
URGI Plant Bioinformatics Facility

Plan de gestion de données créé à l'aide de DMP OPIDoR

Créateurs du PGD : Célia Michotey, Michael Alaux

Affiliation du créateur principal : INRAE - Institut national de recherche pour l'agriculture l'alimentation et l'environnement

Modèle du PGD : INRA - Trame Structure (5 modes de gestion)

Dernière modification du PGD : 16/02/2021

Financier : INRAE - Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement

Résumé du projet :

The URGI, a research unit of INRAE (<https://urgj.versailles.inrae.fr>), hosts a bioinformatic platform (Plant Bioinformatics Facility - doi:[10.15454/1.5572414581735654E12](https://doi.org/10.15454/1.5572414581735654E12)) that supports genetic and genomic research activities on plants and fungi. Platform services cover database design, software engineering, software hosting, data integration and training. The platform activities benefit from the URGI research activities (data integration, repeat annotation, study of genome structure and evolution). It belongs to the "Institut Français de Bioinformatique" (IFB), the french node of the european network of bioinformatics platforms Elixir. It was labelled by the INRAE ISC ("Infrastructure Scientifique Collective") committee and, at the national level, by the GIS IBISA ("Groupement d'Intérêt Scientifique Infrastructures en Biologie Sante et Agronomie") as a national strategic platform. More recently, the platform belongs to the INRAE Research Infrastructure "BioInfOmics". Its management is certified ISO9001 v. 2015. For more informations, see <https://urgj.versailles.inrae.fr/Platform>.

Chercheur Principal : Michaël Alaux

Identifiant ORCID : <http://orcid.org/0000-0001-9356-4072>

Contact pour les Données : Michaël Alaux

Droits d'auteur

Le(s) créateur(s) de ce plan accepte(nt) que tout ou partie de texte de ce plan soit réutilisé et personnalisé si nécessaire pour un autre plan. Vous n'avez pas besoin de citer le(s) créateur(s) en tant que source. L'utilisation de toute partie de texte de ce plan n'implique pas que le(s) créateur(s) soutien(nen)t ou aient une quelconque relation avec votre projet ou votre soumission.

URGI Plant Bioinformatics Facility - Informations générales

Informations sur la structure

[Plant Bioinformatics Facility](#)

- Infrastructure de recherche
- ISC (Infrastructure Scientifique Collective)

Infrastructure de Recherche BioinfOmics

<https://doi.org/10.15454/1.5572414581735654E12>

Nom, Prénom	Courriel	Rôle
Quesneville, Hadi	hadi.quesneville@inrae.fr	Responsable scientifique
Alaux, Michaël	michael.alaus@inrae.fr	Responsable opérationnel

INRAE

- BAP

The platform also include ECODIV (0.8 FTE) and SPE (0.5 FTE) staff.

Datasets are currently acquired through collaborative projects with platform members. They benefit from different types of funding, the main ones being: INRAE; ANR (PIA and non PIA); EU (FP7, H2020).

Our international (e.g. IWGSC) or national data providers outside collaborative projects do not provide us with their sources of funding.

Informations sur le plan de gestion

Mode de gestion 1	GnpIS
Mode de gestion 2	Software
Mode de gestion 3	
Mode de gestion 4	
Mode de gestion 5	

Date	n° de version	Status	Auteur	Affiliation de l'auteur <i>(se reporter à l'annuaire Inra)</i>	Validé par	Validé le
16/02/2021	1	published	Célia Michotey	UR1164 URGI Unité de Recherche Génomique-Info		

<https://doi.org/10.15454/9HM5U>

URGI Plant Bioinformatics Facility - Mode de gestion 1

Présentation générale des données

- Données produites par un tiers
- Données générées par la structure

Provided by the structure:

- Genome annotations (genes and transposable elements from automatic prediction and/or curations)
- Traits ontologies

- Aggregation
- Observation
- Expérimentation
- Analyse

GnpIS stores and integrates genomic data, genetic data and phenotypic data from INRAE researchers and their national and international partners.

- Collection
- Dataset
- Software

Software are described in management mode 2

Plant and fungi genomic and genetic data provided by INRAE units, their projects partners and by the International Wheat Genome Sequencing Consortium (IWGSC).

GnpIS mostly stores textual data:

- Genetic resources (accessions, passport data, images)
- Genomic data (mostly genome annotations, polymorphisms and synteny)
- Genetic data (QTLs and GWAS analysis)
- Phenotypic data (ontologies, observations and experimental data)

Collections (Genetic resources)

- CSV/TSV
- XLS/XLSX
- JSON

Datasets

- CSV/TSV
- XLS/XLSX
- VCF
- BED
- Genbank
- EMBL
- GFF
- Fasta/FastQ
- SAM/BAM
- JSON
- RDF

Recently GnpIS has started to expose some of its data in a semantic representation to improve data integration in other databases (see <https://urqi.versailles.inra.fr/About-us/News/2017/RDF-Phenotyping>).

- Insects and Entomology
- Microorganisms
- Omics
- Biodiversity and Ecology
- Forests and Forest Products
- Plant Breeding and Plant Products
- Plant Health and Pathology

Droits de propriété intellectuelle

It is described in [our terms of use](#). We also describe conditions specific to datasets in [dedicated web pages](#).

URGI encourage users to associate DOI to the deposited datasets and help the data producers to get it with proper metadata in collaboration with [INRAE's open data repository](#) service. It allows to discuss the license associated to data with a default proposition of CC-BY V4.0 for public data.

More generally, we implement in GnpIS the terms of the data management plans of the consortium agreements of the projects producing the data stored, with some data only accessible to defined consortia of users.

The decision of data publication is taken with the submitter.

Confidentialité

- Data subject to the CNIL requirements and RGPD regulation
- Data subject to specific consortium agreements
- Datasets from private partners
- Datasets from public partners, under embargo before publication

An authenticated access is required to access private data.

When data are private, a specific group including all persons who can access the data (e.g. colleagues, project partners) is defined with the data owner in the information system. The data is tagged with this group to defined access rights, so only the persons belonging to the group can access them.

The Authentication is ruled by massively used Apache HTTP authentication system, accounts being created by our internal services on demand. The Authorization is ruled by the database mechanism described above.

The transfer of confidential data to third parties is subject to validation and follow-up by the data owner.

In details, the access of shared private data follows the same procedure as described above, re-using the authentication and authorization schemes under our control.

Partage des données

The data provider is committed to publicly open the data. An embargo period can be defined with respect to the scientific community usage.

The decision of data publication is taken with the scientific manager of the data when they are submitted.

- Update of international genetic resource catalogs

- Update of other information systems
- Re-use for new research purposes
- Support for public policy, expertise
- Trainings

Data are accessible through [web interfaces](#) and [web services APIs](#).

Data can be downloaded in various text formats (CSV/TSV, GFF, VCF ...).

Data are shared through [web interfaces](#) and [web services APIs](#) and can be downloaded in various text formats (CSV/TSV, GFF, VCF, JSON ...). Authentication is required to access private data (see [our terms of use](#)).

Some datasets are also available through:

- Our [ontology portal](#)
- [INRAE's data portal](#)
- Federated or community specific portals ([FAIDARE](#), [Plant Data-Discovery](#), [WheatIS](#), [RARE](#), [Siregal](#))

- Autre

- Public data are shared with anyone (open access)
- Private data are shared with identified users (academic and/or private partners)

- Autre (à préciser dans la zone d'Informations supplémentaires)

We encourage the scientific managers to associate a DOI to the dataset with [INRAE's open data repository](#) service. It allows to discuss the license associated to the data. By default, public data are under the CC-BY V4.0 license.

We can provide support if needed.

Organisation et documentation des données

Data on transposable elements is generated and managed following the diagram below (https://urgi.versailles.inrae.fr/files/gnpis/data_integration_repet.jpg).

Consensus of transposable element libraries are produced by REPET or REPET factory in VRE (Virtual Research Environment). Open data are inserted in RepetDB using standard formats: classification file (tsv), fasta and gff output of REPET. Data are then accessible through RepetDB, an InterMine based information system.

ISO9001 v. 2015 quality procedures exist to explain in details how to manage data in GnpIS (acquisition, validation, integration and visualization in the information system - IS, archiving). The schema below illustrates this data management (https://urgi.versailles.inrae.fr/files/gnpis/data_integration_gnpis.jpg).

Data produced by research teams are submitted to PlantBioinfoPF using standard and in house exchange formats. ETL - Extract Transform Load tools (mainly Talend Open Studio projects and Perl scripts) are used to check the data quality and consistency and to populate GnpIS RDBMS. Data from GnpIS and other IS (such as BrAPI endpoints, Data INRAE or RDF data) are integrated together in Elasticsearch using ETL tools (mainly Bash and Python scripts orchestrated with Nextflow). Data are then accessible through RESTful APIs and web portals (GnpIS, FAIDARE, Plant Data-Discovery, WheatIS, RARE, Siregal).

In the case of forest trees, different kinds of data are managed in various IS with different accessibility. To share this knowledge, we set up an automated data flow to synchronize data shared by multiple IS, as shown in the schema below (https://urgi.versailles.inrae.fr/files/gnpis/forest_interoperability.jpg).

Data produced by research teams are managed in local IS: data acquisition tools, such as Adonis, local databases and files (standards or in house formats). When data are ready to be shared, they are extracted from those local sources and inserted into GnpIS, our global IS. When relevant, data are extracted from GnpIS to be inserted into other IS to further enhance its visibility at national and/or international scale. ETL tools specific to each IS are used to

automatically manage those data flows.

Metadata	Metadata origin and production mode <i>(e.g. manual input, automatic annotation...)</i>	Standard and associated vocabularies	Conditions or frequency update (if applicable) <i>(e.g. change in accessibility)</i>
Passport data of genetic resources	Semi manual by germplasm managers in the GnpIS submission format	<ul style="list-style-type: none"> • Multi-Crop Passport Descriptors (MCPD) • Referential taxonomies (NCBI, TAXREF, Catalogue of Life) • Trait ontologies (CropOntology Trait dictionary, Trait Ontology ...) 	<ul style="list-style-type: none"> • MCPD under the governance of FAO • CropOntology Trait dictionaries updates depends on the communities
Plant phenotyping experiments	Semi-manual by the data producers in the GnpIS submission format	<ul style="list-style-type: none"> • Minimal Informations About Plant Phenotyping Experiments (MIAPPE) • Breeding API (BrAPI) • CropOntology Trait dictionary 	<ul style="list-style-type: none"> • www.miappe.org • https://brapi.org/ • Trait dictionaries updates depends on the communities
Genomic data	Semi-manual by the data producteurs in the GnpIS submission format	EMBL, NCBI recommendations	

GnpIS submission formats ensure that the essential metadata to describe and reuse the dataset is available. If necessary, documents can be attached to the data to provide further information (e.g. readme files), non-proprietary formats being strongly recommended. Moreover, we increasingly associate DOI to datasets and recommend data papers to our users as an improvement of this documentation.

Besides, data can be retrieved in standard formats:

- Trait ontologies can be retrieve in the CropOntology Trait dictionary standard in various formats via [GnpIS web interface](#) or computationally through a [BrAPI compliant web service](#).
- Genetic resources: accessions and their passport data can be retrieved as a MCPD standard compliant CSV format via GnpIS web interface or computationally through a [BrAPI compliant web service](#).
- Phenotyping data can be retrieved as a MIAPPE compliant ISA-Tab format or computationally through a [BrAPI compliant web service](#).
- Polymorphism data can be retrieved as a VCF and CSV format via GnpIS interface.
- Genome annotation data can be retrieved as a GFF3 format via web pages dedicated to the species when GnpIS is the official repository or in international archive as described in the metadata of the GnpIS JBrowse instances.
- Genetic data can be retrieved in a CSV format as there is no internationally agreed standard.

There are tools to produce these metadata:

- [Digital Curation center list of metadata tools](#)
- [RDA \(Research Data Alliance\) metadata directory](#)

ISO9001 v. 2015 quality procedures exist to define in details how to manage data in GnpIS.

ETL tools (scripts in Bash, Perl or Python and Talend Open Studio projects) are used to handle data files and control the data quality and integrity along its management from submission to access in GnpIS portal. Implementation of reproducible ETL workflows are under development using Nextflow.

The trait ontologies we develop and maintain are versioned on a public project of [INRAE's MATHNUM department forgemia](#), a GitLab forge (see [Ontologies](#)).

ISO9001 v. 2015 quality procedures exist to define in details how to manage data in GnpIS, including the steps to

control data quality and integrity.

Steps to check the validity of the submitted files (e.g. format and mandatory content respected), the data quality (e.g. controlled vocabularies/ontologies correctly used) and the dataset consistency (e.g. data and links between them coherent) are implemented in the ETL tools (scripts in Bash, Perl or Python and Talend Open Studio projects) we use to manage datasets in GnpIS. Moreover, the use of RDBMS guarantees the integrity of the data by relying on some business constraints implemented over the years. Last, when an insertion is done, several checks regarding the number of entries are also done to ensure no data is missing neither duplicated.

Stockage et sécurité des données

Data producers can access the service of data deposition by different ways, which are described in the URGI website:

- Via the platform [service-offering](#)
- Via [GnpIS submission form](#)

And specific pages dedicated to the wheat community:

- [Wheat Initiative](#)
- [IWGSC sequence repository](#)

Submitted files are archived on URGI's servers, hosted in INRAE's Ile-de-France data center. The files content is processed for the data to be inserted in the databases making up our information system (RDBMS MySQL and PostgreSQL, NoSQL Elasticsearch).

The trait ontologies we develop and maintain are versioned on a public project of the GitLab forge [forgemia](#) (see [Ontologies](#)).

Datasets: 4.5 To of storage in June 2018

Trait Ontologies: 60 MB in January 2021

Our security policy follows the [INRAE's Research Infrastructures Charter](#).

All submitted data and attached files are stored on URGI's servers, host in INRAE's Ile-de-France data center, and regularly backed up. The databases making up our information system are backed up twice a month and NetApp volumes are backed up twice a day.

Private data are only available through an authentication process. Access rights are given to a specific group including all persons who can access the data (e.g. colleagues, project partners) and defined with the data owner. The data is tagged in GnpIS with this group, so only the persons belonging to the group can access them.

The transfer of confidential data to third parties is submitted to validation and follow up by the data owner.

Private data can be provided using cryptographic based tools, such as secure shell sessions to copy the data to our servers backed by NetApp technology, which is configured to snapshot any copied data twice a day. Access to those copied files is controlled using well known UNIX permissions on Linux servers mounting the NetApp volumes only where needed.

Submitted files are following already mentioned ISO9001 v. 2015 procedures and all steps are logged into our internal JIRA instance (numeric lab book) in a dedicated task.

Trait Ontologies are managed with the functionalities of a GIT forge ([forgemia](#)).

Archivage et conservation des données

Data to keep on the long run are:

- Passport data of genetic resources and associated images
- Processed phenotyping data (not the raw data files from sensors)
- The Trait Ontologies we manage
- TE annotation data

Trait Ontologies are versioned on a public repository of [INRAE's MATHNUM department forgemia](#), a GitLab forge (see [Ontologies](#)). Otherwise, there is no action beyond GnpIS itself.

However, we progressively enforce the publication of the datasets in parallel in [INRAE's data portal](#), which in association with the DOI guarantee an access to the data for 10 years.

Trait Ontologies will be publicly accessible as long as [forgemia](#) (or an equivalent) exists. Alternate solution will be used in the unlikely shut down of those solutions.

Genetic resources and phenotyping data are strategic and conserved as long as INRAE provides means for it.

TE annotations are also versioned and conserved as long as possible, as no open access central repository exists.

For other data, it depends on the interest to be integrated in GnpIS with other datasets and on strategic issues to be discussed with the data provider.

GnpIS is so far a strategic asset of INRAE, which provides basal fundings (human resources and financial support through the URGI platform).

The platform also has access to specific fundings that allow to support GnpIS.

URGI Plant Bioinformatics Facility - Mode de gestion 2

Présentation générale des données

- Données produites par un tiers
- Données générées par la structure

As the code of our software is open, third parties can contribute to it and add new functionalities.

- Code

- Service
- Workflow
- Software

Software are tools we develop:

- Information systems implemented in Java for the backend and Angular or the GWT framework for the frontend. The data layer relies on a PostgreSQL database and an Elasticsearch cluster.
- Genome analysis tools implemented in Python and C++.

Workflow are:

- ETL (Extract Transform Load) tools used to supply our information systems with data. Scripts are developed in Bash, Perl or Python and Talend Open Studio projects.
- Pipelines of analyses tools, such as REPET suites, developed with SnakeMake and Python.

Service are RESTful web services (for instance our implementation of the Breeding API - BrAPI) developed in Java.

Software

- JSON
- Python
- C++
- Java
- TypeScript
- HTML
- SCSS
- YAML
- Markdown

Workflow

- JSON
- SQL
- Bash
- Perl
- Python
- C++
- Talend Open Studio
- Nextflow
- SnakeMake
- Ansible
- DockerFile

- Information management
- Omics

Droits de propriété intellectuelle

Institutions that payed developments of the codes (mainly INRAE).

Confidentialité

GnpIS-coreDB database model.

Our software and ETL codes are not confidential, but the master branches of their repositories are restricted for some actions.

The code of our software and ETL tools are versioned on projects of [INRAE's MATHNUM department forgemia](#), a GitLab forge. We use the application's functionalities to manage the repositories access and grants.

NA.

Partage des données

For our ETLs and software, there is no obligation to share, but we encourage users to engage (e.g. giving feedback, identifying bugs) and developers to improve the code (e.g. fixing bugs, adding new functionalities) to enhance the original repository so that anyone can take advantage of it.

However, sharing the data model of GnpIS-coreDB is prohibited.

- Creation of a new instance dedicated to a specific community
- Improvement of existing functionalities
- Addition of new functionalities to answer new needs

ETL (Extract Transform Load) tools developed with Talend Open Studio must be managed with the dedicated tool ([Talend Open Studio for Data Integration](#), freely available).

Otherwise, no specific software or tool is necessary to read the code.

- GnpIS-coreDB and our ETL are versioned on private repositories of [the GitLab forge forgemia](#) and are available upon request.
- The ETL used to supply FAIDARE with data and the Trait Ontology widget are publicly available on GitHub (see [ETL FAIDARE](#) and [Trait Ontology widget](#)).
- Our other software codes are versioned on public repositories of [the GitLab forge forgemia](#) (see [FAIDARE](#) and [Data Discovery](#)). They are also mirrored on GitHub (see [FAIDARE](#) and [Data Discovery](#)).
- Our genome analysis tools are versioned on private repositories of [the GitLab forge forgemia](#) and some codes are also versioned on public repositories on GitHub (see [TE_finder](#)).

- Autre
- Our ETLs and software are shared with anyone (open access).
- The data model of GnpIS-coreDB is shared following the proprietary license.

- Autre (à préciser dans la zone d'Informations supplémentaires)
- Our software and the ETL used to supply FAIDARE with data are under [BSD 3-Clause License](#): redistribution and use in source and binary forms, with or without modification, are permitted under specific conditions.
- Our other ETL are under [GNU LGPL v3 Licence](#) : everyone is permitted to copy and distribute verbatim copies, but changing it is not allowed.
- The data model of GnpIS-coreDB is under a proprietary license and protected by deposits at the European program deposit agency ([Agence de Protection des Programmes](#)).
- Genome analysis tools are under [CeCILLI v2.1 Licence](#): grants users the right to copy, modify, and distribute the software governed by this license under an open source distribution model.

Organisation et documentation des données

We use the functionalities of a GIT forge ([INRAE's MATHNUM GitLab instance](#)) to manage our software and ETLs codes. Except for Talend Open Studio ETLs that are versioned as is in the main (master) branch of the repository, to change the code of an ETL or a software a feature branch must be created from the master branch and each modification must be versioned in this branch. When the code is ready to be push in production, the feature branch is merged into master through a merge request implying a code review and batteries of tests to succeed.

- Data Discovery is derived from the generic data model collectively defined in [Spannagl et al. 2016](#).
- FAIDARE relies on the [Breeding API \(BrAPI\)](#) specifications, itself relying on MIAPPE standard, and follows the BrAPI community process for its update.
- The Trait Ontology widget is based on the observation variable calls of the [BrAPI](#) and follows the BrAPI community process for its update.

README files are available in each software repository to explain how to contribute, install the prerequisites, build and run the application, install the CI and set up the configuration and authentication.

Tutorials to explain how to use our analyses tools and “how to” documentation to explain how to join our federative portals (see [How to join FAIDARE](#) and [How to join Data-Discovery](#)) are also available alongside the code.

For the ETL tools, a combination of README files versioned in the ETL repository and in house good practice guides stored on our Wiki or SharePoint are available.

The ETL used to supply FAIDARE with data and the Trait Ontology widget are publicly available on GitHub (see [ETL FAIDARE](#) and [Trait Ontology widget](#)). Our other ETLs and software codes are versioned on the GitLab forge [forgemia](#). Contributing files are also available alongside the software code to explain how to manage it in GIT, how to manage the application's data, how to install the development environment and make tests (for instance, see [Contributing to FAIDARE](#)).

As explain in the contributing files, each code modification (e.g. bug fixes, new feature, version bump) must be done in a new branch of the dedicated GIT repository. When the branch is ready to be merged in the master branch, a merge request must be created. At least one core committer from our team review the code before validation and a series of tests is launch and must succeed for the branch to be merged.

For our software that are put in production via a continuous delivery, we also put in place a continuous integration that is automatically launched by GitLab on each commit push or merge request creation (see [.gitlab-ci.yml](#) file in [Data Discovery](#) and [FAIDARE](#) repositories).

Stockage et sécurité des données

Our ETLs and software codes are versioned on a GitLab forge.

Except for Talend Open Studio ETLs that are versioned as is in the main (master) branch of the repository, to change the code of an ETL or a software a feature branch must be pull from the master branch and each modification must be versioned in this branch. When the code is ready to be push in production, the feature branch is merged into master through a merge request.

- Information Systems: 1 GB
- ETLs: 1 GB
- Genome analyses tools: 10 GB

The GitLab forge Forgemia is installed on a VM hosted in INRAE's Toulouse data center.

In order to offer a high guarantee of availability and robustness, the service is virtualized on a server hosted in the data center "L'ARCHE DE DONNÉES Francis Sevila" located in INRAE's Occitanie-Toulouse center. Server administration, daily backups and GitLab's management is handled by a team of system administrators from different units of the INRAE's MATHNUM department in collaboration with the IT team of Toulouse center.

Software versioned on public repositories are in open access so they are publicly available.

Software and ETLs versioned on private repositories are accessible through an LDAP authentication.

We use the functionalities of a GIT forge ([forgemia's GitLab](#) and/or GitHub) to manage our software and ETLs code.

Archivage et conservation des données

ETLs and software codes will not be destroyed.

Some of our GitLab repositories are archived by the [Software Heritage initiative](#) once a year according to the platform decisions.

As our ETLs and software are versioned on GIT forges ([forgemia's GitLab](#) and GitHub) they will be accessible as long as those forges exists.

NA. There is no cost for the platform, forgemia's costs are supported by INRAE's MATHNUM division.

URGI Plant Bioinformatics Facility - Mode de gestion 3

Présentation générale des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Droits de propriété intellectuelle

Question sans réponse.

Confidentialité

Question sans réponse.

Question sans réponse.

Question sans réponse.

Partage des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Organisation et documentation des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Stockage et sécurité des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Archivage et conservation des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

URGI Plant Bioinformatics Facility - Mode de gestion 5

Présentation générale des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Droits de propriété intellectuelle

Question sans réponse.

Confidentialité

Question sans réponse.

Question sans réponse.

Question sans réponse.

Partage des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Organisation et documentation des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Stockage et sécurité des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Archivage et conservation des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

URGI Plant Bioinformatics Facility - Mode de gestion 4

Présentation générale des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Droits de propriété intellectuelle

Question sans réponse.

Confidentialité

Question sans réponse.

Question sans réponse.

Question sans réponse.

Partage des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Organisation et documentation des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Stockage et sécurité des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.

Archivage et conservation des données

Question sans réponse.

Question sans réponse.

Question sans réponse.

Question sans réponse.