



# Quand la recherche scientifique fait de l'Agile.

Histoire d'une équipe de développement dans un milieu académique



- ① Le contexte de la recherche scientifique
- ② Le contexte de la bioinformatique
- ③ Un retour d'expérience



Définir une grille de lecture (re)connue de l'industrie et du service.

productions    modes de production    profils

connaissances

## Resource

## Windshield splitter analysis with the Galaxy metagenomic pipeline

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How many species inhabit our immediate surroundings? A straightforward collection technique suitable for assessing this question is known to anyone who has ever driven a car at highway speeds. The windshield of a moving vehicle is subjected to numerous insect strikes and can be used as a collection device for representative sampling. Unfortunately the analysis of biological material collected in that manner, as with most metagenomic studies, proves to be rather demanding due to the large number of required tools and considerable computational infrastructure. In this study, we use organic matter collected by a moving vehicle to design and test a comprehensive pipeline for phylogenetic profiling of metagenomic samples that includes all steps from processing and quality control of data generated by next-generation sequencing technologies to statistical analyses and data visualization. To the best of our knowledge, this is also the first publication that fulfills a *de novo* requirement providing access to exact analyses and workflows used in the article.

Supplemental material is available online at <http://www.genome.org>. All data and tools described in this manuscript can be downloaded or used directly at <http://galaxyproject.org>. Exact analyses and workflows used in this paper are available at <http://galaxyproject.org/workflows/whindshield-splitter>.

Metagenomics is often thought of as an exclusively microbial enterprise, as one of the first seminal papers was titled "Metagenomic applications of genomics to uncultured microorganisms" (Klappenbach 2004). Because we struggle to know the number of bacterial taxa, the major motivation behind metagenomic studies was the need to understand the diversity of rare environments by direct sampling of potentially unculturable organisms (Steele et al. 2000, 2001; Traves et al. 2000; Finster et al. 2004; Oosting 2004; Vitacek et al. 2005; Gill et al. 2006; Finster et al. 2006; von Mering et al. 2007). However, our understanding of molecular diversity may not be as complete as we would like. The number of distinct eukaryotic taxa, in particular insect taxa is likely far below recorded, the existing confusion about the species number is as striking. For example, Erwin (1982) obtained an estimate of 10 million insect species on the planet. This figure was later debated, and the latest calculations converge on an inflated guess on the order of 10 million (May 1998; Simps 1999; May 1998; Vilgashov 2004). If we accepted these estimates at face value, then only a minute number of insect species have been described to date. For example, as of February 2009 the taxonomy database at the National Center for Biotechnology Information

(NCBI) lists 338,048 species from all branches of life. In this study we apply existing metagenomic methodologies to directly determine the taxonomic composition of biological matter collected by the front end of a moving vehicle. Although our specimen collection strategy is straightforward, we set ourselves the monumental task of taxonomic identification of collected species, because morphological identification is precluded by the destructive nature of the collection procedure. Only DNA sequence analysis is feasible making this study a *de novo* metagenomic.

Metagenomic methodology has been evolving rapidly in the past few years and now includes a diverse array of approaches for profiling (binning) of complex samples (the essential services, see McInerney and Higgins 2009; Traves et al. 2007; Krumholz et al. 2006; Pop and Midgley 2006). Classification procedures make use of a number of sequence alignment and classification techniques. The figure 2006 oligonucleotide-composition (Mashury et al. 2007; McInerney and Higgins 2007; Chaffey et al. 2008), and codon usage (de Bruijn et al. 2004; Traves et al. 2004). Sequence-based methods compare an query read against existing protein markers (Shalizi et al. 2006; Ludwig and Runk 2003; Runk et al. 2007; Yu and Eisen 2006; genomic data (Angly et al. 2006; DeLong et al. 2006; Palmer et al. 2006; Traves et al. 2007). For our study in eukaryotic metagenomics, a homology-based approach is more suitable, as we do not expect complementary properties (i.e., GC content) to be informative in this, as a particular feature of insects. In addition, because we expect high taxonomic complexity within our samples, the coverage of individual eukaryotic genomes will likely be small, rendering protein gene-based approaches unwise. Hence we first cluster the reads by taxonomic phylogenetic profiling of individual samples.

In this approach we use a Bioinformatics PhD degree at NCBI, which relies on the integration of metagenomic reads against existing sequence databases.

## Automation of in-silico data analysis processes through workflow management systems

Pablo Romão

Submitted: 08 August 2007; Accepted: 01 October 2007

## Abstract

Data integration is needed in order to cope with the huge amounts of biological information now available and to perform data mining effectively. Current data integration systems have strict limitations, mainly due to the number of resources, their size and frequency of updates, their heterogeneity and distribution on the Internet. Integration must therefore be achieved by accessing network services through flexible and extensible data integration and analysis network tools. Extensible Markup Language (XML), Web Services and Workflow Management Systems (WMS) can support the creation and deployment of such systems. Many XML languages and Web Services for bioinformatics have already been designed and implemented and some WMS have been proposed. In this article, we review a methodology for data integration in biological research that is based on these technologies. We also briefly describe some of the available WMS and discuss the current limitations of this methodology and the ways in which they can be overcome.

**Keywords:** biological data integration; automation of retrieval and analysis processes; XML; web services; workflow management systems; ontologies

INTRODUCTION  
Some relevant characteristics of biological information

In the post-genomic era, a huge amount of biological and medical information is publicly available. Genome projects contributed only a fraction of all available data. Emerging research domains, like the analysis of mutations and of metabolic pathways, and high-throughput technologies are contributing with even larger amounts of data. The scientific literature remains one of the most important sources of biological information.

This information is increasing at an impressive rate. The size of the European Molecular Biology Laboratory Data Library reached 97,361,640 sequences in 91 releases. It grew by 6.78% since the previous release and by 31.50% in a year. AntipEtopes [1], a microarray experiment database maintained by the European Bioinformatics Institute

(EBI), included 2256 experiments and occupied 1,471,587,000 bytes in June 2007 with an increase of 19.02% from June 2006. As regards the literature, Medline includes >15 000 000 references.

Only a few databases are managed under a coordination effort. This is the case for nucleotide sequence databases available at EBI, National Center for Biotechnology Information (NCBI) and the Japanese National Institute of Genetics that exchange data on a peer-to-peer basis under the framework of the International Nucleotide Sequence Database Collaboration [2]. Instead, databases on similar biological objects can be managed without a common information and data structures. For example, the International Agency for Research on Cancer (Tumor Protein 53 (TP53) somatic mutation database [3], the Universal Mutation Database-TP53 [4] and the Catalogue Of Somatic Mutations in Cancer [5] all refer to mutations of the

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Pablo Romão obtained a Bioinformatics PhD degree at the Polytechnic of Milan. Since 1993 he has been a researcher at the National Cancer Research Institute of Genoa. His interests include biological databases, data modeling and integration, automation of retrieval and analysis processes through scientific tools and programming methods.

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Les productions (revues) sont dans le domaine public.  
Elles *contribuent* à la production de nouvelles connaissances.



**i Program Outline**

This may be adjusted a bit, but will stay within these topics and timepoints:

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**May 15**

05:30 FOOD

**Session 1** | 07:30pm - 09:00pm  
 07:30 Intro  
 07:35 Deploying on the Cloud  
 08:05 Q&A  
 08:15 COFFEE  
 08:30 Integrating and Scaling Analysis Tools  
 09:00 BEER

**May 16**

07:30 FOOD

**Session 2** | 09:00am - Noon  
 09:00 Building scalable Galaxy  
 09:30 Q&A  
 09:40 Libraries and Sample Tracking at NGS Facilities  
 10:10 Q&A  
 10:20 Reproducibility & Transparency: Workflows and Pages  
 11:50 Q&A  
 11:00 COFFEE  
 11:15 Building Custom Genome Browsers with Galaxy Tracker3  
 11:45 Q&A  
 Noon FOOD

**Session 3** | 02:00pm - 09:00pm  
 02:00 Contributed talks  
 05:30 FOOD  
 07:30 Lightning talks  
 09:00 BEER

**May 17**

**Break outs | Q&A and other interactions**  
 07:30 FOOD  
 09:00 Break-out sessions  
 12:00 SEE YA NEXT YEAR

*Genetics and population analysis*

**Bioinformatics challenges for genome-wide association studies**

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Accueil > L'institut > Organisation > Le dispositif de recherche > Un dispositif expérimental unique

## Un dispositif expérimental unique ouvert à la communauté scientifique

L'Inra possède un dispositif expérimental unique pour mener à bien des études tant sur les végétaux, les animaux et leurs produits, ainsi que sur l'environnement agricole. Les fermes et domaines expérimentaux, plateformes technologiques et plateaux techniques permettent également des recherches fondamentales sur des modèles animaux, végétaux ou microbiens divers et complémentaires pour élucider les bases biologiques des grandes fonctions d'intérêt agronomique. Plus récemment, l'Inra a mis en place de nouveaux dispositifs en appui aux recherches sur l'alimentation et l'environnement.

successions d'expériences  
pas de plan au sens strict



snap2objects

Quelle ingénierie pour ce contexte ?  
Quel référentiel adopter ?



**” Individuals and interactions over processes and tools”**

**"Customer collaboration over contract negotiation"**

**” Responding to change over following a plan”**



background commun: les profils nous rapprochent ...

- 1 Le contexte de la recherche scientifique
- 2 Le contexte de la bioinformatique
- 3 Un retour d'expérience



>dmel\_chr2L

```
CGACAATGCACGACAGAGGAAGCAGAACAGATATTTAGATTGCCTCTCATTTTCTCTCCC
ATATTATAGGGAGAAATATGATCGCGTATGCGAGAGTAGTGCCAACATATTGTGCTCTTT
GATTTTTTGGCAACCCAAAATGGTGGCGGATGAACGAGATGATAATATATTCAAGTTGCC
GCTAATCAGAAATAAATTCATTGCAACGTTAAATACAGCACAATATATGATCGCGTATGC
GAGAGTAGTGCCAACATATTGTGCTAATGAGTGCCTCTCGTTCTCTGTCTTATATTACCG
CAAACCCAAAAGACAATACACGACAGAGAGAGAGAGCAGCGGAGATATTTAGATTGCCT
ATTAAATATGATCGCGTATGCGAGAGTAGTGCCAACATATTGTGCTCTCTATATAATGAC
TGCCTCTCATTCTGTCTTATTTTACCGCAAACCCAAATCGACAATGCACGACAGAGGAAG
CAGAACAGATATTTAGATTGCCTCTCATTTTCTCTCCCATATTATAGGGAGAAATATGAT
CGCGTATGCGAGAGTAGTGCCAACATATTGTGCTCTTTGATTTTTTGGCAACCCAAAATG
GTGGCGGATGAACGAGATGATAATATATTCAAGTTGCCGCTAATCAGAAATAAATTCATT
GCAACGTTAAATACAGCACAATATATGATCGCGTATGCGAGAGTAGTGCCAACATATTGT
GCTAATGAGTGCCTCTCGTTCTCTGTCTTATATTACCGCAAACCCAAAAGACAATACAC
GACAGAGAGAGAGCAGCGGAGATATTTAGATTGCCTATTAAATATGATCGCGTATGCC
```

Software

Open Access

## Searching for SNPs with cloud computing

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Stem Genome Biology 2010, 11:207  
<http://genomebiology.com/2010/11/5/207>



### REVIEW

## The case for cloud computing in genome informatics

Lincoln D Stein<sup>1\*</sup>

Software

**PLAST: parallel local alignment search tool for database comparison**Van Hoa Nguyen\*<sup>1</sup> and Dominique Lavenier\*<sup>1,2</sup>

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## GPU computing for systems biology

Lorenzo Dematté and Davide Prandi

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*Sequence analysis*

## **Fast and accurate short read alignment with Burrows–Wheeler transform**

Heng Li and Richard Durbin\*

Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge, CB10 1SA, UK

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Advance Access publication May 18, 2009

Associate Editor: John Quackenbush

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**Manifesto for Agile Software Development**

We are uncovering better ways of developing software by doing it and helping others do it.  
Through this work we have come to value:

- Individuals and interactions** over processes and tools
- Working software** over comprehensive documentation
- Customer collaboration** over contract negotiation
- Responding to change** over following a plan

That is, while there is value in the items on the right, we value the items on the left more.



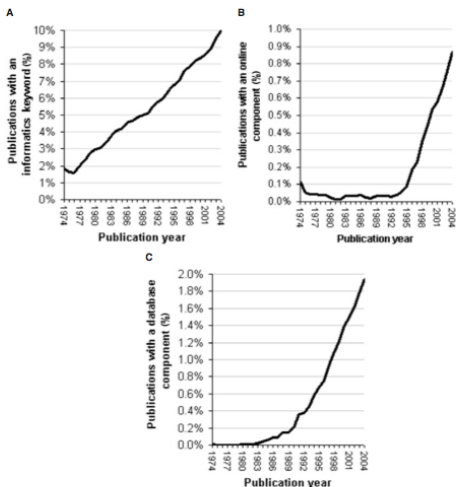
qui sommes nous ?









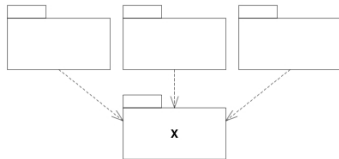


**Figure 1:** Estimated growth in the use of computational methods by year. (See Methods for details) **(A)** Growth in the percentage of publications containing computational keywords. **(B)** Growth in the percentage of publications that include or use online methods or resources. This trend persists even if only the keywords 'internet' and 'online' are used, but is slightly less pronounced. This consideration is pertinent because one would not expect phrases such as 'world wide web' to occur prior to 1994 and would want to ensure this increase is not merely an artifact of a new vocabulary word entering the literature. **(C)** Growth in the use of databases. Databases are not only useful as a means of organizing data, but are important in data-mining efforts.

- ① Le contexte de la recherche scientifique
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1 mois pour l'itération  
une équipe de développement pilote  
des utilisateurs



**Figure 2-25**  
X is a stable package

filer la métaphore des modules logiciels ...

user-stories

features

acceptance-tests

demos



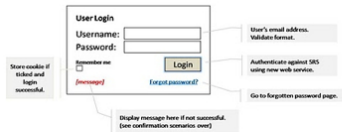
## Example of a User Story



#0001 USER LOGIN Fibonacci Size # 3

As a [registered user], I want to [log in], so I can [access subscriber content].

For new features, annotated wireframes. For bugs, steps to reproduce with screenshots. For non-functional stories, explain scope/standards.



Further information is attached to this story on VSTS Product Backlog.

about the feature.

Note the feature (for a user to log in to a web site) is small, so the story can be **fairly well described on a small card**.

Clearly it's not as detailed as a traditional specification, but **annotating a visual representation** of a small feature at a time, makes it **fairly self explanatory** for team members.

And I would certainly argue it's **more easily digestible than a lengthy specification**, especially for **business colleagues**.

Here is the **back of the card**:

I recently described **User Stories** and the **composition of a User Story Card - Card, Conversation and Confirmation**.

I'm not really sure if you would consider this example to be good, bad or indifferent - I guess it depends what you're used to - but here is an **example** nevertheless!

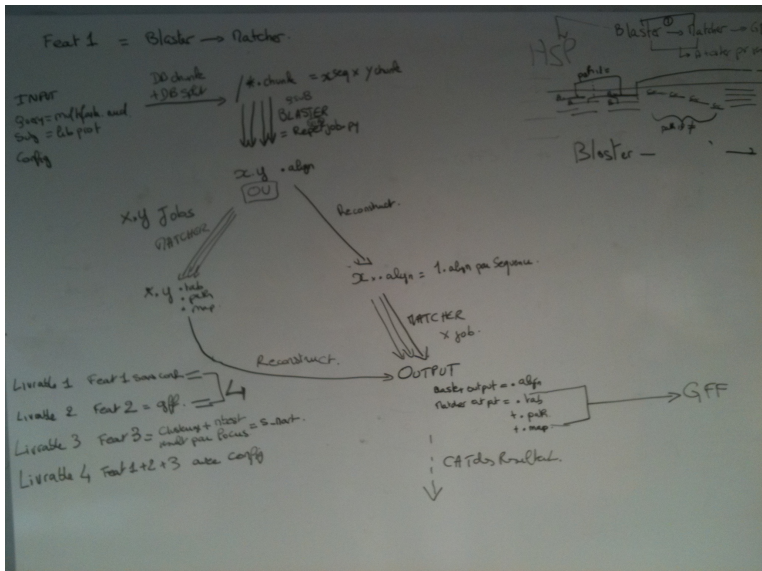
This is the **front of the card**.

The **Card** section describes the user story. The **Conversation** section provides more information

# séquence de mise en place

user-stories → ?  
acceptance-tests → ?

user-stories → ? → features  
acceptance-tests → ? → demos



```
class Test_F_BlasterMatcher2GFF3(unittest.TestCase):
```

```
def setUp(self):
    self._bm2gff3 = BlasterMatcher2GFF3()
    self._bm2gff3.setInputTab("dummy.align.match.tab")
    self._bm2gff3.setInputPath("dummy.align.match.path")
    self._expGFF3File = "exp_dummy.gff"

def tearDown(self):
    os.remove(self._obsGFF3File)

def test_Run(self):
    self._bm2gff3.run()
    self._obsGFF3File = "dummy.gff"
    areFilesIdentical = FileUtils.are2FilesIdentical(
        self._expGFF3File, self._obsGFF3File)
    self.assertTrue(areFilesIdentical)
```

**"Individuals and interactions** over processes and tools"  
confiance

features user-stories **demos** acceptance-tests

## p2: prendre soin du besoin

estimations

rôles

budget



granularité

qui ?

unité de mesure

l'échec

équipe + (n) feature leader + coach

1 = 4 jours		estimations	Backlog Mai	6
<b>TEClassifier</b>	<b>PASTEC</b>		<b>TEClassifier</b>	<b>6</b>
	Filter sur les gènes de l'hôte grâce aux profiles	1	Filter sur les gènes de l'hôte grâce aux profiles REP-617	1
	Modifier complétude grâce au coverage des blast	0,75	Modifier complétude grâce au coverage des blast Seuil raisonable pour TE complet/REP621	0,75
	Calculer taille des TE sans les répétitions terminales utiliser cette longueur pour la classif	2		
	Calculer le coverage du blastX sur le subject et pas la query	1		
	<b>Insertion automatique chado</b>		<b>Insertion automatique chado</b>	
	Validation Fct	1	Validation Fct Chado instertion: functional validation REP-646	1
	Insertion de plusieurs GFF3:		Validation Format (ii) Amélioration output et verbosité Chado insertion: format validation, increase verbosity REP-647	0,75
	(iii) Insertion N gff	1,25		
	<b>blastX2GFF</b>		<b>blastX2GFF</b>	
	Correction API Dbmysql pour accepter les « ' » dans les headers fasta des banques	0,5	Correction API Dbmysql pour accepter les « ' » dans les headers fasta des banques: REP 648	0,5
	Outil de conversion align and path en gff3	1	Outil de conversion align and path en gff3: REP 616	1
	Integration de l'outil de conversion align/path en gff3	1	Integration de l'outil de conversion align/path en gff3 REP 649	1

1 =	Mai -
1 semaine	Semaines
	18 19 20 21
Claire	2,5
Sandie	3
Olivier	1
Marc	1
Hakim	0
Nacer	0
Laetitia	2,25
Jonathan	2,25
Françoise	0
	12
Tps Binôme	6

budget

**"Customer collaboration** over contract negotiation"

features user-stories **demos** acceptance-tests **budget**

## p3: le travail collaboratif

stand-up-meeting      rotation      pair-programming  
collaborative-workspace      code-review      retrospective

# séquence de mise en place

stand-up-meeting   collaborative-workspace   code-review

masse critique



stand-up-meeting

collaborative-workspace

code-review

pair-programming

↓  
rotation

retrospective

pair-programming  
rotation

features user-stories pair-programming code-review demos  
acceptance-tests retrospective budget  
stand-up-meeting rotation

test-first

test-driven

functional-test

continuous-integration

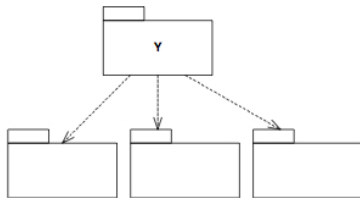
test-first → Build.py

test-first → Build.py  
functional-test → Build.py -c unitary/functional

la non régression

features user-stories pair-programming demos  
continuous-integration acceptance-tests code-review  
retrospective budget test-first  
stand-up-meeting rotation

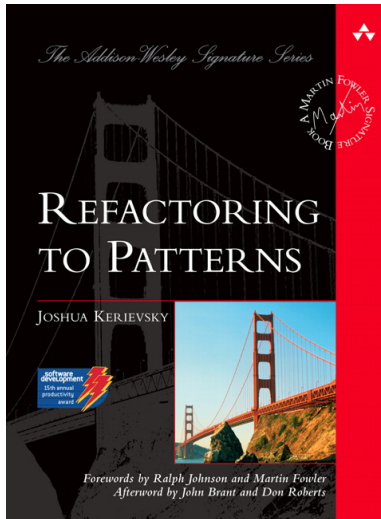
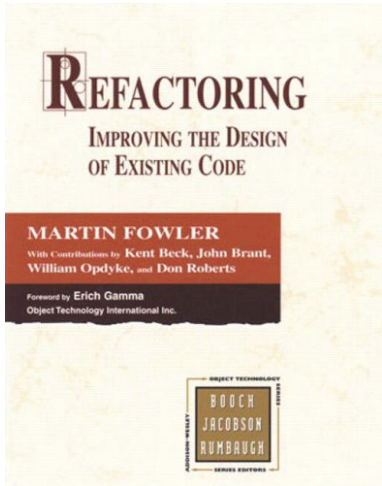




**Figure 2-26**  
Y is instable.

Dave Thomas: "The idea of tracer bullets comes obviously from gunnery artillery. In the heavy artillery days, you would take your gun position, your target position, the wind, temperature, elevation, and other factors, and feed that into a firing table. You would get a solution that said to aim your gun at this angle and elevation, and fire. And you'd fire your gun and hope that your shell landed somewhere close to your target."

"An alternative to that approach is to use **tracer bullets**. If your target is moving, or if you don't know all the factors, you use tracer bullets—little phosphorous rounds intermixed with real rounds in your gun. As you fire, you can actually see the tracer bullets. And where they are landing is where the actual bullets are landing. If you're not quite on target—because you can see if you're not on target—you can adjust your position."



Construisez votre Agilité

M E R C I

Claire Hoede

Sandie Arnoux

Françoise Alfama

Nacer Mohellibi

Dorothee Valdenaire

Marc Bras

Jonathan Kreplak

Laeticia Brigitte

Véronique Jamilloux

Timothée Flutre

Emmanuelle Permal

Michaël Alaux

Sébastien Reboux

Isabelle Luyten

Cyril Pommier

Sophie Durand

Eric Kimmel

Mathias Zytnicki

Nicolas Lapalu

Daphné Verdelet

Baptiste Brault

Aminah Keliet

Joëlle Amselem

Delphine Steinbach

Nathalie Choisne

Hadi Quesneville