

Creation date
November 2004

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Web access
<http://lipm-grpware.toulouse.inra.fr>
<http://lipm-bioinfo.toulouse.inra.fr>
<http://lipm-intranet.toulouse.inra.fr:81/>
<http://bioinfo.genopole-toulouse.prd.fr/inra/>

Organisation and tasks

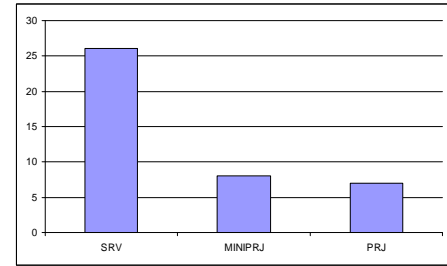
Transparent: everyone can access the list of queries (who and what) on the egroupware forum

Query types:

1. **Service** (short term tasks)
2. **Small Projects** (less than 2 man-months)
3. **Projects** (months to years).

History (nov04-nov06):

	LIPM	MA/AT	CB	CBM	Fd/BC	JB	JV	DB	DRYM	DT	JD/CG	JCPG	PV	Coll.
SRV	1	3	6		2	2	1		2	1		7	1	
MINIPRJ	1		4			1	2	1/2				1/2		
PRJ	3	1	2	1							1	1		3



Project management

Objectives:

- Ensure programming quality (→ ensure maintainability over years)
- Offer the opportunity for collaborators to implement some of the current industry standards (→ requirement for promotion/recruitment)
- Share experience

Three complementary point of views:

- a modeling language: UML (Unified Modeling Language)
- a method to manage development process: XP (eXtreme Programming)
- a philosophy: « no integrism »
- UML and XP have been adapted to the context.
- Coding standards have been developed by several bioinformatics teams (<http://genopole.toulouse.inra.fr/bioinfo/Code/NORMES>)

to standardize and simplify the recurrent tasks in bioinformatics software development were the priorities of the first year

« Low level » perl libraries (<http://lipm-svn.toulouse.inra.fr/svn/lipmutils>)

Logger: log actions/events in structured text files

ParamParser: read parameters from several sources (parameter file, CGI form, command line)

WebBuilder: from a XML file that describes the site structure, the modules build dynamic and normalized web sites

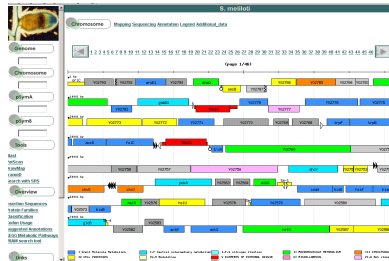
Pili and Sufine: provides the programmers with a generic pipeline architecture

paraloo: provides a generic interface for jobs distribution in order to facilitate pipeline development and migration (open source at: <http://lipm-bioinfo.toulouse.inra.fr/paraloo/>)

Analysis platforms@LIPM

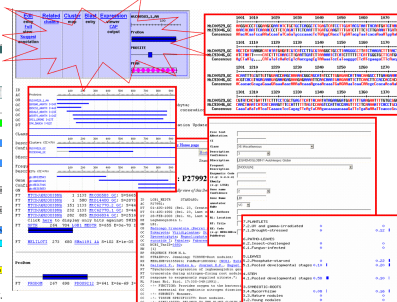
IAnt: Integrated Annotation Tool

Annotation environment and bacteria genome browser
<http://sequence.toulouse.inra.fr/S.mellioti>
<http://sequence.toulouse.inra.fr/R.solanacearum>
Carrere S & Gouzy J. (1998-200X)



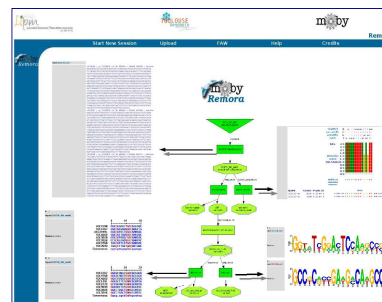
MENS: Medicago EST Navigation System

Environment to cluster, annotate and analyze EST sequences
Gouzy J. (1999-2004)



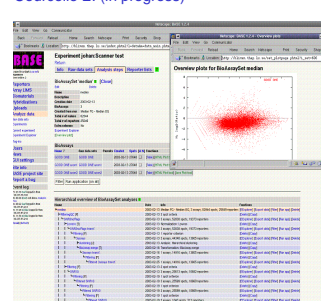
REMORA: a pilot in the ocean of BioMoby web-services

Workflow design using the BioMoby technology
Carrere S & Gouzy J. (2005-)



BASE Installation and database management

BASE - BioArray Software Environment
<http://base.thep.lu.se/>
Courcelle E. (in progress)



On-going genome annotation and comparative genomics projects

Bacteria

- *Xantomonas albilineans* genome annotation (M. Arlat)
- Genome annotation of two *Ralstonia solanacearum* strains (C. Boucher)
- Bacteria phylogenomics (J. Batut)

Eukaryota

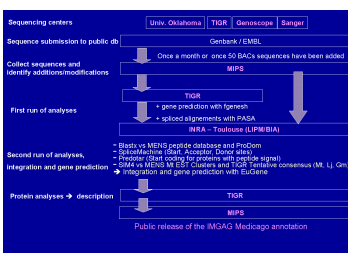
- *Medicago truncatula* genome sequencing and annotation project (F. Debelle, FP6)
- *Meloidogyne incognita* genome annotation / P. Abad (INRA/CNRS Antibes)
- Tomato genome annotation (T. Schiex, UBIA, FP6)
- LEGOO: a bioinformatics gateway towards integrative legume biology (ANR-Genoplante 2007-2010)

Main bioinformatics collaborations

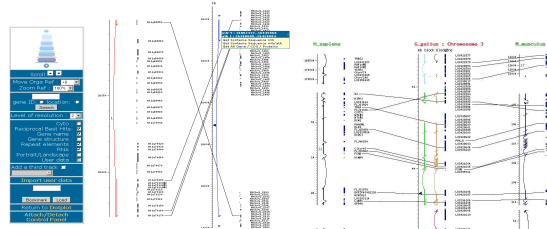
EuGene/IMGAG: International Medicago Genome Annotation Group
MIPS, TIGR, INRA-T (LIPM,BIA), VIB Gent, U. Minnesota

NARCISSE: a mirror view of conserved synteny
<http://bioinfo.genopole-toulouse.prd.fr/narcisse/>

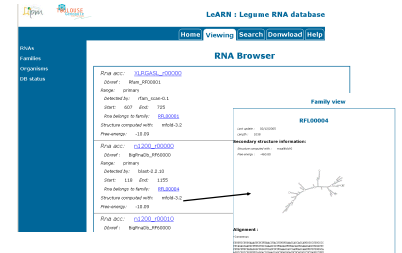
LeARN: Legume RNA database



Gouzy J. & Schiex T (INRA BIA)



Beausse Y. & Faraut T. (INRA LGC); Courcelle E & Gouzy J.



Noiret C. & Gouzy J.; Schiex T & Gaspin C. (INRA BIA)

References (2004-06)

1. Cannon SB et al. Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. *Proc Natl Acad Sci U S A*. 2006 103(40): 14959-64.
2. Carrere S, Gouzy J. REMORA: a pilot in the ocean of BioMoby web-services. *Bioinformatics*. 2006 22(7):900-1.
3. Bontemps C et al. Microarray-based detection and typing of the Rhizobium nodulation gene nodC: potential of DNA arrays to diagnose biological functions of interest. *Appl Environ Microbiol*. 2005 71(12):8042-8.
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7. Jallouf O et al. H. Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. *Nature*. 2004 431(7011):948-57.
8. El Yahyaoui F et al. Expression profiling in Medicago truncatula identifies more than 750 genes differentially expressed during nodulation, including many potential regulators of the symbiotic program. *Plant Physiol*. 2004 36:3159-76.
9. Ferreres L et al. FixI-regulated genes evolved through duplication in Sinorhizobium meliloti. *Microbiology*. 2004 150:2335-45.
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Date de création
juin 1993

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Web access
<http://lipm-grpware.toulouse.inra.fr/egroupware>

Conseil, assistance et formation des utilisateurs

Isabelle Gairin & Marcel Tantolin

Administration des ressources informatiques

- 128 Windows dont 25 portables
- 10 Stations Linux (debian) dont 1 portable
- 6 imprimantes réseaux

Serveur Bureauque
Xeon 2.8Gz, 500Gb RAID5



Serveur Bureauque Windows 2000 Terminal Server
Pentium 800Mhz; 36Gb RAID 1



• **Serveur Bioinformatique**
bi processor Xeon 3.6Gz,
• 8Gb of memory, 1.2 Tb RAID 5



Cluster de calcul
18 processors Pentium Xeon > 2.6 Gz



• **Serveur Bioinformatique Web**



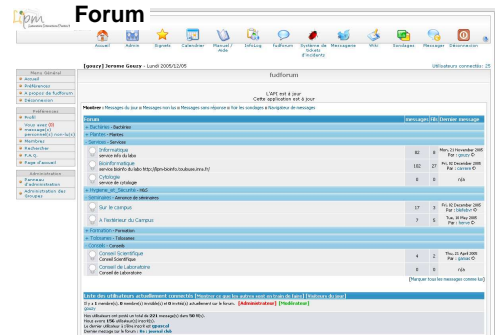
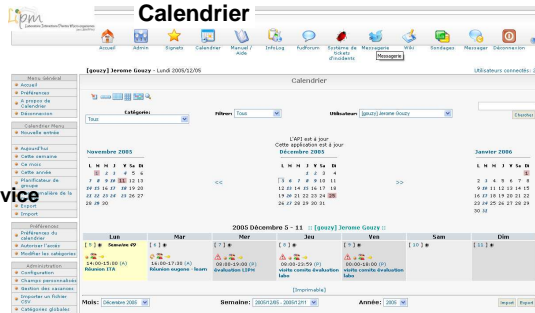
Isabelle Gairin, Marcel Tantolin & Jérôme Gouzy

Jérôme Gouzy & Emmanuel Courcelle

Favoriser le travail collaboratif

EGROUPWARE: un portail pour:

- Organiser des réunions (calendrier partagé)
- Partager l'information et les connaissances
- Afficher les demandes et réalisations du service

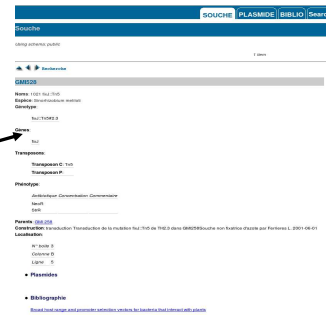
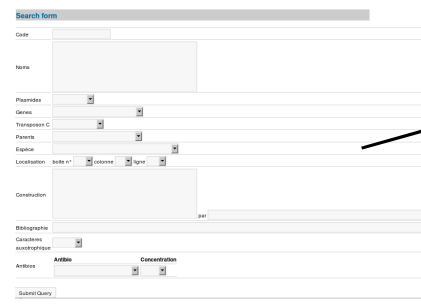
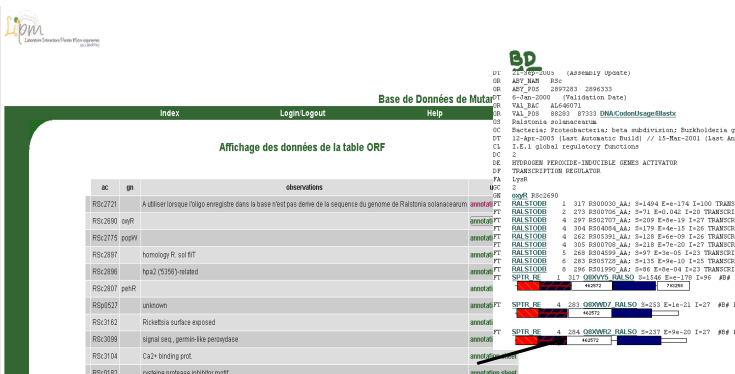


Isabelle Gairin, Marcel Tantolin, Jérôme Gouzy

Développements logiciels

BDMI: Insertion Mutants Database (Carrere S.)

▪ **CLISM: Collection LIPM Informatisée de Souches Microbiennes (en cours, Courcelle E., Carrere S.)**



▪ **Base de Données Graines (Gouzy J + externalisation)**

▪ **PHYLARRAY: Gestion des données pour la "Comparative genomic hybridization" (Carrere S.)**

