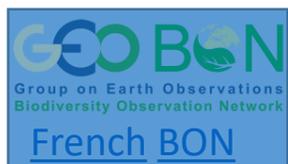
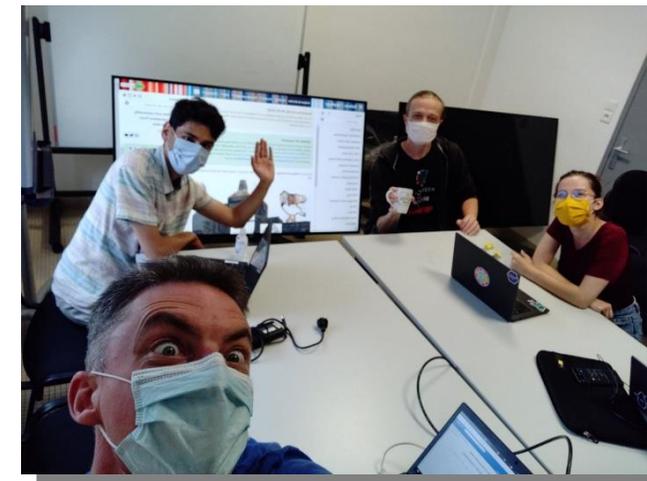


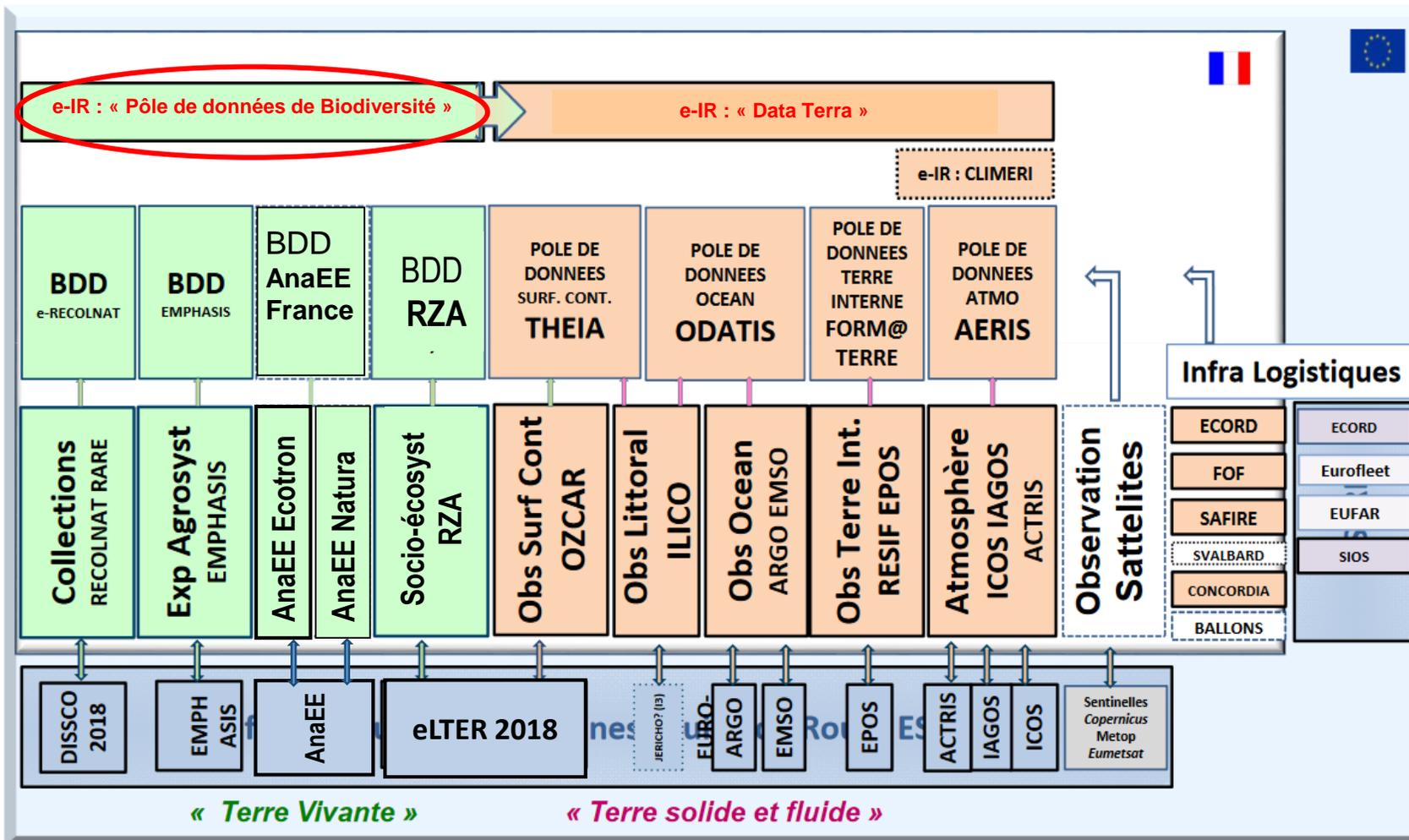
Pôle national de données de Biodiversité de la donnée de biodiversité au calcul scientifique via la métadonnée



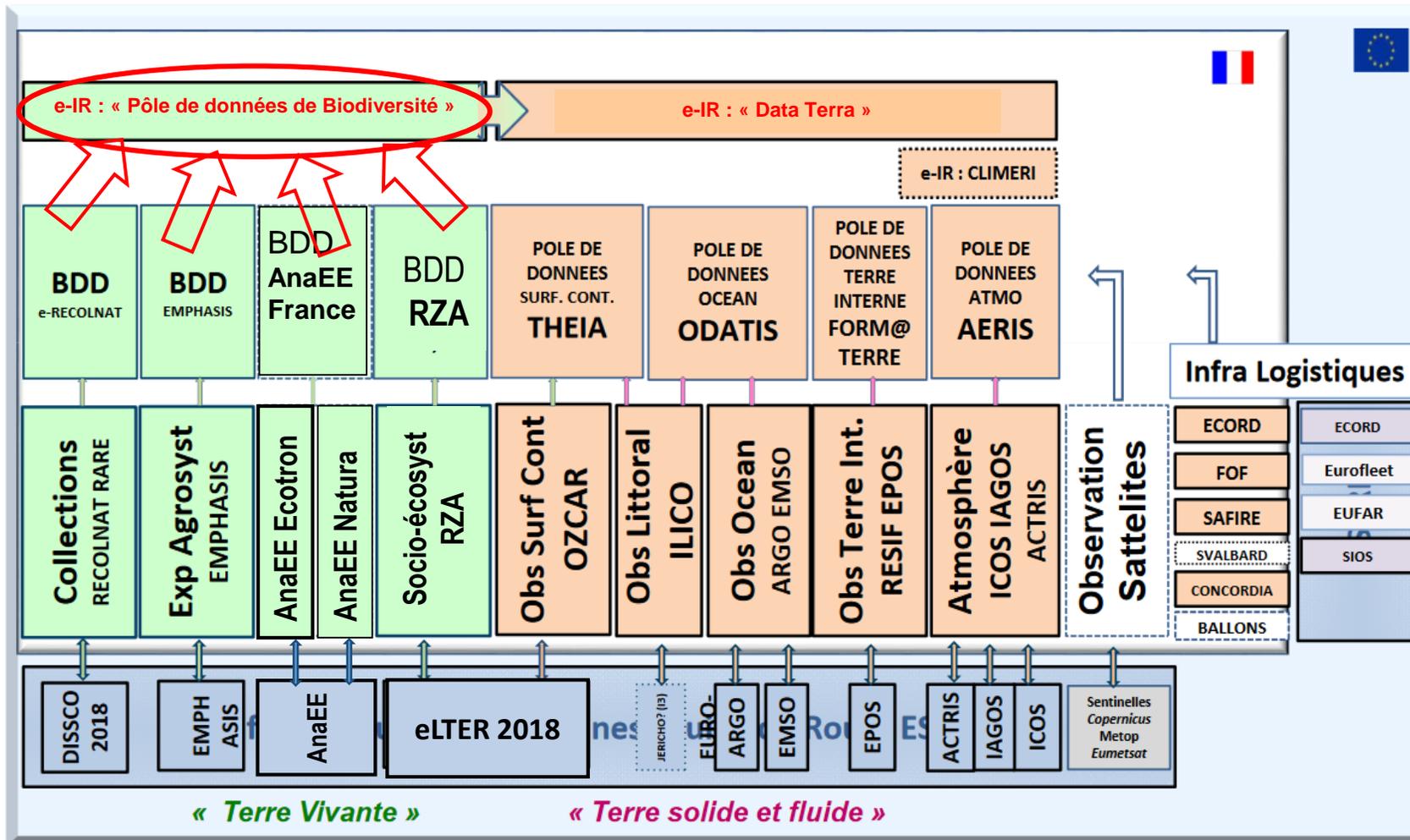
Yvan LE BRAS, Chef de projet (UMS PatriNat)
 Sandrine Pavoine, MNHN (UMR CESCO)
 Anne-Sophie ARCHAMBEAU, GBIF-France (UMS PatriNat)
 Cécile CALLOU, Dir UMS BBEES (CNRS-MNHN)
 Aurélie DELAUDAUD (FRB)
 Dominique JOLY, DAS CNRS (INEE)
 Thomas Milon, Chef de projet "Système d'information sur la biodiversité" (UMS PatriNat)
 Laurent PONCET, Dir. UMS PatriNat, en charge du Centre de données (MNHN)
 Jean-Denis VIGNE, DGD-Recherche, expertise, valorisation, enseignement MNHN

#PNDB @Yvan2935 @earnaud @ColineRoyaux @jusana_photos
Yvan.le-bras@mnhn.fr, elie.arnaud@mnhn.fr,
coline.royaux@mnhn.fr, julien.sananikone@mnhn.fr

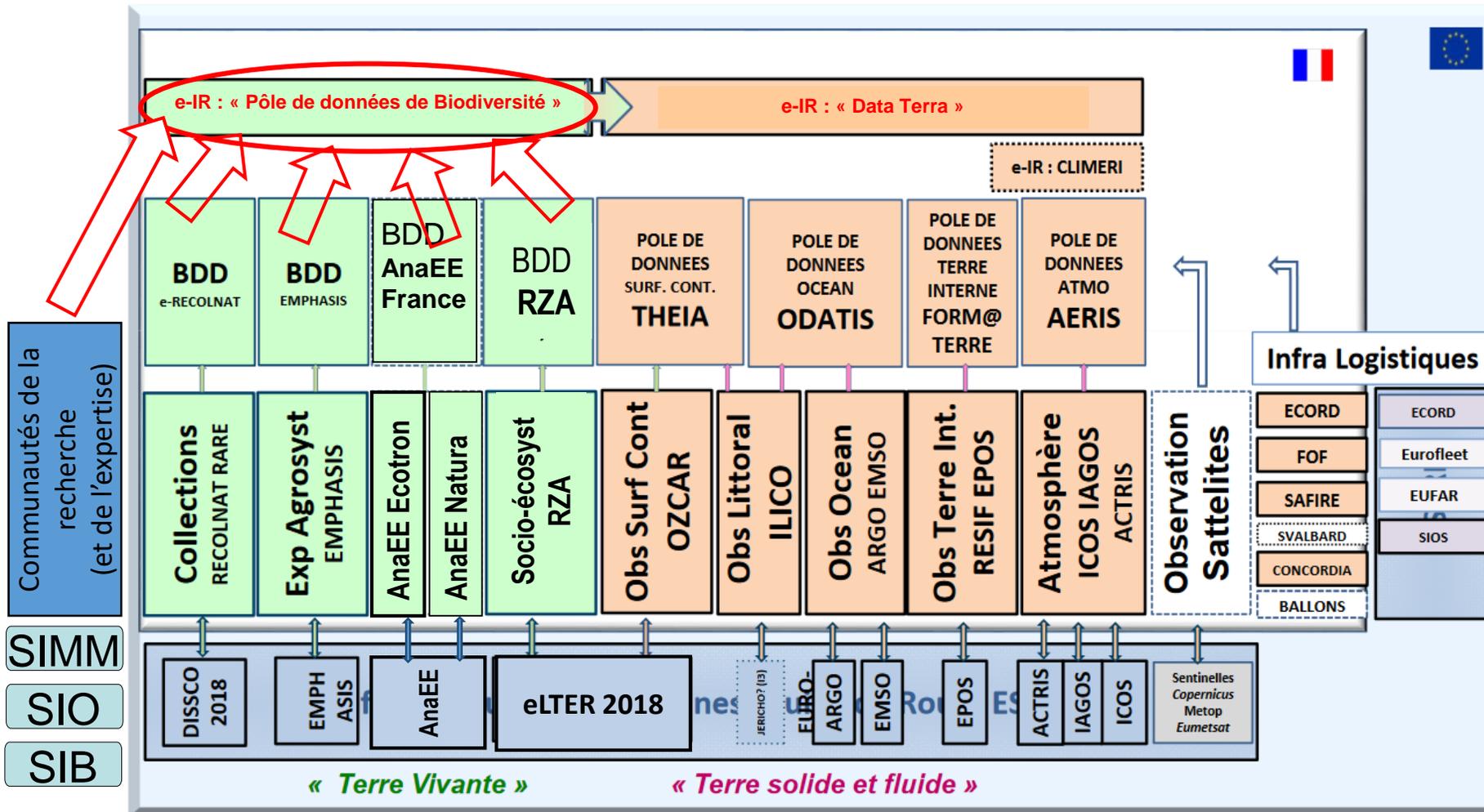




Interface « terre vivante » IR

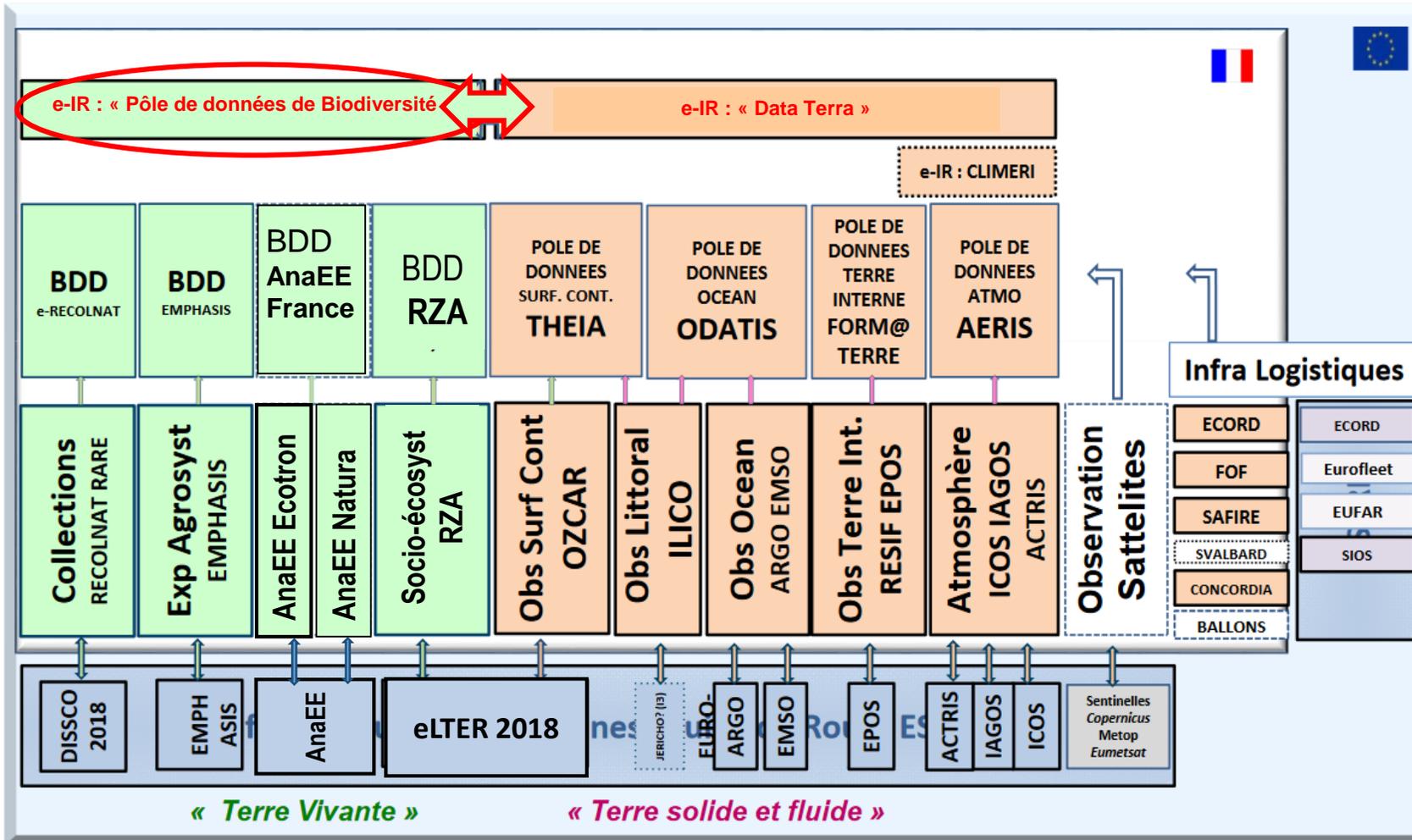


Interface « terre vivante » IR + chercheurs surtout via organismes + SI fédérateurs OFB

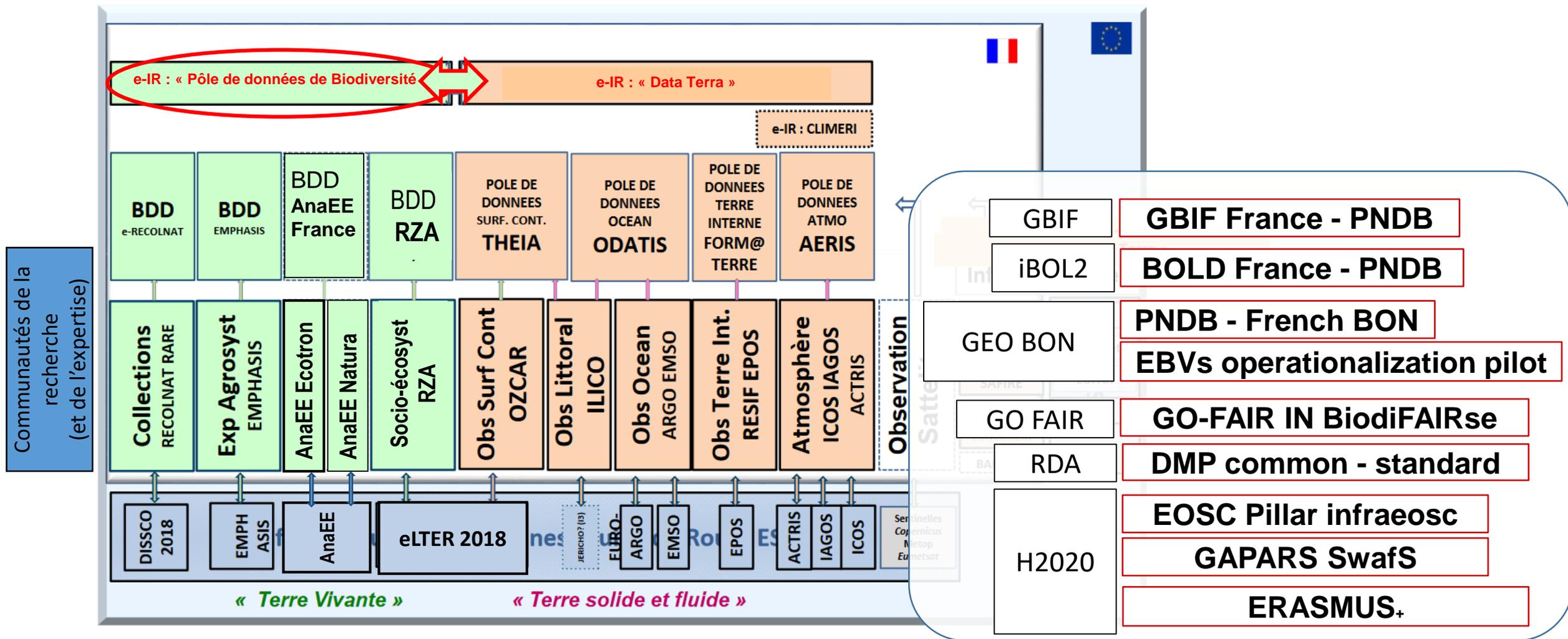


Interface « terre solide » IR

Communautés de la recherche (et de l'expertise)



Cohérence avec les dispositifs internationaux



Le PNDB, e-Infrastructure nationale de recherche

- **Infrastructure numérique** inscrite sur la feuille de route du MESRI depuis mars 2018

- **Consortium maître d'ouvrage :**

(22 partenaires institutionnels, avec le soutien financier du MESRI)



- **Maître d'œuvre :**

MNHN depuis mars 2018 (UMS PatriNat)

- **Gouvernance :**

Comité de pilotage
Conseil scientifique
Comité exécutif

Comités d'experts scientifique :

1. Variabilité génétique des populations domestiques ou sauvages
2. Espèces, traits fonctionnels, communautés
3. Ecosystèmes et socio-écosystèmes, variables SHS : structures et fonctions
4. Données, scénarios, modélisation ; télédétection

Cahier des charges du PNDB

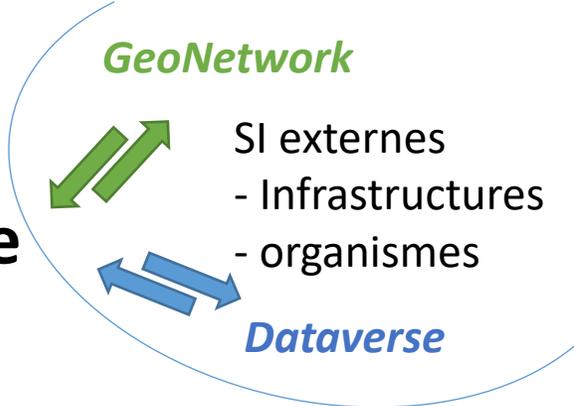
10 lignes de force

1. Orientation FAIR (aussi FAIR et *Open* que possible)
2. Relier/mutualiser avec les composantes existantes du Syst. Terre-Env.
3. Articuler/mutualiser avec le SIB-SIMM
4. Offrir des services à valeur ajoutée
5. Privilégier la qualité (*quality data*), au-delà de la quantité (*big data*),
6. Promouvoir la flexibilité des services (« à la carte »)
7. Développer, faciliter et favoriser la description fine des données
8. Viser une portée internationale (couverture & utilisation)
9. Articuler le PNDB avec les initiatives européennes et internationales
10. Pour commencer, s'appuyer sur un petit nombre de cas d'étude
(preuve de concept)

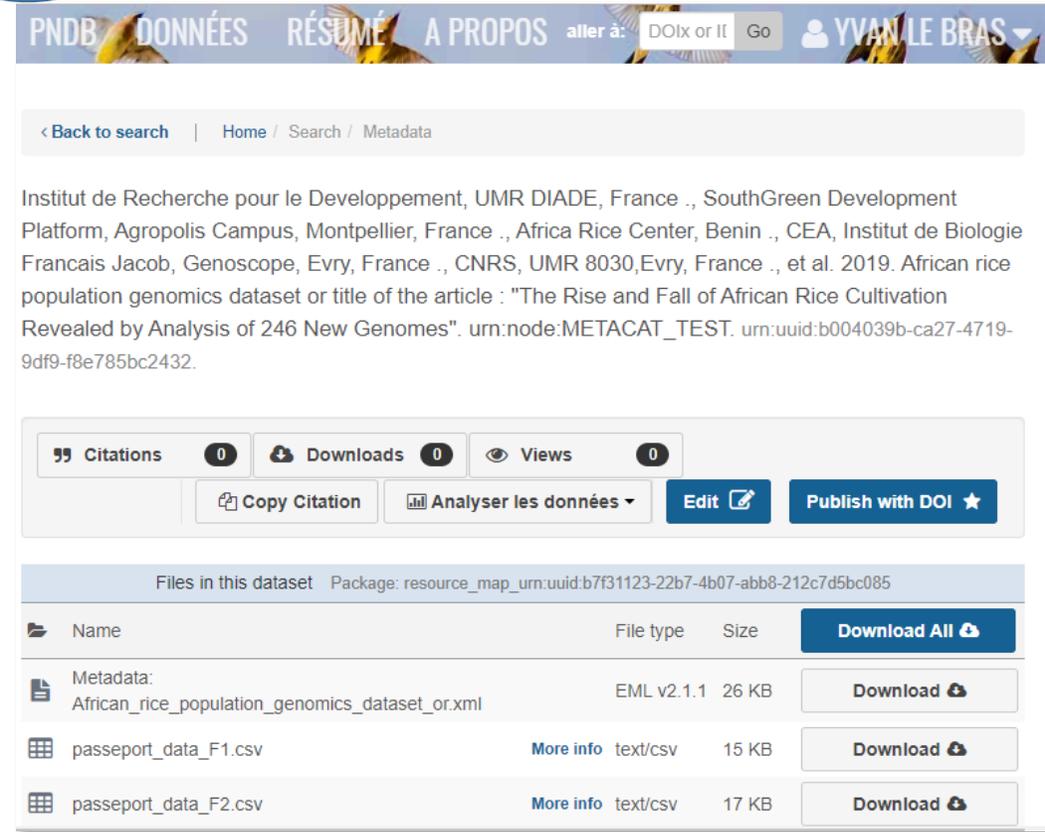
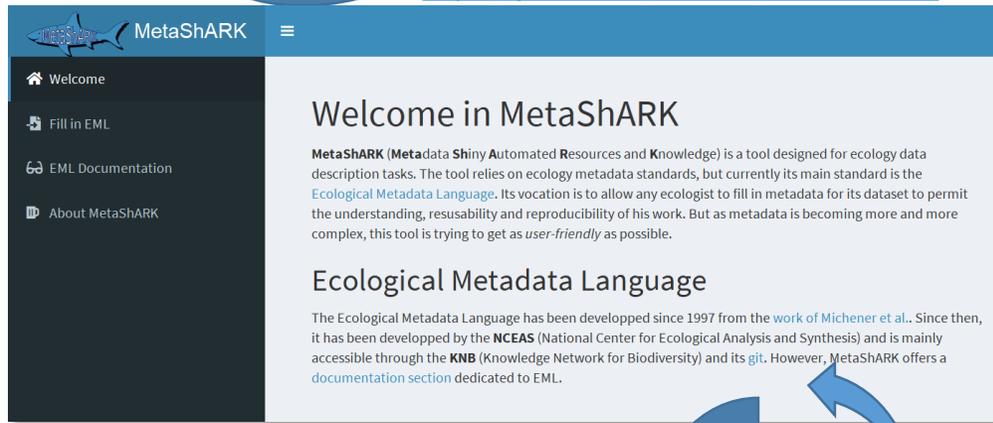
3 volets

1. Accès aux métadonnées et données
2. Animation et accompagnement
3. Accès aux outils de traitement, de couplage, d'analyse (calcul)

Le paysage (méta)données via l' Ecological Metadata Language

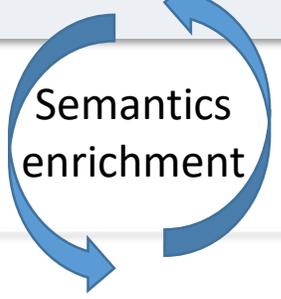


- dataset1
- dataset2
- script1
- article1
- protocol1



R EML Assembly Line
<https://ediorg.github.io/EMLassemblyline/index.html>

EML



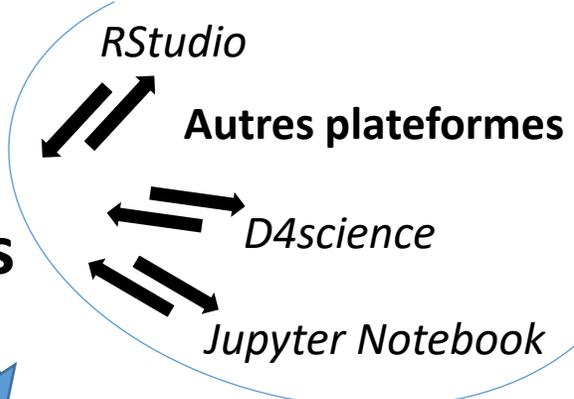
cedarr

CEDAR R package for API linking in an R interface.
<https://github.com/earnaud/cedarr>

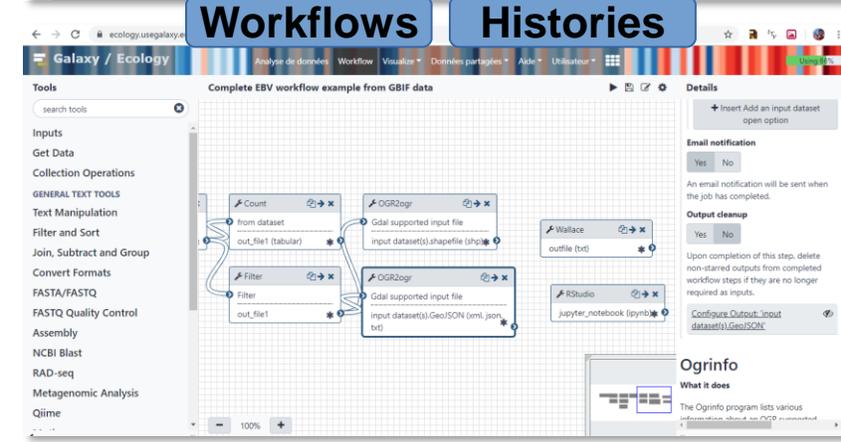
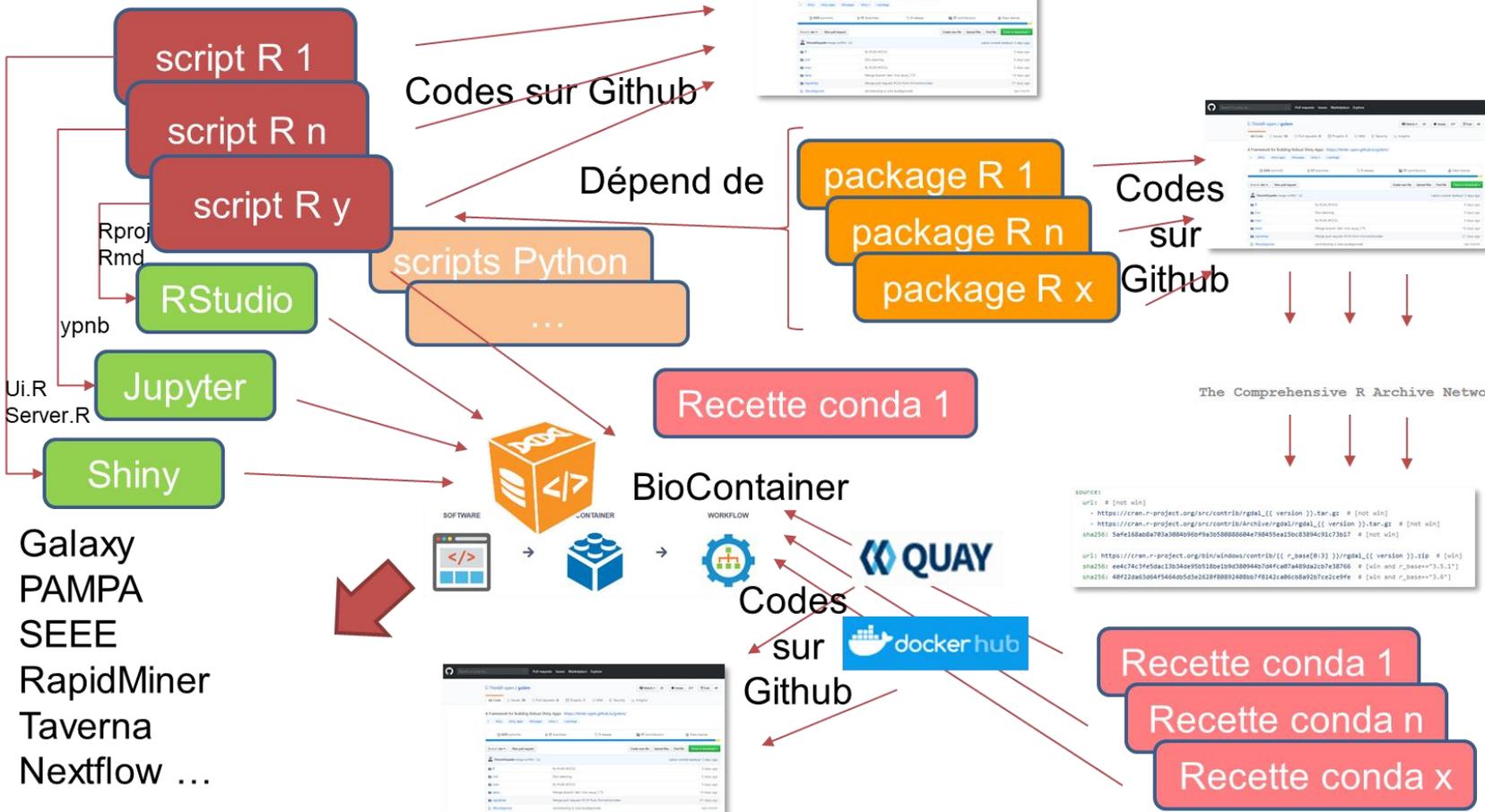
Portail de données métadonnées :
<https://openstack-192-168-100-101.genouest.org/metacatui>
<http://data.test.pndb.fr/data> <https://data.pndb.fr/data>

Le paysage analyse via Github, Conda, Containers, Cloud et Galaxy

Codes + dépendances → Containers



Machines virtuelles (local ou cloud)
Galaxy



- Galaxy
- PAMPA
- SEEE
- RapidMiner
- Taverna
- Nextflow ...

Les projets

FNSO - OpenMetaPaper

ANR Challenge IA & Biodiversité

GBIF

GBIF France - PNDB

iBOL2

BOLD France - PNDB

GEO BON

PNDB - French BON

EBVs operationalization pilot

GO FAIR

GO-FAIR IN BiodiFAIRse

RDA

DMP common - standard

H2020

EOSC Pillar infraeosc

GAPARS SwafS

ERASMUS+

Merci de votre attention



PNDB team

Coline Royaux – Ingénieure développement scientifique R / Galaxy (workflows Galaxy pour calcul indicateurs espèces / communautés)



Elie Arnaud – Ingénieur développement scientifique via R Shiny / connaissance métadonnées



<https://www.pndb.fr/>

Démo saisie et publication données / métadonnées MetaShARK

<https://youtu.be/OVViSMzRGtw>

Démo portail de données et métadonnées

<https://youtu.be/STwsYDHEt2A>

Démo Galaxy Europe

- <https://youtu.be/HeIAHggX6D4>

- [Essential biodiversity variables on Galaxy: implementing the PAMPA application](#)

- [Producing biodiversity indicators from citizen science projects: update of birds and bats monitoring schemes on Galaxy-F](#)

Julien Sananikone – Ingénieur DevOps / administration système & réseau / développeur web

Yvan Le Bras – Béta testeur Yvan.le-bras@mnhn.fr



Visitez la version préliminaire du site web du PNDB pour suivre le projet

<https://www.pndb.fr/>

PNDB Outils ▾ Animation ▾ Projets ▾ FAQ

Pôle National de Données de Biodiversité!

Un pôle de données au service des scientifiques produisant, gérant et analysant des données de biodiversité

[Accéder aux données »](#)

[Tester MetaShaRK »](#)

En 2018, le Ministère de l'Enseignement supérieur, de la recherche et de l'innovation a inscrit sur sa feuille de route la création d'une nouvelle infrastructure intitulée Pôle National de données de biodiversité (PNDB). Les missions du PNDB s'inscrivent dans une approche FAIR (Facile à trouver, Accessible, Intéropérable, Réutilisable), et consistent à :

1. fournir un accès aux jeux de données et de métadonnées, à des services associés et à des produits dérivés des analyses
2. promouvoir l'animation scientifique pour identifier les lacunes et favoriser l'émergence de dispositifs portés par des communautés d'utilisateurs et producteurs
3. faciliter le partage des pratiques avec les autres communautés de recherche, favoriser le partage des données et leur réutilisation, s'insérer dans la réflexion de la future infrastructure Système Terre.
4. favoriser la cohérence avec les efforts nationaux, européens et internationaux relatifs à l'accès et à l'exploitation des données de recherche sur la biodiversité, à la promotion de produits et services.

Le PNDB est porté par le Muséum national d'Histoire naturelle, plus particulièrement par l'UMS 2006 PatriNat, unité MNHN CNRS et AFB. Le projet est en lien étroit avec la FRB et plusieurs de ses institutions fondatrices (AFB, BRGM, CIRAD, CNRS, Ifremer, INERIS, INRA, IRD, IRSTEA, MNHN, Univ. Montpellier).

Portail de données

MetaShark

Galaxy

Visitez le portail de données du PNDB et jouez avec les premiers jeux de données-métadonnées

<https://data.pndb.fr/>

PNDB DONNÉES RÉSUMÉ A PROPOS aller à: DOIx or II Go CONNEXION

PÔLE NATIONAL DE DONNÉES DE BIODIVERSITÉ

Un pôle de données au service des scientifiques produisant, gérant et analysant des données de biodiversité

Exemple: espèces invasives

brgm Géosciences pour une Terre durable
cirad LA RECHERCHE AGRONOMIQUE POUR LE DÉVELOPPEMENT
cnrs
FRB FONDATION POUR LA RECHERCHE SUR LA BIODIVERSITÉ
Ifremer
INERIS maîtriser le risque pour un développement durable

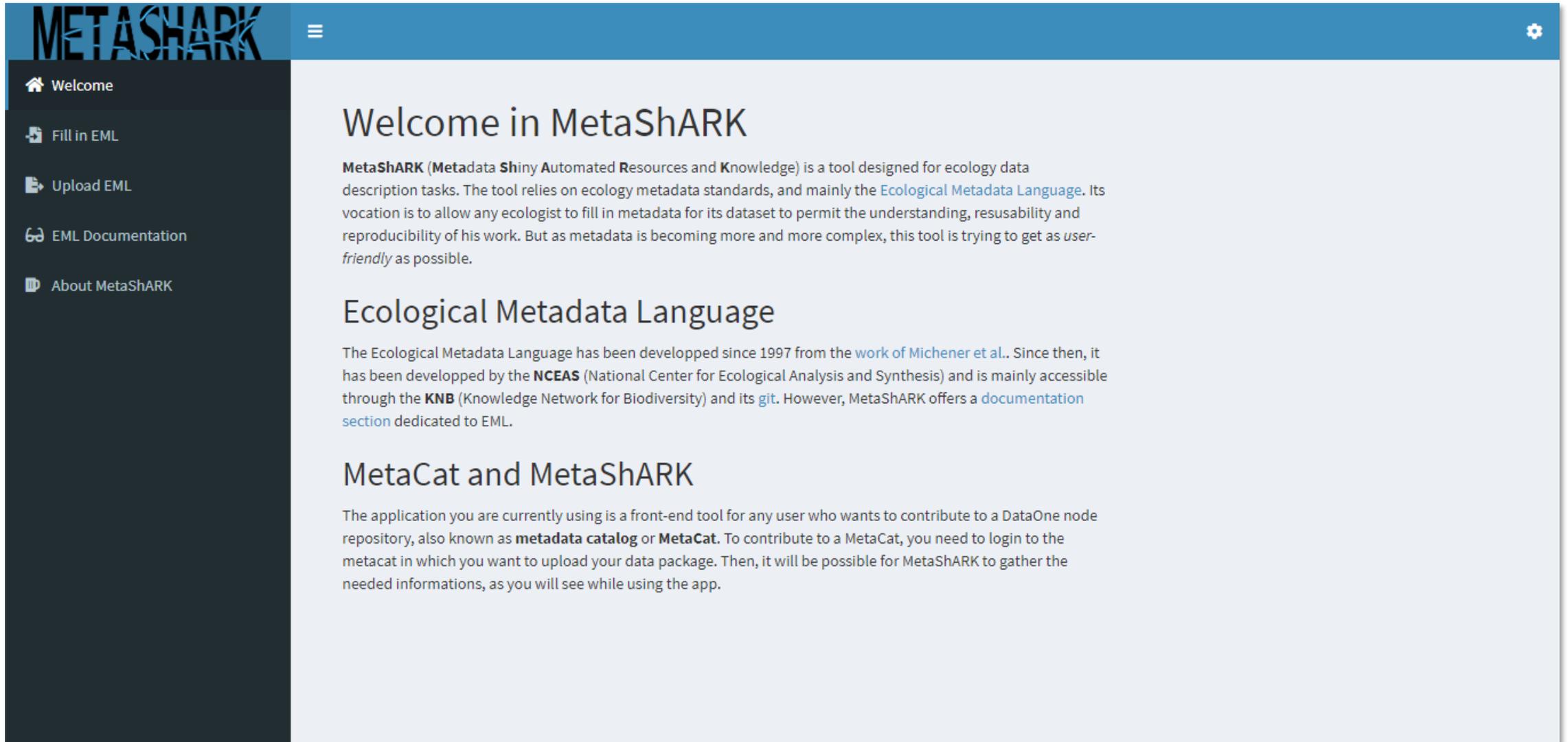
INRAE
IRD Institut de Recherche pour le Développement FRANCE
MUSÉUM NATIONAL D'HISTOIRE NATURELLE
OFB OFFICE FRANÇAIS DE LA BIODIVERSITÉ
Météo France

En 2018, le Ministère de l'Enseignement supérieur, de la recherche et de l'innovation a inscrit sur sa feuille de route la création d'une nouvelle infrastructure intitulée Pôle National de données de biodiversité (PNDB). Les missions du PNDB s'inscrivent dans une approche FAIR (Facile à trouver, Accessible, Intéropérable, Réutilisable), et consistent à :

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2. promouvoir l'animation scientifique pour identifier les lacunes et favoriser l'émergence de dispositifs portés par des communautés d'utilisateurs et producteurs

Testez l'interface de saisie de données et métadonnées du PNDB

<https://metashark.test.pndb.fr/>



The screenshot shows the MetaShARK web application interface. The top navigation bar is blue and contains the 'METASHARK' logo on the left, a hamburger menu icon in the center, and a gear icon for settings on the right. A dark grey sidebar on the left contains a list of navigation items: 'Welcome' (home icon), 'Fill in EML' (document icon), 'Upload EML' (upload icon), 'EML Documentation' (book icon), and 'About MetaShARK' (info icon). The main content area has a light blue background and features the following sections:

Welcome in MetaShARK

MetaShARK (**M**etadata **S**hiny **A**utomated **R**esources and **K**nowledge) is a tool designed for ecology data description tasks. The tool relies on ecology metadata standards, and mainly the [Ecological Metadata Language](#). Its vocation is to allow any ecologist to fill in metadata for its dataset to permit the understanding, resusability and reproducibility of his work. But as metadata is becoming more and more complex, this tool is trying to get as *user-friendly* as possible.

Ecological Metadata Language

The Ecological Metadata Language has been developed since 1997 from the [work of Michener et al.](#). Since then, it has been developed by the **NCEAS** (National Center for Ecological Analysis and Synthesis) and is mainly accessible through the **KNB** (Knowledge Network for Biodiversity) and its [git](#). However, MetaShARK offers a [documentation section](#) dedicated to EML.

MetaCat and MetaShARK

The application you are currently using is a front-end tool for any user who wants to contribute to a DataOne node repository, also known as **metadata catalog** or **MetaCat**. To contribute to a MetaCat, you need to login to the metacat in which you want to upload your data package. Then, it will be possible for MetaShARK to gather the needed informations, as you will see while using the app.

Testez la plateforme d'analyse / couplage de données du PNDB <https://ecology.usegalaxy.eu/>

The image displays four screenshots of the Galaxy / Ecology web interface:

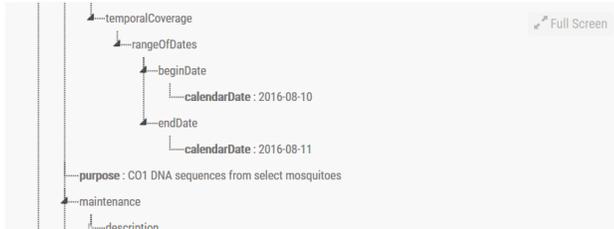
- Top-left:** A world map showing data points (red dots) with a sidebar containing tool categories like 'GIS Data Handling', 'Animal Detection on Acoustic Recordings', 'STATISTICS AND VISUALISATION', and 'MISCELLANEOUS TOOLS'.
- Top-right:** A 'History' panel showing a search bar and a list of workflows, including 'treat biodiversity data & tuto GBIF data handling' (23 shown, 16 deleted, 395.98 MB) and '20: Species occurrences'.
- Bottom-left:** A workflow editor for 'Complete EBV workflow example from GBIF data' showing a sequence of tool nodes: 'Count', 'Filter', 'OGR2ogr', 'Wallace', and 'RStudio'.
- Bottom-right:** A 'Your workflows' table listing various workflows with columns for Name, Tags, Owner, Steps, and Published status.

Tutoriels : <https://training.galaxyproject.org/>

Codes sources : <https://github.com/65MO/Galaxy-E>
<https://github.com/galaxyecology/tools-ecology>

Pourquoi ce fameux *Ecological Metadata Language* ?

Les LTER -> THE exemple US & Australie



Attribute Metadata

A fundamental part of EML metadata is a description of the attributes (usually columns) of a text file (usually a csv file) containing the data being described. This is the heart of many EML files.

```
attributes <-
tibble::tribble(
  ~attributeName, ~attributeDefinition, ~formatString, ~definition,
  "run_num", "which run number (=block). Range: 1 - 6. (integer)", NA, "which run numbe",
  "year", "year, 2012", "YYYY", NA,
  "day", "Julian day. Range: 170 - 209.", "DDD", NA,
  "hour.min", "hour and minute of observation. Range 1 - 2400 (integer)", "hhmm", NA,
  "i.flag", "is variable Real, Interpolated or Bad (character/factor)", NA, NA,
  "variable", "what variable being measured in what treatment (character/factor).", NA, NA,
  "value.i", "value of measured variable for run_num on year/day/hour.min.", NA, NA,
  "length", "length of the species in meters (dummy example of numeric data)", NA, NA,
```



<p>Bird Survey Data, Warra Tall Eucalypt SuperSite, Silvicultural Systems Trial/ External Control Track, 1998-2010</p> <p>Five-minute counts of birds (seen or hear) observed during >5 separate visits made each year to each of 20 points located at 50-metre intervals along "Bird Track". The dataset contains records made initially in 1998 and ...</p> <p>6602 birds bird survey Warra</p> <p>QC 3 PUBLISHED 2013-06-03 LAST UPDATED 2016-04-03 docid: lloyd.502.11</p>	<p>Wardlaw Forestry Tasmania</p>
<p>Coarse Woody Debris Greater Than 40 cm Diameter, Warra Tall Eucalypt SuperSite, Core 1 ha, 2015</p> <p>The dataset comprises measurements carried out in 2015 of all pieces of coarse woody debris greater than 40 cm diameter at the small end within the Core 1 ha plot at the Warra Supersite. The measurements include: ...</p> <p>0802 0807 0705 Warra forest vegetation biomass carbon</p> <p>QC 1 PUBLISHED 2016-04-03 LAST UPDATED 2016-04-07 docid: supersite.616.4</p>	<p>Wardlaw Forestry Tasmania</p>

Pourquoi ce fameux Ecological Metadata Language ?

Les LTER -> THE exemple US & Australie



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    "year", "year, 2012", "YYYY", NA,
    "day", "Julian day. Range: 170 - 209.", "DDD", NA,
    "hour.min", "hour and minute of observation. Range 1 - 2400 (integer)", "hhmm", NA,
    "i.flag", "is variable Real, Interpolated or Bad (character/factor)", NA, NA,
    "variable", "what variable being measured in what treatment (character/factor).", NA, NA,
    "value.i.", "value of measured variable for run.num on year/day/hour.min.", NA, NA,
    "length", "length of the species in meters (dummy example of numeric data)", NA, NA,
  )
```



EML (MTD std) <https://ropensci.github.io/EML/articles/creating-EML.html>

EML Assembly Line <https://ediorg.github.io/EMLassemblyline/index.html>

Metacat (data portal) <https://github.com/NCEAS/metacatui>

OAI-PMH (harvesting)

NCEAS / EDI / KNB

DataOne



Pourquoi ce fameux *Ecological Metadata Language* ?

Les LTER -> THE exemple Europe

The screenshot displays the DEIMS-SDR website interface. At the top, there is a navigation menu with links for Home, Discovery, Documentation, Network, and Login. Below the menu, the breadcrumb trail reads: Home » Dataset » Discovery » Leaf Colors in the subalpine Zone. The main title of the page is 'Leaf Colors in the subalpine Zone'. The content is organized into several sections: 'Basic Information' containing related site information, an abstract, keywords, and contact details; 'Dates' showing the data range from August 4, 2016, to September 3, 2016; 'Downloads' with buttons for EML, ISO GMI, ISO GMD, and BDP; and 'Additional Information' with expandable sections for 'Methodology' and 'Other', where the language is listed as 'eng'. On the right side, there is a 'Geographic' section featuring a map of the island of Réunion with a blue polygon highlighting the study area. The map includes labels for various locations such as Saint-Denis, Saint-Paul, Saint-André, Saint-Benoit, Sainte-Rose, Saint-Leu, Le Tampon, Saint-Pierre, and Saint-Philippe. A 'Click for more details' link is provided below the map.

Pourquoi ce fameux *Ecological Metadata Language* ?

Les LTER -> THE exemple Europe

~2010

Drupal Ecological Information Management System



Dataset Metadata Model

Scope

The dataset metadata model (DSMM) is based on requirements defined by the target stakeholder groups. The user requirements for the content were harmonized with the [INSPIRE metadata regulation](#) and implemented using [Ecological Metadata Language \(EML\) metadata specification, version 2.1.1](#). EnvEurope focused on the EML metadata standard (stemming from the US LTER activities) but also provides an interface to discover ISO compliant metadata based on XSLT transformation EML2ISO developed in the project and Geonetwork opensource CSW implementation.

Documentation Main menu

Tutorials Metadata Models EnvThes Thesaurus

Network Login

list Links

ILTER US-LTER LTER Europe

Quick start

registry) is an information
around the globe, along with the
S-SDR describes a wide range of
ilities, parameters measured and
products associated with the sites.

Do you need any help?
[Read our tutorials](#)

Is something not working?
have any change request?
[Provide feedback](#)

Do you want your site or research
to be on DEIMS-SDR?
[Contact us](#)

Site and Dataset Registry

2019-04-08 08:45

2019-04-05 18:21

2019-04-05 17:52

2019-04-05 14:14

2019-04-04 18:06

2019-04-04 16:38

Available Resources

 Sites Find out about the international network of ecosystem research, monitoring and experimentation sites.	 Datasets Find out about the available dataset metadata records from the network.
 Sensors Find out about deployed sensors used to generate data.	 Data Products Find out about data products published or contributed.

We've published a paper about DEIMS-SDR: [10.1016/j.ecoinf.2019.01.005](https://doi.org/10.1016/j.ecoinf.2019.01.005)

ProTip! Use the [DEIMS.ID](#) to reference sites in papers.



2018

DEIMS-SDR
Dynamic
Ecological
Information
Management
System



Pourquoi ce fameux Ecological Metadata Language ?

Amazing EML

Language + Modules -> flexibility!

4 sources

2 derivations

Entry Name: Total_Aromatic_Alkanes_PWS.csv

Description: Combined dataset from PAH, Alkane and Sample tables documenting samples collected after the Exxon Valdez oil spill in Prince William Sound, AK

Object Name: Total_Aromatic_Alkanes_PWS.csv

Online Distribution Info: <https://on.dataone.org/inv2/resolve?um:uuid:44108a76-4056-4d58-b1b3-94b054e3f9f9>

Size: 2901033 byte

Text Format: Number of Header Lines: 1

Record Delimiter: #nGA

Attribute Orientation: column

Field Delimiter: .

Number of Records: 12142

Provenance tracking!

Semantic Module functionality Example

Principle

Write annotations: kind of "sentence" composed with:

- a subject
- a property
- a property's value

Semantics!

(similar to RDF statement)

An annotation is added inside an *Attribute* as its direct child (cf. example).

```
<attribute id="att.12">
  <attributeName>biomass</attributeName>
  ...
  <annotation>
    <propertyURI label="of characteristic">http://ecoinformatics.org/oboe/oboe.1.2/oboe-core.owl#ofCharacteristic</propertyURI>
    <valueURI label="Mass">http://ecoinformatics.org/oboe/oboe.1.2/oboe-characteristics.owl#Mass</valueURI>
  </annotation>
  <annotation>
    <propertyURI label="of entity">http://ecoinformatics.org/oboe/oboe.1.2/oboe-core.owl#ofEntity</propertyURI>
    <valueURI label="Plant Sample">http://example.com/example-vocab-1.owl#PlantSample</valueURI>
  </annotation>
</attribute>
```

Data Table

Data: <https://pasta.lternet.edu/package/data/eml/knb-lter-and/4541/3/f3232065a859b5ec150596b4af4a0158>

Name: HF02001

Identifier: 1

Description: Multi-scale tracer tests: Dye tracer test concentration breakthrough curves

Number of Records: 0

Number of Columns: 14

Time Period

Begin: 2003-06-14

End: 2003-06-21

Constraint:

Name:	PRIMARY
Primary Key:	HF02001.DATANUM
Key:	HF02001.SITENAME
Name:	NOTNULL
Key:	HF02001.BASIN_REG
Key:	HF02001.CONCEN
Key:	HF02001.DATANUM

Constraints definition!

A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	DBCODE	ENTITY	SITE	SITENAME	TEST	DATANUM	DATE	TIME	CONCEN	MASSFLUX	DISCHARGE	BASIN_REG	TEMP
2	HF020	1	TT-S	CC-IOTT_ALC	IOTT	1	01/09/2003	16790 0.010	2.88	202.3	MACX		M
3	HF020	1	TT-S	CC-IOTT_ALC	IOTT	2	01/09/2003	20390 0.100	30.88	202.2	MACX		M
4	HF020	1	TT-S	CC-IOTT_ALC	IOTT	3	01/09/2003	23990 0.460	92.41	202.1	MACX		M
5	HF020	1	TT-S	CC-IOTT_ALC	IOTT	4	01/09/2003	27590 0.850	170.92	202.0	MACX		M
6	HF020	1	TT-S	CC-IOTT_ALC	IOTT	5	01/09/2003	31190 1.240	249.64	201.9	MACX		M
7	HF020	1	TT-S	CC-IOTT_ALC	IOTT	6	01/09/2003	34790 1.580	318.12	201.8	MACX		M
8	HF020	1	TT-S	CC-IOTT_ALC	IOTT	7	01/09/2003	38390 1.980	398.62	201.7	MACX		M
9	HF020	1	TT-S	CC-IOTT_ALC	IOTT	8	01/09/2003	41990 2.350	473.07	201.6	MACX		M
10	HF020	1	TT-S	CC-IOTT_ALC	IOTT	9	01/09/2003	45590 2.670	537.28	201.5	MACX		M
11	HF020	1	TT-S	CC-IOTT_ALC	IOTT	10	02/09/2003	49190 3.010	605.33	201.4	MACX		M
12	HF020	1	TT-S	CC-IOTT_ALC	IOTT	11	02/09/2003	52790 3.300	663.34	201.2	MACX		M
13	HF020	1	TT-S	CC-IOTT_ALC	IOTT	12	02/09/2003	56390 3.560	714.84	201.0	MACX		M

+ = uniq ID

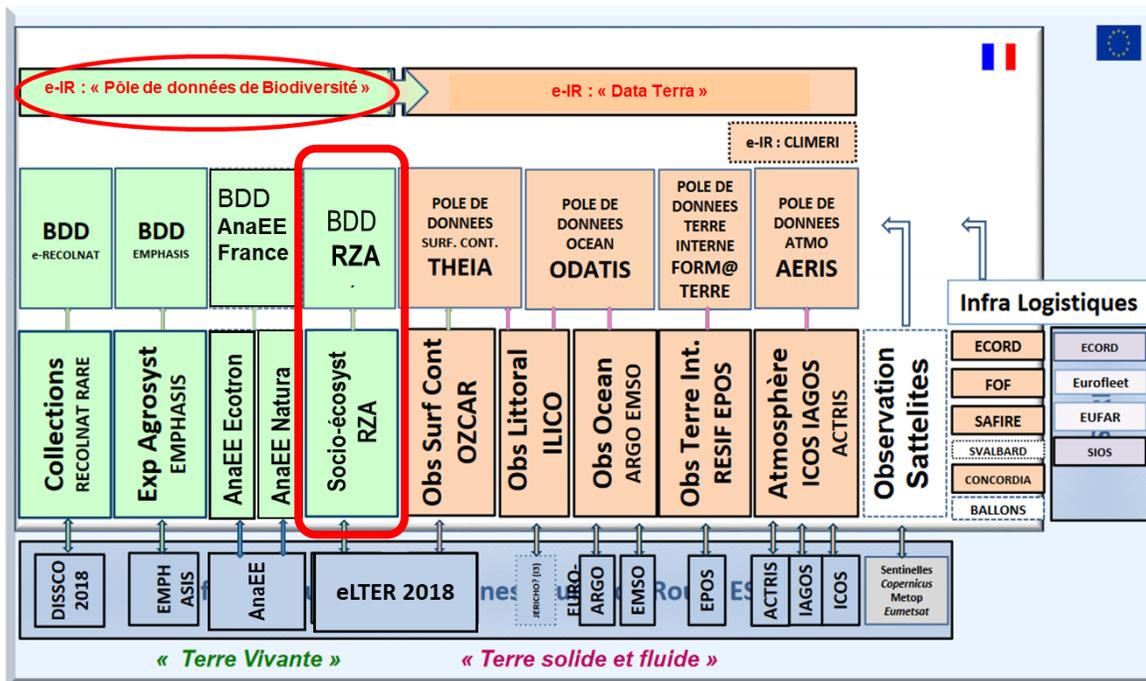
DRYAD

Hastie, Gordon D., Russell, Debbie J. F., Lopper, Paul, Elliott, Jim, Wilson, Ben, et al. 2017. JApEcol_Hastie_etal_seal_telemetry_data_Dryad. Dryad Digital Repository. <https://doi.org/10.5061/dryad.vt2b3?ver=2018-07-26T02:32:33.167+00:00>

Deploy Analytics environment on the cloud!

Proposition de rôle via BED

- Liens communautés ZA -> PNDB
- Support technique PNDB
- Retours / conseils vis-à-vis initiatives internationales (GEO BON dont EBV / DataOne ..)



Démonstrations !!!!!!!

Structuration

Accessible FAIR

Reproductible

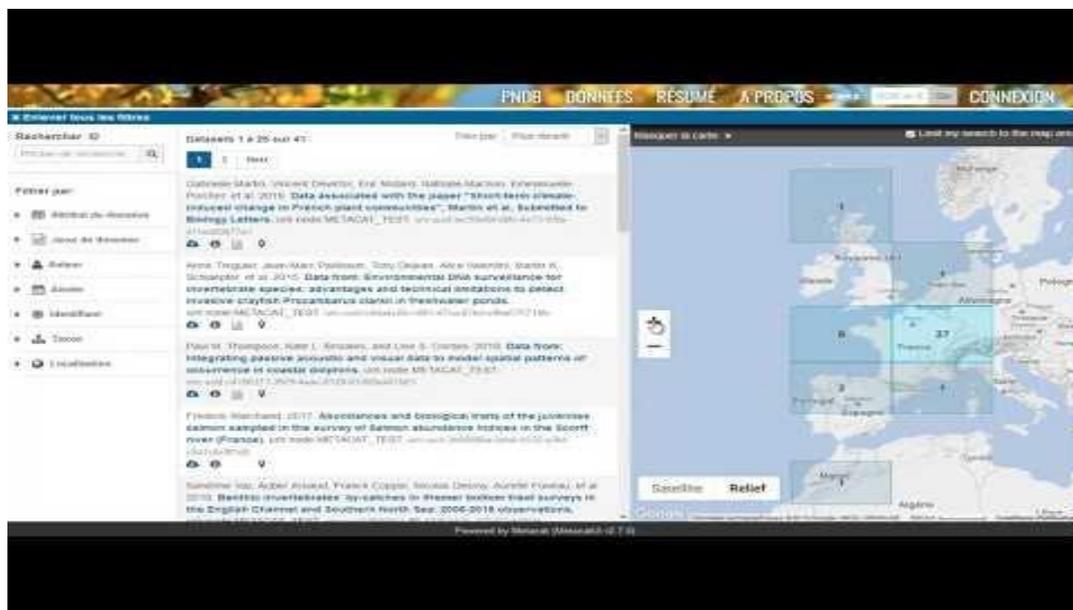
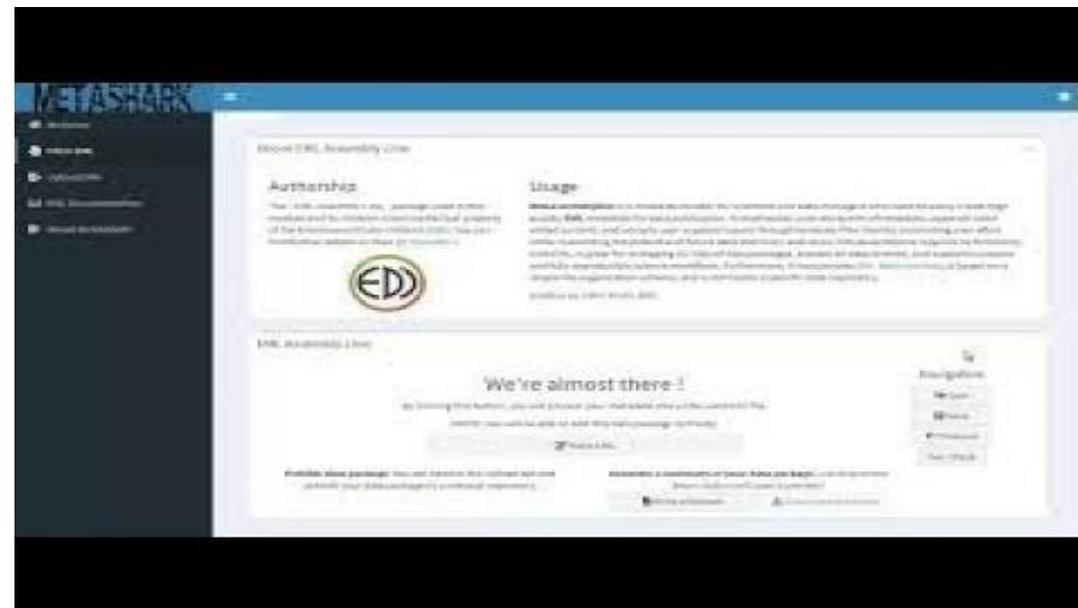
Analyse

Collaboratif

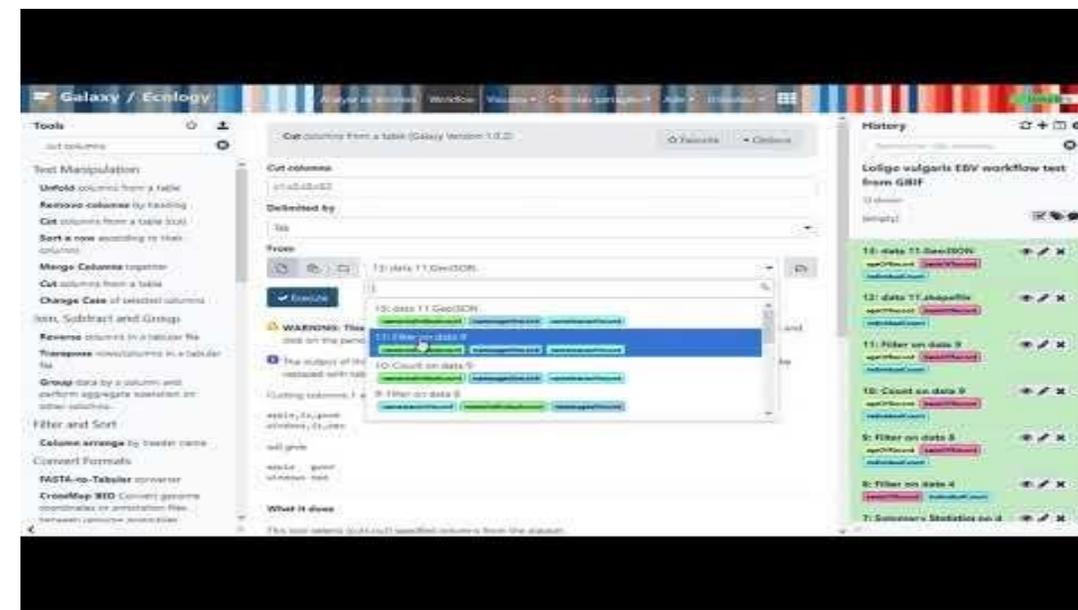
Publication

Démo saisie et publication données / métadonnées MetaShARK

<https://youtu.be/OVViSMzRGtw>



Démo portail de données et métadonnées basé sur Metacat/metacatui/Geoserver <https://youtu.be/STwsYDHet2A>



Démo plateforme d'analyse de données de biodiversité via Galaxy Europe <https://youtu.be/HelAHggX6D4>

MetaShARK



Au début était l'EML

Ecological Metadata Language (by [knb](#))

Au début était l'EML

Ecological Metadata Language (by [knb](#))

Solutions techniques existantes

- MetaCAT (→ [DataONE](#))
- Morpho (écriture métadonnées)

Au début était l'EML

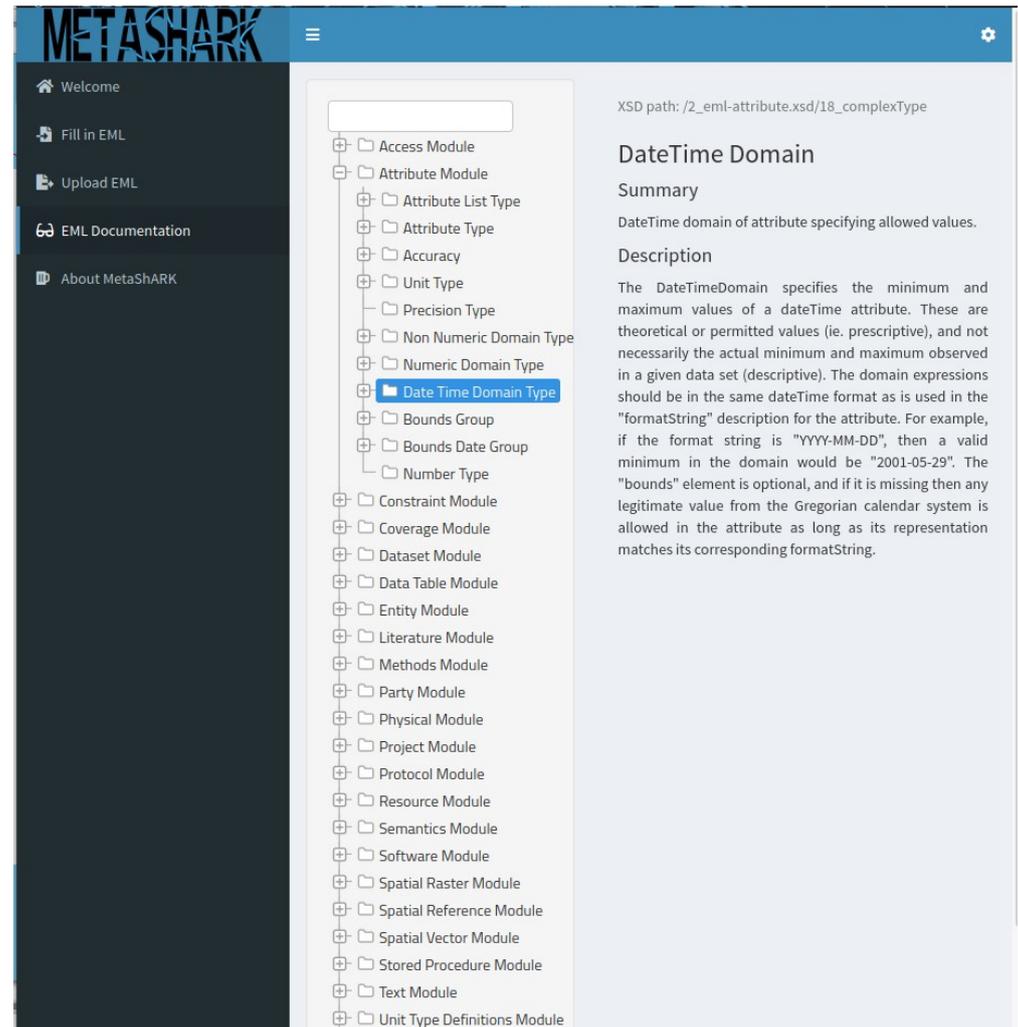
Ecological Metadata Language (by )

Solutions techniques existantes

- MetaCAT (→ )
- **Morpho (écriture métadonnées)**
 - **MetaShARK =**
EML Assembly Line (by ) + Travail de stage 2019

Documentation

- Localisation
- Interactions
- Recherche
- Utilisation
- Infos techniques



The screenshot displays the METASHARK documentation interface. The left sidebar contains navigation links: Welcome, Fill in EML, Upload EML, EML Documentation (selected), and About MetaSHARK. The main content area shows a tree view of modules, with 'Date Time Domain Type' highlighted. The right panel displays the XSD path: /2_eml-attribute.xsd/18_complexType. The page title is 'DateTime Domain', followed by a 'Summary' section stating 'DateTime domain of attribute specifying allowed values.' and a 'Description' section explaining that the DateTimeDomain specifies the minimum and maximum values of a dateTime attribute, including details on format strings and the optional 'bounds' element.

METASHARK

Welcome

Fill in EML

Upload EML

EML Documentation

About MetaSHARK

Access Module

Attribute Module

Attribute List Type

Attribute Type

Accuracy

Unit Type

Precision Type

Non Numeric Domain Type

Numeric Domain Type

Date Time Domain Type

Bounds Group

Bounds Date Group

Number Type

Constraint Module

Coverage Module

Dataset Module

Data Table Module

Entity Module

Literature Module

Methods Module

Party Module

Physical Module

Project Module

Protocol Module

Resource Module

Semantics Module

Software Module

Spatial Raster Module

Spatial Reference Module

Spatial Vector Module

Stored Procedure Module

Text Module

Unit Type Definitions Module

XSD path: /2_eml-attribute.xsd/18_complexType

DateTime Domain

Summary

DateTime domain of attribute specifying allowed values.

Description

The `DateTimeDomain` specifies the minimum and maximum values of a `dateTime` attribute. These are theoretical or permitted values (ie. prescriptive), and not necessarily the actual minimum and maximum observed in a given data set (descriptive). The domain expressions should be in the same `dateTime` format as is used in the "formatString" description for the attribute. For example, if the format string is "YYYY-MM-DD", then a valid minimum in the domain would be "2001-05-29". The "bounds" element is optional, and if it is missing then any legitimate value from the Gregorian calendar system is allowed in the attribute as long as its representation matches its corresponding `formatString`.

Saisie

Etape 2: téléchargement des fichiers à décrire

- Fichiers tableurs
(pour l'instant)
- Description de
chaque fichier

EML Assembly Line Step 2/9: Data Files

Disclaimers:

- Until now, only table files are supported.
- Selecting a file will immediately upload it: beware of heavy files (> 5 Mb).

Select data file(s) from your dataset

Load files No file selected

Select files to delete (all files here will be kept otherwise)

Base_de_données_Lorraine__table3observation.txt

Data table name	Data remote location
Base_de_données_Lorrain	https://github.com/earnat

Data Table Description

Content of
Base_de_données_Lorraine__table3observation.txt

Base_de_données_Lorraine__table1observateur.txt

Data table name	Data remote location
Base_de_données_Lorrain	https://github.com/earnat

Data Table Description

Content of

Navigation

Quit

Save

Next

Files size:
225.9 Kb

Help

Saisie

Etape 3&4: attributs

- Typage + explication des attributs (=variables)
- Définition des modes possibles des variables catégorielles
- “Custom units”

EML Assembly Line Step 3/9: Attributes

Even if EML Assembly Line automatically infers most of your data's metadata, some steps need you to check out. Please check the following attribute, and fill in at least the mandatory elements.*

attributes_Base_de_données_Lorraine__table3observation.txt

code_observateur

code_sortie

code_observation

Describe the attribute*

Description for code_observation

Detected class (change if misdetected)

character

Code for missing value (max 1 word)

Lorem Ipsum

Explain Missing Values

Lorem Ipsum

Preview:

data
31122019_CCA_CM_A1
30122019_CCA_CM_B1
30122019_CCA_CM_B2
30122019_CCA_CM_A1
30122019_CCA_CM_A2

secteur observation

Saisie

Etape 5: couverture géographique

- Définition en employant des colonnes du jeu de données
- Définition manuelle, site par site

The screenshot shows a software interface for data assembly. At the top, it says 'EML Assembly Line' with a progress bar where the fifth step, 'Step 5/9: Geographic Coverage', is highlighted in green. Below this, there is instructional text: 'You can fill in geographic coverage through two methods: either by choosing columns from your file, or using the custom input UI. If both are filled, the software will prefer to save the columns, but on proceeding to next step, the choice will be yours.' and 'Make sure all of your locations are stored in a single file, under 3 to 5 columns: one for the site description and one or two others for latitude and longitude. Southern latitude and western longitude shall be noted with negative values.'

The main form area is titled 'Use dataset's geographic variables'. It contains three sections for column selection:

- Choose a column for sites:** A dropdown menu with 'code_observation' selected.
- Choose a column for latitude:** A text input field containing 'latitude'.
- Choose a column for longitude:** A text input field containing 'longitude'.

Below these fields is a button labeled 'Fill geographic template'. At the bottom of the interface, there is a section labeled 'Lorem Ipsum' and a field containing 'secteur_observation'.

Saisie

Etape 6: couverture taxonomique

- Définition en employant des colonnes du jeu de données
- Connection à des ressources terminologiques (GBIF, ITIS)

EML Assembly Line Step 6/9: Taxonomic Coverage

Files containing taxonomic references
Base_de_données_Lorraine_table3observation.t

Columns from selected files
nom_scientifique

Select one or both taxonomic name notation
 scientific
 common

Select taxonomic authority.ies
Global Biodiversity Information Facility (GBIF)

latitude

Choose a column for longitude:
longitude

Fill geographic template
Lorem Ipsum

secteur_observation

Saisie

Etape 8: “détails”

- Abstract
- Méthodes
- Durée
- Mots-clés
- Informations additionnelles

The screenshot shows a web form titled "EML Assembly Line" with a progress indicator showing 8 out of 9 steps completed. The current step is "Step 8/9: Miscellaneous". The form includes a "DISCLAIMER" section with two bullet points: "Do not use special characters, symbols, formatting, or hyperlinks (URLs are acceptable)." and "Any file selected will not be overwritten but will be used as a template." Below the disclaimer are five input fields: "Abstract*", "Methods*", "Keywords*", "Temporal coverage", and "Additional Info". At the bottom, there are two more input fields: "Name of organization the person is associated with*" (containing "UBO") and "Email address*" (containing "iwan.leberre@univ-brest.fr").

EML Assembly Line Step 8/9: Miscellaneous

DISCLAIMER

- Do not use special characters, symbols, formatting, or hyperlinks (URLs are acceptable).
- Any file selected will not be overwritten but will be used as a template.

Abstract*

Methods*

Keywords*

Temporal coverage

Additional Info

Name of organization the person is associated with* UBO

Email address* iwan.leberre@univ-brest.fr

Saisie

Etape 9: écriture

- Génération de .xml “EML-valide”
- Possibilité de proto-data paper (*emldown*)

The screenshot shows a web interface for the 'EML Assembly Line' at Step 9/9: 'Make EML'. The page has a progress indicator with 9 blue dots, the 9th being green. The main heading is 'We're almost there !'. Below it, a text block explains that clicking the 'Make EML' button will process metadata into an EML-valid XML file, with a note that the package can be edited further. A 'Make EML' button with a pencil icon is centered. Below this, there are two columns of text: 'Publish data package' (with instructions to go to the Upload tab) and 'Generate a summary of your data package' (with a note that clicking the button will open a preview). A 'Download emldown' button with a download icon is positioned below the second column. At the bottom, there is an 'Additional Info' section with two input fields: 'Name of organization the person is associated with*' (containing 'UBO') and 'Email address*' (containing 'iwan.leberre@univ-brest.fr').

Résultats

- Data package téléchargeable
- *eml*down succinct

Project name Home Temporal coverage Geographic coverage Data tables Custom units Other entities

2020-07-13

Data table(s) 2

Other entity(ies) 1

Abstract

AxIOM is a sample-based dataset (n = 187 samples) documenting occurrences of amphipod crustaceans associated to *Posidonia oceanica* seagrass meadows from Mediterranean Islands (Corsica, Sardinia). In total, it contains 10720 records of specimens belonging to 72 species spanning 29 families. Samples were collected over different periods 3 consecutive years, both during the day and during the night. A nested hierarchical sampling design was set up, and multiple sampling methods were combined to ensure a holistic view of the taxocenosis. The dataset package is composed of two data files: one describing sampling events, and the other reporting occurrence data of amphipod crustaceans.

Metadata Provider

Author list

Keywords

- Samplingevent,Amphipoda,Crustacea,Posidonia oceanica,Seagrass,Mediterranean,Corsica,Sardinia,Islands,Revellata Bay,Tavolara - Punta Coda Cavallo Marine Protected Area,Hierarchical sampling design,IA_BiodivNet

Project name Home Temporal coverage Geographic coverage Data tables Custom units Other entities

Data tables

dwca-axiom-v1.4__occurrence.txt , 281 records, Content of dwca-axiom-v1.4__occurrence.txt

Physical: dwca-axiom-v1.4__event.txt

attribute name	definition	format, unit or codes
id	Description for id	
eventID	Description for eventID	
parentEventID	Description for parentEventID	
samplingProtocol	Description for samplingProtocol	Litter = Value: Litter for attribute: samplingProtocol Net = Value: Net for attribute: samplingProtocol Trap1 = Value: Trap1 for attribute: samplingProtocol Trap2 = Value: Trap2 for attribute: samplingProtocol Airlift = Value: Airlift for attribute: samplingProtocol
sampleSizeValue	Description for sampleSizeValue	dimensionless
sampleSizeUnit	Description for sampleSizeUnit	square metre = Value: square metre for attribute: sampleSizeUnit
samplingEffort	Description for samplingEffort	Complete collection of litter fragments = Value: Complete collection of litter fragments for attribute: samplingEffort 150 net strokes = Value: 150 net strokes for attribute: samplingEffort 9 traps = Value: 9 traps for attribute: samplingEffort 2 minutes of aspiration = Value: 2 minutes of aspiration for attribute: samplingEffort
eventDate	Description for eventDate	YYYY-MM-DD
eventTime	Description for eventTime	YYYY-MM-DD
eventRemarks	Description for eventRemarks	Main sampling region = Value: Main sampling region for attribute: eventRemarks Sampling zone (design scale >1000 m) = Value: Sampling zone (design scale >1000 m) for attribute: eventRemarks Sampling site (design scale ~100m) = Value: Sampling site (design scale ~100m) for attribute: eventRemarks Sampling sector (design scale ~10m) = Value: Sampling sector (design scale ~10m) for attribute: eventRemarks Day = Value: Day for attribute: eventRemarks Night = Value: Night for attribute: eventRemarks
waterBody	Description for waterBody	Calvi Bay = Value: Calvi Bay for attribute: waterBody Tavolara-Punta Coda Cavallo Marine Protected Area = Value: Tavolara-Punta Coda Cavallo Marine Protected Area for attribute: waterBody Gulf of Olbia = Value: Gulf of Olbia for attribute: waterBody
island	Description for island	Corsica = Value: Corsica for attribute: island Sardinia = Value: Sardinia for attribute: island

Résultats

- Data package téléchargeable
- *emldown* succinct
- Mise en ligne possible vers MetaCAT

Exemple *Study of specific diversity of phytoplankton populations*, F. Rigault-Jalabert ([lien](#))

WIPs

- EML Annotation: connection aux ontologies
- Mise en ligne: réparation en cours
- Galaxyfication
- Conversion vers d'autres standards (DwC, SINP, ISO 19k+, ...)
- Sessions personnalisées + profilage des utilisateurs par communauté

Galaxy-E : une instance de Galaxy dédiée à l'analyse de données en Ecologie

Coline Royaux



Plateforme web pour le partage et le traitement des données de recherche

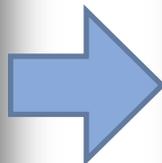
Permet un accès facilité à l'analyse cloud et au Calcul Haute Performance par l'interfaçage de n'importe quel langage informatique

Quatre principes clés

- ✓ Accessibilité
- ✓ Reproductibilité
- ✓ Transparence
- ✓ Peer review

```
direction="wide")
tab[is.na(tab)] <- 0
# filename <- "touverUNNom"
# chemin <- paste(rep,filename,sep="/")
# write.table(tab, chemin)
colnames(tab) <- sub("nombre.", "", colnames(tab))
return(tab)
}

## sous jeux de donnees si choix d espece d annee ou d un pourcentage de carres
makeSousTab <- fonction(tab,vecSp=NULL,echantillon=1,
methodeEchantillon="carre",vecannees=NULL) {
cat(" -- Fabrication du sous jeu de donnees --\n")
flush.console()
## reduction de la table à certaine espèces
if(!is.null(vecSp)) {
cat(" selection", length(vecSp), "espece(s):\n -> ")
cat(vecSp)
cat("\n")
tab <- data.frame(carre = tab$carre, annee = tab$annee, tab[,vecSp])
colnames(tab) <- c("carre", "annee", vecSp)
}
## reduction de la table pour certaines annees
if(!is.null(vecannees)) {
tab <- subset(tab, annee=>vecannees[1] & annee <= vecannees[2])
}
## reduction de la table par une proportion de carre suivie
if(echantillon != 1) {
if(echantillon < 1 & echantillon > 0) {
nbinit <- nrow(tab)
if(methodeEchantillon == "global") {
nb <- round(nrow(tab)*echantillon)
cat(" echantillonnage", echantillon*100,
"% des donnees par la methode", methodeEchantillon, "\n")
cat(" -> conservation de", nb, "lignes sur", nbinit, "\n")
flush.console()
tab <- tab[sample(1:nrow(tab))[1:nb], ]
} else {
if (methodeEchantillon == "carre") {
cat(" echantillonnage", echantillon*100,
"% des carrees par la methode", methodeEchantillon, "\n")
nbcarreinit <- length(unique(tab$carre))
chat=sample(unique(tab$carre),
length(unique(tab$carre))*echantillon, replace=F)
cat(" -> conservation de", length(chat), "carrees sur",
nbcarreinit)
tab=subset(tab, subset = carre %in% chat)
cat(" (", nrow(tab), " lignes sur ", nbinit, ")\n", sep="")
} else {
stop("Methode d echantillonnage non reconnue")
}
}
}
```



Calculate community metrics calculate community metrics from abundance data (Galaxy Version 0.0.1)

Input file



No tabular dataset available.

Observation data file, with location, year, species and abundance.

Choose the community metrics you want to compute

Select/Unselect all

All

Presence/absence, Species richness, Simpson and Shannon index are systematically computed.

Execute

Calculate community metrics from abundance data

Le workflow Galaxy PAMPA

Calculate community metrics calculate community metrics from abundance data (Galaxy Version 0.0.1)

Input file
No tabular dataset available.

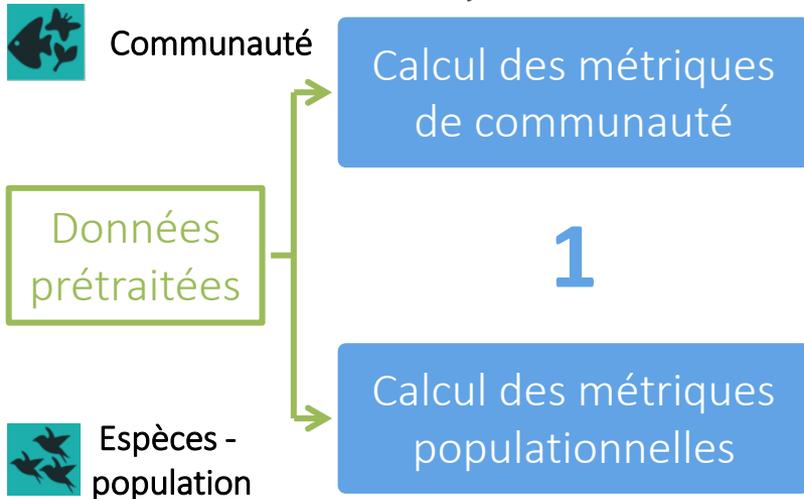
Observation data file, with location, year, species and abundance.

Choose the community metrics you want to compute
Select/Unselect all
All

Presence/absence, Species richness, Simpson and Shannon index are systematically computed.

Execute

Calculate community metrics from abundance data



Calculate presence absence table calculate presence absence table from observation data (Galaxy Version 0.0.1)

Input file
No tabular dataset available.

Observation data file, with location, year, species and abundance.

Email notification
Yes No

Send an email notification when the job completes.

Execute

Calculate presence absence table from abundance data



Le workflow Galaxy PAMPA

Calculate community metrics calculate community metrics from abundance data (Galaxy Version 0.0.1)

Input file
 No tabular dataset available.

Observation data file, with location, year, species and abundance.

Choose the community metrics you want to compute
 Select/Unselect all

Presence/absence, Species richness, Simpson and Shannon index are systematically computed.

Compute GLM on community data Compute a GLM of your choice on community data (Galaxy Version 0.0.1)

Input metrics file
 No tabular dataset available.

Metrics data file, with location, year, and metrics informations that can be used as interest variable.

Untaxids informations file
 No tabular dataset available.

Untaxids file, with all informations available about untaxids.

Response variables
 Select/Unselect all

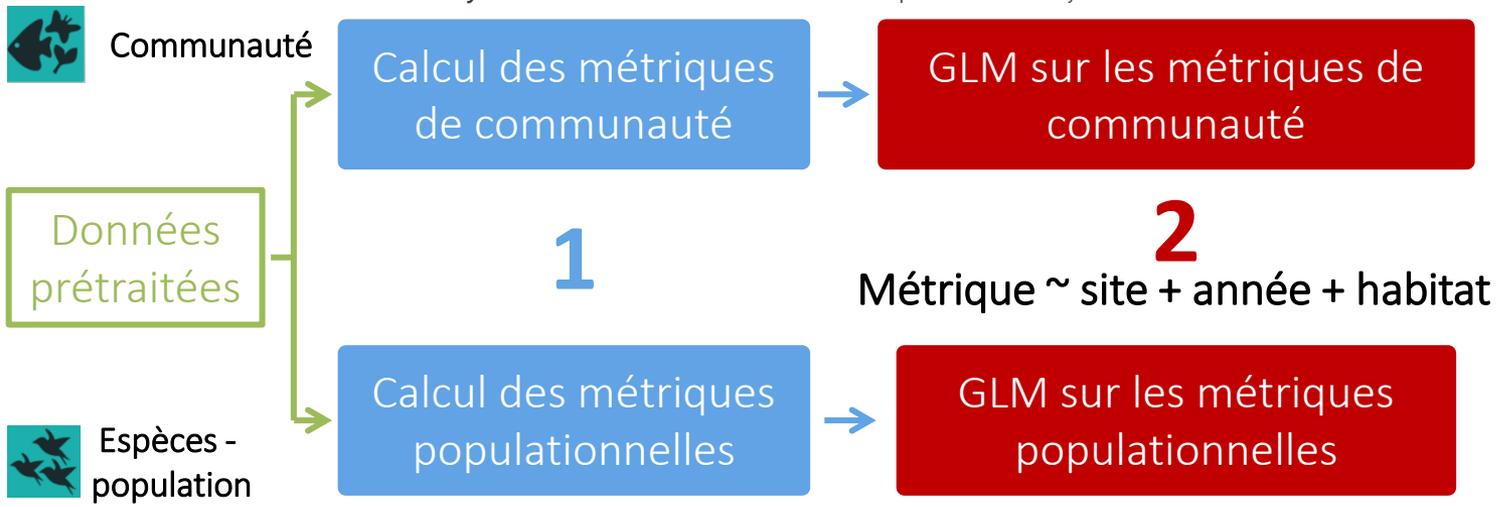
Choose the response variables you want to include in your analysis.

Random effect ?
 Select/Unselect all

Allocates a random effect on site or year makes your model more reliable as random events on a peculiar site or year can affect populations, it takes account of pseudoreplication. However, avoid applying it on a less than 10 levels variable (less than 10 different sites and/or year).

Calculate community metrics from abundance data

Compute GLM on community data with selected interest variables



Calculate presence absence table calculate presence absence table from observation data (Galaxy Version 0.0.)

Input file
 No tabular dataset available.

Observation data file, with location, year, species and abundance.

Email notification

Send an email notification when the job completes.

Compute GLM on population data Compute a GLM of your choice on population data (Galaxy Version 0.0.1)

Input metrics file
 No tabular dataset available.

Metrics data file, with location, year, and metrics informations that can be used as interest variable.

Untaxids informations file
 No tabular dataset available.

Untaxids file, with all informations available about untaxids.

Interest variable from metrics file
 Missing columns in referenced dataset.

Choose the field of the interest variable.

Response variables
 Select/Unselect all

Choose the response variables you want to include in your analysis.

Random effect ?
 Select/Unselect all

Allocates a random effect on site or year makes your model more reliable as random events on a peculiar site or year can affect populations, it takes account of pseudoreplication. However, avoid applying it on a less than 10 levels variable (less than 10 different sites and/or year).

Calculate presence absence table from abundance data

Compute GLM on population data with selected interest variables

Le workflow Galaxy PAMPA



Calculate community metrics calculate community metrics from abundance data (Galaxy Version 0.0.1)

Input file
No tabular dataset available.

Observation data file, with location, year, species and abundance.

Choose the community metrics you want to compute
Select/Unselect all
All

Presence/absence, Species richness, Simpson and Shannon index are systematically computed.

Execute

Compute GLM on community data Compute a GLM of your choice on community data (Galaxy Version 0.0.1)

Input metrics file
No tabular dataset available.

Metric data file, with location, year, and metrics informations that can be used as interest variable.

Unlobs informations file
No tabular dataset available.

Unlobs file, with all informations available about unlobs.

Response variables
Select/Unselect all
Year Site Habitat

Choose the response variables you want to include in your analysis.

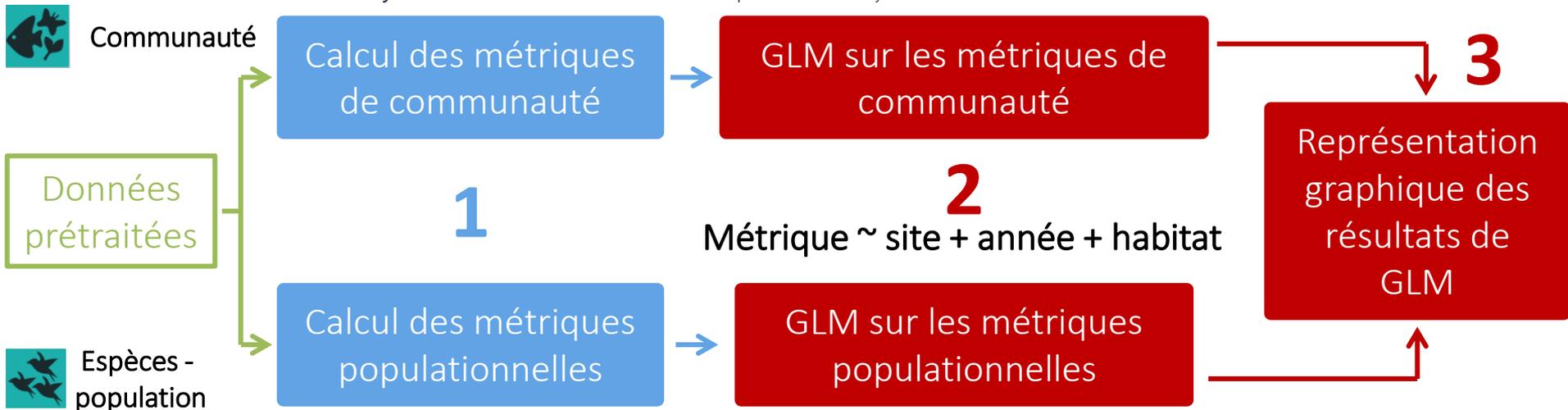
Random effect ?
Select/Unselect all
Site

Allocate a random effect on site or year makes your model more reliable as random events on a peculiar site or year can affect populations, it takes account of pseudoreplication. However, avoid applying it on a less than 10 levels variable (less than 10 different sites and/or year).

Execute

Calculate community metrics from abundance data

Compute GLM on community data with selected interest variables



Calculate presence absence table calculate presence absence table from observation data (Galaxy Version 0.0.)

Input file
No tabular dataset available.

Observation data file, with location, year, species and abundance.

Email notification
Yes No

Send an email notification when the job completes.

Execute

Compute GLM on population data Compute a GLM of your choice on population data (Galaxy Version 0.0.1)

Input metrics file
No tabular dataset available.

Metric data file, with location, year, and metrics informations that can be used as interest variable.

Unlobs informations file
No tabular dataset available.

Unlobs file, with all informations available about unlobs.

Interest variable from metrics file
Missing columns in referenced dataset.

Choose the field of the interest variable.

Response variables
Select/Unselect all
Year Site Habitat

Choose the response variables you want to include in your analysis.

Random effect ?
Select/Unselect all
Site

Allocate a random effect on site or year makes your model more reliable as random events on a peculiar site or year can affect populations, it takes account of pseudoreplication. However, avoid applying it on a less than 10 levels variable (less than 10 different sites and/or year).

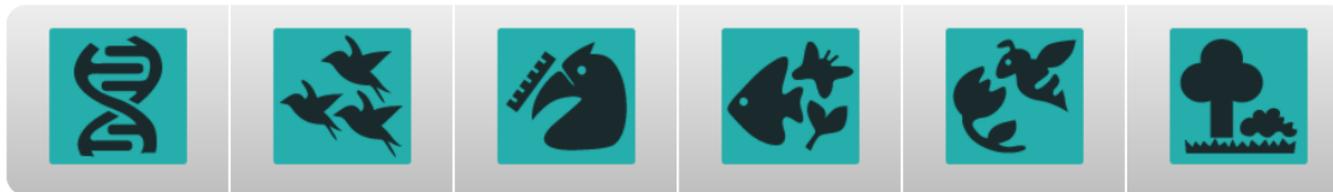
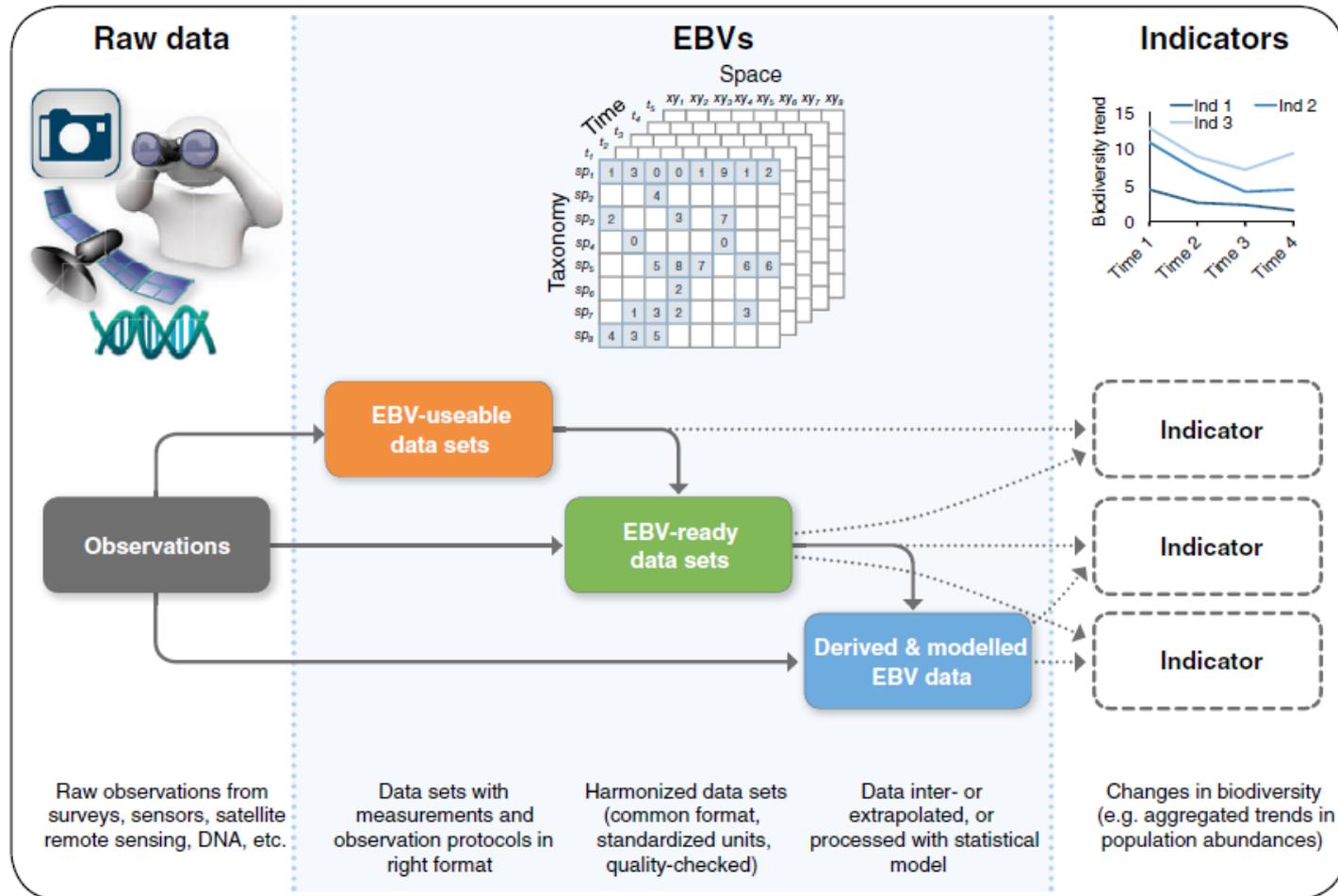
Execute

Calculate presence absence table from abundance data

Compute GLM on population data with selected interest variables



Les Variables Essentielles de Biodiversité (EBV)



Genetic composition

Species population

Species traits

Community composition

Ecosystem function

Ecosystem structure

Kissling *et al.* 2017

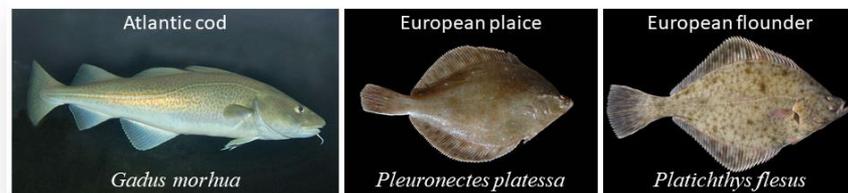


Tutoriel sur données de pêche (CPUE)

<https://bit.ly/2VjDTaQ>

Compute and analyze Essential Biodiversity Variables with PAMPA toolsuite

By:  Coline Royaux



Overview

🔍 Questions

- How to evaluate properly species populations and communities biological state with abundance data?
- How does trawl exploited populations of Baltic sea, Southern Atlantic and Scotland are doing over time?
- How to compute and analyze Essential Biodiversity Variables (EBV) on abundance data?

🎯 Objectives

- Upload data from DATRAS portal of ICES
- Pre-process population data with Galaxy
- Learning how to use an Essential Biodiversity Variables (EBV) scientific workflow from raw data to graphical representations
- Learning how to construct a Generalized Linear (Mixed) Model from a usual ecological question
- Learning how to interpret a Generalized Linear (Mixed) Model

📋 Requirements

- [Introduction to Galaxy Analyses](#)

🕒 **Time estimation:** 2 hours

📄 Supporting Materials

[📄 Datasets](#) [🔗 Workflows](#) [🌐 Available on these Galaxies](#) ▾

📅 **Last modification:** Nov 19, 2020



Introduction

Upload and pre-processing of the data

Compute Essential Biodiversity Variables

Introduction

This tutorial aims to present the PAMPA Galaxy workflow and how to use it to compute Essential Biodiversity Variables (EBV) from species abundance data and analyse it through generalized linear (mixed) models (GLM and GLMM). This workflow made up of 5 tools will allow you to process temporal series data that include at least `year`, "location" and species sampled along with abundance value and, finally, generate article-ready data products.

Outils Galaxy-E généralisable

Variables primaires similaires

Données Suivi Temporel des Oiseaux Communs

	carre	annee	espece	abond
1	2	2016	ACCGEN	0
2	2	2017	ACCGEN	0
3	2	2018	ACCGEN	0
4	2	2019	ACCGEN	0
5	183	2016	ACCGEN	0
6	183	2017	ACCGEN	0
7	183	2018	ACCGEN	0
8	183	2019	ACCGEN	0

Données de caméras sous-marines

	UnitObs	rotation	codeSp	sexe	taille	classe_taille	poids	nb_ind
1	AS140155	3	Hemifasc	-999	-999	P	-999	1
2	AS140159	1	Nasosp.	-999	-999	P	-999	3
3	AS140159	3	Gompvari	-999	-999	P	-999	1
4	AS140160	3	Gompvari	-999	-999	P	-999	1
5	AS140099	2	Parumult	-999	-999	P	-999	1
6	AS140088	1	Varilout	-999	-999	P	-999	1
7	AS140088	2	Gompvari	-999	-999	P	-999	2
8	AS140041	1	Nasosp.	-999	-999	P	-999	5
9	AS140044	1	Parumult	-999	-999	P	-999	4

Données de pêche

	Survey	Year	Quarter	Area	AphiaID	Species	LngtClass	CPUE_number_per_hour
1	BITS	1991	1	22	126281	Anguilla anguilla	0	0.000000
2	BITS	1991	1	22	126281	Anguilla anguilla	720	0.009160
3	BITS	1991	1	22	126417	Clupea harengus	0	0.000000
4	BITS	1991	1	22	126417	Clupea harengus	80	0.075785
5	BITS	1991	1	22	126417	Clupea harengus	85	0.088277
6	BITS	1991	1	22	126417	Clupea harengus	95	0.037892
7	BITS	1991	1	22	126417	Clupea harengus	100	0.063293
8	BITS	1991	1	22	126417	Clupea harengus	105	0.012492
9	BITS	1991	1	22	126417	Clupea harengus	110	0.618357

Données Vigie - Chiro

	participation	Nuit	num_micro	groupe	espece	nb_contacts
1	55de2cd52121b1000d27430e	2015-07-26	0	bat	Barbar	1
2	55de2cd52121b1000d27430e	2015-07-26	0	bush-cricket	Barfis	1
3	55de2cd52121b1000d27430e	2015-07-26	0	noise	noise	5022
4	55de2cd52121b1000d27430e	2015-07-26	0	bush-cricket	Decalb	5
5	55de2cd52121b1000d27430e	2015-07-26	0	bush-cricket	Tyllil	18
6	55de2cd52121b1000d27430e	2015-07-26	0	bat	Nyclei	1
7	55de2cd52121b1000d27430e	2015-07-26	0	bush-cricket	Phanan	269

- Site
- Année
- Espèce
- Occurrence

Atomisation

Actuellement, en écologie...

Un script R pour chaque fichier de données

```
      ,direction="wide")
  tab[is.na(tab)] <- 0
  # filename <- "trouverUnNom"
  # chemin <- paste(rep,filename,sep="/")
  # write.table(tab, chemin)
colnames(tab) <- sub("nombre.", "", colnames(tab))
  return(tab)
}

## sous jeux de donnees si choix d espece d annee ou d un pourcentage de carres
makeSousTab <- function(tab,vecSp=NULL,echantillon=1,
  methodeEchantillon="carre",vecannees=NULL) {
  cat(" -- Fabrication du sous jeu de donnees --\n")
  flush.console()
  ## reduction de la table à certaine espèces
  if(!is.null(vecSp)) {
    cat(" selection", length(vecSp), "espece(s):\n -> ")
    cat(vecSp)
    cat("\n")
    tab <- data.frame(carre = tab$carre, annee = tab$annee, tab[,vecSp])
    colnames(tab) <- c("carre", "annee", vecSp)
  }
  ## reduction de la table pour certaines annees
  if(!is.null(vecannees)) {
    tab <- subset(tab, annee >= vecannees[1] & annee <= vecannees[2])
  }
  ## reduction de la table par une proportion de carre suivie
  if(echantillon != 1) {
    if(echantillon < 1 & echantillon > 0) {
      nbinit <- nrow(tab)
      if(methodeEchantillon == "global") {
        nb <- round(nrow(tab)*echantillon)
        cat(" echantillonnage", echantillon*100,
          "% des donnees par la methode", methodeEchantillon, "\n")
        cat(" -> conservation de", nb, "lignes sur", nbinit, "\n")
        flush.console()
        tab <- tab[sample(1:nrow(tab))[1:nb],]
      } else {
        if (methodeEchantillon == "carre") {
          cat(" echantillonnage", echantillon*100,
            "% des carrees par la methode", methodeEchantillon, "\n")
          nbcarreinit <- length(unique(tab$carre))
          chat=sample(unique(tab$carre),
            length(unique(tab$carre))*echantillon, replace=F)
          cat(" -> conservation de", length(chat), "carrees sur",
            nbcarreinit)
          tab=subset(tab, subset = carre %in% chat)
          cat(" (" , nrow(tab), " lignes sur " , nbinit, ")\n", sep="")
        } else {
          stop("Methode d echantillonnage non reconnue")
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Atomisation

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```

Atomisation

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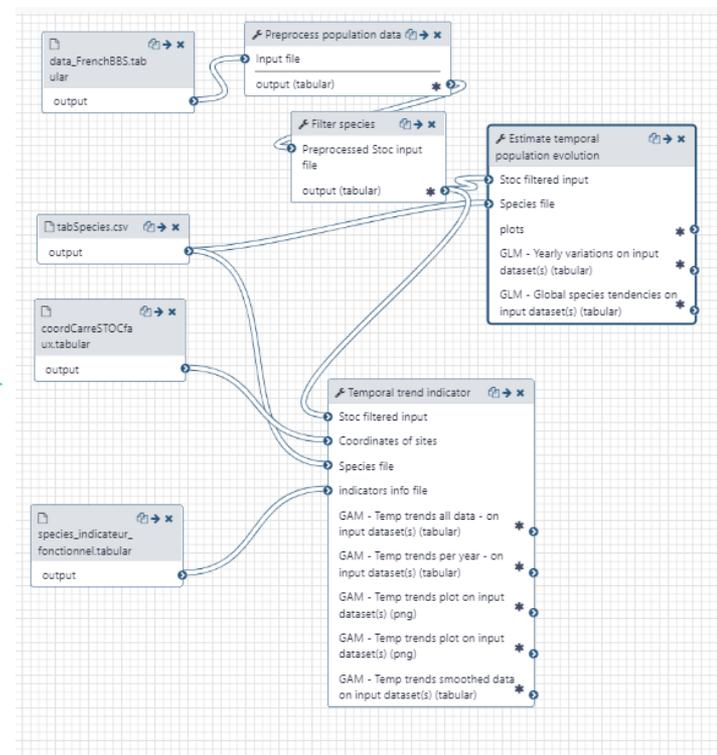
```
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Avec Galaxy...

Plusieurs scripts R atomisés pour analyser différents fichiers de données



Atomisation

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Un script R pour chaque fichier de données

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