence, robotics, **biology**, and organisational sciences

Coordination is the process of building programs by gluing together active pieces [Carriero and Gelernter 92]

Active pieces here can mean processes, objects with threads, agents, or whole applications

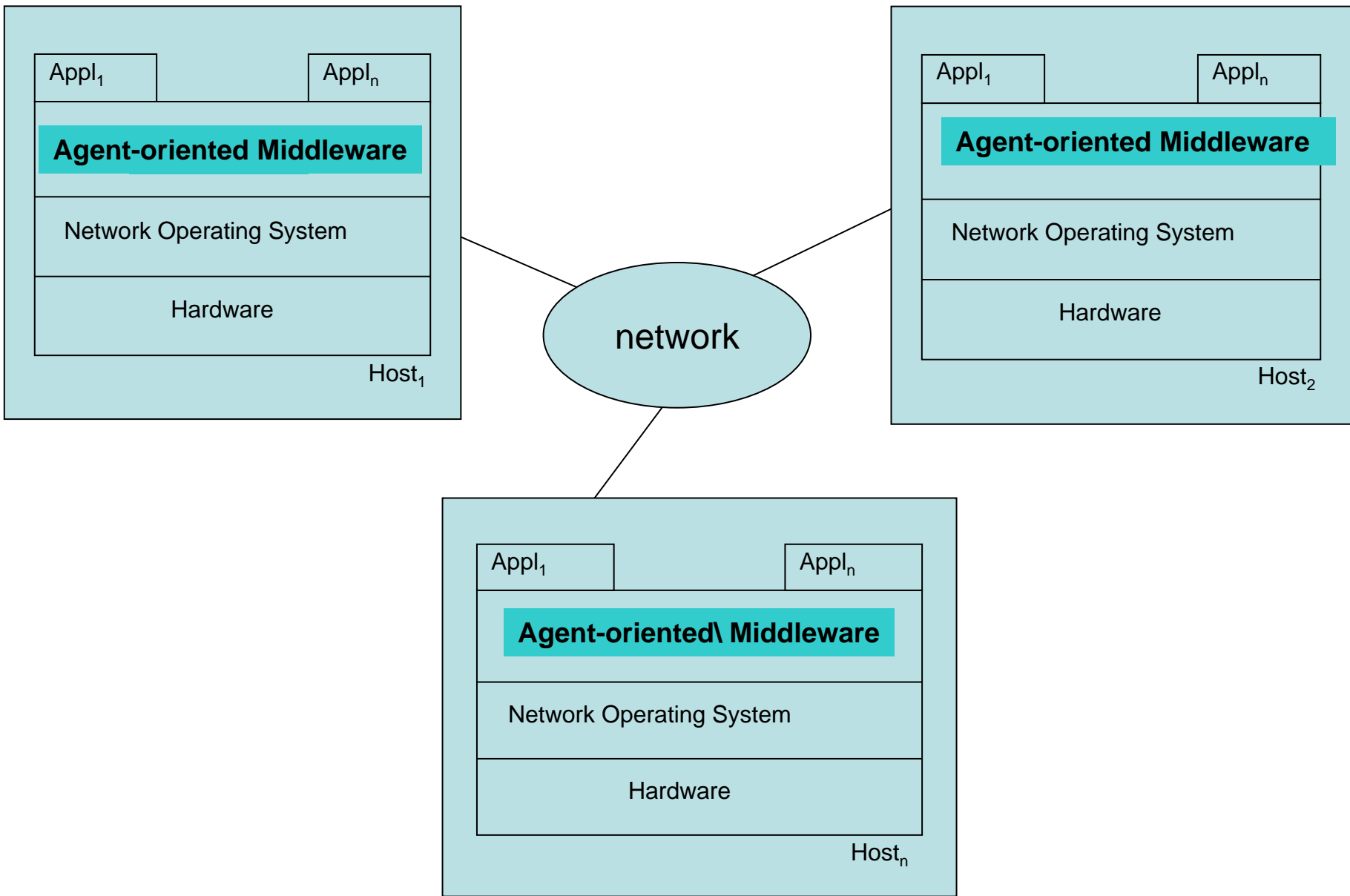
programming = coordination + computation

Workflow-based Activity Coordination



Internet and Coordination

The Internet can be enhanced by **coordination middleware** to a programmable platform offering support for large-scale groupware, agent-based applications, and high-performance computational services (eg. the GRID)



a)

Web applications

Middleware

Network operating
System

Distributed System Architecture

Application Layer

Presentation Layer

Session Layer

Transport Layer

Network Layer

Datalink Layer

Physical Layer

OSI/RM

b)

What is a Coordination Model?

A coordination model is the formal basis (semantics) for a coordination language;

It proved that it is possible to “**think in a coordinated way**” abstracting from low level mechanisms for concurrent, parallel, or distributed programming

A *coordination model* is an **abstract** (semantic) **framework** useful to study and understand problems in designing concurrent and distributed programs

“A coordination model is the **glue** that binds separate activities into an ensemble” [CarGel92]

Historically, Linda was introduced as a new model for parallel programming, more flexible and high level wrt its competitors (“Linda Is Not aDA”)

What is a Coordination Model? Cont.

In other words, a coordination model provides a minimum **framework** in which the interaction of individual agents can be expressed

Coordination framework covers the issues of **dynamic agent creation** and **destruction**, **control** of communication **flows** among agents, control of spatial distribution and **mobility of agents**, as well as **synchronization** and **distribution** of actions over time

What is coordination language?

A **Coordination language** is the linguistic embodiment of a coordination model, and consists of some coordination mechanisms that are added to an *host* (sequential) language

In practice, a coordination language includes clearly defined mechanisms for **communication**, **synchronization**, **distribution**, and **concurrency control**.

References

[Malone and Crowston '94]

T. Malone and K. Crowstone, *The interdisciplinary study of coordination*, ACM Computing Survey, vol.26, no.1, pp.87-119, 1994

[Gelernter and Carriero '92]

N. Carriero and D. Gelernter, *Coordination languages and their significance*, Communication of ACM, vol.35, no.2, 1992

Digital Library

- ACM

- www.acm.org

- User-id: emerelli
 - Pwd: costanza

- IEEE

- www.computer.org

- User-id: miaweb
 - Pwd: memacu02

A case study

- Distributed Applications in Bioinformatics Domain
- Activity-based applications
- Tool integration distributed middleware
- Agent-based coordination model

The Tool Integration Problem in Activity-Based Applications

Problem: To *integrate and coordinate multiple software tools* for retrieving and integrating heterogeneous, distributed and frequently redundant data

Objective: To *integrate and coordinate several software tools* in order to provide a uniform way and an high level of abstraction for users

Aim: To define an *integrated environment* freeing the user from the need to know details on data repository and to coordinate the intermediate steps of an experiment (tasks)

Proposed Approach: To define an application as a workflow of tasks; to coordinate the execution of cooperative tasks by using software agent tools

Activity-Based Application in Bioinformatics Domain

Problem: To find the crystallographic structure of the 10 proteins more similar to that of a given genetic sequence, e.g., *atggag ... tga*,

Objective: To use several Bioinformatics Software Tools available on Internet in order to find the wanted result

1. Select the **10 proteins more similar to the given sequence *atggag ... tga***

- by using **BLASTn** in **GenBank** at [NCBI](#)

1st Activity

2. Search for the **PDB ID (crystallographic structure identifier)** of each selected proteins,

- by using **BLASTp** in **SWISS-PROT** at **EMBL-EBI**
- by retrieving from **PubMed** via [Entrez Retrieval System](#) at **NCBI**, abstracts containing PDB-ID information

2nd Activity

3. Search for the **Crystallographic Structure of any selected PDB ID**

- find 3-D biological macromolecular structure in [Protein DataBank](#) repository

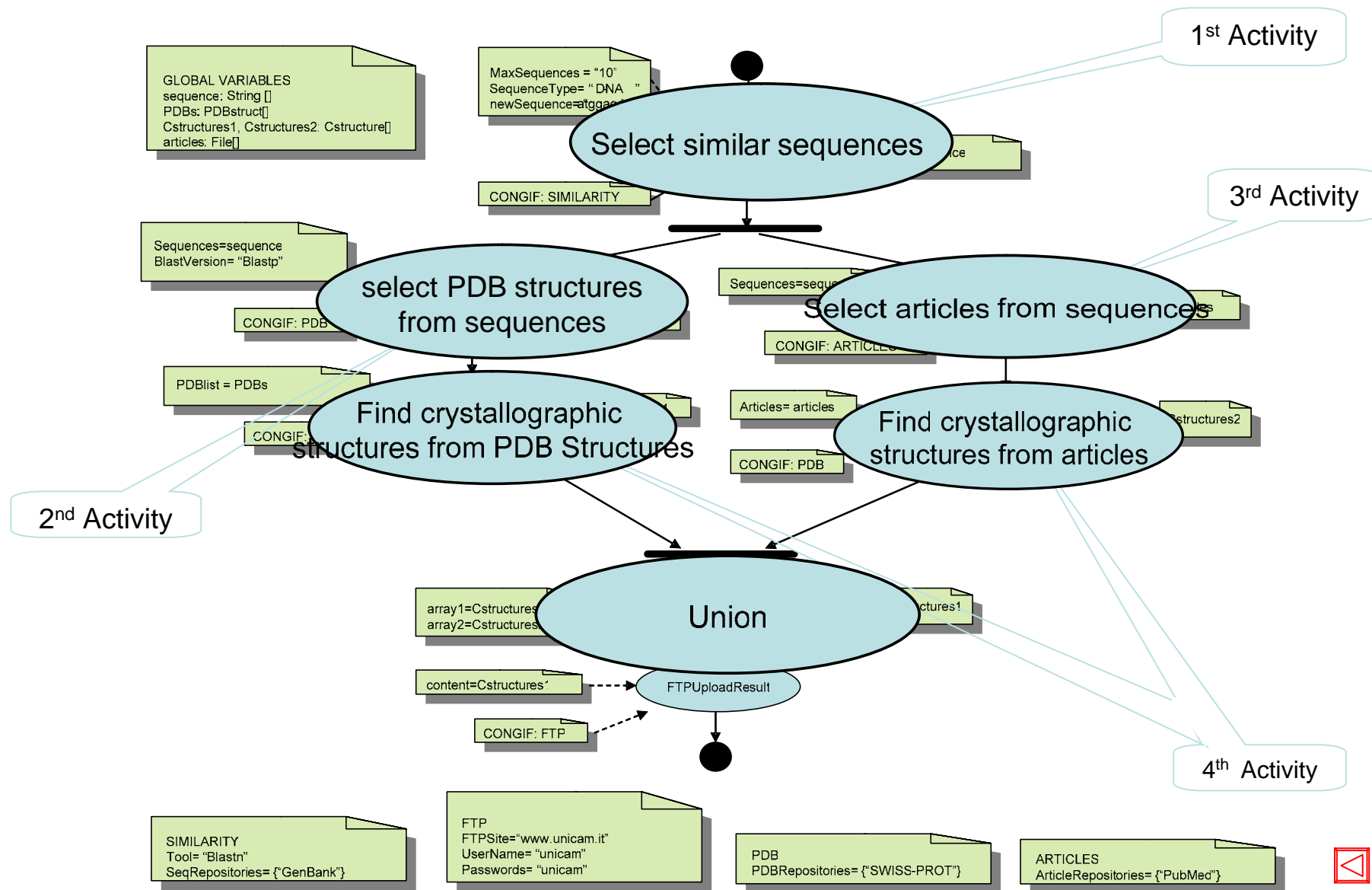
3rd Activity

4th Activity

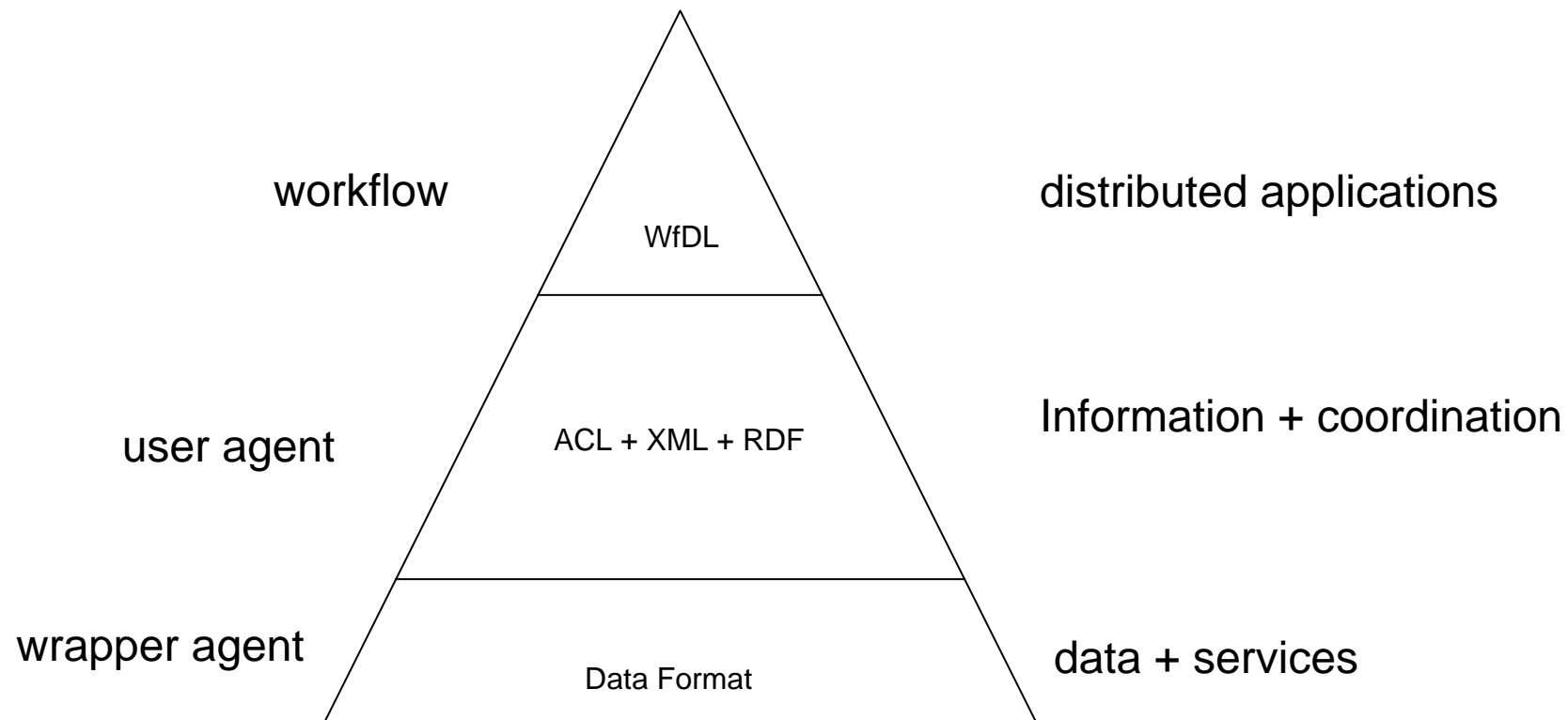
Aim: the automatic execution of the activities by **coordinating several Bioinformatics tools**, freeing the Bioscientist from the need to know details on data and to continuous interact with remote sites.

By defining an **integrated environment** supporting activity coordination data and services integration large scale distributed management system in order to automatically execute an experiment

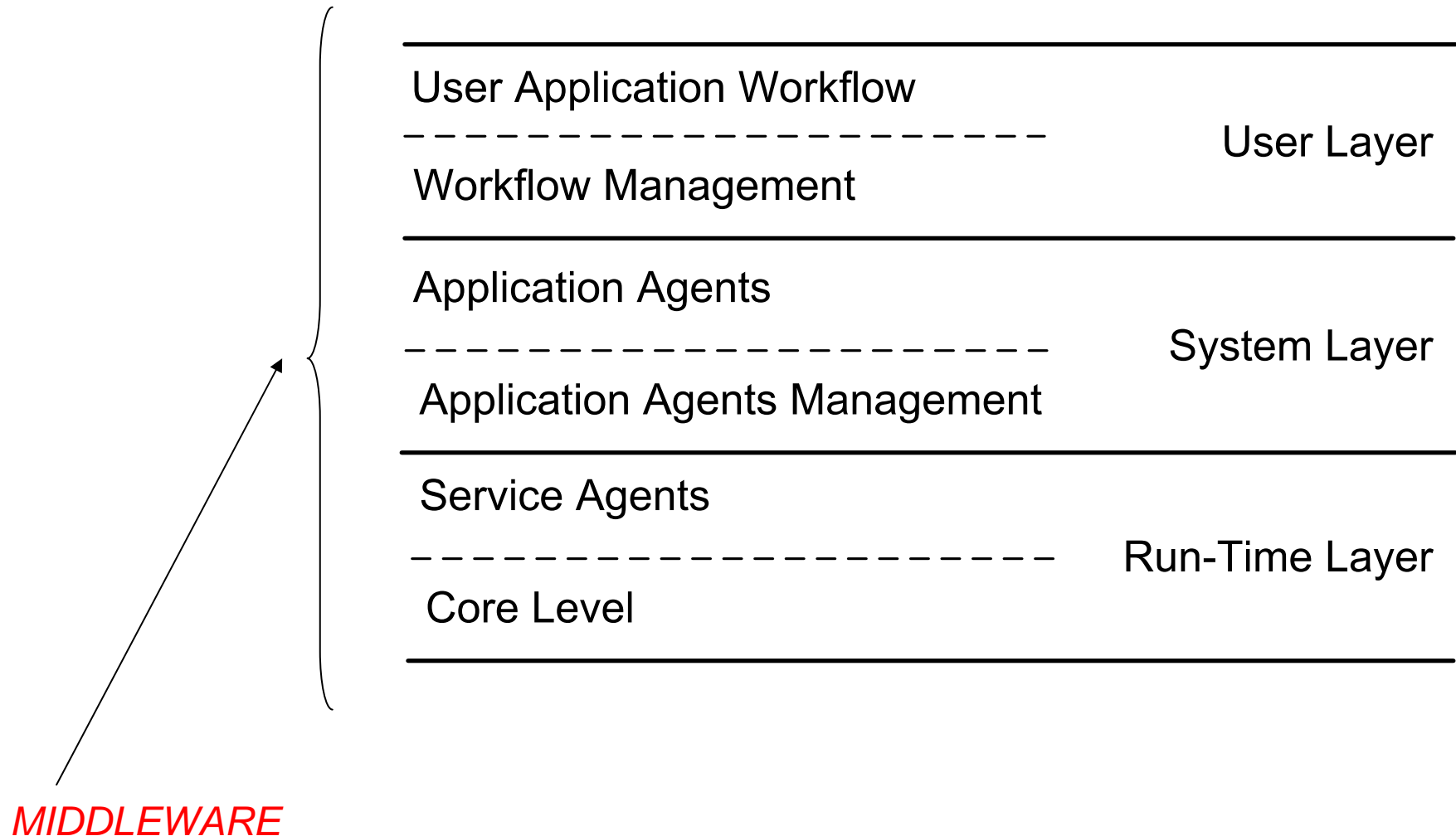
Workflow-based Activity Coordination



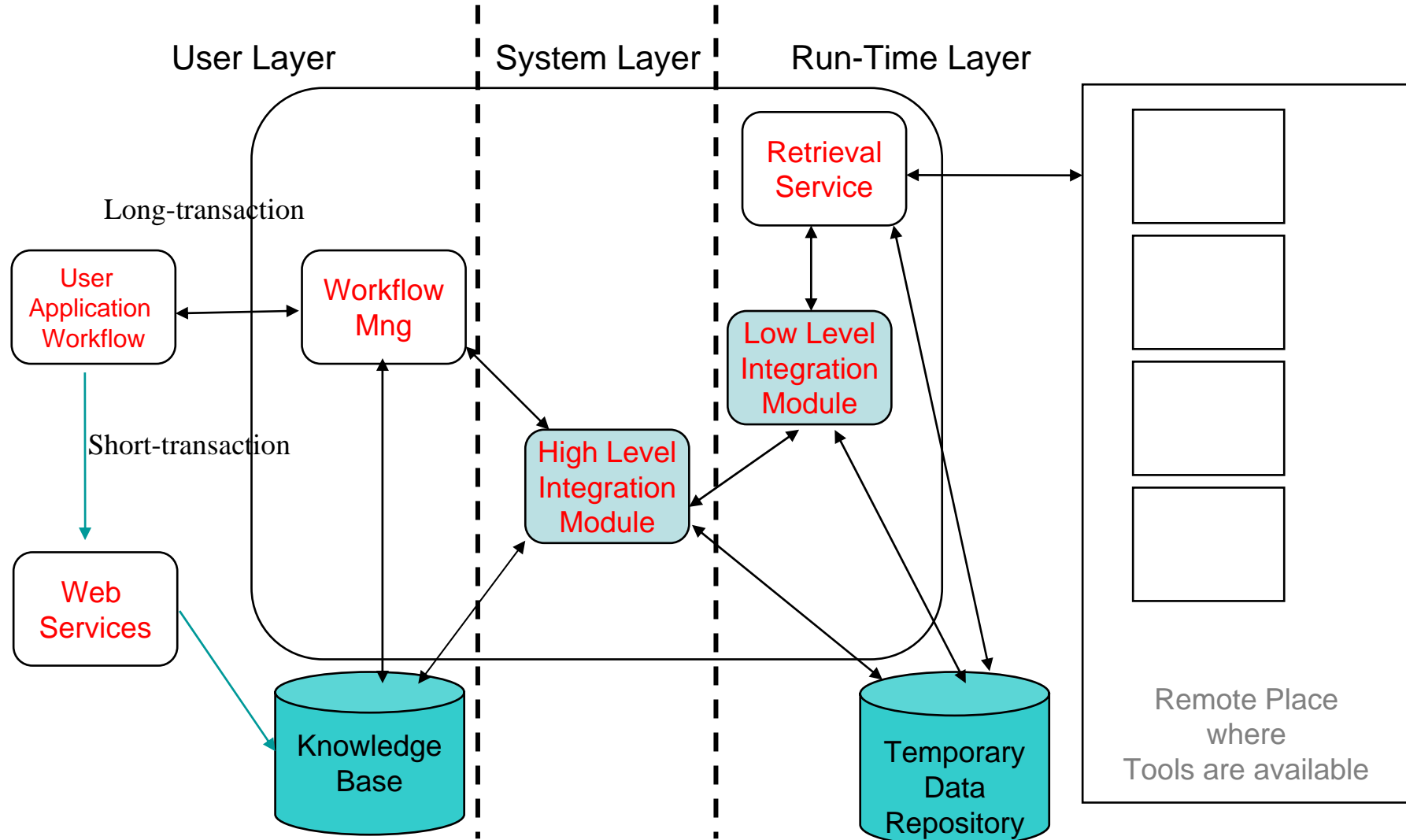
From Data to Knowledge and vice versa



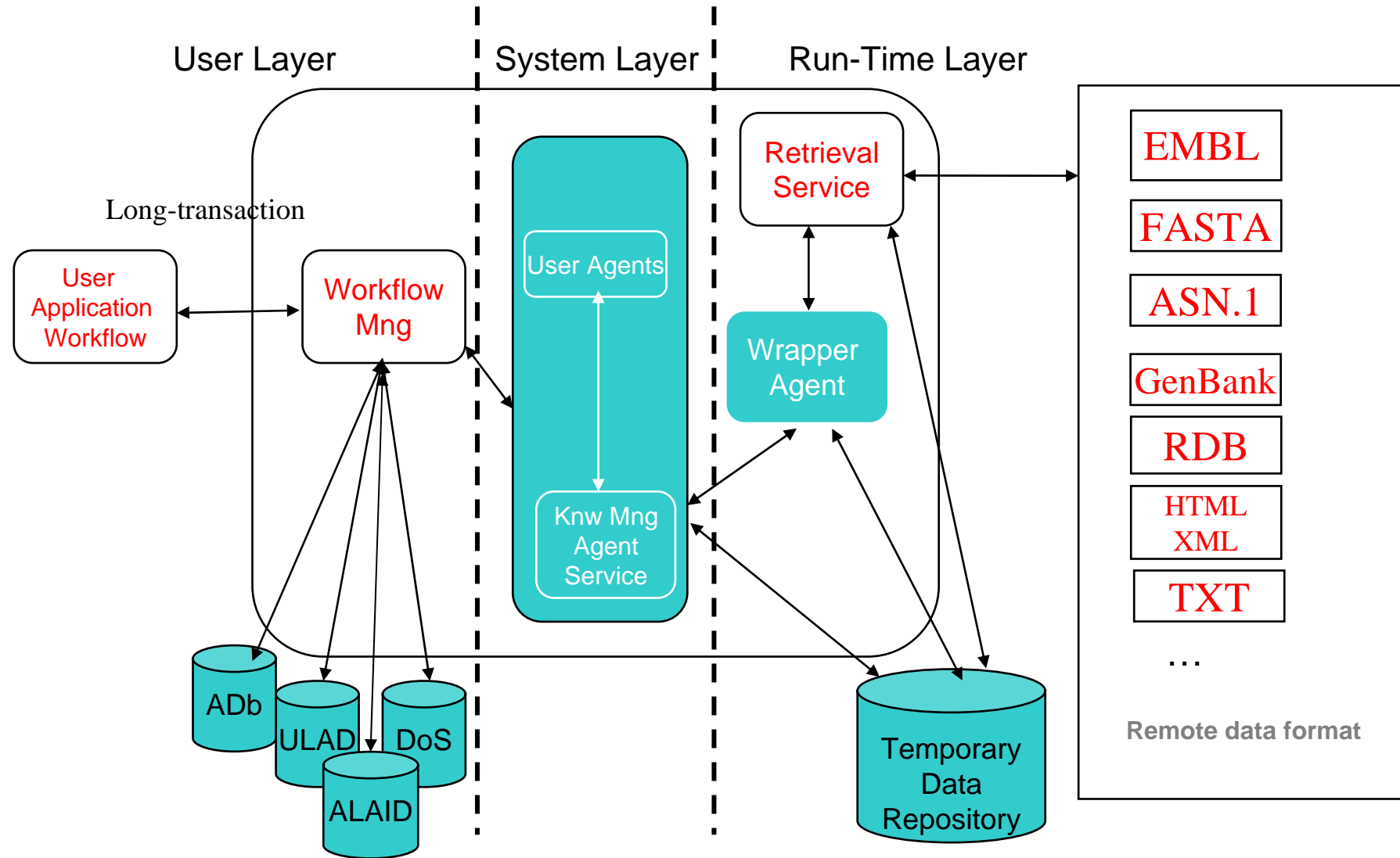
Software Architecture



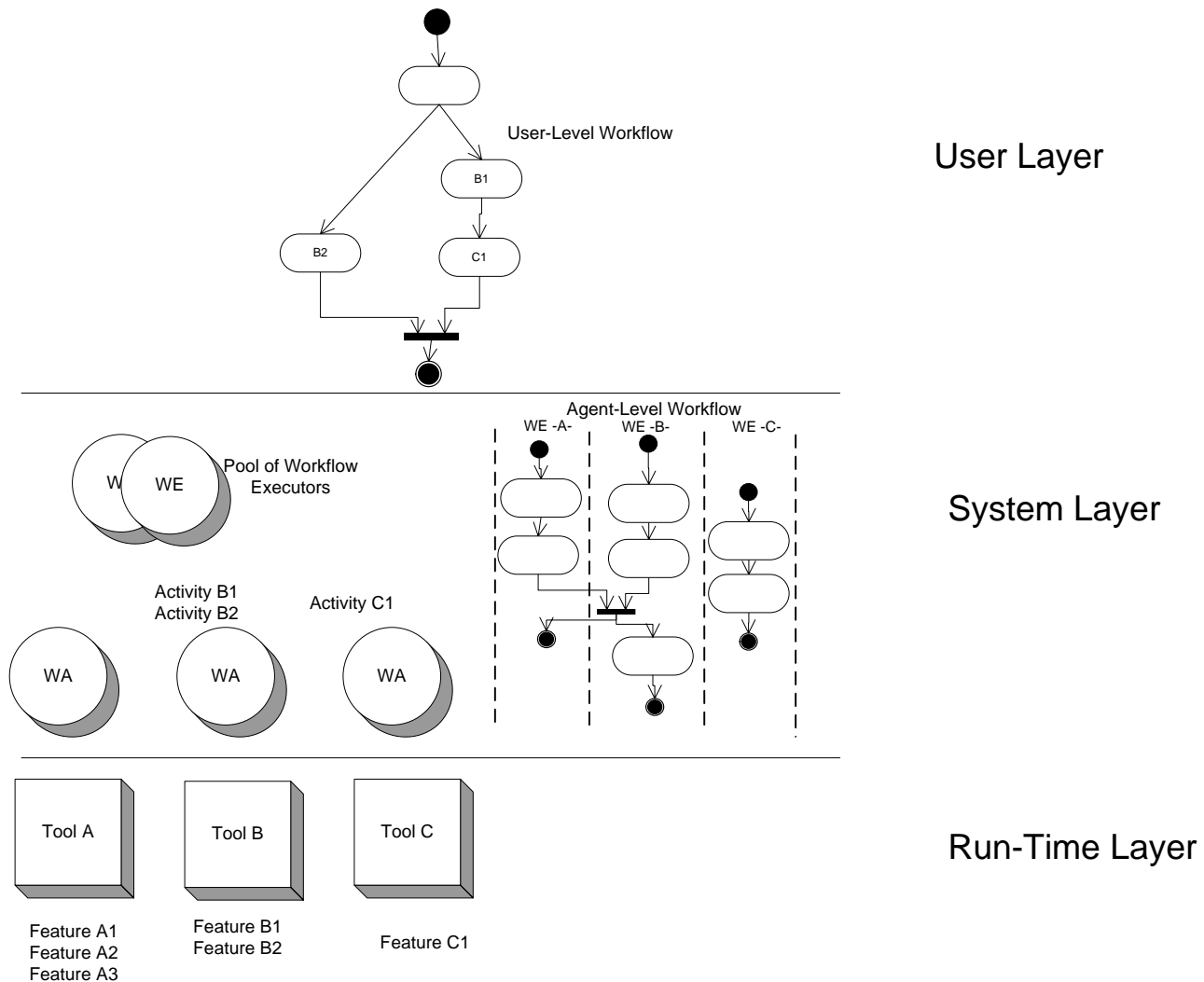
A general system's architecture



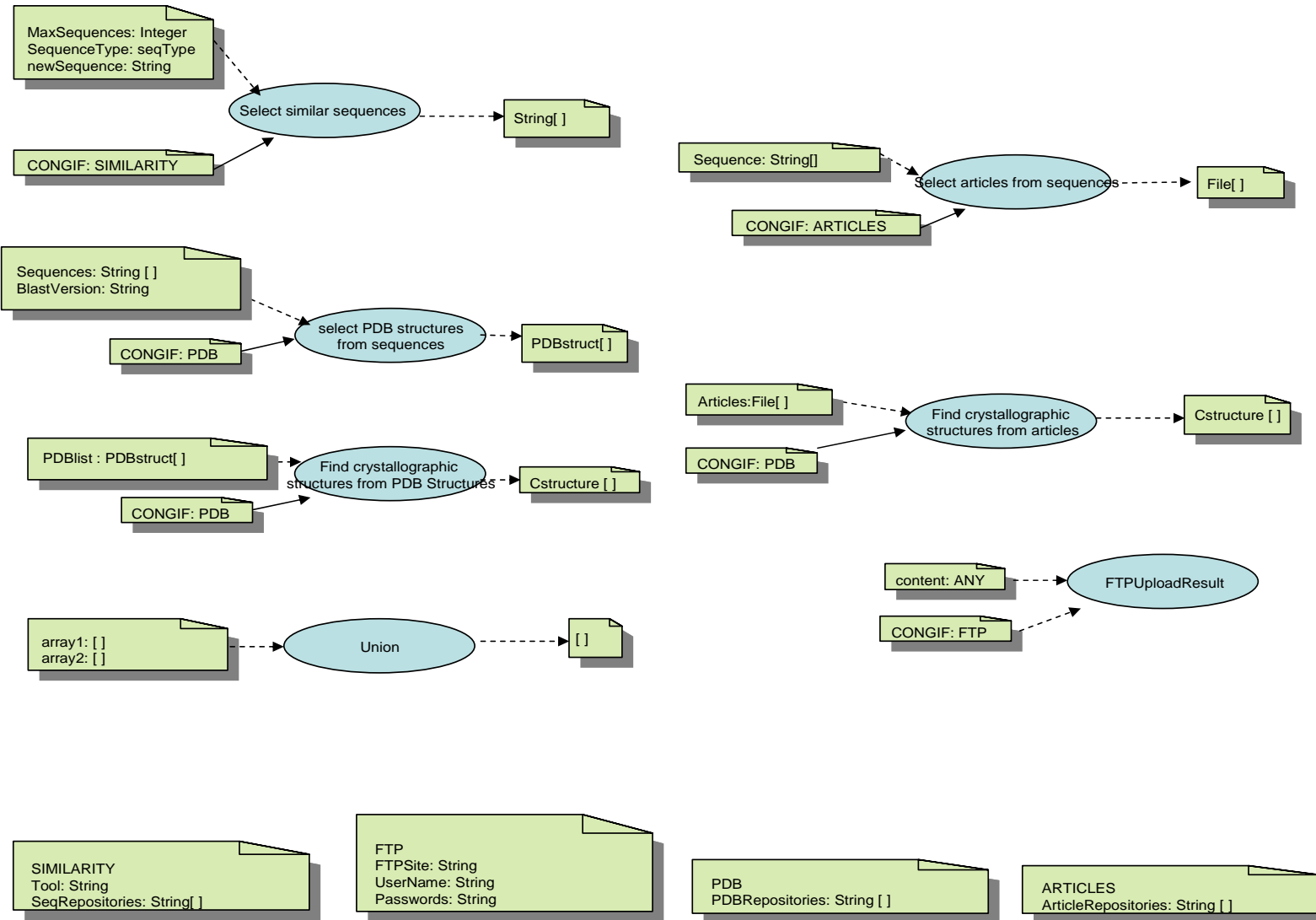
Agent-based System Architecture



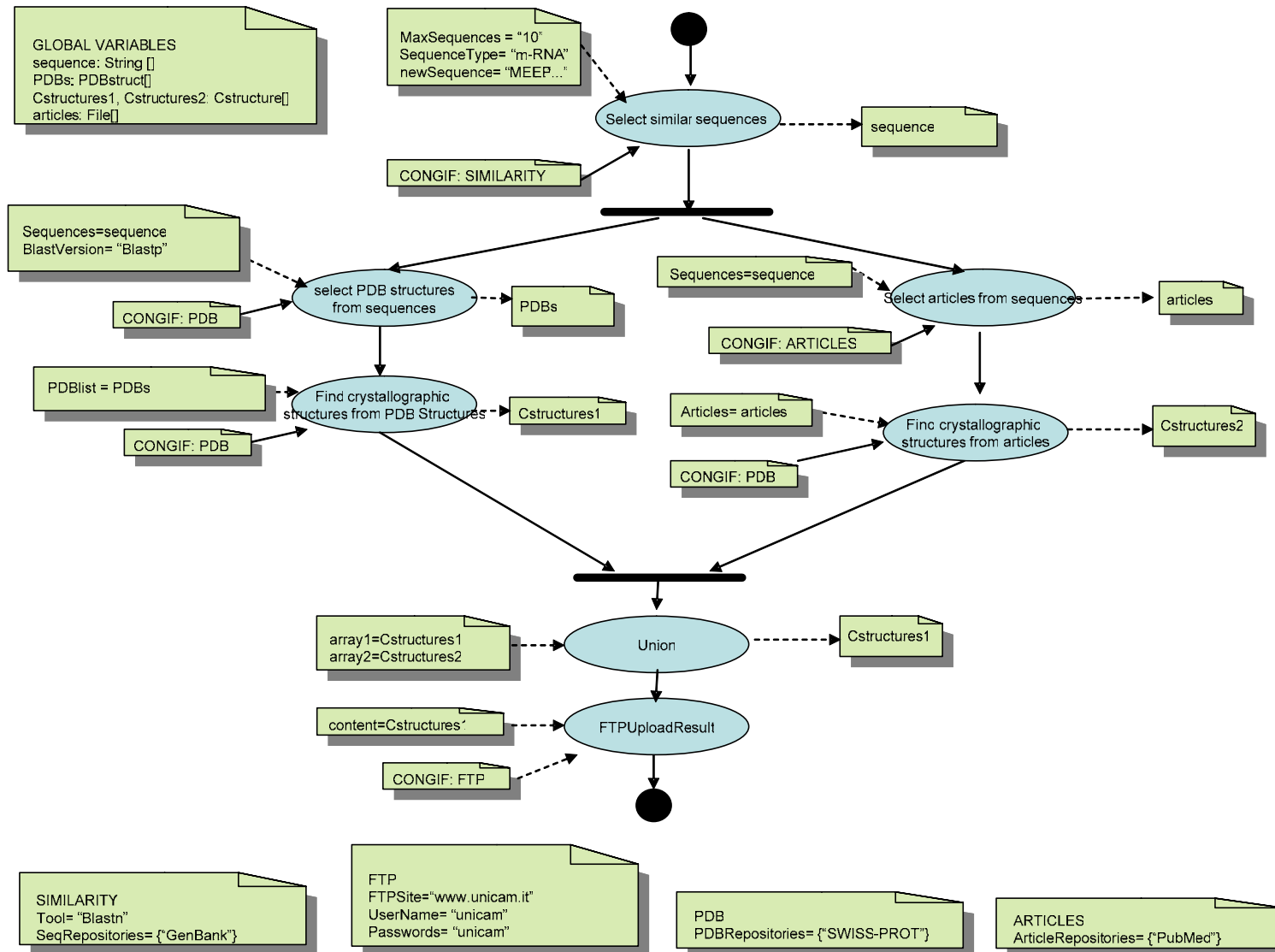
PEGAA: The Agent-based Middleware



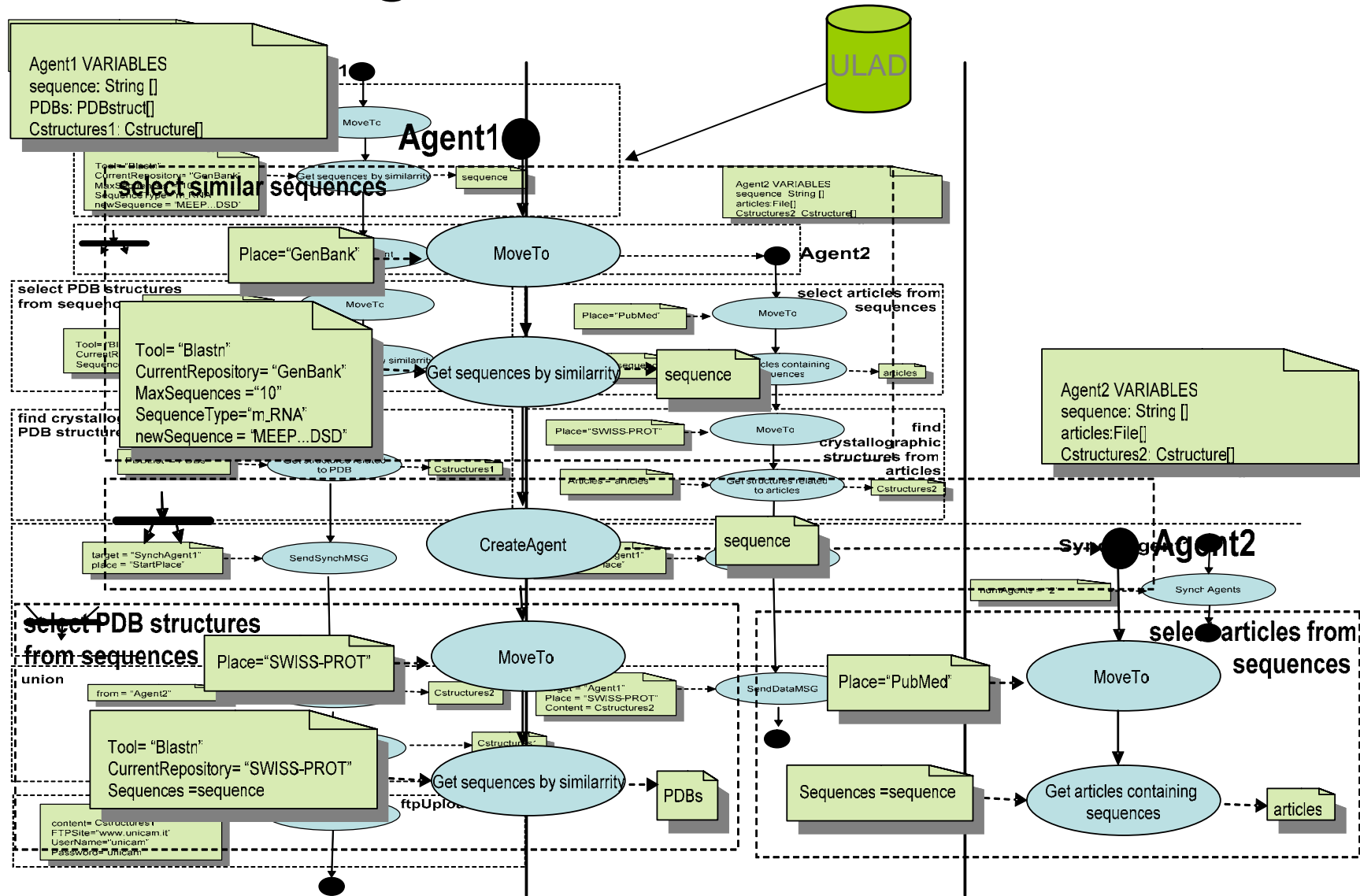
Activity Database (ADb)



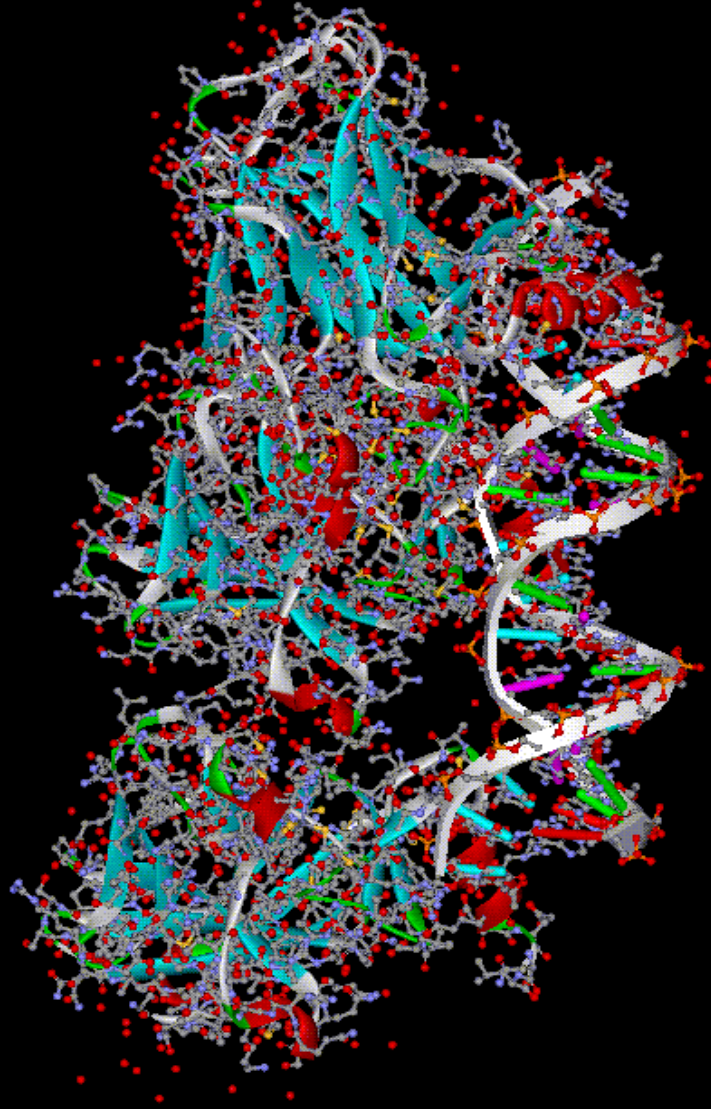
User Level Workflow



Agent level workflow



P53 Crystallographic Structure



*... one of those selected
by the bioworkflow*

A case study

- Distributed Application in Bioinformatics Domain
- Activity-based application
- Tool integration distributed middleware
- Agent-based coordination model
- What for “coordination language?”

NCBI – Home page

The image shows a screenshot of the NCBI (National Center for Biotechnology Information) home page as it appeared in the early 2000s. The browser window title is "National Center for Biotechnology Information". The page features a navigation bar with links to PubMed, Entrez, BLAST, OMIM, Books, TaxBrowser, and Structure. A search bar is present with a dropdown menu set to "Nucleotide" and a search term "MEEEP...DSD" entered. The main content area is divided into several sections:

- SITE MAP**: A vertical sidebar on the left containing links to "Guide to NCBI resources", "About NCBI" (describing the science behind the resources), "GenBank" (sequence submission support), "Literature databases" (PubMed, OMIM, Books and PubMed Central), "Molecular databases" (sequences, structures, and taxonomy), "Genomic biology" (human genome, whole genomes), and "Tools" (data mining).
- What does NCBI do?**: A central section explaining that NCBI was established in 1988 as a national resource for molecular biology information, creating public databases, conducting research in computational biology, and developing software tools for genome data analysis.
- Hot Spots**: A list of featured resources including Clusters of orthologous groups, Electronic PCR, Gene expression omnibus, Genes and disease, Human genome resources, Human/mouse homology maps, LocusLink, Malaria genetics & genomics, Map Viewer, MHC, Mouse genome resources, NCBI Handbook, ORF finder, Reference sequence project, and Retrovirus.
- PubMed Central**: A highlighted box describing it as an archive of life sciences journals, offering free fulltext, 80,000 articles from over 100 journals, and being linked to PubMed and fully searchable.
- NCBI Web Site Search**: A highlighted box announcing a new function in Entrez that allows users to search the NCBI website and ftp site directly from the Entrez pulldown menu.
- RefSeq**: A partially visible section at the bottom left.

A red square icon with a white left-pointing arrow is located in the bottom right corner of the browser window.

NCBI – main databses

NCBI HomePage - Microsoft Internet Explorer

File Modifica Visualizza Preferiti Strumenti ?

Indietro [Back] [Forward] [Home] [Stop] [Refresh] [Search] Cerca Preferiti Multimedia [Print] [Mail] [Share] [Connect To]

Indirizzo <http://www.ncbi.nlm.nih.gov/> Vai Collegamenti Norton AntiVirus

NCBI National Center for Biotechnology Information

National Library of Medicine National Institutes of Health

PubMed Entrez BLAST OMIM Books TaxBrowser Structure

Search PubMed for [] Go

SITE MAP
Guide to NCBI resources

About NCBI
The science of our resources: an introduction for researchers, educators and the public.

GenBank
Sequence submission support and software

Literature databases
PubMed, OMIM, Books and PubMed Central

Molecular databases
Sequences, structures, and taxonomy

Genomic

What does NCBI do?

Established in 1988 as a national resource for molecular biology information, NCBI creates databases, conducts research in computational biology, develops software for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease. [More...](#)

Hot Spots

- ▶ Clusters of orthologous groups
- ▶ Electronic PCR
- ▶ Gene expression omnibus
- ▶ Genes and disease
- ▶ Human genome resources
- ▶ Human/mouse homology maps
- ▶ LocusLink
- ▶ Malaria genetics & genomics
- ▶ Map Viewer
- ▶ MHC
- ▶ Mouse genome resources

PubMed Central

An archive of life sciences journals

- Free fulltext
- 80,000 articles from over 100 journals
- Linked to PubMed and fully searchable

Use of PubMed Central requires no registration or fee. Access it from any computer with an Internet connection.

dbMHC

A new NCBI resource that provides a platform for genetic

Operazione completata

Start [Icons] Eudora - [tool-Integratio...] Microsoft PowerPoint NCBI HomePage - Mic... << 17.40



NCBI – site map

NCBI Site Map

PubMed Entrez BLAST OMIM Taxonomy Structure

This site map is also a **guide to NCBI resources**. Each link leads to a **brief description of the resource** on this page, then to the resource itself. A **Quick Links** table is also available. It provides only an alphabetical list of the major resources with **direct links** to those resources, bypassing the descriptions.

RESOURCE CATEGORIES

About NCBI

[programs and services](#), [NCBI handbook](#), [what's new](#), [NCBI News](#), [postdoctoral fellowships](#), [organizational structure](#), [contact information](#), [e-mail lists](#), [site search](#)

GenBank

[overview](#), [submit sequences](#), [submit genomes](#), [sample record](#), [GenBank divisions](#), [statistics](#), [release notes](#), [international collaboration](#), [FTP GenBank](#)

Molecular Databases

[nucleotides](#), [proteins](#), [structures](#), [taxonomy](#)

Literature Databases

[PubMed](#), [PubMedCentral](#), [OMIM](#), [Books](#), [Citation Matcher](#)

Genomes and Maps

[organism collections](#) (including [Entrez Genomes](#), [Map Viewer](#), and [UniGene](#)), [human](#), [mouse](#), [rat](#), [cow](#), [zebrafish](#), [Drosophila](#), [nematode](#), [plant genomes](#), [yeast](#), [malaria](#), [microbial genomes](#), [viruses](#), [viroids](#), [plasmids](#), [eukaryotic organelles](#)

Tools

[Entrez](#), [LinkOut](#), [Cubby](#), [BLAST](#), [nucleotide sequence analysis](#), [protein sequence analysis](#), [3-D structure display and similarity searching](#)

Research at NCBI

[Computational Biology Branch \(CBB\)](#), [senior](#)

ALPHABETICAL INDEX

WITH LINKS TO RESOURCE DESCRIPTIONS
(To bypass descriptions, use the [Quick Links](#) table.)

About NCBI	Genomes and Maps	PubMed
ASN.1	GEO (Expression)	PubMed Central
BankIt	Glossaries	RefSeq
BLAST	HTGs	Research at NCBI
Books	HomoloGene	Retroviruses
CDART	Human Genome Resources	SAGEmap
CDD	Human-Mouse Homology Maps	Science Primer
CGAP	LinkOut	Seminars
Clones	LocusLink	Sequin
Cn3D	Malaria	Site Search <small>NEW</small>
Coffee Break	Map Viewer	SKY/CGH
COGs	MGC	Software Engineering
Computational Biology Branch	Microbial Genomes	Spidey
dbEST	MMDB	Structures
dbGSS	Model Maker <small>NEW</small>	Submit Data
dbSNP	Mutation Databases	Taxonomy



NCBI - Entrez

Entrez Home - Microsoft Internet Explorer

File Modifica Visualizza Preferiti Strumenti ?

Indietro Cerca Preferiti Multimedia

Indirizzo <http://www.ncbi.nlm.nih.gov/Entrez/> Vai Collegamenti Norton AntiVirus

NCBI Entrez search and retrieval system

PubMed Entrez BLAST OMIM Books Taxonomy Structure

Search PubMed for Go Clear

About Entrez

SITE MAP

PubMed Help help documentation for PubMed

Entrez Help help documentation

Entrez Tutorial **NEW** tutorial for the Entrez system

The Entrez Databases cross-references and information

Batch Entrez upload a file of GI or accession numbers to retrieve sequences

Making WWW Links to Entrez linking to PubMed and GenBank

LinkOut external links to related resources

Entrez is a retrieval system for searching several linked databases. It provides access to:

- [PubMed](#): biomedical literature
- [Nucleotide](#): sequence database (GenBank)
- [Protein](#): sequence database
- [Structure](#): three-dimensional macromolecular structures
- [Genome](#): complete genome assemblies
- [Books](#): BookShelf online books
- [Domains](#): conserved domains (CDD)
- [3D Domains](#): domains from Entrez Structure
- [GEO](#): Gene Expression Omnibus
- [GEO Datasets](#): curated GEO data sets
- [Journals](#): journals in Entrez
- [MeSH](#): medical subject headings
- [NCBI Web Site](#): NCBI Web site search
- [OMIM](#): Online Mendelian Inheritance in Man
- [PMC](#): full-text digital archive of life sciences journal literature
- [PopSet](#): population study datasets
- [SNP](#): single nucleotide polymorphisms
- [Taxonomy](#): organisms in GenBank
- [UniGene](#): gene-oriented clusters of transcript sequences
- [UniSTS](#): markers and mapping data

Pre-computed similarity searches are available for most database records, which produce a list of related sequences, structure neighbors, as well as related articles.

Operazione completata

Start Eudora - [tool-Integratio... Microsoft PowerPoint Entrez Home - Micros... 17.48



PDB –Home page

The screenshot shows the PDB Home page in a web browser. The browser's address bar is empty, and the taskbar at the bottom shows various icons. The page layout includes a navigation menu at the top, a main content area with a search box and news section, and a sidebar on the left with links to deposit data and current holdings. A red circle highlights the search input field, and a red square highlights a back button in the bottom right corner.

DEPOSIT data
[DOWNLOAD files](#)
[browse LINKS](#)
[BETA TEST new features](#)
[BETA mmCIF and XML files](#)

Current Holdings
21838 Structures
Last Update: 22-Jul-2003
[PDB Statistics](#)


Molecule of the Month:
[Src Tyrosine Kinase](#)

The Protein Data Bank (PDB) is operated by Rutgers, The State University of New Jersey; the San Diego Supercomputer Center at the University of California, San Diego; and the Center for Advanced Research in Biotechnology of the National Institute of Standards and Technology -- three members of the [Research Collaboratory for Structural Bioinformatics \(RCSB\)](#). The PDB is supported by funds from the [National Science Foundation](#), the [Department of Energy](#), and two units of the National Institutes of Health: the [National Institute of General Medical Sciences](#) and the [National Library of Medicine](#).

PDBB
PROTEIN DATA BANK

Welcome to the PDB, the single worldwide repository for the processing and distribution of 3-D biological macromolecular structure data.

[RCSB Home](#) [Contact Us](#) [Help](#)

[Did you find what you wanted?](#)

[ABOUT PDB](#) | [DATA UNIFORMITY](#) | [RECENT FEATURES](#) | [USER GUIDES](#) | [FILE FORMATS](#) | [EDUCATION](#) | [STRUCTURAL GENOMICS](#) | [PUBLICATIONS](#) | [SOFTWARE](#)

Search the Archive 

Enter a **PDB ID** or keyword [Query Tutorial](#)

query by PDB id only match exact word
 [remove sequence homologs](#)

[SearchLite](#) keyword search form with examples
[SearchFields](#) customizable search form
[Status Search](#) find entries awaiting release

News [Complete News Newsletter](#) [pdb-I Archive Subscribe](#)

22-Jul-2003
[Demonstrations, Posters, and More: PDB at the ACA Annual Meeting and the 17th Symposium of the Protein Society](#)
The PDB would like to thank those ISMB 2003 attendees who provided valuable feedback at our demonstration session and exhibit during this worthwhile event. PDB staff members will also participate in several other meetings in the near future, including the annual meetings of the Protein Society and the American Crystallographic Association... [\[MORE...\]](#)

PDB Mirrors
Please bookmark a mirror site
[San Diego Supercomputer Center*](#)
[Rutgers University*](#)
[National Institute of Standards and Technology*](#)
[Cambridge Crystallographic Data Centre, UK](#)
[National University of Singapore](#)
[Osaka University, Japan](#)
[Universidade Federal de Minas Gerais, Brazil](#)
[Max Delbrück Center for Molecular Medicine, Germany](#)

OTHER SITES
**RCSB partner*

In citing the PDB please refer to:
H.M. Berman, J. Westbrook, Z. Feng, G. Gilliland, T.N. Bhat, H. Weissig, I.N. Shindyalov, P.E. Bourne: [The Protein Data Bank](#), *Nucleic Acids Research*, **28** pp. 235-242 (2000)

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NCBI - BLAST

The screenshot shows a Microsoft Internet Explorer browser window displaying the NCBI BLAST Basic Overview page. The address bar shows the URL http://www.ncbi.nlm.nih.gov/BLAST/blast_overview.html. The browser's menu bar includes File, Modifica, Visualizza, Preferiti, and Strumenti. The toolbar contains navigation buttons like Indietro, Avanti, and home, along with search and utility icons. The page content features the NCBI logo and a navigation menu with links to PubMed, Entrez, BLAST, OMIM, Taxonomy, and Structure. The main heading is "Basic Overview", followed by a list of links: "What is BLAST?", "What is the best BLAST for me?", "How can I access the BLAST services at NCBI?", and "What is the StandAlone WWW BLAST Server?". Below this is a section titled "Q: What is BLAST?" with a detailed paragraph explaining the BLAST algorithm. Another section, "Q: What is the Best BLAST for me?", discusses different BLAST tools and provides a link to a "BLAST Program Selection Guide". A final section, "Q: How can I access the NCBI's BLAST services?", is partially visible. The browser's status bar at the bottom shows "Operazione completata" and the system tray includes the Start button, taskbar icons for Eudora, Microsoft PowerPoint, and the current browser window, along with the system clock showing 17.53.

http://www.ncbi.nlm.nih.gov/BLAST/blast_overview.html - Microsoft Internet Explorer

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Indietro Avanti Home Cerca Preferiti Multimedia

Indirizzo http://www.ncbi.nlm.nih.gov/BLAST/blast_overview.html Vai Collegamenti Norton AntiVirus

NCBI BLAST

PubMed Entrez BLAST OMIM Taxonomy Structure

Basic Overview

- [What is BLAST?](#)
- [What is the best BLAST for me?](#)
- [How can I access the BLAST services at NCBI?](#)
- [What is the StandAlone WWW BLAST Server?](#)

Q: What is BLAST?

BLAST[®] (Basic Local Alignment Search Tool) is a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. The BLAST programs have been designed for speed, with a minimal sacrifice of sensitivity to distant sequence relationships. The scores assigned in a BLAST search have a well-defined statistical interpretation, making real matches easier to distinguish from random background hits. BLAST uses a heuristic algorithm that seeks local as opposed to global alignments and is therefore able to detect relationships among sequences that share only isolated regions of similarity ([Altschul et al. 1990](#)). For a better understanding of BLAST, you can refer to the [BLAST Course](#), which explains the basics of the BLAST algorithm. There is also a description of BLAST services located [here](#). Also for details on BLAST and theory of similarity search, see the [References](#) section.

Q: What is the Best BLAST for me?

There are many different types of BLAST available from the main [BLAST web page](#). Choosing the right one depends on the type of sequence you are searching with (long, short, nucleotide protein), and the desired database. In order to help guide you to the right service for your search please consult the "[BLAST Program Selection Guide](#)".

This guide provides information on what database and BLAST service (megaBLAST, translation BLAST etc) is ideal for your search. Plus there is also additional information describing how the tools work and why they are best for certain types of searches.

Q: How can I access the NCBI's BLAST services?

Operazione completata

Start Eudora - [tool-Integratio... Microsoft PowerPoint <http://www.ncbi.nlm...> 17.53



NCBI – ASN.1

ASN.1 Summary - Microsoft Internet Explorer

File Modifica Visualizza Preferiti Strumenti ?

Indietro Cerca Preferiti Multimedia

Indirizzo <http://www.ncbi.nlm.nih.gov/Sitemap/Summary/asn1.html> Vai Collegamenti Norton AntiVirus

ASN.1 Summary

PubMed Entrez BLAST OMIM Taxonomy Structure

NCBI Home

Site Map
brief and complete versions

About NCBI
general and contact information

GenBank
submit your sequence, general information

Molecular Databases
nucleotides, proteins, structures and taxonomy

Literature Databases
PubMed, PubRef, OMIM, Citation Matcher

Genomes and Maps
maps, the human

ASN.1, or Abstract Syntax Notation One, is an International Standards Organization (ISO) data representation format used to achieve interoperability between platforms. NCBI uses ASN.1 for the storage and retrieval of data such as nucleotide and protein sequences, structures, genomes, and MEDLINE records. It permits computers and software systems of all types to reliably exchange both the data structure and content.

The documentation for the NCBI Software Development ToolKit contains information about the ASN.1 specification. The toolkit documentation is quite large (over 300 pages) and can be downloaded as the MS Word file [sdk.doc.Z](#) from the NCBI FTP site. Please see the [readme](#) file in that directory for more information.

The NCBI Software Development ToolKit (known as the "[NCBI Toolbox](#)") is a set of software and data exchange specifications used by NCBI to produce portable, modular software for molecular biology. The software in the Toolbox is primarily designed to read ASN.1 format records. It is available to the public in the [toolbox/ncbi_tools](#) directory of NCBI's ftp site, and can be used in its own right or as a foundation for building tools with similar properties. The readme files in the [toolbox](#) and [toolbox/ncbi_tools](#) directories of the FTP site contain more information about the toolbox and ASN.1.

The following **publications** might also be of interest.

Operazione completata Internet



NCBI - fomats

NCBI Sequence Viewer - Microsoft Internet Explorer

File Modifica Visualizza Preferiti Strumenti ?

Indirizzo <http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=4680228&db=Nucleotide&dopt=GenBank>

NCBI

CGCTCAGGATAGGACTTCGCGCTAGAGATCGGATCCCGGATGATTATATAGCTCGATGATC
TTCTCTATATCCGCGGATGGGCTATATACACACACGCGGATAGCAGCTGATCTA
CCCCATGCTTTCGATACGCTTTCGATACGCTTTCGATACGCTTTCGATACGCTTTCGATACG
CACAGATACGCTTTCGATACGCTTTCGATACGCTTTCGATACGCTTTCGATACGCTTTCGATACG

Nucleotide

PubMed Nucleotide Profile Genome Structure PMC Taxonomy OMIM Books

Search Nucleotide for [] Go Clear

Limits Preview/Index History Clipboard Details

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1: AF1182 Summary ASN.1 Nb... [gi:4680228] Link

FASTA

LOCUS TinySeq XML 1748 bp mRNA linear PRI 17-APR-2000

DEFINITION GenBank Mb-5 mRNA, partial cds.

ACCESSION GBSeq XML

VERSION GI List :4680228

KEYWORDS Graphics

SOURCE XML human)

ORGANISM default

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1748)

AUTHORS Amler, L.C., Bauer, A., Corvi, R., Dihlmann, S., Praml, C.,
Cavenee, W.K., Schwab, M. and Hampton, G.M.

TITLE Identification and characterization of novel genes located at the
t(1;15)(p36.2;q24) translocation breakpoint in the neuroblastoma
cell line NGP

JOURNAL Genomics 64 (2), 195-202 (2000)

MEDLINE [20195630](#)

PUBMED [10729226](#)

REFERENCE 2 (bases 1 to 1748)

AUTHORS Amler, L.C. and Hampton, G.M.

TITLE Direct Submission

JOURNAL Submitted (06-JAN-1999) Genos Biosciences, 11099 North Torrey Pines
Road, La Jolla, CA 92037, USA

FEATURES Location/Qualifiers

source 1..1748
/organism="Homo sapiens"
/mol_type="mRNA"

Operazione completata

Start Eudora - [tool-Integratio... Microsoft PowerPoint NCBI Sequence View... 17.39



- Sistemi distribuiti e coordinazione
- Modelli di coordinazione
- Architetture software
- Linguaggi di coordinazione
- Middleware per la coordinazione
- Agenti software e coordinazione

Sistemi distribuiti e coordinazione

- Coordination-based systems
 - TIBCO's Rendezvous Bus
 - Sun Microsystem's Jini

Articoli

La parte di coordinazione di un sistema distribuito gestisce la comunicazione e la cooperazione tra processi. Rappresenta “glue” che lega le attività dei processi come se fosse unica.

- D. Gelernter and N. Carriero, *Coordination languages and their significance*, *Communication of ACM*, vol.35, no.2, pp.96-107, Feb. 1992

Una tassonomia di modelli di coordinazione per agenti mobili, generalizzabile ad altri tipi di sistema distribuito

- G. Cabri, L. Leonardi and F. Zambonelli, *Mobile-Agent coordination models for Internet Applications*, *IEEE Computer*, vol.33, no.2, pp.82-89, feb. 2000

Modelli di coordinazione

- Direct coordination
- Meeting-oriented coordination

Architetture software e coordinazione

Linguaggi di coordinazione

- LINDA

Middleware per la coordinazione

Agenti sw e coordinazione

- CCS: un calcolo di base per la concorrenza, semantiche operazionali ed osservazionali, assiomatizzazioni
- Pi-calcolo: un calcolo con mobilità di interconnessioni,
- semantiche operazionali ed osservazionali, sistemi di tipo.
-