

The logo for Gen2Bio features the word 'Gen' in blue, '2' in green, and 'Bio' in red. The '2' is stylized with a white outline and a green-to-yellow gradient. A registered trademark symbol (®) is located to the upper right of the 'Bio' text.

Gen2Bio®

Jeudi 3 avril 2014  
à Saint-Malo

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E-BIOGENOUEST : DÉMONSTRATIONS ET  
ÉCHANGES AUTOUR DES OUTILS DE  
L'ENVIRONNEMENT VIRTUEL DE RECHERCHE

Intervenant(s) : Yvan Le Bras, Cyril Monjeaud, Olivier  
Collin



# E-BIOGENOUEST

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Programme fédérateur Biogenouest co-financé par les Régions Bretagne et Pays de la Loire

- 24 mois
- Lancé depuis Mai 2012
- Porteur : Olivier Collin (IRISA) – Animateur : Yvan Le Bras (IRISA)
  - Tester une approche e-Science en Sciences de la vie
  - Proposer une structuration e-Science dans le Grand Ouest



# Optimiser / Standardiser

Kahn. On the future of genomic data. Science (2011)  
vol. 331 (6018) pp. 728-9

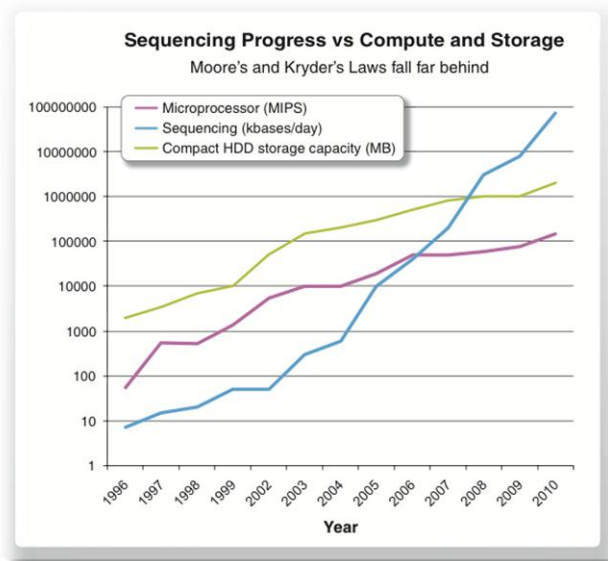
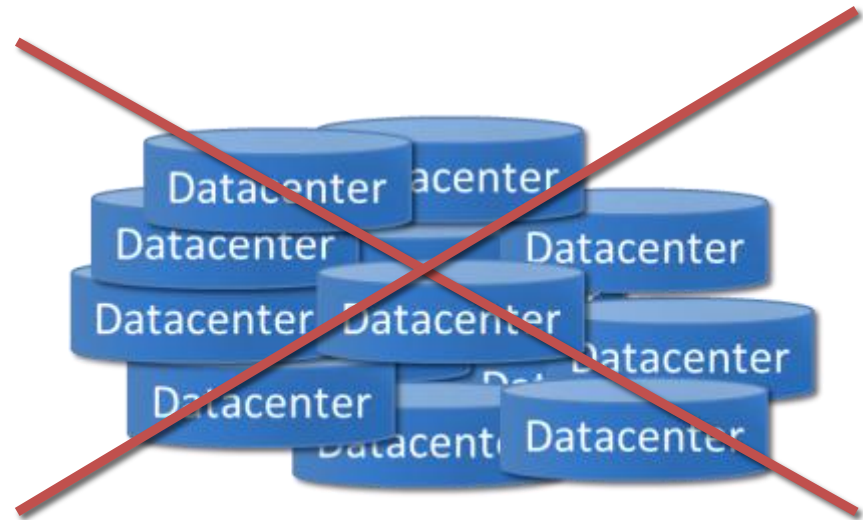


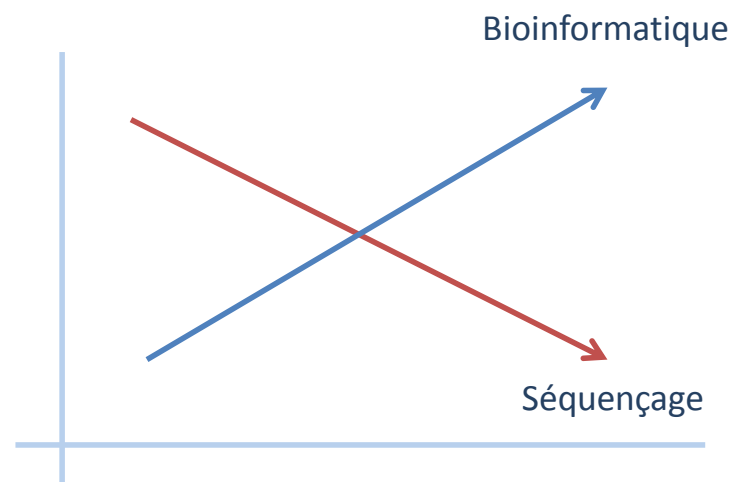
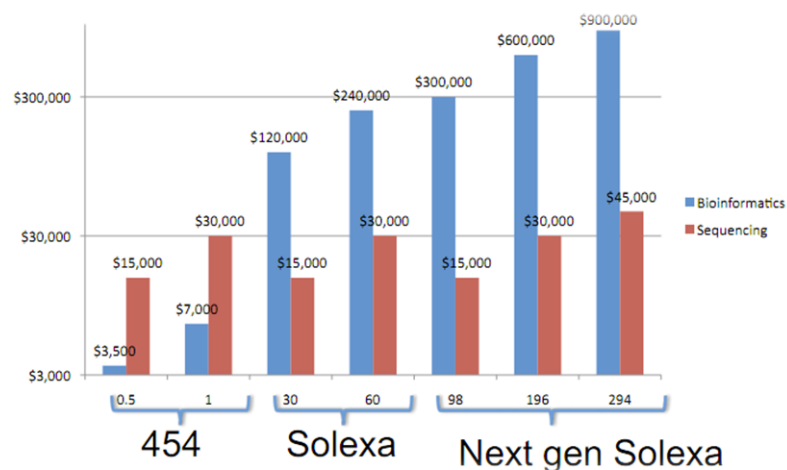
Fig. 1. A doubling of sequencing output every 9 months has outpaced and overtaken performance improvements within the disk storage and high-performance computation fields.



- Code, algorithmes, calcul, stockage, réseau, bonnes pratiques
- Prévoir interopérabilité, langage commun, vocabulaire contrôlé, ontologies



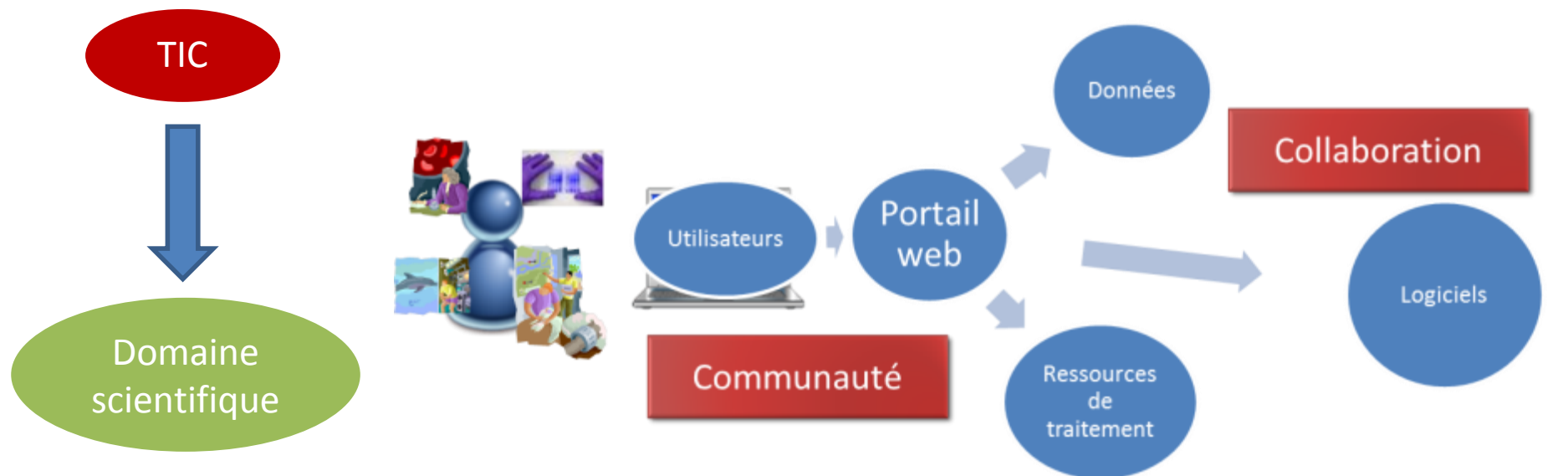
# People paradox



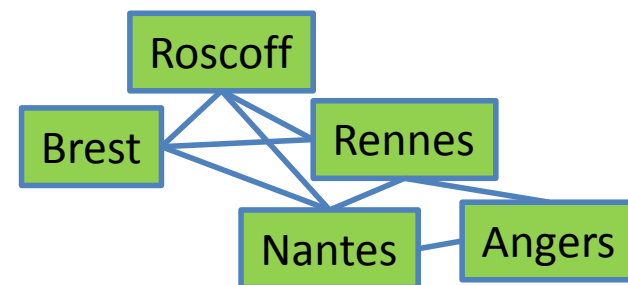
Using Clouds for Metagenomics: A Case Study Wilkening et al.  
IEEE cluster 2009

- Défis : Manque RH, Evolution des usages
- Solutions : mutualisation, science citoyenne, Environnement virtuel de recherche

# Solution : e-Science



- Une démarche e-Science
- Un environnement virtuel de recherche



# L'APPROCHE E-SCIENCE

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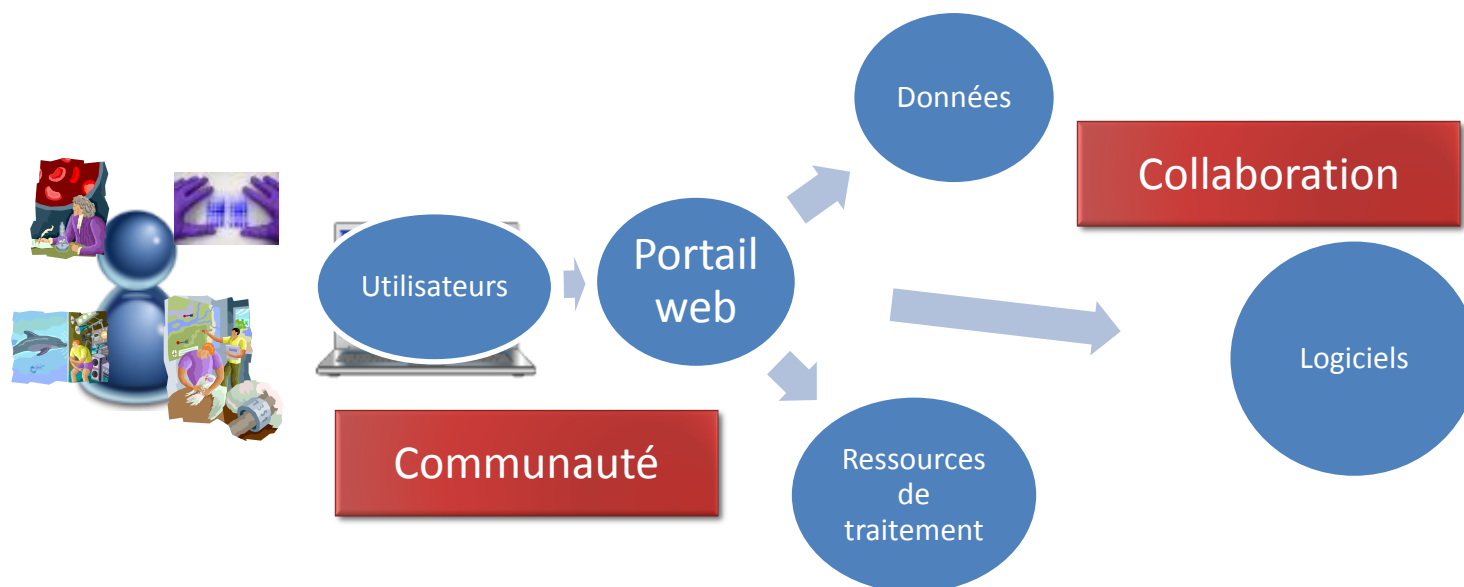
# e-Science

- e-Science = Science + TIC
- « *Research done through distributed global collaboration enabled by the internet, using very large data collections, terascale computing resources and high performance visualization* » (Sir John Taylor - 2001)
- e-Science : trois volets
  - Calcul: grille, cloud
  - Stockage
  - Outils collaboratifs
- Pas d'initiative française purement e-Science

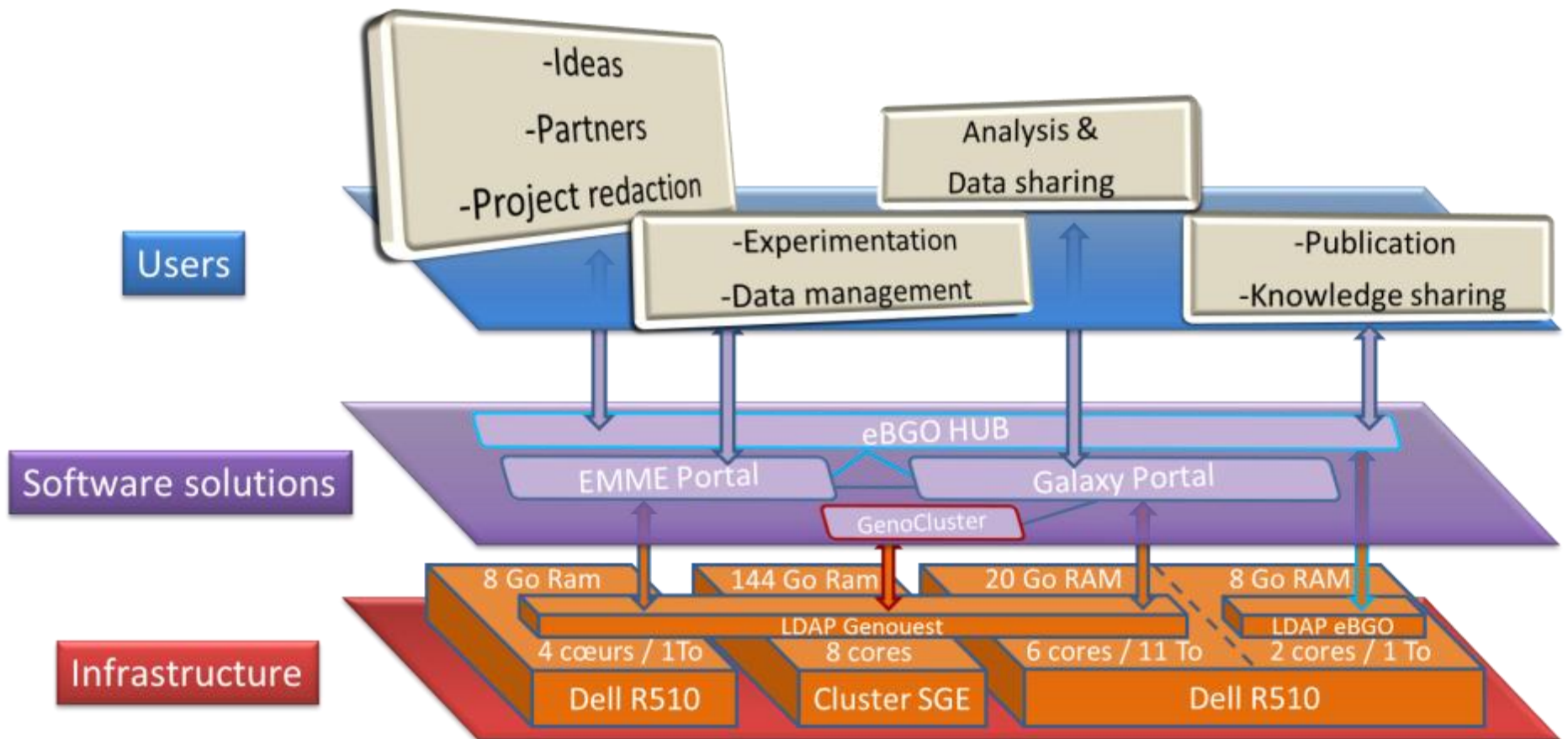
# Caractéristiques e-Science

- Caractère distribué, pas de point central...
- ... n'empêche pas un guichet unique!

## Environnement de Recherche Virtuel



# e-infrastructure test : le VRE eBiogenouest



# LE VRE

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Un environnement virtuel de recherche en sciences de la vie



# Un début de structuration e-Science?

Invite partners



record your data/metadata

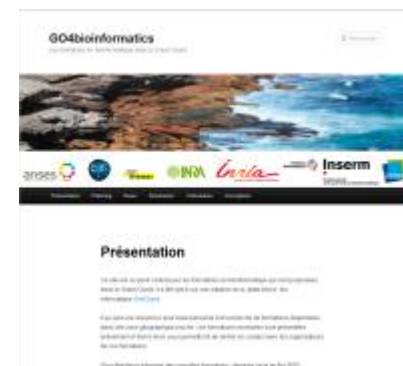


Have an idea & create a group



analyse & share your data/metadata

Training



Write & manage a new Project



# Un début de structuration e-Science?

## Le HUB eBGO

HUBzero pour partager les connaissances et gérer les groupes et projets

### Informations

125 utilisateurs

69 Projets

40 Groupes

495 ressources

...



# Un début de structuration e-Science?

## eBGO : Collaboration

The screenshot displays the eBGO website interface. At the top left is the eBGO logo with navigation links: Discover, e-Infrastructure, Community, About, and Support. A user profile for Yvan Le Bras is visible in the top right. A dark banner features statistics on the left: Galaxy by GenOuest statistics, 22729 jobs run to date, 15 jobs run this month, and 1 jobs run today. The center of the banner contains a call to action: 'Use e-Biogenouest Hub to' with sub-points: 'Create or join Groups and Projects for collaboration', 'Contribute Resources for education, training or knowledge sharing', 'Follow e-biogenouest project & e-Science point of view', and 'Manage or Analyse data'. Below the banner, a central message reads 'Welcome to ebgoHUB : The e-Science initiative of Biogenouest'. The main content area is divided into three columns: 'Featured Resources' with links to 'iMarine Gateway', 'Journal du CNRS Mai 2013', and a blog post; a 'Utilize' section with 'HUBzero users documentation' and 'eBGO HUB video tutorials'; and 'Community Polls' with a poll about bioinformatics tool usage and a 'Who are you?' section with radio button options for student and professional status. A search bar and a 'Popular Tags' section are also present.

Galaxy by GenOuest statistics

22729 jobs run to date  
15 jobs run this month  
1 jobs run today

Use e-Biogenouest Hub to

Create or join [Groups](#) and [Projects](#) for collaboration

Contribute [Resources](#) for education, training or knowledge sharing

Follow [e-biogenouest project](#) & [e-Science point of view](#)

[Manage](#) or [Analyse](#) data

Welcome to ebgoHUB : The e-Science initiative of **Biogenouest**

**Featured Resources**

- [iMarine Gateway](#) - in [Linked Resources](#)
- [Journal du CNRS Mai 2013 : Portail collaboratif du CNRS Core](#) - in [Linked Resources](#)
- ★ [Testons le blog avec Jaccard](#) by [Guillaume Collet](#) - in [Blogs](#)

Keyword or phrase:

Popular Tags: [Galaxy](#) [AVGS](#) [Data analysis](#) [Training](#) [Genomics](#)  
[Data management](#) [Population Genomics](#) [Tutorial](#) [Bio-informatics](#) [Data](#)  
[HUBzero](#) [eBGO HUB](#) [Tools](#) [More tags >](#)

[Courses](#), [Datasets](#), [Downloads](#), [Linked Resources](#), [Manuals](#), [Ph.D. Thesis](#), [Presentation Slides](#), [Publications](#), [Reports](#), [Seminars](#), [Series](#), [Tools](#), [Tutorials](#), [Workshops](#)... [All Categories >](#)

**Utilize**

View tutorials and read about how to use the numerous features of a hub. We show you how to add content, customize your dashboard, create groups, and more..

- [HUBzero users documentation](#)
- [eBGO HUB video tutorials](#)

**Community Polls**

How much time do you spend using Bioinformatics tools ?

- Less than 20%
- From 20 to 40%
- From 40 to 60%
- From 60 to 80%
- More than 80%

[Results...](#)

**Who are you?**

- Graduate student
- Undergraduate student
- High school or elementary student
- College faculty
- Professional scientist/engineer

# Un début de structuration e-Science?

## eBGO : Collaboration

The screenshot shows the eBGO website interface. At the top left is the eBGO logo. The navigation bar includes links for Discover, e-Infrastructure, Community, About, and Support. A user profile for 'Yvan Le Bras' is visible in the top right. A dropdown menu is open under 'Discover', listing Resources, What's New, Share, Tags, Wiki, Tweets, Citations, Events, and Feedback. A blue callout box with the text 'Partage de ressources' is overlaid on the page. The main content area displays a list of resources under the heading 'Resources'. Each resource entry includes a title, date, contributor(s), a brief description, and a star rating. A sidebar on the right contains a 'Time period' filter set to 'Past Quarter' and a 'Go' button. Below this is a category list with counts: All Categories (50), Events (2), Resources (44), Downloads (12), Linked Resources (11), Presentation Slides (15), Publications (4), Seminars (1), Tutorials (1), and Wiki Pages (4).

**Partage de ressources**

**Resources**

- [Biogenouest - Réunion des DU 2014 - Présentation projet e-Biogenouest première partie](#)  
21 Mar 2014 | Presentation Slides | Contributor(s): [Yvan Le Bras](#), [Olivier Collin](#) | ☆☆☆☆ 0.0 out of 5 stars  
Première partie de la présentation du projet fédérateur e-Biogenouest, posant le contexte dans lequel se place ce projet fédérateur.  
<https://www.e-biogenouest.org/resources/694>
- [Biogenouest - Réunion des DU 2014 - La démarche Qualité de PRISM](#)  
21 Mar 2014 | Presentation Slides | Contributor(s): François Mariette | ☆☆☆☆ 0.0 out of 5 stars  
"La démarche qualité de la plate-forme PRISM, une chance ou une contrainte ?" - Par François Mariette, coordinateur de la plate-forme.  
<https://www.e-biogenouest.org/resources/692>
- [Biogenouest - Réunion des DU 2014 - Présentation projet e-Biogenouest seconde partie](#)  
19 Mar 2014 | Presentation Slides | Contributor(s): [Yvan Le Bras](#), [Olivier Collin](#) | ☆☆☆☆ 0.0 out of 5 stars  
Seconde partie de la présentation du projet fédérateur e-Biogenouest, reprenant succinctement, en 5 diapos, les informations majeures de la première partie de la présentation et présentant en 3 ...  
<https://www.e-biogenouest.org/resources/690>
- [Biogenouest - Réunion des DU 2014 - Bilan et perspectives](#)  
19 Mar 2014 | Presentation Slides | Contributor(s): Catherine Boyen | ☆☆☆☆ 0.0 out of 5 stars  
Présentation du rapport d'évaluation de Biogenouest rendu par le comité d'experts extérieurs en janvier 2014. Point sur les perspectives 2014-2017. Par Catherine Boyen, membre du Comité ...  
<https://www.e-biogenouest.org/resources/688>
- [Biogenouest - Réunion des DU 2014 - Présentation des plates-formes et des missions](#)  
19 Mar 2014 | Presentation Slides | Contributor(s): [Roxanne Amelot](#) | ☆☆☆☆ 0.0 out of 5 stars  
Présentation du réseau des plates-formes Biogenouest par Roxanne Amelot, chargée de communication de Biogenouest.  
<https://www.e-biogenouest.org/resources/686>

Time period: Past Quarter [Go]

All Categories: 50  
Events: 2  
Resources: 44  
Downloads: 12  
Linked Resources: 11  
Presentation Slides: 15  
Publications: 4  
Seminars: 1  
Tutorials: 1  
Wiki Pages: 4

sis.bioinformatics.analysis.txt



# Un début de structuration e-Science?

## eBGO : une porte d'entrée vers l'e-Infrastructure



**Une porte vers les outils du VRE**

**HUB-eBGO** is an open, web-based platform for scientific collaboration in Life Sciences. It represents the gate towards a Western France Virtual Research Environment aiming at disseminate e-Science concepts into Life Sciences. This VRE is a first step to go towards e-Infrastructure development in Western France. This VRE give access to Computing resources and to several tools helping scientist to :

### Manage, Analyse, Share Data and Metadata

The **Emme** Experimental Metadata Management Environment.

The EMME project aims at facilitating the data integration and exchange among different entities of Biogenouest. In recent years, the volume and diversity of data from biological and biomedical technologies have greatly increased. This is due to multi-omics approaches performed on new species. EMME suggests the use of tools developed by the ISA team to manage experimental metadata and BiolnVdex (BII) submission. Thus, information and data from each experiment will be more easily available. ISA (Investigation / Study / Assay) infrastructure is the first to suggest a general format and a free software suite for biologists and bioinformaticians in order to: Facilitate experimental metadata local management (ie sample characteristics, technology and type of measurement, sample-related data) for studies using one or more technologies; Encourage users to use ontologies and "minimum information checklists"; Standardize the studies to submit them in public repositories such as international ENA (genomics), PRIDE (proteomics) and ArrayExpress (transcriptomics).

The **Galaxy@Genouest** web-based platform.

**Galaxy** is an open, web-based platform for accessible, reproducible, and transparent computational biomedical research. Accessible: Users without programming experience can easily specify parameters and run tools and workflows. Reproducible: Galaxy captures information so that any user can repeat and understand a complete computational analysis. Transparent: Users share and publish analyses via the web and create Pages, interactive, web-based documents that describe a complete analysis.

### Collaborate

The **HUB-eBGO** web platform for scientific collaboration.

This Hub is a resource for research, education and collaboration in Life Sciences. It hosts various resources which will help you learn about e-science, including Online Presentations, Courses, Learning Modules, Animations, Teaching Materials, and more. These resources come from contributors in our scientific community, and are used by visitors .



<http://www.biogenouest.org/einfrastructure/data>

# Un début de structuration e-Science?

## eBGO : Collaborons

**eBGO** Discover e-Infrastructure **Community** About Support

Members  
Groups  
Projects  
Questions & Answers  
Polls

Groupes, projets, forums, ...

Create User Group

### Groups

**What are groups?**  
Groups are an easy way to share content and conversation, either privately or with the world. Many times, a group already exists for a specific interest or topic. If you can't find one you like, feel free to start your own.

**How do groups work?**  
Groups can either be public, restricted (users may read a brief description or overview but not view content) or completely private. Every group has a wiki, a pool of resources, and a discussion board for talking.

**Questions?**  
Groups FAQ  
Group Guidelines

**Find a group**

Search  Search

Browse the list of available groups

A list of all public and restricted groups. Private groups are not listed.

Search group names and public descriptions. Private groups do not show up in results.

### My Groups

- Bioimaging** (Manager)
- CoordinGO** (Manager)
- eBiogenouest** (Manager)
- Galaxy User Group Grand Ouest** (Manager)
- Genouest Core Facility** (Manager)
- GO4Training** (Manager)
- L'intranet de Biogenouest** (Manager)
- Cloud group**
- e-Learning**
- France Génomique**
- Galaxy@Genouest.org Admins** (Manager)
- GO4Thesis** (Manager)
- IMPACT**
- Moby user group**

# Un début de structuration e-Science?

## eBGO : Gestion de groupes

The screenshot displays the eBGO website interface. At the top, the eBGO logo is followed by navigation links: Discover, e-Infrastructure, Community, About, and Support. A user profile for 'Yvan Le Bras' is visible in the top right corner.

The main content area is titled 'Galaxy@Genouest.org Admins' with an 'Overview' tab selected. Below the title is a breadcrumb trail: Administration > Development > Galaxy > Genouest > Tools.

The 'ABOUT THE GROUP' section contains an information icon and the text: 'The "Galaxy@Genouest.org Admins" group gathers the people developing the Genouest Galaxy-dev and Galaxy instance.' Below this is a 'Linked Galaxy groups:' section with a bulleted list:

- [Symbiose](#) : UMR CNRS 6074 IRISA-INRIA
- [GenOuest](#) : Biogenouest Bio-informatics core facility
- eBiogenouest project:
  - [eBiogenouest admin](#)
  - [eBiogenouest & Griote coordination](#)
  - [Citizen Science](#)
- [Mobyfe User Group](#)
- Galaxy groups:
  - [Galaxy@genouest.org admins](#) : GenOuest Galaxy instance administration
  - [GUGGO](#) : Groupe des Utilisateurs de Galaxy du Grand Ouest / Galaxy User Group Grand Ouest

The 'GROUP MEMBERS' section is located below and includes a 'View all members' link. It displays a grid of member profiles, each with a profile picture, name, and affiliation:

- Edouard Hirchaud (Université Nantes)
- Mathieu Charles
- Claudia Heriveau (INRIA)
- Coline Thomas (CNRS)
- Yvan Le Bras (CNRS)
- Mathieu Bahin (CNRS)
- Anthony Bretaudeau (INRA)
- Aurélien ROULT (INSERM)
- Cyril Monjeaud (CNRS)

A sidebar on the left contains a 'Group Manager' dropdown and an 'Overview' menu with items like 'Galaxy by GenOuest', 'Members' (9), 'Wiki' (41), 'Messages', 'Resources' (2), 'Discussion' (1), 'Blog', 'Wish List' (2), 'Projects', and 'Calendar'. A 'Discoverability' section in the sidebar shows 'Hidden', 'Join Policy: Invite Only', and 'Created: 16 May, 2013'.



# Un début de structuration e-Science?

## eBGO : Gestion de projets

The screenshot displays the eBGO project management interface. At the top, the eBGO logo is on the left, and navigation links for 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support' are in the center. On the right, a user profile for 'Yvan Le Bras' is visible. The main content area shows a project titled 'Galaxy@GenOuest (galaxy)' by 'Cyril Monjeaud'. A left sidebar contains navigation options: 'Updates' (2), 'Info', 'Team' (28), 'Files', 'To-do' (28), and 'Notes' (5). The main content is divided into 'Updates' and 'Latest Activity'. The 'Updates' section has a search bar with the text 'Got an update?'. The 'Latest Activity' section lists several updates by 'Yvan Le Bras', including 'Intégrer les outils phylogénétique d'Osiris Bitbucket' (1 day ago), 'Améliorer Structure pour pouvoir modifier k facilement sans reuploader un nouveau fichier de paramètre et pouvoir faire plusieurs runs avec des k dif' (1 month ago), 'Intégrer CRAC pour RNA-seq' (2 months ago), 'Installer et intégrer STACKS pour analyses RAD-seq' (2 months ago), and 'Add .cg datatype for Carthage' (3 months ago). A right sidebar contains 'To-do' and 'Notes' sections. The 'To-do' section lists tasks like 'install TESS tools ...' and 'Integrate Arlequin ...'. The 'Notes' section includes 'Ask to the System Administrator to ...' and 'Add a display application'.

eBGO Discover e-Infrastructure Community About Support

Yvan Le Bras ylebras

Project manager

### Galaxy@GenOuest (galaxy)

Public project by Cyril Monjeaud

#### Updates

Got an update?

#### Latest Activity

- Yvan Le Bras posted a to-do item: *Intégrer les outils phylogénétique d'Osiris Bitbucket* 1 day ago  
+ Comment · 1 Comment · 1 new  
[https://bitbucket.org/osiriis\\_phylogenetics/osiriis\\_phylogenetics](https://bitbucket.org/osiriis_phylogenetics/osiriis_phylogenetics)  
Yvan Le Bras · 1 day ago
- Yvan Le Bras checked off a to-do item: *Améliorer Structure pour pouvoir modifier k facilement sans reuploader un nouveau fichier de paramètre et pouvoir faire plusieurs runs avec des k dif* 1 month ago
- Yvan Le Bras posted a to-do item: *Améliorer Structure pour pouvoir modifier k facilement sans reuploader un nouveau fichier de paramètre et pouvoir faire plusieurs runs avec des k dif* 2 months ago  
+ Comment
- Yvan Le Bras posted a to-do item: *Intégrer CRAC pour RNA-seq* 2 months ago  
+ Comment · 1 Comment  
<http://www.atgc-montpellier.fr/crac/>  
Yvan Le Bras · 2 months ago
- Yvan Le Bras checked off a to-do item: *Installer et intégrer STACKS pour analyses RAD-seq* 2 months ago  
<http://creskolab.uoregon.edu/stacks/>  
Yvan Le Bras · 4 months ago  
Outils créés, tests en cours  
Yvan Le Bras · 3 months ago
- Yvan Le Bras checked off a to-do item: *Add .cg datatype for Carthage* 3 months ago
- Yvan Le Bras posted a to-do item: *intégrer FDIIST pour pop genomics à utiliser comme bayescan après STACKS* 3 months ago  
+ Comment

#### To-do

See all

- install TESS tools ...  
Aurélien R. | overdue by 3 months | 1 comment
- install hapik  
Aurélien R. | overdue by 3 months | 1 comment
- Integrate Arlequin ...  
Cyril M. | overdue by 3 months | 0 comments

#### Notes

See all

- Ask to the System Administrator to ...
- Developments
- Add a display application

# Un début de structuration e-Science?

## eBGO : Gestion de projets

**eBGO** Discover e-Infrastructure Community About Support

Yvan Le Bras ylebras

### Gestion de tâches

**Galaxy@GenOuest** (galaxy)  
Public project by Cyril Monjeaud

Project manager

**To-do**

Showing all 28 outstanding to-do item(s). Sort by:  new and ordered  due date

- Propose a Web form to test .xml and wrappers developed by members of ebgo HUB (Yvan Le Bras)
- Create a resource share category corresponding to scripts prepared for integration into Galaxy (Yvan Le Bras)
- Problème des job\_working directory non supprimés à l'issu d'un job avorté. (Cyril Monjeaud)
- Put example files for each kind of bio-analysis in the shared libraries part (Yvan Le Bras)
- Modify Velvet tools scripts adding "ulimit -v 90000000" (bash execution) before every run to allocate only 90Go ram maximum (Yvan Le Bras)
- Optimize Velvet & Velvet optimizer options to use less than a maximum amount of RAM (Yvan Le Bras)
- Add pca tools and refection of data in previous pca (using eigenfactory) (Yvan Le Bras)
- créer une visu interactive prenant sorties de clustering pour metre en face l'arbre phylogénétique correspondant avec un seuil dessus pr modifier k (Yvan Le Bras)
- Propose VM for Genocloud & virtualization on personal computer (Cyril Monjeaud)
- install hapflk (Aurélien ROULT) due 07/06/2013 (overdue)
- install TESS tools http://membres-timc.imag.fr/Olivier.Francois/te (Aurélien ROULT) due 08/28/2013 (overdue)
- install pops tools http://membres-timc.imag.fr/Olivier.Francois/pops (Aurélien ROULT)
- install LFMM tool http://membres-timc.imag.fr/Eric.Frichot/lfmm (Aurélien ROULT)
- Integrate Arlequin /softs/local/galaxy/arlequin to Galaxy (Cyril Monjeaud) due 07/09/2013 (overdue)
- Use a Cloud Galaxy Dev instance to help people contribute to our Galaxy instance (Cyril Monjeaud)
- install sNMF /home/genouest/admin@genouest.org (Aurélien ROULT)
- Remove all previous toolshed installed tools and install new proteomics tools from net (Yvan Le Bras)
- Modifier minia pour la dernière version http://minia.genouest.org/ (Yvan Le Bras)
- Intégrer Soap De Novo 2 (Cyril Monjeaud)
- Modifier le ToolFactory pour l'améliorer (Cyril Monjeaud)
- Pb avec les MAF indices et multiz4way (Cyril Monjeaud)
- Intégrer SWARM (Yvan Le Bras)

**To-do Lists**

- Administration
- Lien Recherche-Service
- Population Genetics
- Proteomics
- Scripts & tools sharing
- Tools Dev
- Training
- Use
- Visualization

My To-do's - 13 item(s)

Completed - 26 item(s)

# Un début de structuration e-Science?

## eBGO : Profil de membre

The screenshot displays the eBGO member profile dashboard for Yan Le Bras. The interface is organized into several sections:

- Header:** Includes the eBGO logo and navigation links: Discover, e-Infrastructure, Community, About, Support. The user's name and profile picture are shown in the top right.
- Left Sidebar:** A navigation menu with options: Dashboard (selected), Profile, Account, Groups (19), Points (20), Contributions (161), Usage, Favorites (14), Messages (203), Resume, Blog (5), and Projects (34).
- Profile Section:** Shows the user's name "Yvan Le Bras" and a "Dashboard" link. A "Personalize Dashboard" button is also present.
- My Groups:** A list of groups with roles: L'intranet de Biogenouest (manager), Bioimaging (manager), Cloud group (approved), CoordinaGO (manager), eBiogenouest (manager), e-Learning (approved), France Génomique (approved), Galaxy@Genouest.org Admins (manager), Genouest Core Facility (manager), and GO4Thesis (manager). Buttons for "All My Groups", "All Groups", and "New Group" are at the bottom.
- My Projects:** A list of projects: Add Galaxy Visualization (manager), Analyse Entérovirus cardiaque (manager), analyses\_prot (collaborator), APECS Cetorhinus maximus ... (manager), Bioinfo Academy (manager), Cantine Bio-informatique 2013 (manager), Cloud project (collaborator), Contribute 2 Galaxy (manager), Détection des amorces pour ... (collaborator), eBiogenouest (manager), ECS: Evolution of Cooperation ... (collaborator), EMME project ... (manager), EvalBGO (manager), FaSTRAD (manager), FG "Mapping" (collaborator), and Galaximaging (manager).
- My Tickets:** Three sections: Submitted Tickets, Assigned Tickets, and Tickets On My Contributions, all showing "You have no active tickets at this time." Buttons for "All My Tickets" and "New Ticket" are provided.
- My Messages:** A list of messages: "You are now a member of project amorcesdiopcarpon" (01 Apr 2014 11:11 AM), "Group 'radseq' Updated" (18 Mar 2014 11:31 AM), "Group 'guggo' Membership Cancelled" (11 Mar 2014 04:06 PM), "Support, Ticket" (20 Jan 2014 03:45 PM), and "Support, Ticket #17 comment" (20 Jan 2014 10:27 AM). Buttons for "All My Messages" and "Settings" are at the bottom.
- My Wishes:** Divided into Submitted and Assigned Wishes. Submitted wishes include: "#10: Proposer une journée cantine ..." (Accepted), "#9: Illustrate the group" (Pending), "#7: Add a Galaxy instance for NGS ..." (Pending), "#6: Facilitate multi-resources sharing" (Pending), "#4: Add a picture for the group" (Pending), and "#1: Logo creation for GenOuest". Assigned wishes include: "#8: Link GUGGO to the IFB France ..." (Accepted).

# Un début de structuration e-Science?

## EMME

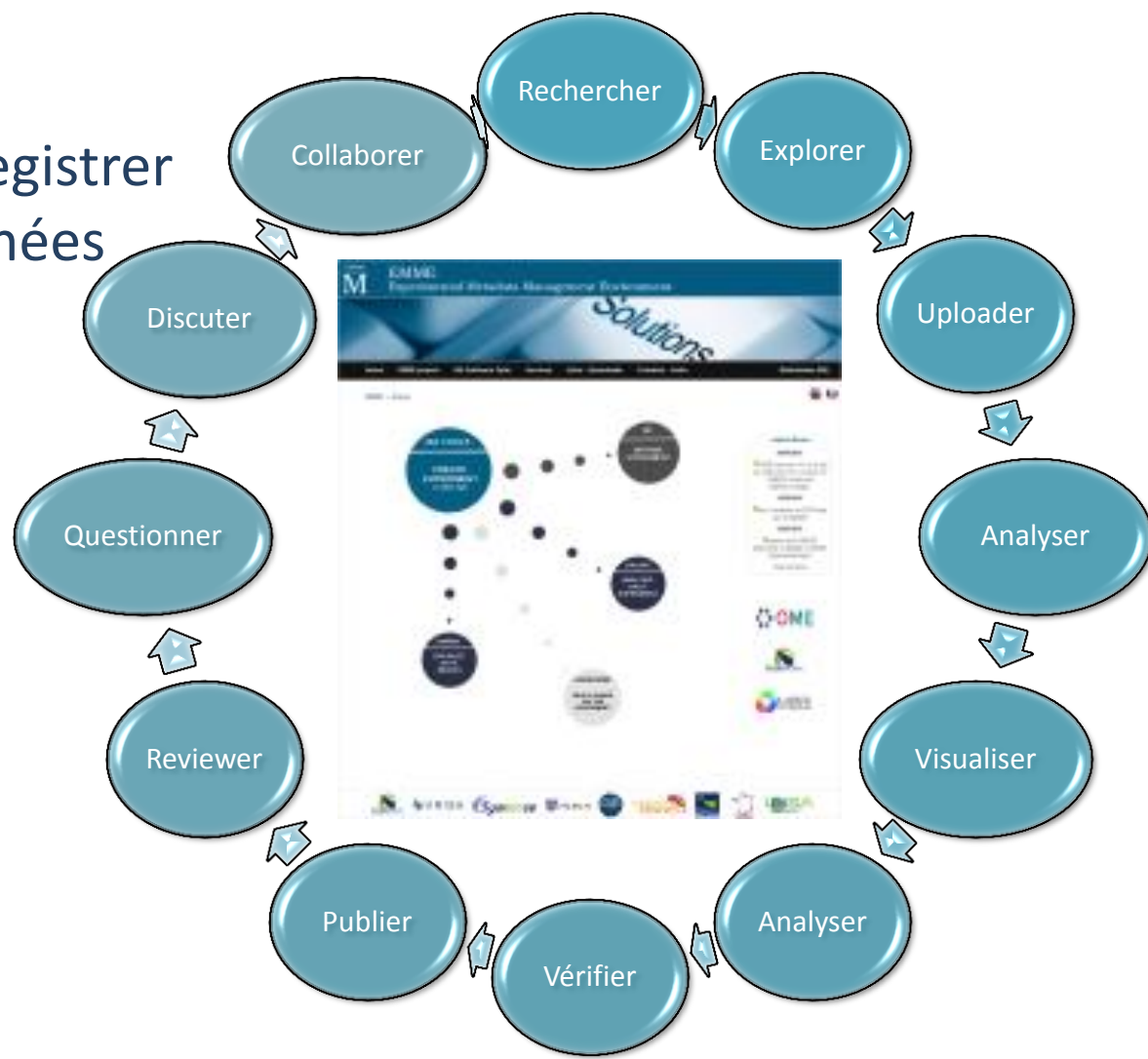
suite ISA tools pour enregistrer données et métadonnées

### Protocoles existant

Métabolomique  
Protéomique  
Génomique  
Bio-informatique

### Protocoles sur mesure

Colorimétrie  
Dosage d'ions plasmatique  
...



# Un début de structuration e-Science?

## EMME suite ISA tools : isacreator configurator

The screenshot shows the eBGO website interface. The navigation menu includes 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support'. Under 'e-Infrastructure', there are sub-menus for 'Data-centered World', 'Education', and 'Processing resources'. The 'Data-centered World' menu is expanded, showing 'Metadata management' and 'Data temporary repository'. The 'Metadata management' menu is further expanded, showing 'ISA tools suite' and 'Browse Experiments'. The main content area is titled 'ISA' and contains three paragraphs describing the tools: 'ISAconfigurator', 'ISAcreeator', and 'ISAconverter'. Below the text is a logo for 'isacreator configurator' and a note about Java Web start. A large blue callout box on the left contains text about existing protocols. The bottom right corner of the screenshot shows the text 'Powered by HUBzero® a Purdue project'.

ISA

**ISAconfigurator** : Java Application for curators to customize and regulate the fields displayed in ISAcreeator, by declaring some required fields and specifying allowed values (e.g. from a set of ontologies term).

**ISAcreeator** : friendly Java application with which the "experimentalists" can include or edit experimental metadata and validate the ISA-Tab files formatted according to the specified configuration (via the ISAconfigurator).

**ISAconverter** : Java application to validate and convert ISA-Tab files into several other tabular or XML formats to submit into public repositories such as ENA (genomics), PRIDE (proteomics) and ArrayExpress (transcriptomics).

These applications are launched by Java Web start.

During the first launch, a directory named `ISA_metadata` will be created in your home directory.

Protocoles existant  
Métabolomique, Protéomique,  
Génomique  
Protocoles sur mesure  
Bio-informatique, Protéomique  
ICPL, ...

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# Un début de structuration e-Science?

## EMME suite ISA tools : isacreator

The screenshot displays the eBGO website interface. At the top, the navigation menu includes 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support'. A dropdown menu is open under 'e-Infrastructure', listing categories such as 'Data-centered World', 'Education', 'Processing resources', 'Metadata management', 'Data analysis', and 'Genocluster FTP'. The 'Data analysis' category is selected, showing sub-items: 'Data temporary repository', 'ISA tools suite', and 'Browse Experiments'. The user profile 'Yvan Le Bras' is visible in the top right corner.

### ISA

**ISAconfigurator** : Java Application for curators to customize and regulate the fields displayed in ISAcreeator, by declaring some required fields and specifying allowed values (e.g. from a set of ontologies term).

**ISAcreeator** : friendly Java application with which the "experimentalists" can include or edit experimental metadata and validate the ISA-Tab files formatted according to the specified configuration (via the ISAconfigurator).

**ISAconverter** : Java application to validate and convert ISA-Tab file into several other tabular or XML formats to submit into public repositories such as ENA (genomics), PRIDE (proteomics) and ArrayExpress (transcriptomics).

These applications are launched by Java Web start.

During the first launch, a directory named **ISA\_metadata** will be created in your home directory. This last one will contain all configurations and ISA-tab files created with this software suite.

The bottom section shows a browser window displaying the 'isacreator' login page. The page features the 'isacreator' logo, a 'please login' prompt, and input fields for 'username' (containing 'ylebras') and 'password'. There are also buttons for 'createprofile', 'login', and 'exit'. To the right of the browser window, a 'Discover' sidebar lists 'What's New', 'Resources', 'Topics', 'Tags', and 'Knowledge Base'. A large blue 'Login' button is prominently displayed. A 'Learn' sidebar lists 'About us', 'Terms of use', 'Privacy Policy', 'Abuse Policy', and 'Copyright Infringement'. The footer indicates the site is 'Powered by HUBzero®' and a 'Purdue project'.

# Un début de structuration e-Science?

## EMME suite ISA tools : isacreator

The screenshot shows the eBGO website interface. At the top, there is a navigation menu with links for 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support'. A dropdown menu is open under 'e-Infrastructure', listing categories like 'Data-centered World', 'Education', 'Processing resources', 'Metadata management', 'Data analysis', and 'Genocluster FTP'. A sub-menu is open under 'Data analysis', showing 'Data temporary repository', 'ISA tools suite', and 'Browse Experiments'. The main content area is titled 'ISA' and contains descriptions for 'ISAconfigurator', 'ISAcreeator', and 'ISAconverter'. Below the text are three icons representing the tools. A blue box with the text 'Choix de la configuration' is overlaid on the bottom right of the screenshot. At the bottom, there is a footer with 'Discover', 'Learn', 'What's New', 'About us', 'Knowledge Base', 'Copyright Infringement', and 'Powered by HUBzero® - Purdue project'.

eBGO Discover e-Infrastructure Community About Support

Data-centered World → Metadata management → Data temporary repository

Education → Data analysis → ISA tools suite

Processing resources Genocluster FTP Browse Experiments

### ISA

**ISAconfigurator** : Java Application for curators to customize and regulate the fields displayed in ISAcreeator, by declaring some required fields and specifying allowed values (e.g. from a set of ontologies term).

**ISAcreeator** : friendly Java application with which the "experimentalists" can include or edit experimental metadata and validate the ISA-Tab files formatted according to the specified configuration (via the ISAconfigurator).

**ISAconverter** : Java application to validate and convert ISA-Tab files into several other tabular or XML formats to submit into public repositories such as ENA (genomics), PRIDE (proteomics) and ArrayExpress (transcriptomics).

isacreator configurator isacreator converter

These applications are launched by Java Web start.

During the first launch, a directory named **ISA\_metadata** will be created in your home directory. This last one will contain all configurations and ISA-tab files created with this software suite.

selected configuration to load

- EMME\_config
- EMME\_config\_2014**
- EMME\_config\_2014\_test
- isaconfig-2014226
- isaconfig-2014226fin
- isaconfig-default\_v2011-02-18

filtercontents [Q] J

search loadselected exit

Discover Learn

What's New About us

Knowledge Base Copyright Infringement

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**Choix de la configuration**



# Un début de structuration e-Science?

## EMME suite ISA tools : isacreator

The image shows a screenshot of the eBGO website. At the top, there is a navigation bar with the eBGO logo and links for Discover, e-Infrastructure, Community, About, and Support. A dropdown menu is open under e-Infrastructure, showing options like Data-centered World, Education, Processing resources, Metadata management, Data analysis, Genocluster FTP, Data temporary repository, ISA tools suite, and Browse Experiments. The user profile for Yvan Le Bras is visible in the top right corner.

Below the navigation bar, the page title is "ISA". The main content area contains three paragraphs describing the tools:

- ISAconfigurator** : Java Application for curators to customize and regulate the fields displayed in ISAcreeator, by declaring some required fields and specifying allowed values (e.g. from a set of ontologies term).
- ISAcreeator** : friendly Java application with which the "experimentalists" can include or edit experimental metadata and validate the ISA-Tab files formatted according to the specified configuration (via the ISAconfigurator).
- ISAconverter** : Java application to validate and convert ISA-Tab file into several other tabular or XML formats to submit into public repositories such as ENA (genomics), PRIDE (proteomics) and ArrayExpress (transcriptomics).

Below the text, there are three icons representing the tools: isacreator configurator, isacreator, and converter. A note states: "These applications are launched by Java Web start. During the first launch, a directory named ISA\_metadata will be created in your home directory. This last one will contain all configurations and ISA-tab files created with this software suite."

At the bottom, there is a screenshot of the isacreator application's main menu. The menu items are:

- create new experiment description
- load an existing isatab file
- merge isatab files
- settings
- load another configuration
- logout
- exit

A blue button with the text "Ouverture / création d'un projet" is overlaid on the right side of the screenshot. The footer of the website includes "Discover", "Learn", "What's New", "About us", and "Powered by HUBzero - Purdue project".

# Un début de structuration e-Science?

## EMME suite ISA tools : isacreator

The screenshot displays the eBGO website interface. At the top, the navigation menu includes 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support'. A dropdown menu is open under 'e-Infrastructure', showing options like 'Data-centered World', 'Education', 'Processing resources', 'Metadata management', 'Data analysis', 'Genocluster FTP', 'Data temporary repository', 'ISA tools suite', and 'Browse Experiments'. The 'ISA tools suite' option is highlighted.

Below the navigation, the page title is 'ISA'. The main content area contains three descriptions:

- ISAconfigurator** : Java Application for curators to customize and regulate the fields displayed in ISAcreeator, by declaring some required fields and specifying allowed values (e.g. from a set of ontologies term).
- ISAcreeator** : friendly Java application with which the "experimentalists" can include or edit experimental metadata and validate the ISA-Tab files formatted according to the specified configuration (via the ISAconfigurator).
- ISAconverter** : Java application to validate and convert ISA-Tab files into several other tabular or XML formats to submit into public repositories such as ENA (genomics), PRIDE (proteomics) and ArrayExpress (transcriptomics).

Below the text, there are three icons representing the tools: 'isacreator configurator', 'isacreator', and 'converter'. A large blue button in the bottom right corner of the screenshot reads 'Choix d'un projet préexistant'.

The 'isacreator configurator' application window is shown in the foreground, displaying a list of projects to load:

- select ISA-TAB to load
- [-] Bioinformatics2012
- [-] ET\_experiment
- [-] Proteomics2011
- [-] RADSticklebackHohenlohe
- [-] TroutGenomicsLeBrasThesis2007-2010Fin
- [-] TroutGenomicsLeBrasThesis2007-2010Test

At the bottom of the application window, there is a search bar labeled 'filtercontents', a 'search' button, and a 'loadselected' button. A '< back' button is also visible.

# Un début de structuration e-Science?

## EMME suite ISA tools : isacreator



The screenshot displays the 'isacreator' web application interface. The top navigation bar includes 'eBGO Discover e-Infrastructure Community About Support' and a user profile for 'Yvan Le Bras'. The main content area is titled 'studydefinition' and contains several sections for defining a study:

- Study description:** Includes fields for 'Study Identifier', 'Study Title', 'Study Description', 'Study Submission Date', and 'Study Public Release Date'. The 'Study Description' field contains text about next-generation sequencing technology and a genome scan of threespine stickleback.
- STUDY ASSAYS:** Includes a 'add new assay(s)' button and a list of assays such as 'genome sequencing' and 'Illumina'.
- STUDY DESIGN DESCRIPTORS:** Includes a 'add a new design column' button and fields for 'Field Name' and 'Study Design Type'.
- STUDY PUBLICATIONS:** Includes a 'add a new publication column' button and fields for 'Field Name', 'Study PubMed ID', 'Study Publication DOI', 'Study Publication Author List', 'Study Publication Title', and 'Study Publication Status'.
- STUDY FACTORS:** Includes a 'add a new factor column' button and fields for 'Field Name', 'Study Factor Name', and 'Study Factor Type'.
- STUDY PROTOCOLS:** Includes a 'add a new protocol column' button and a table for defining protocols.

A blue callout box on the right side of the interface contains the text 'Description du projet'. At the bottom left, there is an 'information' section with a diagram showing a study containing information about samples, treatments, assays, and associated assays.

Field Name	protocol	protocol	protocol	protocol	protocol	protocol	protocol	protocol
Study Protocol Name	nucleic acid extraction	library construction	nucleic acid sequencing	sequence assembly	Building loci	Read depth analysis	Cleaning sequencing data	RADseq data analysis
Study Protocol Type	nucleic acid extraction	library construction	nucleic acid sequencing	sequence assembly	Building loci	Read depth analysis	Cleaning sequencing data	RADseq data analysis
Study Protocol Description								
Study Protocol URI								
Study Protocol Version								
Study Protocol Parameters Name		library selection;libr...	base caller;quality sco...		RAD clean...	RAD analysis tools ...	RAD cleaning tool;RAD c...	RAD analysis tools ve...

# Un début de structuration e-Science? IS..

## EMME suite ISA tools : isacreator

The screenshot displays the 'isacreator' web application interface. The main window shows a table titled 'Sample Definitions' with columns for 'Row No.', 'Source Name', 'Factor Value[population]', 'Factor Value[environment]', 'Characteristic[organism]', 'Protocol REF', and 'Sample Name'. The table lists 64 samples, each with a unique identifier and associated metadata.

Row No.	Source Name	Factor Value[population]	Factor Value[environment]	Characteristic[organism]	Protocol REF	Sample Name
1	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke1	
2	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke2	
3	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke3	
4	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke4	
5	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke5	
6	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke6	
7	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke7	
8	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke8	
9	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke9	
10	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke10	
11	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke11	
12	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke12	
13	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke13	
14	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke14	
15	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke15	
16	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke16	
17	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke17	
18	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke18	
19	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke19	
20	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke20	
21	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke21	
22	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke22	
23	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke23	
24	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke24	
25	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke25	
26	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke26	
27	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke27	
28	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke28	
29	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke29	
30	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke30	
31	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke31	
32	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke32	
33	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke33	
34	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke34	
35	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke35	
36	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke36	
37	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke37	
38	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke38	
39	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke39	
40	Rabbit Slough	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke40	
41	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke41	
42	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke42	
43	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke43	
44	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke44	
45	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke45	
46	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke46	
47	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke47	
48	Bear Paw	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke48	
49	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke49	
50	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke50	
51	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke51	
52	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke52	
53	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke53	
54	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke54	
55	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke55	
56	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke56	
57	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke57	
58	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke58	
59	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke59	
60	Boot Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke60	
61	Mud Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke61	
62	Mud Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke62	
63	Mud Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke63	
64	Mud Lake	Freshwater	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke64	
65	Recombination Row	Oceanic	NCBITaxon:Gasterosteus aculeatus	sample collection	sticke65	

The interface includes a navigation menu at the top with options like 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support'. A user profile for 'Yvan Le Bras' is visible in the top right. The bottom of the screen features an 'information' icon and a 'Powered by HUBzero' logo.

Description d'une étude  
du projet

# Un début de structuration e-Science?

# ISA

## EMME suite ISA tools : isacreator

The screenshot displays the 'isacreator' web application interface. At the top, there is a navigation menu with 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support'. The main content area shows a table titled 'Assay measuring genome sequencing using e.g. OBI:nucleotide sequencing'. The table has columns for 'Row No.', 'Sample Name', 'Protocol REF', 'Extract Name', 'Protocol REF', 'Parameter Value[library source]', 'Pa...', 'Para...', 'Para...', 'Protocol REF', and 'Derived Data File'. The rows list various assays, such as '1|sticckel1', '2|sticckel2', etc., up to '64|sticckel64'. Each row contains detailed information about the assay, including the sample name, protocol reference, extract name, and the derived data file URL. A 'converter' button is visible on the right side of the interface. In the bottom right corner, there is a blue callout box with the text: 'Description d'une expérience de l'étude du projet'.

Row No.	Sample Name	Protocol REF	Extract Name	Protocol REF	Parameter Value[library source]	Pa...	Para...	Para...	Protocol REF	Derived Data File
1 sticckel1	nucleic acid extra...	lane 4, 10-Oct-2008_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
2 sticckel2	nucleic acid extra...	lane 4, 10-Oct-2008_2	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
3 sticckel3	nucleic acid extra...	lane 4, 10-Oct-2008_3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
4 sticckel4	nucleic acid extra...	lane 4, 10-Oct-2008_4	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
5 sticckel5	nucleic acid extra...	lane 4, 10-Oct-2008_5	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
6 sticckel6	nucleic acid extra...	lane 4, 10-Oct-2008_6	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
7 sticckel7	nucleic acid extra...	lane 4, 10-Oct-2008_7	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
8 sticckel8	nucleic acid extra...	lane 4, 10-Oct-2008_8	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
9 sticckel9	nucleic acid extra...	lane 4, 10-Oct-2008_9	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
10 sticckel10	nucleic acid extra...	lane 4, 10-Oct-2008_2	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
11 sticckel11	nucleic acid extra...	lane 4, 10-Oct-2008_3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
12 sticckel12	nucleic acid extra...	lane 4, 10-Oct-2008_4	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
13 sticckel13	nucleic acid extra...	lane 4, 10-Oct-2008_5	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
14 sticckel14	nucleic acid extra...	lane 4, 10-Oct-2008_6	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
15 sticckel15	nucleic acid extra...	lane 4, 10-Oct-2008_7	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
16 sticckel16	nucleic acid extra...	lane 4, 10-Oct-2008_8	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
17 sticckel17	nucleic acid extra...	lane 4, 27-Jan2009_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
18 sticckel18	nucleic acid extra...	lane 4, 27-Jan2009_2	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
19 sticckel19	nucleic acid extra...	lane 4, 27-Jan2009_3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
20 sticckel20	nucleic acid extra...	lane 4, 27-Jan2009_4	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
21 sticckel21	nucleic acid extra...	lane 4, 27-Jan2009_5	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
22 sticckel22	nucleic acid extra...	lane 4, 27-Jan2009_6	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
23 sticckel23	nucleic acid extra...	lane 4, 27-Jan2009_7	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
24 sticckel24	nucleic acid extra...	lane 4, 27-Jan2009_8	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
25 sticckel25	nucleic acid extra...	lane 4, 27-Jan2009_9	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
26 sticckel26	nucleic acid extra...	lane 4, 27-Jan2009_10	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
27 sticckel27	nucleic acid extra...	lane 4, 27-Jan2009_11	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
28 sticckel28	nucleic acid extra...	lane 4, 27-Jan2009_12	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
29 sticckel29	nucleic acid extra...	lane 4, 27-Jan2009_9	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
30 sticckel30	nucleic acid extra...	lane 4, 27-Jan2009_10	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
31 sticckel31	nucleic acid extra...	lane 4, 27-Jan2009_11	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
32 sticckel32	nucleic acid extra...	lane 4, 27-Jan2009_12	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
33 sticckel33	nucleic acid extra...	lane 4, 22-May-2009_13	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
34 sticckel34	nucleic acid extra...	lane 4, 22-May-2009_14	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
35 sticckel35	nucleic acid extra...	lane 4, 22-May-2009_15	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
36 sticckel36	nucleic acid extra...	lane 4, 22-May-2009_16	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
37 sticckel37	nucleic acid extra...	lane 4, 22-May-2009_17	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
38 sticckel38	nucleic acid extra...	lane 4, 22-May-2009_18	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
39 sticckel39	nucleic acid extra...	lane 4, 22-May-2009_19	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
40 sticckel40	nucleic acid extra...	lane 4, 22-May-2009_20	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
41 sticckel41	nucleic acid extra...	lane 4, 22-May-2009_13	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
42 sticckel42	nucleic acid extra...	lane 4, 22-May-2009_14	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
43 sticckel43	nucleic acid extra...	lane 4, 22-May-2009_15	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
44 sticckel44	nucleic acid extra...	lane 4, 22-May-2009_16	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
45 sticckel45	nucleic acid extra...	lane 4, 22-May-2009_17	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
46 sticckel46	nucleic acid extra...	lane 4, 22-May-2009_18	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
47 sticckel47	nucleic acid extra...	lane 4, 22-May-2009_19	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
48 sticckel48	nucleic acid extra...	lane 4, 22-May-2009_20	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
49 sticckel49	nucleic acid extra...	lane 6, 22-May-2009_9	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
50 sticckel50	nucleic acid extra...	lane 6, 22-May-2009_10	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
51 sticckel51	nucleic acid extra...	lane 6, 22-May-2009_11	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
52 sticckel52	nucleic acid extra...	lane 6, 22-May-2009_12	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
53 sticckel53	nucleic acid extra...	lane 6, 22-May-2009_13	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
54 sticckel54	nucleic acid extra...	lane 6, 22-May-2009_14	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequen	...	ftp://ftp-trace.ncbi.nlm...
55 sticckel55	nucleic acid extra...	lane 6, 22-May-2009_15	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
56 sticckel56	nucleic acid extra...	lane 6, 22-May-2009_16	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
57 sticckel57	nucleic acid extra...	lane 6, 22-May-2009_17	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
58 sticckel58	nucleic acid extra...	lane 6, 22-May-2009_18	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
59 sticckel59	nucleic acid extra...	lane 6, 22-May-2009_19	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
60 sticckel60	nucleic acid extra...	lane 6, 22-May-2009_20	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
61 sticckel61	nucleic acid extra...	lane 6, 22-May-2009_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
62 sticckel62	nucleic acid extra...	lane 6, 22-May-2009_2	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
63 sticckel63	nucleic acid extra...	lane 6, 22-May-2009_3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
64 sticckel64	nucleic acid extra...	lane 6, 22-May-2009_4	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...
65 sticckel65	nucleic acid extra...	lane 7, 22-May-2009_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing	...	ftp://ftp-trace.ncbi.nlm...



# Un début de structuration e-Science?

# ISA

## EMME suite ISA tools : isacreator

The screenshot shows the eBGO web interface with the 'ISA tools suite' menu open. The 'isacreator' application window is active, displaying a table of ISA tab data. The table has the following columns: Sample Name, Protocol REF, Extract Name, Protocol REF, Parameter Value[library source], Parameter Value[library strategy], Parameter Value[library selection], Parameter Value[library layout], and Protocol REF. A 'Validation Successful' message is overlaid on the table. The table contains 65 rows of data, each representing an ISA tab entry.

Sample Name	Protocol REF	Extract Name	Protocol REF	Parameter Value[library source]	Parameter Value[library strategy]	Parameter Value[library selection]	Parameter Value[library layout]	Protocol REF
1 jstckel1	nucleic acid extra...	lane 4, 10-Oct-2008_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
2 jstckel2	nucleic acid extra...	lane 4, 10-Oct-2008_2	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
3 jstckel3	nucleic acid extra...	lane 4, 10-Oct-2008_3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
4 jstckel4	nucleic acid extra...	lane 4, 10-Oct-2008_4	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
5 jstckel5	nucleic acid extra...	lane 4, 10-Oct-2008_5	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
6 jstckel6	nucleic acid extra...	lane 4, 10-Oct-2008_6	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
7 jstckel7	nucleic acid extra...	lane 4, 10-Oct-2008_7	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
8 jstckel8	nucleic acid extra...	lane 4, 10-Oct-2008_8	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
9 jstckel9	nucleic acid extra...	lane 4, 10-Oct-2008_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
10 jstckel10	nucleic acid extra...	lane 4, 10-Oct-2008_2	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
11 jstckel11	nucleic acid extra...	lane 4, 10-Oct-2008_3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
12 jstckel12	nucleic acid extra...	lane 4, 10-Oct-2008_4	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
13 jstckel13	nucleic acid extra...	lane 4, 10-Oct-2008_5	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
14 jstckel14	nucleic acid extra...	lane 4, 10-Oct-2008_6	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
15 jstckel15	nucleic acid extra...	lane 4, 10-Oct-2008_7	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
16 jstckel16	nucleic acid extra...	lane 4, 10-Oct-2008_8	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
17 jstckel17	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
18 jstckel18	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
19 jstckel19	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
20 jstckel20	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
21 jstckel21	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
22 jstckel22	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
23 jstckel23	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
24 jstckel24	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
25 jstckel25	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
26 jstckel26	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
27 jstckel27	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
28 jstckel28	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
29 jstckel29	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
30 jstckel30	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
31 jstckel31	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
32 jstckel32	nucleic acid extra...	lane 4, 27-3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
33 jstckel33	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
34 jstckel34	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
35 jstckel35	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
36 jstckel36	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
37 jstckel37	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
38 jstckel38	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
39 jstckel39	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
40 jstckel40	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
41 jstckel41	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
42 jstckel42	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
43 jstckel43	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
44 jstckel44	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
45 jstckel45	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
46 jstckel46	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
47 jstckel47	nucleic acid extra...	lane 4, 22-N	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
48 jstckel48	nucleic acid extra...	lane 4, 22-May-2009_20	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
49 jstckel49	nucleic acid extra...	lane 6, 22-May-2009_9	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
50 jstckel50	nucleic acid extra...	lane 6, 22-May-2009_10	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
51 jstckel51	nucleic acid extra...	lane 6, 22-May-2009_11	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
52 jstckel52	nucleic acid extra...	lane 6, 22-May-2009_12	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
53 jstckel53	nucleic acid extra...	lane 6, 22-May-2009_13	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
54 jstckel54	nucleic acid extra...	lane 6, 22-May-2009_14	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
55 jstckel55	nucleic acid extra...	lane 6, 22-May-2009_15	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
56 jstckel56	nucleic acid extra...	lane 6, 22-May-2009_16	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
57 jstckel57	nucleic acid extra...	lane 6, 22-May-2009_17	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
58 jstckel58	nucleic acid extra...	lane 6, 22-May-2009_18	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
59 jstckel59	nucleic acid extra...	lane 6, 22-May-2009_19	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
60 jstckel60	nucleic acid extra...	lane 6, 22-May-2009_20	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
61 jstckel61	nucleic acid extra...	lane 6, 22-May-2009_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
62 jstckel62	nucleic acid extra...	lane 6, 22-May-2009_2	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
63 jstckel63	nucleic acid extra...	lane 6, 22-May-2009_3	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
64 jstckel64	nucleic acid extra...	lane 6, 22-May-2009_4	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing
65 jstckel65	nucleic acid extra...	lane 7, 22-May-2009_1	library construction	GENOMIC	OTHER	RAD	SINGLE	nucleic acid sequencing

Validation de l'ISAtab

# Un début de structuration e-Science?

# ISA

## EMME suite ISA tools : isacreator

The screenshot displays the eBGO website interface. At the top, the navigation menu includes 'Discover', 'e-Infrastructure', 'Community', and 'About Support'. A dropdown menu is open, showing 'Data-centered World' with sub-items 'Metadata management' and 'Data temporary repository', and 'Education' with sub-items 'Data analysis' and 'ISA tools suite'. The 'ISA tools suite' option is highlighted.

The main content area shows the 'ISAcreator' tool interface. It features a table with columns for 'Sample Name', 'Protocol REF', 'Extract Name', 'Protocol REF', 'Parameter Value[library source]', 'Parameter Value[library strategy]', 'Parameter Value[library selection]', and 'Parameter Value[library layout]'. The table lists various samples (e.g., 3jstckel1, 3jstckel2) and their associated protocols and parameters.

Overlaid on the table is a dialog box titled 'Conversion de l'ISAtab'. It contains two sections: '1. Choose your conversion target(s):' and '2. Choose the output directory'. The first section has a 'start conversion' button. The second section has a 'start conversion' button. There are also checkboxes for 'SRA' and 'X All'.

At the bottom right, there is a 'converter' button and a 'Policy' link. The footer includes 'Powered by HUBzero® - Purdue project'.



# Un début de structuration e-Science? ISA

## EMME suite ISA tools : isacreator

The screenshot displays the eBGO website interface. At the top, the navigation menu includes 'Discover', 'e-Infrastructure', 'Community', 'About', and 'Support'. A dropdown menu is open under 'e-Infrastructure', showing options like 'Data-centered World', 'Education', and 'Processing resources'. The 'ISA tools suite' option is highlighted.

The main content area shows the 'ISA Creator' tool. It features a table with columns for 'Sample Name', 'Protocol REF', 'Extract Name', 'Protocol REF', 'Parameter Value[library source]', 'Parameter Value[library strategy]', 'Parameter Value[library selection]', and 'Parameter Value[library layout]'. The table lists various samples (e.g., 1|sticke11, 2|sticke12) and their associated protocols and parameters.

On the right side of the interface, there is a 'converter' button and a 'Policy' section. A large blue banner at the bottom right reads 'Création de l'ISArchive'.

At the bottom of the page, there is a footer that says 'Powered by HUBzero® - Purdue project'.

# Un début de structuration e-Science?

**GALAXY by GenOuest**  
pour analyser et partager les  
données

## Informations

22729 jobs

105 utilisateurs

Plus de 800 outils

-NGS

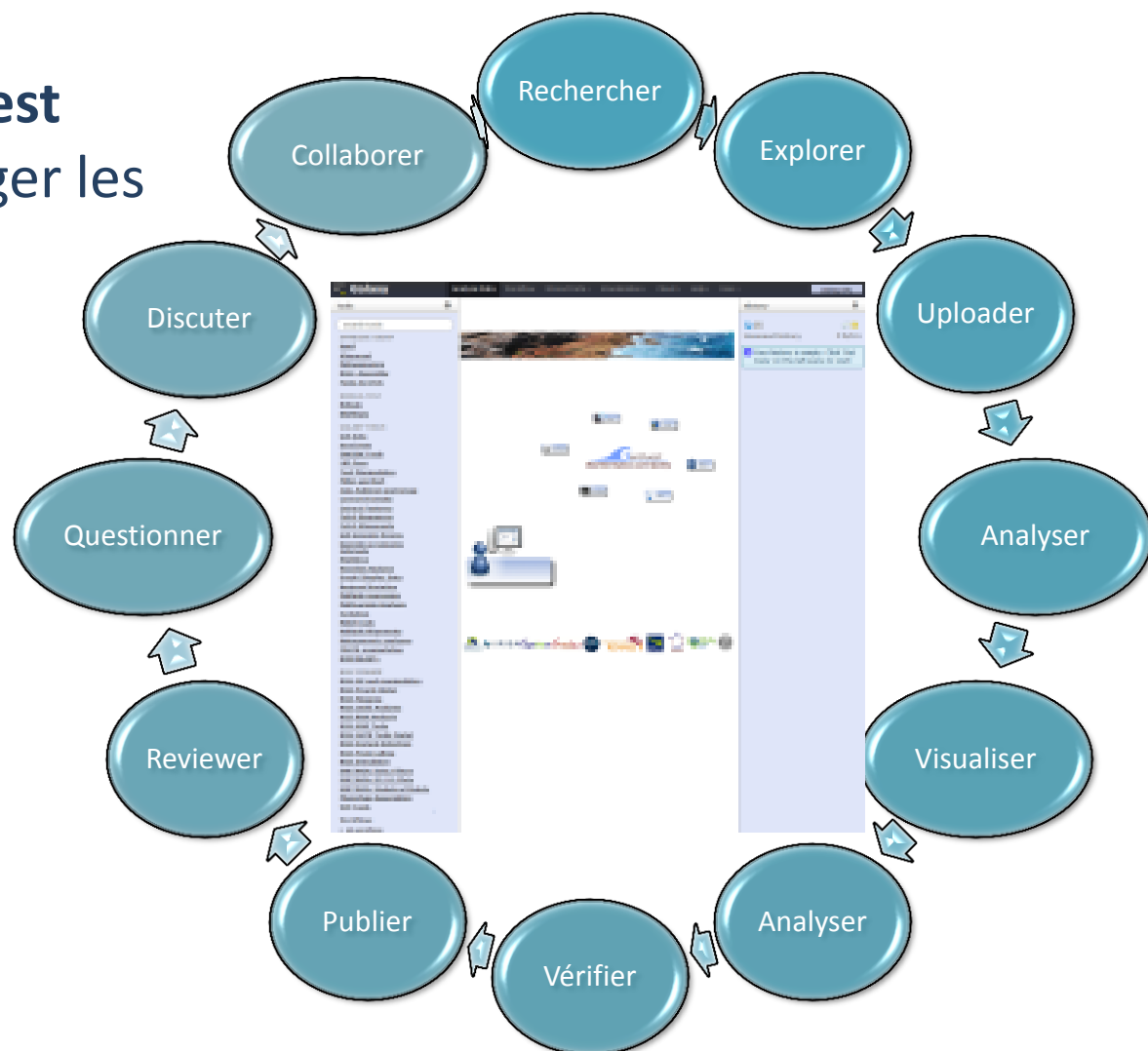
-Génomique des populations

-Génétique quantitative

-Protéomique

-Nombreux utilitaires

-...



# Un début de structuration e-Science?

## Galaxy by GenOuest : Traitement de l'ISArchive

The screenshot displays the Galaxy by GenOuest web interface. At the top, the eBGO logo and navigation menu (Discover, e-Infrastructure, Community, About, Support) are visible. A user profile for Yan Le Bras is in the top right. The main content area features a blue button labeled "Upload de l'ISArchive". Below this, the "Upload File (version 1.1.4)" tool is active, with a modal window open for file selection. The modal window has a title "Download data directly from web or upload files from your disk" and a table with the following data:

Name	Size	Type	Genome	Space	Tab	Status
RADSticklebackHohenlohe_archive.zip	8.3 KB	Auto-detect	Unspecified (?)			100% ✓

Below the table, there is a "Choose files" button and a "Create file" button. The modal also includes "Start", "Pause", "Reset", and "Close" buttons. The background interface shows various tool categories on the left and a history panel on the right.

# Un début de structuration e-Science?

## Galaxy by GenOuest : Traitement de l'ISArchive

The screenshot displays the Galaxy by GenOuest web interface. At the top, the eBGO logo and navigation links (Discover, e-Infrastructure, Community, About, Support) are visible. A user profile for 'Yvan Le Bras' is in the top right. A blue callout box in the center reads 'Décompression de l'ISArchive'. The main content area shows the 'Decompress an ISArchive (version 1.0.0)' tool configuration. The 'ISArchive file' field contains '1: RADSticklebackHohenlohe\_archive.zip'. Below the field is an 'Execute' button. The 'Tool documentation' section explains that the tool decompresses ISArchive files into zip format, extracting Investigations, Studies, and Assays files. The 'Created and integrated by' section lists Cyril Monjeaud and GenOuest Bio-informatics Core Facility. The 'History' panel on the right shows the execution history, with the current job '1: RADSticklebackHohenlohe\_archive.zip' highlighted in green.

Galaxy by GenOuest

Tools [Load Data](#)

isa

**dev-tools**

[Decompress an ISArchive](#) in zip format

**ISA-Tab toolkit**

[Download external data files from an ISA-Tab](#) into the history

[Load or unload your ISArchive](#) into the EMME BioInvIndex (BI1)

[View and import studies](#) from the EMME BioInvIndex (BI1) in an ISArchive

**Workflows**

- All workflows

**Decompress an ISArchive (version 1.0.0)**

**ISArchive file:**

1: RADSticklebackHohenlohe\_archive.zip

ISArchive must be in zip format

[Execute](#)

**Tool documentation**

This tool simply decompresses an ISArchive file in a zip format. Only Investigations, Studies and Assays files are extracted.

**Created and integrated by:**

Cyril Monjeaud  
GenOuest Bio-informatics Core Facility  
UMR 6074 IRISA INRIA-CNRS-UR1 Rennes (France)  
[support@genouest.org](mailto:support@genouest.org)

If you use this tool in Galaxy, please cite :  
Y. Le Bras, A. Roult, C. Monjeaud, M. Bahin, O. Quenez, C. Heriveau, A. Bretaudeau, O. Sallou, O. Collin, Towards a Life Sciences Virtual Research Environment : an e-Science initiative in Western France, JOBIM 2013.

**History**

Hohenlohe 2010 RADseq Stickleback  
8.1 KB

1: RADSticklebackHohenlohe\_archive.zip

# Un début de structuration e-Science?

## Galaxy by GenOuest : Traitement de l'ISArchive

The screenshot displays the Galaxy by GenOuest web interface. At the top, the eBGO logo and navigation menu (Discover, e-Infrastructure, Community, About, Support) are visible. The user profile for 'Yvan Le Bras' is in the top right. The main content area shows a workflow titled 'Log de la décompression' in a blue box. The workflow steps are:

- 1: RADSticklebackHohenlohe\_archive.zip
- 2: isa-extraction (Hohenlohe 2010 RADseq)
- 3: isa-extraction (s.Thr eespine.Stickleback.RADseq.txt)
- 4: isa-extraction (a.Hohenlohe.pop.genomics.stickleback.rad.genome.sequencing.nucleotide.sequencing.txt)
- 5: isa-extraction (a.threespine.stickleback.radseq.genome.sequencing.nucleotide.sequencing.txt)
- 6: isa-extraction (i.Investigation.txt)

The right-hand 'History' panel shows the output of the first step, 'Hohenlohe 2010 RADseq', which is a 167.9 KB file in 'isatab' format. A preview of the file content is shown below the history entry.

**Log de la décompression**





# Un début de structuration e-Science?

## Galaxy by GenOuest : Récupération des données

The screenshot displays the Galaxy by GenOuest web interface. At the top, the eBGO logo and navigation menu (Discover, e-Infrastructure, Community, About, Support) are visible. A user profile for Yvan Le Bras is in the top right. A blue callout box in the center reads "Téléchargement des données brutes pointées par les URL". The main content area shows the configuration for the 'isa' tool, which is used to download external data files from an ISA-Tab format. The tool options include downloading raw data files, derived data files, assignment files, image files, spot picking files, and acquisition parameter files. The 'Assay file in ISA-Tab format (isatab)' dropdown is set to '5: isa-extraction (a.threespine.stickleback.radseq.genome.sequencing.nucleotide.sequencing.txt)'. The 'Execute' button is visible at the bottom of the tool configuration. On the left, there are sections for 'Tools' (dev-tools, ISA-Tab toolkit, Workflows) and 'History' (listing previous tool runs with file names and sizes). On the right, a preview of the output data is shown, including a table with columns for Sample Name, Protocol REF, and Extract Name.

Galaxy by GenOuest

Tools

**dev-tools**

- Decompress an ISArchive in zip format
- ISA-Tab toolkit**
  - Download external data files from an ISA-Tab into the history
  - Load or unload your ISArchive into the EMME BioInvIndex (BII)
  - View and import studies from the EMME BioInvIndex (BII) in an ISArchive
- Workflows**
  - All workflows

**Download external data files from an ISA-Tab (version 1.0.0)**

**Assay file in ISA-Tab format (isatab):**

5: isa-extraction (a.threespine.stickleback.radseq.genome.sequencing.nucleotide.sequencing.txt)

Data links are only present in the assay file

**Download raw data files:**

Raw Data File, Raw Spectral Data File, Array Data File, Array Data Matrix File, Free Induction Decay Data File

**Download derived data files:**

Derived Data File, Derived Spectral Data File, Derived Array Data File, Derived Array Data Matrix File

**Download assignment files:**

Peptide Assignment File, Protein Assignment File, Post Translational Modification Assignment File (into a mass spectrometry experiment)

**Download image files:**

Image File (into a Gel Electrophoresis experiment)

**Download spot picking files:**

Spot Picking File (into a Gel Electrophoresis experiment)

**Download acquisition parameter files:**

Acquisition Parameter Data File (into a NMR experiment)

**Tool documentation**

This tool parse an assay file in ISA-Tab format and download only files with a web URL (<http://>, <ftp://>).

**Created and integrated by:**

Cyril Monjeaud

**History**

Hohenlohe 2010 RADseq Stickleback  
167.9 KB

7: isa-extraction (a.hohenlohe.pop.genomics.stickleback.rad.genome.sequencing.RAD.analysis.bioinformatics.analysis.txt)

6: isa-extraction (i.Inv.estliation.txt)

5: isa-extraction (a.threespine.stickleback.radseq.genome.sequencing.nucleotide.sequencing.txt)

101 lines  
format: isatab, database: 2

1	2	3	4
"Sample Name"	"Protocol REF"	"Extract Name"	
"Parameter Value[quality scorer]"	"Term a File"		
"stickel1"	"nucleic acid extraction"		
/SRP001/SRP001747/SRP0034310/SRP0034310.sra"			
"stickel2"	"nucleic acid extraction"		

4: isa-extraction (a.hohenlohe.pop.genomics.stickleback.rad.genome.sequencing.nucleotide.sequencing.txt)

3: isa-extraction (s.Threespine.Stickleback.RADseq.txt)

2: isa-extraction

1: RADSticklebackHohenlohe\_archive.zip

# Un début de structuration e-Science?

## Galaxy by GenOuest : Récupération des données

The screenshot shows the Galaxy by GenOuest web interface. At the top, there is a navigation bar with the eBGO logo and links for Discover, e-Infrastructure, Community, About, and Support. A user profile for Yan Le Bras is visible in the top right corner. The main content area is titled "Galaxy by GenOuest" and displays a "History" table with columns for tool names, URLs, and status. The table contains several rows of data, including tool names like "download-external\_data\_files.log" and "isa-extraction", along with their respective URLs and status indicators (OK or ACCESS PROBLEM). A blue button labeled "Log du download" is positioned in the center of the page. On the right side, a "History" panel shows a list of downloaded files, including "Hohenlohe 2010 RADseq Stickleback" and several "download-external\_data\_files.log" files, each with a size and a download icon.

Tools

isa

**dev-tools**

- [Decompress an ISAArchive in zip format](#)
- ISA-Tab toolkit**
- [Download external data files from an ISA-Tab into the history](#)
- [Load or unload your ISAArchive into the EMME BioInvIndex \(BII\)](#)
- [View and import studies from the EMME BioInvIndex \(BII\) in an ISAarchive](#)

**Workflows**

- All workflows

ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034312/SRR034312.sra	ACCESS PROBLEM	--
ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034315/SRR034315.sra	OK	SRR034315.sra
ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034314/SRR034314.sra	OK	SRR034314.sra
ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034311/SRR034311.sra	OK	SRR034311.sra
ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034310/SRR034310.sra	OK	SRR034310.sra
ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034313/SRR034313.sra	OK	SRR034313.sra
ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034316/SRR034316.sra	OK	SRR034316.sra

Please refresh your history if all data files are not present

**History**

**Hohenlohe 2010 RADseq Stickleback**  
4.2 GB

**14: download-external\_data\_files.log (SRR034315.sra)**  
760.2 MB  
format: sra, database: 2  
Binary sra file

**13: download-external\_data\_files.log (SRR034313.sra)**

**12: download-external\_data\_files.log (SRR034310.sra)**

**11: download-external\_data\_files.log (SRR034316.sra)**

**10: download-external\_data\_files.log (SRR034314.sra)**

**9: download-external\_data\_files.log (SRR034311.sra)**

**8: download-external\_data\_files.log**

**7: isa-extraction (a.hohenlohe.pop.genomics.stickleback.rad.genome.sequencing.RAD.analysis.bioinformatics.analysis.txt)**

**6: isa-extraction (i.Inv.estigation.txt)**

**Log du download**



# Un début de structuration e-Science?

## Galaxy by GenOuest : Analyse des données

The screenshot shows the Galaxy by GenOuest web interface. At the top, the eBGO logo and navigation menu (Discover, e-Infrastructure, Community, About, Support) are visible. The user's name, Yvan Le Bras, is in the top right corner. The main content area is titled "Galaxy by GenOuest".

The interface is divided into several panels:

- Tools:** A sidebar on the left with a search bar containing "isa" and a "Load Data" button. It lists various tools like "Decompress an ISAArchive" and "ISA-Tab toolkit".
- Upload File (version 1.1.4):** The central panel where a file is being uploaded. It shows "File Format" set to "Auto-detect", "File" size as "0.1 KB", and "Status" as "100%". A table below shows the file details:

Name	Size	Type	Genome	Space	Tab	Status
New File	0.1 KB	Auto-detect	Unspecified (?)			100%

The URL/Text field contains the following text:

```
ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034312/SRR034312.sra
```

Below the table, there is a message: "You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file." and a note: "You can Drag & Drop files into this box." At the bottom of the dialog, there are buttons for "Choose files", "Create file", "Start", "Pause", "Reset", and "Close".

On the right side, the "History" panel shows a list of previous jobs, including "Hohenlohe 2010 RADseq Stickleback" and several "download-external\_data\_files.log" jobs.

A blue callout box in the bottom right corner contains the text: "Récupération du fichier manquant (indiqué par un ACCESS PROBLEM)".

# Un début de structuration e-Science?

## Galaxy by GenOuest : Analyse des données

The screenshot displays the Galaxy by GenOuest web interface. At the top, the eBGO logo and navigation links (Discover, e-Infrastructure, Community, About, Support) are visible. The user profile for Yvan Le Bras is shown in the top right. The main content area features a 'Tools' sidebar on the left and a 'History' panel on the right. A central dialog box titled 'Download data directly from web or upload files from your disk' is open, showing two sections for file uploads. The first section, 'New File', shows a file of 0.5 KB with 'Auto-detect' type and 'Unspecified (?)' genome. The second section, 'New File', shows a file of 79 b with 'Auto-detect' type and 'Unspecified (?)' genome. Both sections contain a table of data with columns for Name, Size, Type, Genome, Space, and Status. The 'History' panel on the right lists various past entries, including 'Hohenlohe 2010 RADseq Stickleback' and several 'download-external\_data\_files.log' files.

**Download data directly from web or upload files from your disk**

Name	Size	Type	Genome	Space	Tab	Status
New File	0.5 KB	Auto-detect	Unspecified (?)			100%
GGTT	Rabbit Slough	7	SRRO34310			
GGCC	Rabbit Slough	8	SRRO34310			

Name	Size	Type	Genome	Space	Tab	Status
New File	79 b	Auto-detect	Unspecified (?)			100%
GGAA						
GGTT						
GGCC						

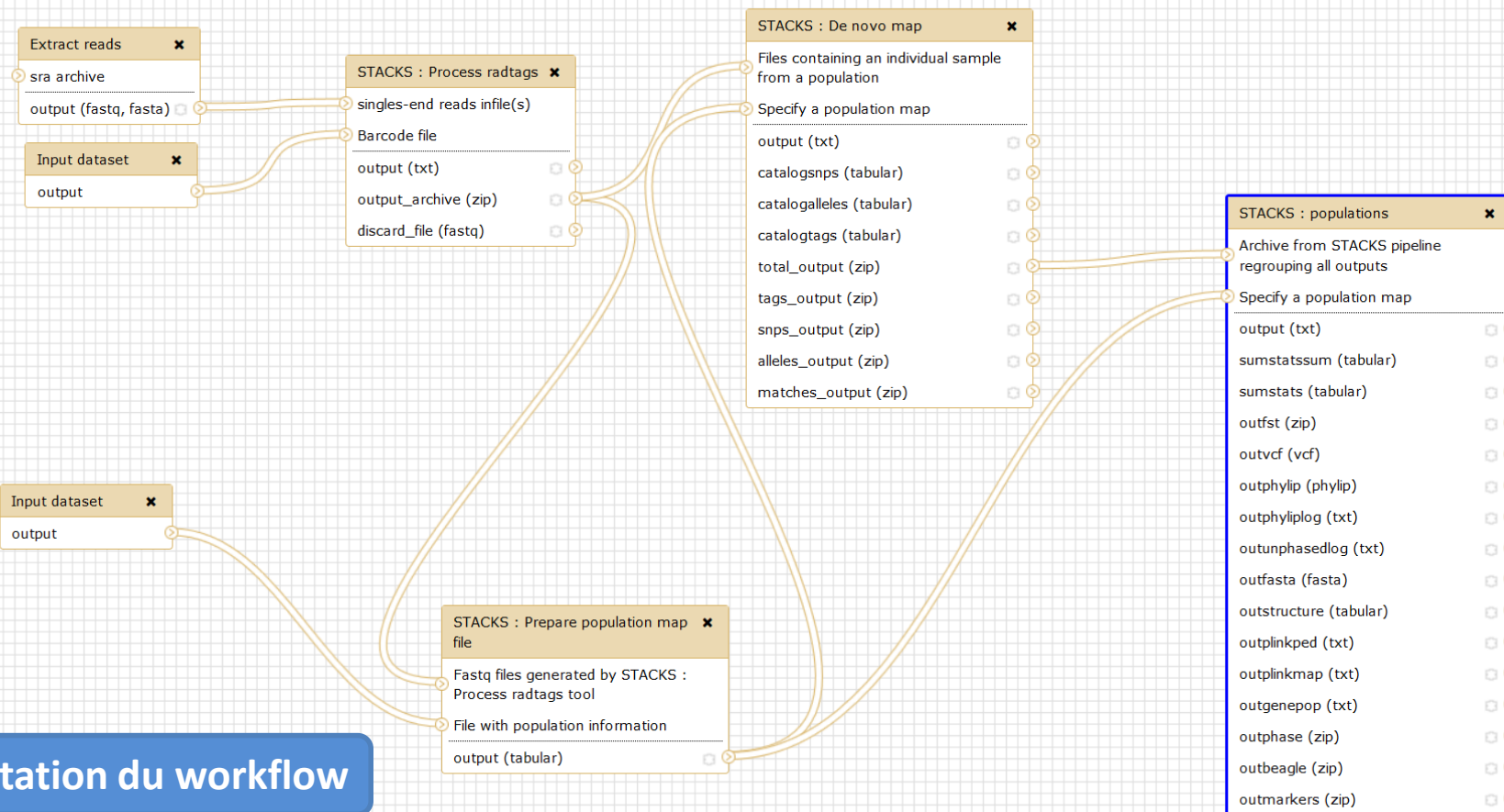
Choose files Create file Start Pause Reset Close

**Ajout du fichier de barcode et du lien barcode - population**

# Un début de structuration e-Science?

## Galaxy by GenOuest : workflow

Workflow Canvas | STACKS pipeline denovo population from sra binary



Présentation du workflow

# Un début de structuration e-Science?

## Galaxy by GenOuest : workflow



Discover e-Infrastructure Community About Support

Yvan Le Bras ylebras

Galaxy by GenOuest

Tools

stacks

### dev-tools

- [STACKS : Process radtags](#) Run the STACKS cleaning script
- [STACKS : Prepare population map file for STACKS denovomap and refmap](#)
- [STACKS : Reference map](#) Run the STACKS ref\_map.pl wrapper
- [STACKS : De novo map](#) Run the STACKS denovo\_map.pl wrapper
- [STACKS : assemble read pairs by locus](#) Run the STACKS sort\_read\_pairs.pl and exec\_velvet.pl wrappers
- [STACKS : populations](#) Run the STACKS populations program
- [STACKS : genotypes](#) Run the STACKS genotypes program
- [Map with BWA for STACKS](#) from zip file with fastq-sanger files
- [Map paired-end with BWA for STACKS](#)

### Workflows

- All workflows

## Running workflow "STACKS pipeline denovo population from sra binary"

Expand All Collapse

### Step 1: Extract reads (version 1.1.1)

**select input type**  
SRA archive in current history

**sra archive**

**minimum spot ID**  
⌵

**maximum spot ID**  
⌵

**minimum read length**  
⌵

**split spot by read pairs**  
Yes ⌵

**aligned or unaligned reads**  
both ⌵

**aligned region**  
⌵

**mate-pair distance (from-to){unknown}**  
⌵

**filter by value**  
None ⌵

**select output format**  
fastq ⌵

**filter by spot-groups**  
⌵

**apply left and right clips**  
No ⌵

### Step 2: Input dataset

**Barcode**


Sélection des fichiers et paramètres d'entrée du workflow

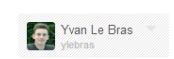
History

- Hohenlohe 2010 RADseq Stickleback**  
4.2 GB
- 17: Barcodes SRR34310 : Pasted entry**
- 16: Detailed barcode and population map SRR034310**
- 15: ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034312/SRR034312.sra**
- 14: download-external\_data\_files.log (SRR034315.sra)**
- 13: download-external\_data\_files.log (SRR034313.sra)**
- 12: download-external\_data\_files.log (SRR034310.sra)**
- 11: download-external\_data\_files.log (SRR034316.sra)**
- 10: download-external\_data\_files.log (SRR034314.sra)**
- 9: download-external\_data\_files.log (SRR034311.sra)**
- 8: download-external\_data\_files.log**
- 7: isa-extraction (a.hohenlohe.pop.genomics.stickleback.rad.genome.sequencing.RAD.analysis)**

# Un début de structuration e-Science?

## Galaxy by GenOuest : Analyse des données

 eBGO Discover e-Infrastructure Community About Support



### Galaxy by GenOuest

Tools Load Data

stacks

**dev-tools**

- [STACKS : Process radtags](#) Run the STACKS cleaning script
- [STACKS : Prepare population map file for STACKS](#) denovomap and refmap
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- [STACKS : populations](#) Run the STACKS populations program
- [STACKS : genotypes](#) Run the STACKS genotypes program

[Map with BWA for STACKS](#) from zip file with fastqsanger files

[Map paired-end with BWA for STACKS](#)

✓ Successfully ran workflow "STACKS pipeline denovo population from sra binary". The following datasets have been added to the queue:

- 18: Extract reads on data 14
- 17: Barcodes SRR34310 : Pasted entry
- 16: Detailed barcode and population map SRR034310
- 19: results.log with STACKS : Process radtags on data 18, data 17, and data 18: demultiplexed and cleaned reads
- 20: all\_files.zip with STACKS : Process radtags on data 18, data 17, and data 18: demultiplexed and cleaned reads
- 21: population\_map.txt with STACKS : Prepare population map file on data 20, data 16, and data 20
- 22: result.log with STACKS : De novo map on data 20, data 20, and data 21
- 23: catalog.snps with STACKS : De novo map on data 20, data 20, and data 21
- 24: catalog.alleles with STACKS : De novo map on data 20, data 20, and data 21
- 25: catalog.tags with STACKS : De novo map on data 20, data 20, and data 21
- 26: total\_output.zip with STACKS : De novo map on data 20, data 20, and data 21
- 27: result.log with STACKS : populations on data 21 and data 26
- 28: sumstats\_summary.tsv with STACKS : populations on data 21 and data 26
- 29: sumstats.tsv with STACKS : populations on data 21 and data 26
- 30: fst.zip with STACKS : populations on data 21 and data 26

**Exécution du workflow**

History

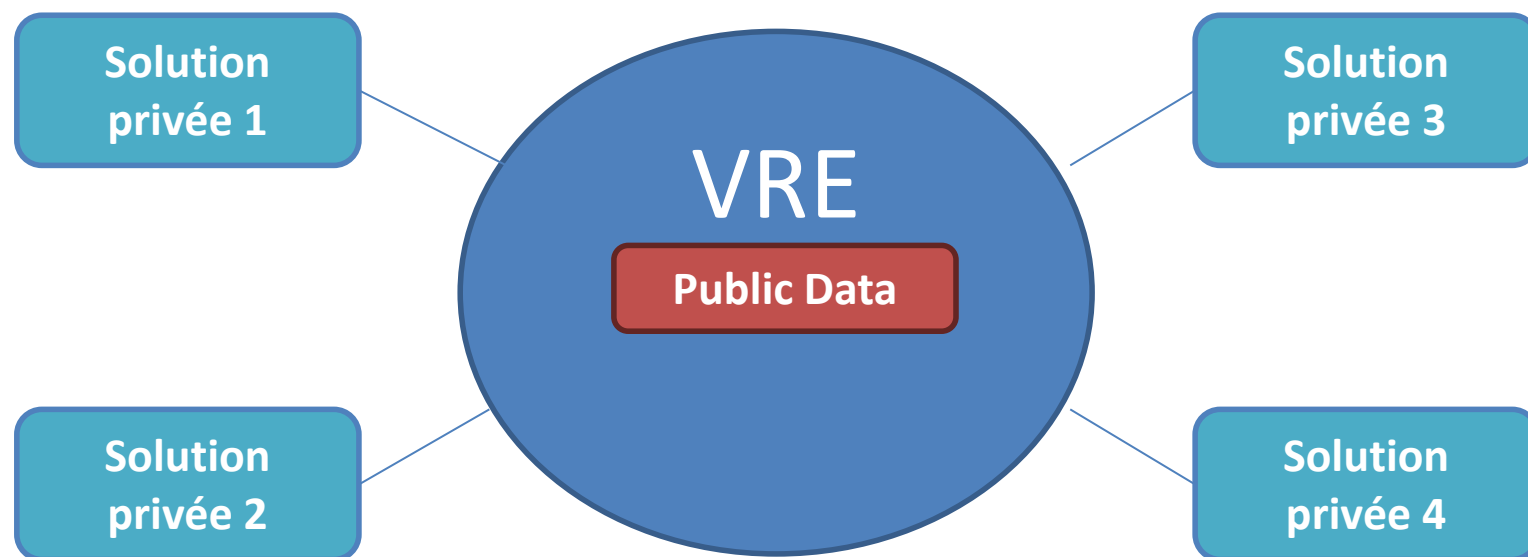
Hohenlohe 2010 RADseq Stickleback  
4.2 GB

- 17: Barcodes SRR34310 : Pasted entry
- 16: Detailed barcode and population map SRR034310
- 15: ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByStudy/sra/SRP/SRP001/SRP001747/SRR034312/SRR034312.sra
- 14: download-external\_data\_files.log (SRR034315.sra)
- 13: download-external\_data\_files.log (SRR034313.sra)
- 12: download-external\_data\_files.log (SRR034310.sra)
- 11: download-external\_data\_files.log (SRR034316.sra)
- 10: download-external\_data\_files.log (SRR034314.sra)
- 9: download-external\_data\_files.log (SRR034311.sra)
- 8: download-external\_data\_files.log
- 7: isa-extraction (a.hohenlohe\_pop.genomics.stickleback.rad.genome.sequencing\_RAD.analysis.bioinformatics.analysis.txt)

Workflows



- All workflows

# Et les solutions privées ?





# I have a dream...

- Pour les scientifiques en sciences de la vie et environnement
  - **Optimiser** son temps (programmation vs compréhension)
  - **Préserver** (données et processus analytiques)
  - **Accéder, partager et visualiser** de n'importe où
  - Une aide à la **gestion** de projet ...
- Pour les développeurs
  - Améliorer l'utilisation des algo et outils : Bioinfo **Recherche**  **Service**
  - Accélérer la mise en production
- Pour la gestion des infrastructures
  - **Optimiser** l'utilisation (stockage, calcul et réseaux...)
- Infrastructure **pour** la donnée  infrastructure **de** donnée

# Merci de votre attention

La plate-forme Bio-informatique GenOuest



Le groupe Symbiose IRISA/INRIA  
*GenOuest-Dyliss-Genscale*



Cyril Monjeaud



Olivier Collin



eBGO HUB (*collaboration*) <http://www.e-biogenouest.org/>

EMME portal (*data management*) <http://emme.genouest.org/>

Galaxy instance (*data analysis*) <http://galaxy.genouest.org/>

GO4Bioinformatics (*education*) <http://go4bioinformatics.genouest.org/>