

Architektura dużych projektów bioinformatycznych

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Wykład 5. - Od systemów LI(M)S do Galaxy
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Problem?



"Think this is bad? You should see the inside of my head."

Zarządzanie danymi w bioinformatyce

- Dostępne i powtarzalne wyniki badań
(Accessible and reproducible research)
- RREnvironment, RRSystem, RRPublishing
- Systemy LI(M)S, Zarządzanie protokołami
(Labkey, BASE, etc...)
- Literate programming (WEB, sweave, etc...)
- Systemy RRS – MeV, GenePattern,
GenomeSpace, Galaxy

COMPUTER SCIENCE

Accessible Reproducible Research

Jill P. Mesirov

Scientific publications have at least two goals: (i) to announce a result and (ii) to convince readers that the result is correct. Mathematics papers are expected to contain a proof complete enough to allow knowledgeable readers to fill in any details. Papers in experimental science should describe the results and provide a clear enough protocol to allow successful repetition and extension.

Over the past ~35 years, computational science has posed challenges to this traditional paradigm—from the publication of the four-color theorem in mathematics (1), in which the proof was partially performed by a computer program, to results depending on computer simulation in chemistry, materials science, astrophysics, geophysics, and climate modeling. In these settings, the scientists are often sophisticated, skilled, and innovative programmers who develop large, robust software packages.

As use of computation in research grows, new tools are needed to expand recording, reporting, and reproduction of methods and data.



between two types of acute leukemia, based on

guage that can produce all of the text, figures,

Pakiety LIMS

- Laboratory Information Management Software
- Zyskuje popularność od lat 80tych XX w. (era PC)
- Obecnie w zasadzie dwie możliwości:
 - desktop (w oparciu o lokalną bazę danych)
 - Klient-serwer, zwykle przez sieć www, choć istnieją jeszcze rozwiązania z lokalną bazą danych w modelu klient serwer

Budowa pakietu LIMS

- Baza danych odczynników
- Baza przeprowadzonych analiz
- Linie komórkowe, populacje zwierząt laboratoryjnych
- Eksperymenty przeprowadzane na bieżąco
- Artykuły i rysunki, wyniki częściowe
- Coraz większe rozmiary danych pośrednich

Pakiety LIMS

- Rynek rozczłonkowany pomiędzy bardzo wiele rozwiązań komercyjnych, często bardzo specjalizowanych:

Accelrys LIMS from Accelrys

AgiLIMS from AgiLab

ApolloLIMS from Common Cents Systems, Inc

benchsys benchsys

Biotracker from Ocimum Bio Solutions

Biotracker Lite from Ocimum Bio Solutions

CaliberLIMS from Caliber Technologies Pvt. Ltd.

Care Med LIS from Medcare International

CCLAS from Ventyx, an ABB company, formerly Mincom (company)

Clarity LIMS from GenoLogics Life Sciences

CloudLIMS from CloudLIMS

Cyberlab in Cloud (Toplab) from Megaweb websites: Megaweb and TOPLAB

Darwin from Thermo Fisher Scientific

ELab from LabLynx

Element LIMS from Promium

eQMS::LIMS Pardus d.o.o. [1]

Exemplar Biomarker Discovery from Sapios Sciences

Exemplar Dx LIMS from Sapios Sciences

Exemplar Research LIMS from Sapios Sciences

Galileo from Thermo Fisher Scientific

LABAsistan from Tenay Medical Software

LABbase from Analytik Jena

LabPlus PRÉVENTION EXPERT CONSEIL INC. (PEC)

LabSoft LIMS from Computing Solutions Inc.

LABVANTAGE from LABVANTAGE Solutions

Labware from LabWare

LABWORKS from PerkinElmer

Labway-LIMS from Ambidata Digital Innovation Solutions & Consulting

LDMS from Frontier Science and Technology Research Foundation

Matrix Gemini from Autoscribe

MetaField Lab from Agile Frameworks, LLC

Nautilus from Thermo Fisher Scientific

ProlabQ from Open-Co

readyLIMS from Analytik Jena

Result Point from Accelerated Technology Laboratories, Inc

SampleManager from Thermo Fisher Scientific

Sample Master from Accelerated Technology Laboratories, Inc

Select Agent Inventory (SAI) Management System Foxspire

SchuyLab from Schuyler House, Inc

SIMATIC IT Unilab from Siemens

SLims from Genohm

Solution Laboratoire from Limseo

SmartLims from SmartSoft, Inc

STARLIMS from STARLIMS Corporation

StrainControl Laboratory Manager from DNA Globe

TITAN from Accelerated Technology Laboratories, Inc

TremoLAB from Binsol S.A. www.binsol.com.ar

Watson from Thermo Fisher Scientific

webLIMS from LabLynx

WinLIMS from QSI Corporation N

NuGenesis from Waters Corporation www.Waters.com

Od niedawna również oprogramowanie open source

- Labkey Server (apache license)
- MISO (GPLv3)
- BIKA LIMS (AGPLv3)
- Typowy model to komercyjna firma rozwijająca oprogramowanie i świadcząca usługi wsparcia
- Często dużo tańsze od rozwiązań komercyjnych, ale wymagające większego know-how na miejscu, popularne w dużych instytucjach

Pakiety typu open lab notebook

... there is a URL to a laboratory notebook that is freely available and indexed on common search engines. It does not necessarily have to look like a paper notebook but it is essential that all of the information available to the researchers to make their conclusions is equally available to the rest of the world

- —Jean-Claude Bradley



Dla eksperymentów mikromacierzowych

- System BASE

BMC Bioinformatics



Software

Open Access

BASE - 2nd generation software for microarray data management and analysis

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Do eksperymentów sekwencjonowania

- Galaxy server

The screenshot shows the Galaxy web interface at <https://usegalaxy.org>. The left sidebar contains a list of tools categorized under 'Tools' and 'NGS TOOLBOX BETA'. The main content area features a 'Try Galaxy on the Cloud' banner with the text 'Now you can have a personal Galaxy within the infinite Universe'. To the right is a 'Tweets' section showing three tweets from the 'Galaxy Project' account (@galaxyproject). The first tweet is about the Fall 2014 Galaxy User Group Grand Ouest (GUGGO) Events Report. The second tweet is about the Next Generation Data Analysis Workshop at UCRiverside. The third tweet is about a Research Specialist at Michigan State University. Below the tweets is a 'Tweet to @galaxyproject' input field. The right sidebar shows a 'History' panel with an empty history named 'Unnamed history'.

Tools

- search tools
- Get Data
- Lift-Over
- Text Manipulation
- Convert Formats
- FASTA manipulation
- Filter and Sort
- Join, Subtract and Group
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- Genome Diversity

NGS TOOLBOX BETA

- Phenotype Association
- NGS: QC and manipulation
- NGS: Mapping
- NGS: SAM Tools
- NGS: GATK Tools (beta)
- NGS: Peak Calling
- NGS: RNA-seq
- NGS: Picard (beta)
- NGS: Variant Analysis

Galaxy

New high performance job execution options are available! See [the wiki](#) for more information.

Analyze Data Workflow Shared Data Visualization Cloud Help User

Using 0%

History

search datasets

Unnamed history
0 bytes

This history has been deleted

This history is empty. You can load your own data or get data from an external source

Tweets

Follow

Galaxy Project @galaxyproject 41m Fall 2014 Galaxy User Group Grand Ouest (GUGGO) Events Report: Tools, User Group, RAD-Seq: bit.ly/1vquY0m #usegalaxy @Biogenoust

Galaxy Project @galaxyproject 31 Oct Next Generation Data Analysis Workshop, Dec 5-8, 2014 @UCRiverside bit.ly/ucrworkshops #usegalaxy Expand

Galaxy Project @galaxyproject 31 Oct Research Specialist, Institute for Cyber-Enabled Research, Michigan State University, United States bit.ly/13pqd0T #usegalaxy Expand

Tweet to @galaxyproject

PENN STATE

JOHNS HOPKINS UNIVERSITY

The Galaxy Team is a part of the Center for Comparative Genomics and Bioinformatics at Penn State, and the Department of Biology and at Johns Hopkins University.

TACC

This instance of Galaxy is utilizing infrastructure generously provided by the iPlant Collaborative at the Texas Advanced Computing Center, with support from the National Science Foundation.