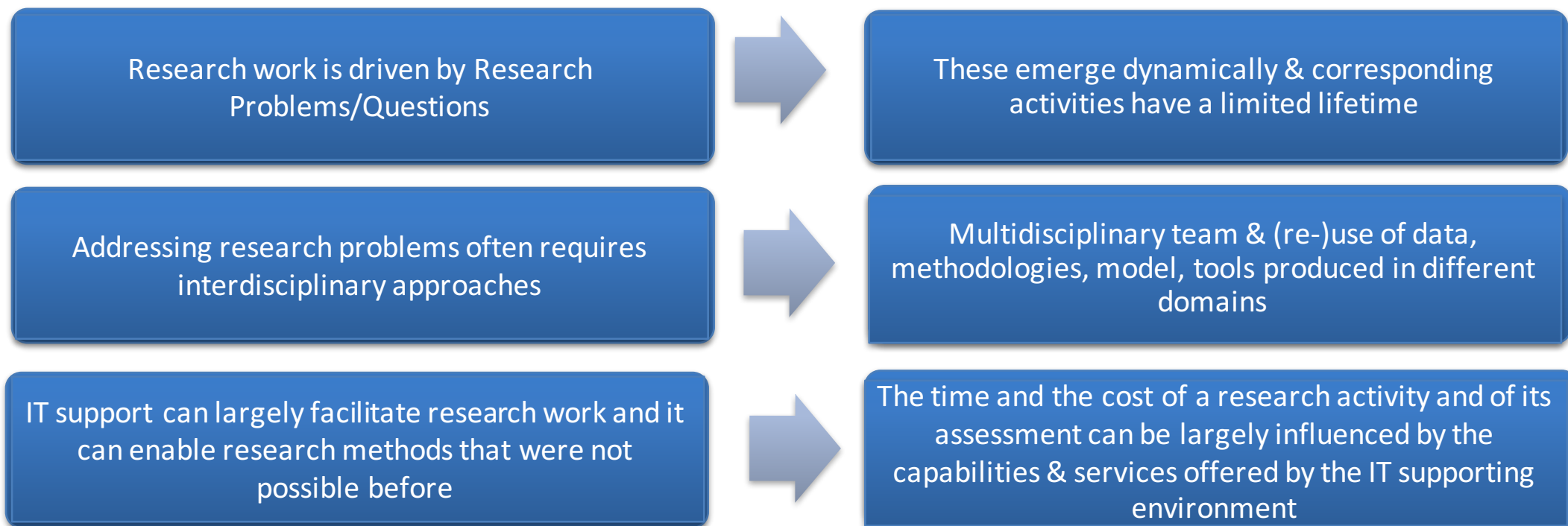


Virtual Research Environments as-a-Service

Donatella Castelli

CNR-ISTI

donatella.castelli@isti.cnr.it



www.d4science.org



+50 heterogeneous data providers, over a billion quality records
+20,000 processes/month
99,7% service availability

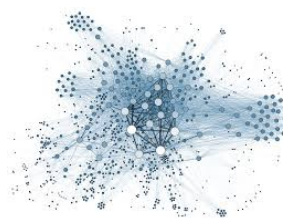
D4Science services: supporting the entire data mgmt lifecycle



Metadata generation and management



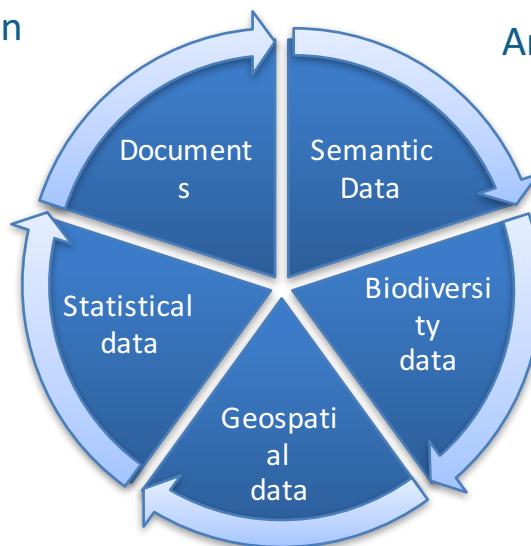
Harmonisation



Analytics



Sharing



Cloud storage

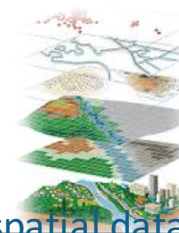
Cloud computing



Multi-platform: R,
Java, Fortran



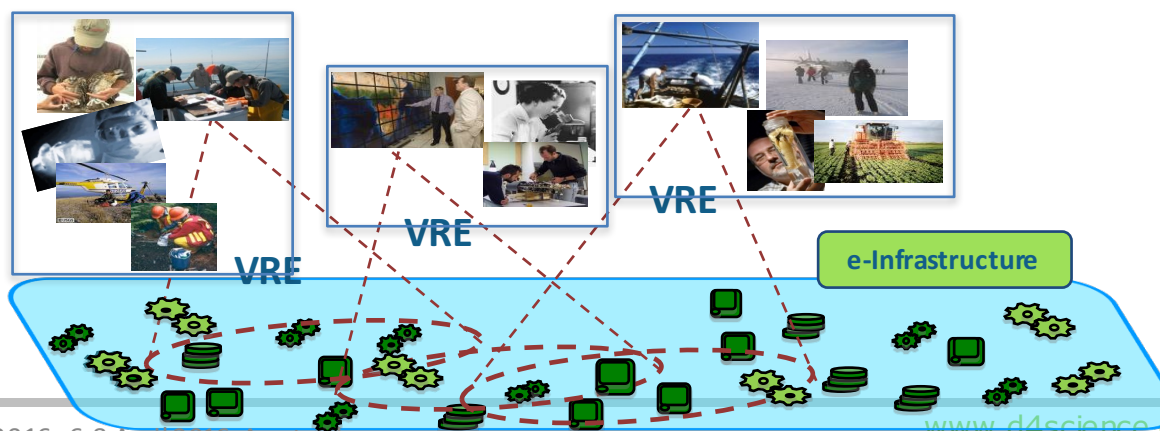
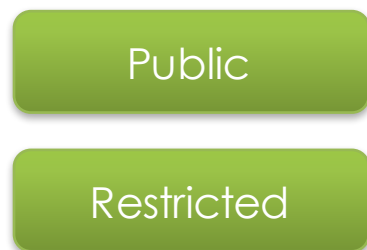
Databases



Geospatial data
www.d4science.org
Store

Virtual Research Environment

- **web-based working environment**
- providing access to services and resources tailored to serve the needs of the research team **in addressing a research question**
- **open and flexible** with respect to service offering and lifetime
- providing fine-grained **controlled sharing** of both intermediate and final research results
- **Low cost of creation and operation**



Name: MyPersonalVRE
 Designer: Pasquale Pagano (pasquale.pagano)
 VRE Manager: Leonardo Candela (leonardo.candela)
 Description: The environment for my research

Life time
 From: November 22, 2014
 To: November 22, 2015

1. Specify VRE metadata (including policies)

- Taxonomic Data Comparison
- ConnectCube
- Enhanced Documents Management
- Information Objects Discovery
- Messaging
- Shared Workspace
- Social Networking Facilities
- GeosCube
- Geospatial Data Discovery
- Geospatial Data Processing
- StatsCube

2. Select applications

Available Resources for Occurrence and Taxonomic Data Discovery

Name	Description	Se
CatalogueOfLife	A virtual biodiversity repository of Catalogue of L...	
GBIF	A virtual biodiversity repository of GBIF data. T...	
BrazilianFlora	A virtual biodiversity repository of List of Sp...	
ITIS	A virtual biodiversity repository of ITIS data.	
WoRDSS	A virtual biodiversity repository of WoRDSS da...	
OBIS	A virtual biodiversity repository of OBIS data. The...	
WoRMS	A virtual biodiversity repository of WoRMS data. Th...	
ASFIS	Runtime Resource for ASFIS Plugin	
IRMNG	A virtual biodiversity repository of IRMNS data. The...	

4. Select data collections

Available Resources for Statistical Service

Name	Description	Se
_OBS...	Algorithm returning most observed species in a sp...	
OBIS_SPECIES_OBSERVATIONS_PER_MEOW_AREA	Algorithm returning most observed species in a specific years range (from OBIS database).	
STDBSCHEMA	Algorithm that allows to view the schema names of...	
Intersection	GIS intersection process. The native algorithm is i...	
Spread	Spread	
SPECIES_OBSERVAT...	Algorithm returning most observed species in a sp...	
OCCURRENCES_DU...	A transducer algorithm that produces a duplicate fr...	
XYEXTRACTOR_TABLE	An algorithm to extract values associated to a table...	


3. Configure applications

Hardware setup and software deployment completely hidden

Evolving needs of its users completely supported

D4Science offer VREs to ...

Environmental Science, Marine biodiversity, Fisheries&Aquaculture science, Culture Heritage, Social data mining, Geothermal Science, Smart cities



Parthenos
Access Info



SmartArea
Access Info



SoBigData.eu
Access Info



SoBigData.it
Access Info



gCube
Access Info




iMarine
Access Info

Supported Projects

D4Science is supporting the operation of a series of diverse Initiatives Communities of Practice and Projects.



ARIADNE
Access Info



BlueBridgeProject
Access Info




DESCRAMBLE
Access Info




EFG
Access Info



EGIEngage
Access Info




EGIP
Access Info



ENVRI
Access Info



ENVRIplus
Access Info



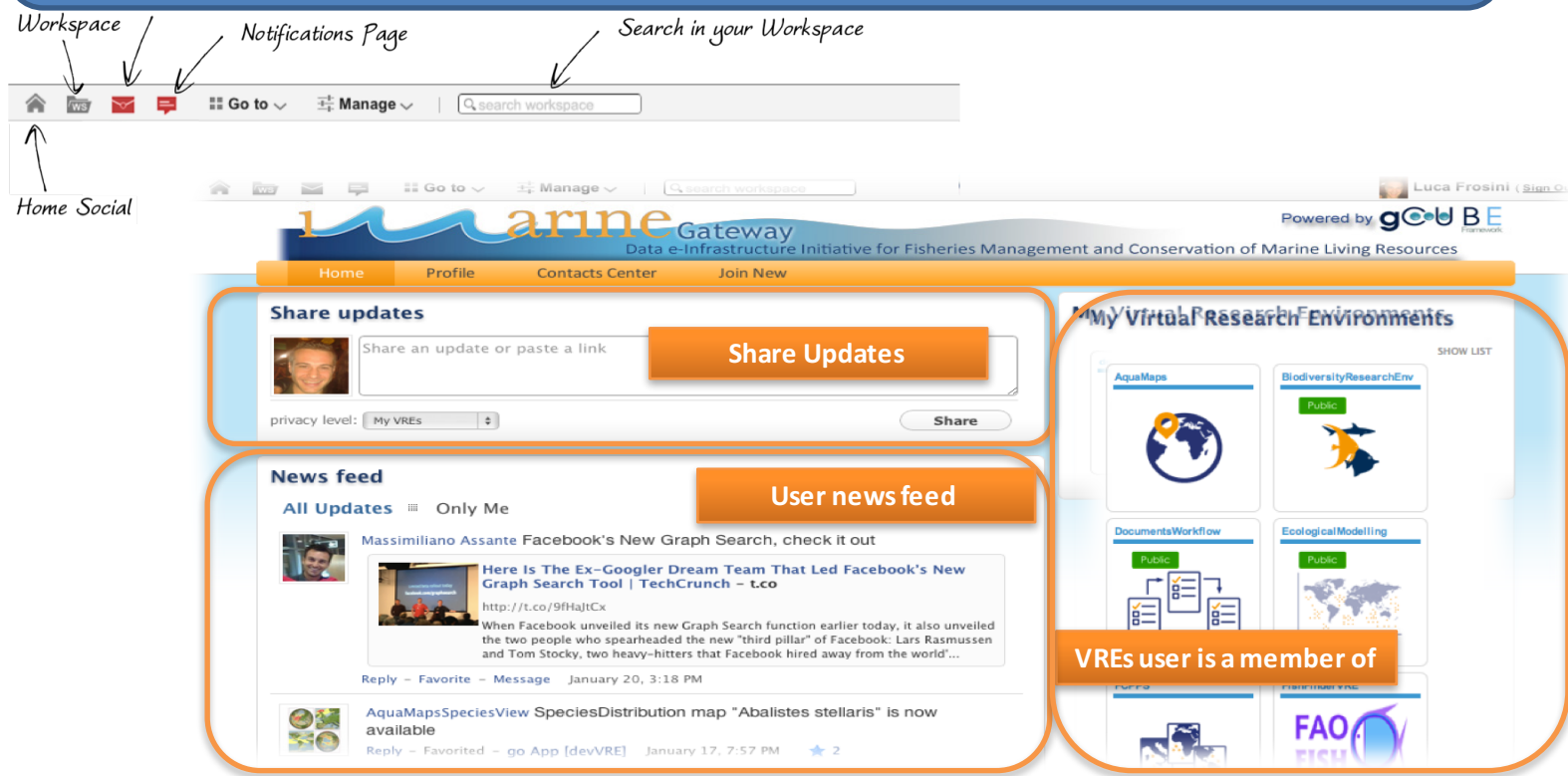
OpenIt
Access Info



PGFA-UFMT
Access Info

*+50 VREs
2000 scientists in 44
countries*

A single point to
 Get status and updates from applications and other users they are interested in
 Get notifications about messages, jobs completion, new generated products, etc.



Workspace

Notifications Page

Search in your Workspace

Home Social

Share updates

Share Updates

News feed

User news feed

My Virtual Research Environments

VREs user is a member of

Luca Frosini (Sign Out)

Powered by **GOUBE**


Home Profile Contacts Center Join New

Here Is The Ex-Googler Dream Team That Led Facebook's New Graph Search Tool | TechCrunch - Lco


AquaMapsSpeciesView SpeciesDistribution map "Abalistes stellaris" is now available

- Folders can be shared
- Including documents, datasets, software & computations

Workspace Public Link

 Create links to files in your Workspace to download them. You can send the links to anyone by pasting them into Workspace Message, your emails, instant messages, etc.

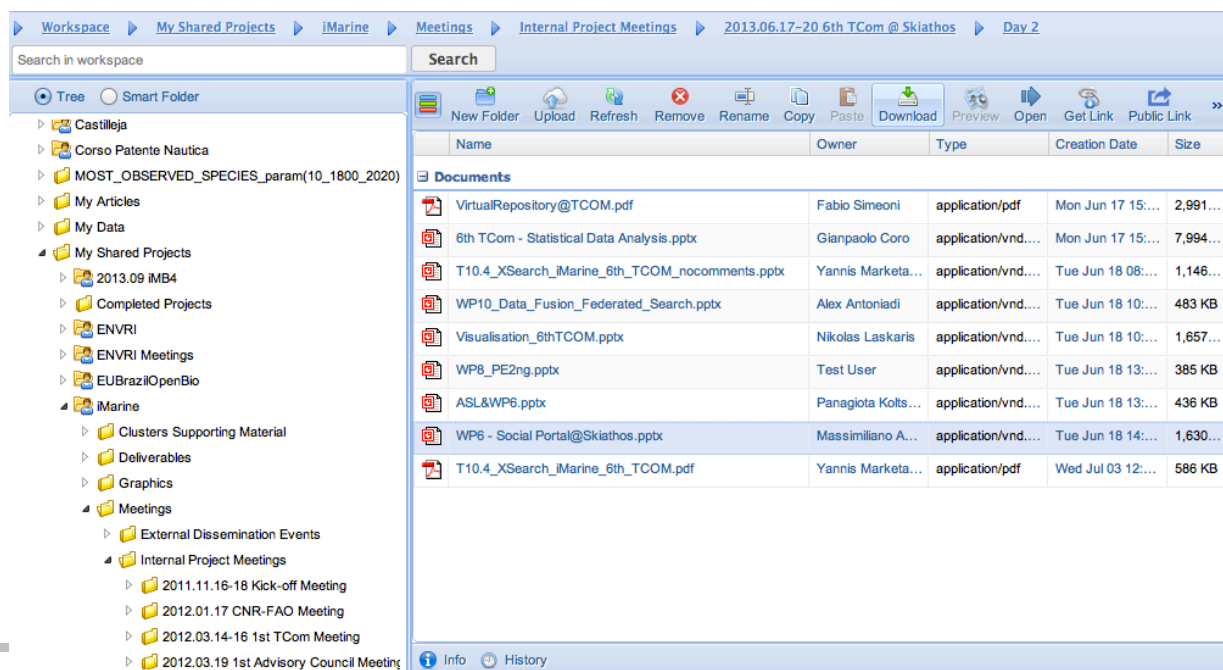
Workspace Share Folders and Files

 The quickest way to share something is using the Share Folder. Locate the folder with the files you want to share and then click 'Share'

Workspace Upload Files and Archives

You can upload files in the Workspace in several ways:

- 1 - Drop your files from Desktop;
- 2 - Click 'Upload' and Browse Files;
- 3 - Upload a zip file to unzip directly its content in the Workspace.

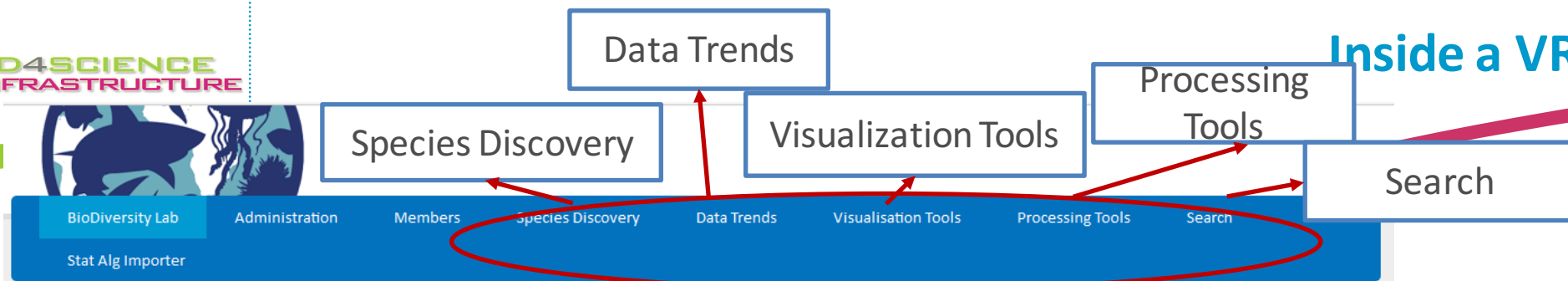


The screenshot shows the workspace interface with a breadcrumb path: Workspace > My Shared Projects > iMarine > Meetings > Internal Project Meetings > 2013.06.17-20 6th TCom @ Skiathos > Day 2. A search bar is at the top. The left sidebar shows a tree view with folders like 'My Shared Projects' and 'Meetings'. The main area displays a table of documents:

Name	Owner	Type	Creation Date	Size
Documents				
VirtualRepository@TCOM.pdf	Fabio Simeoni	application/pdf	Mon Jun 17 15:...	2,991...
6th TCom - Statistical Data Analysis.pptx	Gianpaolo Coro	application/vnd...	Mon Jun 17 15:...	7,994...
T10.4_XSearch_iMarine_6th_TCOM_nocomments.pptx	Yannis Marketa...	application/vnd...	Tue Jun 18 08:...	1,146...
WP10_Data_Fusion_Federated_Search.pptx	Alex Antoniad	application/vnd...	Tue Jun 18 10:...	483 KB
Visualisation_6thTCOM.pptx	Nikolas Laskaris	application/vnd...	Tue Jun 18 10:...	1,657...
WP8_PE2ng.pptx	Test User	application/vnd...	Tue Jun 18 13:...	385 KB
ASL&WP6.pptx	Panagiota Kolts...	application/vnd...	Tue Jun 18 13:...	436 KB
WP6 - Social Portal@Skiathos.pptx	Massimiliano A...	application/vnd...	Tue Jun 18 14:...	1,630...
T10.4_XSearch_iMarine_6th_TCOM.pdf	Yannis Marketa...	application/pdf	Wed Jul 03 12:...	586 KB



Inside a VRE



BioDiversity Lab Administration Members Species Discovery Data Trends Visualisation Tools Processing Tools Search

Stat Alg Importer

Your Stats in BiodiversityLab



POSTS YOU GOT
4 ★ 6 0

Top Topics

#unfao

Recently updated in BiodiversityLab folder

- results.csv
- Mola mola (scientific name)...
- faoceanarea_T20.csv
- UPMC_Coro_iMarine2015_V2.0....

Show all ...

Service Auth. Token

..... Show

Invite whoever's missing

e-mail address

Send Invite



Share an update or a link, use "@" to mention and "#" to add a topic

Share with: BiodiversityLab + Notification to members



Share



Gianpaolo Coro Dear VRE participants,

Three new algorithms are available among the processing tools:
1 - Ecompath With Ecosim: available in the Stock Assessment category, the Ecompath With Ecosim algorithm executes the EwE engine on user-provided models and configuration files. This implementation accepts a model and a configuration file as input; the result of the analysis is returned as a zip archive. This is the result of a joint work activity between IRD, Engineering and CNR.
References: Ch...

[See More](#)

Reply - Favorite March 03, 11:31 AM ★ 2



Roberto Cirillo Dear all,

due to an extraordinary maintenance in one of the D4Science site, the following capabilities will not be ensured from Thursday March 3rd 06:30 CET to Friday March 4th 17:00 CET.
Access to Asfis, Brazil...

[See More](#)

Reply - Favorite March 01, 3:01 PM



Gianpaolo Coro Dear VRE members, the following algorithms are now available among the Processing Tools to process vessel, fisheries and environmental data:

Estimate Fishing Activity

An algorithm that estimates activity hours (fishing or other) from vessels trajectories, adds bathymetry information to the table and classifies (point-by-point) fishing activity of the involved vessels according to two algorithms: one based on speed (activity class speed output column).

[See More](#)



Leave Group



BiodiversityLab

The BiodiversityLab is a VRE designed to provide a collection of applications that allow scholars to perform complete experiments about single individuals or groups of marine species. The VRE allows to:

- inspect species maps;
- produce a species distribution map by means of either an expert system (AquaMaps) or a machine learning model (e.g. Neural Networks);
- analyse species observation trends;
- inspect species occurrence data;
- inspect species descriptions and characteristics;
- perform analysis of climatic changes and of their effects on species distribution;
- produce GIS maps for geo ...

[See more](#)

Questions? Ask the managers

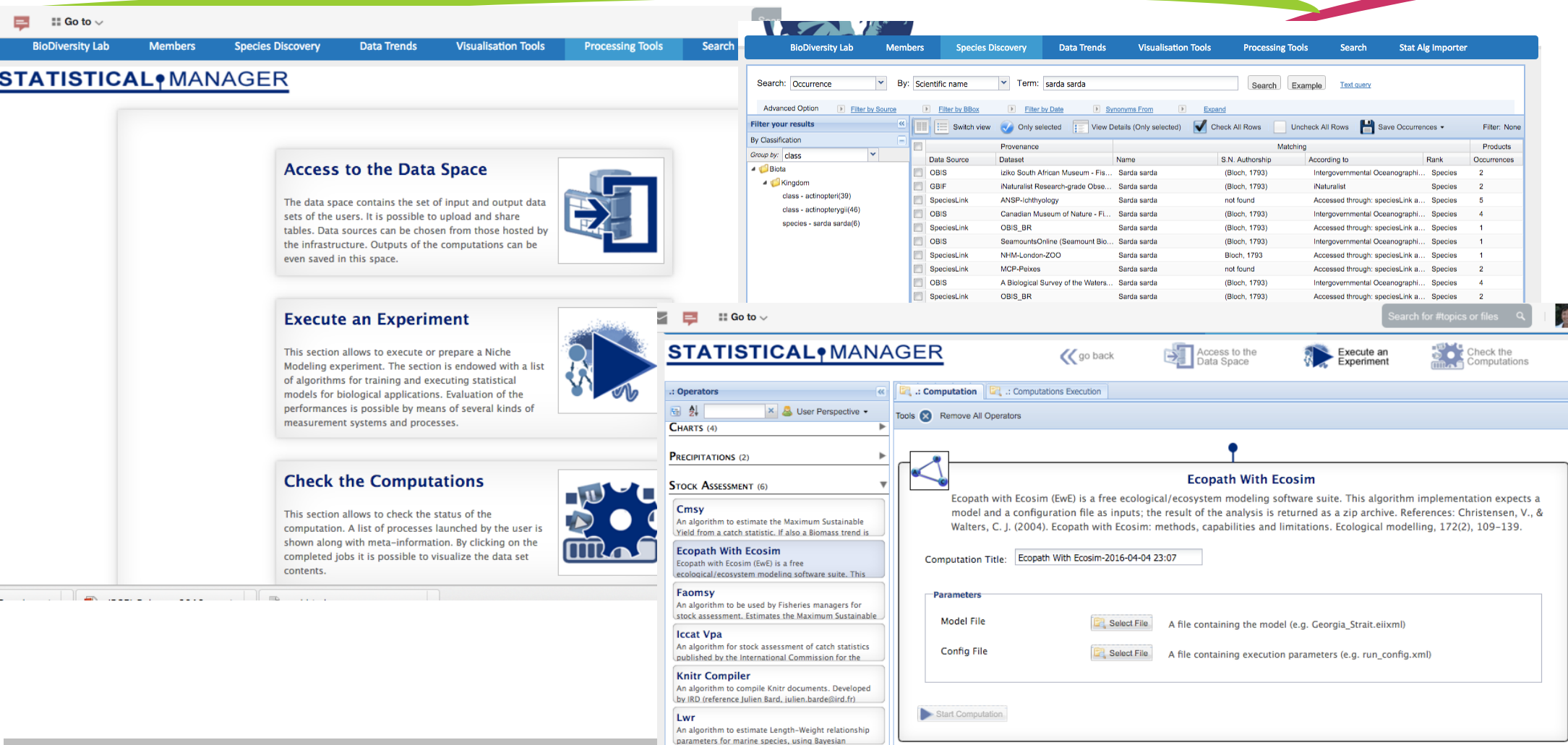
e.org

STATISTICAL MANAGER

Access to the Data Space

Execute an Experiment

Check the Computations



The screenshot displays the Statistical Manager web interface. At the top, there is a navigation bar with tabs for BioDiversity Lab, Members, Species Discovery, Data Trends, Visualisation Tools, Processing Tools, Search, and Stat Alg Importer. Below this, a search interface is shown with filters for Occurrence, Scientific name, and Term (sarda sarda). A table of search results is displayed, listing various data sources and their associated species. On the left side, there are three main sections: 'Access to the Data Space', 'Execute an Experiment', and 'Check the Computations'. The 'Check the Computations' section is expanded, showing a list of operators including Cmsy, Ecopath With Ecosim, Faomsy, Iccat Vpa, Knitr Compiler, and Lwr. The 'Ecopath With Ecosim' operator is selected, and its configuration page is shown, including a description of the software, a computation title, and parameter selection options for the Model File and Config File.

i marine Gateway
Data e-Infrastructure Initiative for Fisheries Management and Conservation of Marine Living Resources

Powered by **D4SCIENCE.ORG**

Home Profile Explore Research Environments

How-to Share Public Link Upload Don't show this again Hide

StatisticalAlgorithmsImporter > VPA_WORKFLOW

Search by name

Tree Smart Folder

- workspace
 - VRE Folders
 - 2015_Sept_21-22-RDP_Workshop
 - AgINFRA+
 - Articles
 - Datasets
 - Draft Presentazioni Kick-off BlueBridge
 - Draft Presentazioni TCOM@Rome@FAO
 - EGI-Engage-D2.6 Shared Folder
 - Experiments
 - Groups
 - ICCAT_BFT_Stock_Assessment
 - Maps Comparison-2016-02-18 19_32
 - Meetings and presentations
 - Other Shares
 - Projects
 - quickrankdeploy
 - SAI Examples
 - StatisticalAlgorithmsImporter
 - Complex_WPS4R_Annotation
 - Simple_WPS4R_Annotation
 - Single_R_Script_Example
 - VPA_WORKFLOW**
 - SupportFolder
 - test_WPS_VPA
 - Training

Documents

- stat_algo.project
- Local_VPA_WF_CN.R

Folders

- Target

Tools: New Folder, Upload, Refresh, Delete, Rename, Copy, Paste, Download, Preview, Open, Get Link, Public Link, Upload Archive, Change Permissions

Name	Owner	Type	Last Update	Size
stat_algo.project				
Local_VPA_WF_CN.R				
Target				

Project Explorer

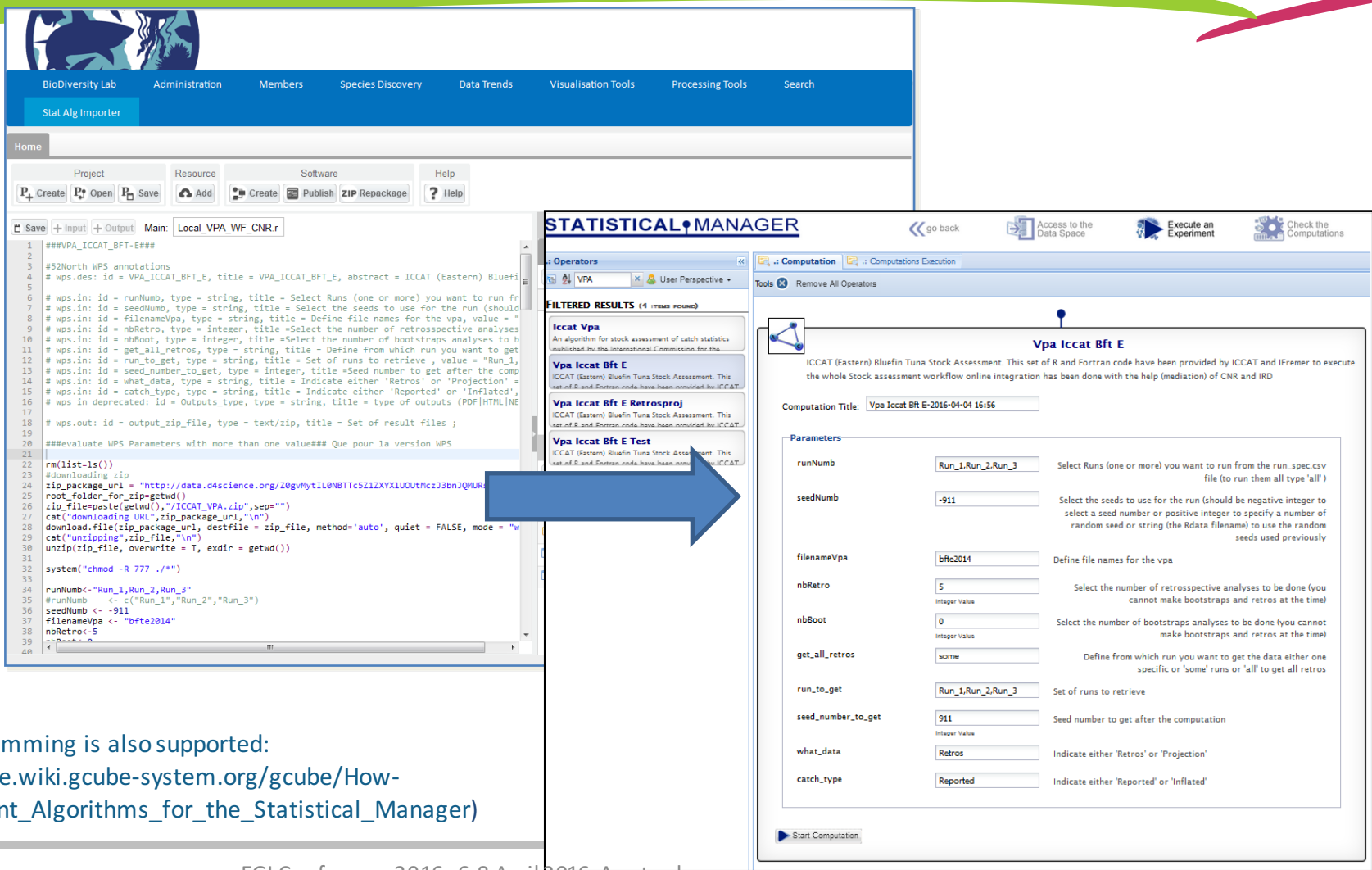
Name
Target
Local_VPA_WF_CN.R
stat_algo.project

```

1 ##VPA_ICCAT_BFT-Ess
2
3 #52North WPS annotations
4 # wps.des: id = VPA_ICCAT_BFT_E, title = VPA_ICCAT_BFT_E, abstract = ICCAT (Eastern) Bluefi
5
6 # wps.in: id = runLump, type = string, title = Select Runs (one or more) you want to run fr
7 # wps.in: id = seedNum, type = string, title = Select the seeds to use for the run (shoul
8 # wps.in: id = filenameVpa, type = string, title = Define file names for the vpa, value =
9 # wps.in: id = nboot, type = integer, title =Select the number of retrospective analysi
10 # wps.in: id = nboot, type = integer, title =Select the number of bootstraps analysi
11 # wps.in: id = get_all_retros, type = string, title = Define from which run you want to
12 # wps.in: id = run_to_get, type = string, title = Set of runs to retrieve , value =
13 # wps.in: id = seed_number_to_get, type = integer, title =Seed number to get after the comp
14 # wps.in: id = what_data, type = string, title = Indicate either 'Retros' or 'Projection' =
15 # wps.in: id = catch_type, type = string, title = Indicate either 'Reported' or 'Inflated',
16 # wps.in deprecated: id = Outputs_type, type = string, title = type of outputs (PDF|HTML|W
17
18 # wps.out: id = output_zip_file, type = text/zip, title = Set of result files ;
19
20 ##evaluate WPS Parameters with more than one value## Que pour la version WPS
21
22
23 rm(list=ls())
24 #load the zip
25 zip_package_url = "http://data.d4science.org/20/vlyt1L0NBttc5212XVX1U0V1Mc33bn3QURs2N1HW
26 # folder_for_zip=getwd()
27 zip_package_url = "http://data.d4science.org/20/vlyt1L0NBttc5212XVX1U0V1Mc33bn3QURs2N1HW
28 cat("Downloading URL",zip_package_url,"\n")
29 download.file(zip_package_url, destfile = zip_file, method="auto", quiet = FALSE, mode = "w
30 cat("unzipping",zip_package_url,"\n")
31 unzip(zip_file, overwrite=T, exdir = getwd())
32
33 system("chmod +R 777 ./")
34
35 runNum<-"Run_1,Run_2,Run_3"
36 runNum = c(c("Run_1","Run_2","Run_3")
37 seedNum <- 911
38 filenameVpa <- "prte2014"
39 nRetros=5
40 nBoot=5
41
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```

3 Items Edit Administrator Admin

Prepare software through a Web interface



The screenshot displays the Statistical Manager web interface. On the left, a code editor shows R script for the 'Vpa Iccat Bft E' operator. On the right, a configuration panel allows users to set parameters for this operator.

Code Editor (Left):

```

1  ##VPA_ICCAT_BFT-E###
2
3  #52North WPS annotations
4  # wps.des: id = VPA_ICCAT_BFT_E, title = VPA_ICCAT_BFT_E, abstract = ICCAT (Eastern) Bluefi
5
6  # wps.in: id = runNum, type = string, title = Select Runs (one or more) you want to run fr
7  # wps.in: id = seedNum, type = string, title = Select the seeds to use for the run (should
8  # wps.in: id = filenameVpa, type = string, title = Define file names for the vpa, value =
9  # wps.in: id = nbRetros, type = integer, title =Select the number of retrospective analyses
10 # wps.in: id = nbBoot, type = integer, title =Select the number of bootstraps analyses to b
11 # wps.in: id = get_all_retros, type = string, title = Define from which run you want to g
12 # wps.in: id = run_to_get, type = string, title = Set of runs to retrieve , value = "Run_1,
13 # wps.in: id = seed_number_to_get, type = integer, title =Seed number to get after the comp
14 # wps.in: id = what_data, type = string, title = Indicate either 'Retros' or 'Projection' =
15 # wps.in: id = catch_type, type = string, title = Indicate either 'Reported' or 'Inflated',
16 # wps.in deprecated: id = Outputs_type, type = string, title = type of outputs (PDF|HTML|NE
17
18 # wps.out: id = output_zip_file, type = text/zip, title = Set of result files ;
19
20 ###evaluate WPS Parameters with more than one value### Que pour la version WPS
21
22 rm(list=ls())
23 #downloading zip
24 zip_package_url = "http://data.d4science.org/Z0gVHytIL0NBTTc5Z1ZXYLU0UtMcZ33bnJQUR
25 root_folder_for_zip=getwd()
26 zip_file=paste(getwd(),"/ICCAT_VPA.zip",sep="")
27 cat("downloading URL",zip_package_url,"n")
28 download.file(zip_package_url, destfile = zip_file, method='auto', quiet = FALSE, mode = "w
29 cat("unzipping",zip_file,"n")
30 unzip(zip_file, overwrite = T, exdir = getwd())
31
32 system("chmod -R 777 ./")
33
34 runNum<- "Run_1,Run_2,Run_3"
35 #runNum <- c("Run_1","Run_2","Run_3")
36 seedNum <- -911
37 filenameVpa <- "bft2014"
38 nbRetros<-5
39
40

```

Configuration Panel (Right):

Vpa Iccat Bft E

ICCAT (Eastern) Bluefin Tuna Stock Assessment. This set of R and Fortran code have been provided by ICCAT and Ifremer to execute the whole Stock assessment workflow online integration has been done with the help (mediation) of CNR and IRD

Computation Title:

Parameters:

- runNum: Select Runs (one or more) you want to run from the run_spec.csv file (to run them all type 'all')
- seedNum: Select the seeds to use for the run (should be negative integer to select a seed number or positive integer to specify a number of random seed or string (the Rdata filename) to use the random seeds used previously
- filenameVpa: Define file names for the vpa
- nbRetros: Select the number of retrospective analyses to be done (you cannot make bootstraps and retros at the time)
- nbBoot: Select the number of bootstraps analyses to be done (you cannot make bootstraps and retros at the time)
- get_all_retros: Define from which run you want to get the data either one specific or 'some' runs or 'all' to get all retros
- run_to_get: Set of runs to retrieve
- seed_number_to_get: Seed number to get after the computation
- what_data: Indicate either 'Retros' or 'Projection'
- catch_type: Indicate either 'Reported' or 'Inflated'

(JAVA programming is also supported:
https://gcube.wiki.gcube-system.org/gcube/How-to_Implement_Algorithms_for_the_Statistical_Manager)

Execute the process and analyse the results

STATISTICAL MANAGER

Access to the Data Space | Execute an Experiment | Check the Computations

Operators: VPA | User Perspective

Tools: Remove All Operators

FILTERED RESULTS (4 ITEMS FOUND)

- iccat Vpa**
An algorithm for stock assessment of each statistics published by the International Commission for the
- Vpa Iccat Bft E**
ICCAT (Eastern) Bluefin Tuna Stock Assessment. This set of R and Fortran code have been provided by ICCAT and IFramer to execute the whole Stock assessment workflow online integration has been done with the help (mediation) of CNR and IRD
- Vpa Iccat Bft E Retrosprogr**
ICCAT (Eastern) Bluefin Tuna Stock Assessment. This set of R and Fortran code have been provided by ICCAT
- Vpa Iccat Bft E Test**
ICCAT (Eastern) Bluefin Tuna Stock Assessment. This set of R and Fortran code have been provided by ICCAT

Vpa Iccat Bft E

ICCAT (Eastern) Bluefin Tuna Stock Assessment. This set of R and Fortran code have been provided by ICCAT and IFramer to execute the whole Stock assessment workflow online integration has been done with the help (mediation) of CNR and IRD

Computation Title:

Parameters:

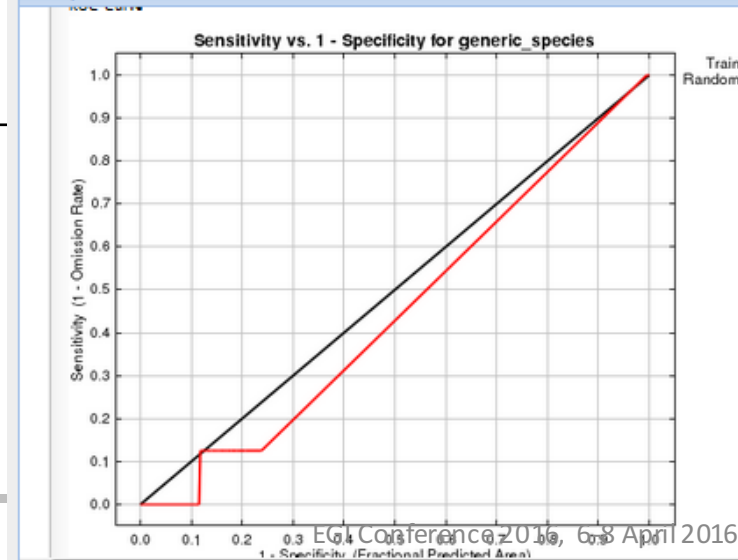
- runNumb: Select Runs (one or more) you want to run from the run_spec.csv file (to run them all type "all")
- seedNumb: Select the seeds to use for the run (should be negative integer to select a seed number or positive integer to specify a number of random seed or string (the Rdata filename) to use the random seeds used previously
- filenameVpa: Define file names for the vpa
- nbRetro: Select the number of retrospective analyses to be done (you cannot make bootstraps and retros at the time)
- nbBoot: Select the number of bootstraps analyses to be done (you cannot make bootstraps and retros at the time)

Computation of **Vpa Iccat Bft E**
Mon Apr 04 16:59:19 GMT+200 2016
Created, the id is 203618

Running, 10.00% Complete

2... Aquamaps Suitable-2016-04-04 16:06 | Aquamaps Suitable | LOCAL | 04/04/2016 | 04/04/2016 | Complete

Computation Viewer



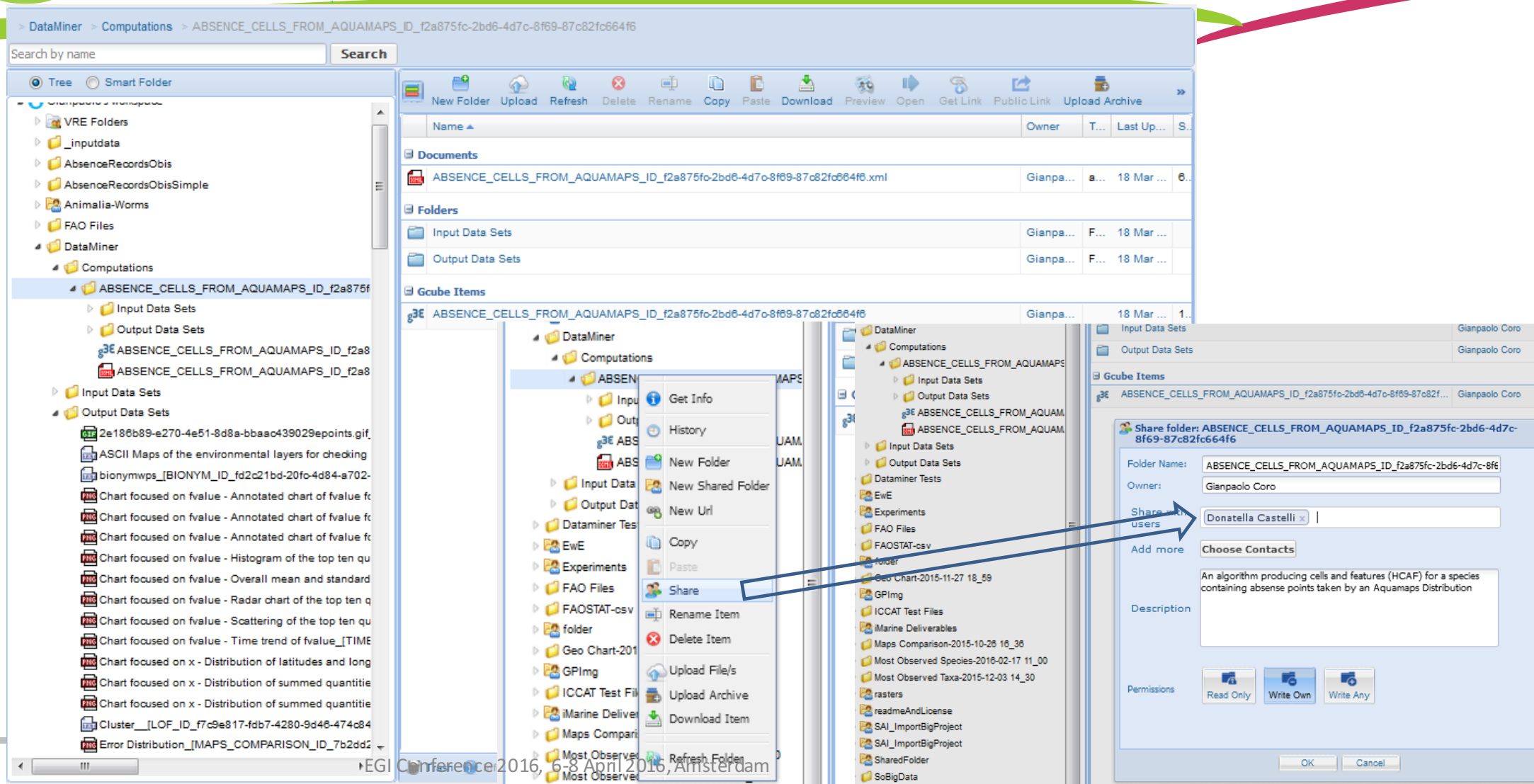
Computations

Id	Cat.	Name	Operator	Infrastructure	Start Date	End Date	Status
2...		Vpa Iccat Bft E					100%
2...		Bionym-2016-04					Complete
2...		Bionym Local-2					Complete
2...		Max Ent Niche					Complete
2...		Cmsy-2016-04					Complete
2...		Occurrences Me					Complete
2...		Occurrences Di					Complete
2...		Occurrences Entr					Complete
2...		Most Observed					Complete
2...		Xyextractor-201					Complete
2...		Raster Data Pu					Complete
2...		Aquamaps Suit					Complete
2...		Aquamaps Suit					Complete

Data Set bionout

source_data	target_data_so...	target_data_bu...	matching_score	target_data_so...	target_data_id
gadus morhua	Gadus morhua	Linnaeus, 1758	1	FISHBASE	FISHBASE:69
gadus morhua	Gadus macroce...	Tilesius, 1810	0.6557879	FISHBASE	FISHBASE:308
gadus morhua	Galeus murinus	(Collett, 1904)	0.61730766	FISHBASE	FISHBASE:808
gadus morhua	Gadella maraldi	(Risso, 1810)	0.60377014	FISHBASE	FISHBASE:2011
gadus morhua	Gadus ogac	Richardson, 1836	0.6	FISHBASE	FISHBASE:309
gadus morhua	Garra microfontis	Chu & Cui, 1987	0.5807359	FISHBASE	FISHBASE:604...
gadus morhua	Garra mamshuca	Knupp, 1983	0.565873	FISHBASE	FISHBASE:278...
gadus morhua	Garra mullya	(Sykes, 1839)	0.5611111	FISHBASE	FISHBASE:244...
gadus morhua	Lates mariae	Steindachner, 1...	0.5555556	FISHBASE	FISHBASE:9898
gadus morhua	Gadella macrura	Sazonov & Shc...	0.55379087	FISHBASE	FISHBASE:608...
gaddus morhoua	Gadus morhua	Linnaeus, 1758	0.9388889	FISHBASE	FISHBASE:69
gaddus morhoua	Gadus macroce...	Tilesius, 1810	0.6557879	FISHBASE	FISHBASE:308
gaddus morhoua	Gadella maraldi	(Risso, 1810)	0.60377014	FISHBASE	FISHBASE:2011
gaddus morhoua	Garra microfontis	Chu & Cui, 1987	0.5807359	FISHBASE	FISHBASE:604...
gaddus morhoua	Galeus murinus	(Collett, 1904)	0.5728632	FISHBASE	FISHBASE:808
gaddus morhoua	Gadus ogac	Richardson, 1836	0.5611111	FISHBASE	FISHBASE:309
gaddus morhoua	Garra ornata	(Nichols & Gris...	0.5418836	FISHBASE	FISHBASE:115...
gaddus morhoua	Gadella norops	Paulin, 1967	0.54183006	FISHBASE	FISHBASE:469...
narhtus morhoua	Gadella tenra	Paulin & Robert	0.540565	FISHBASE	FISHBASE:423

Store and share “research objects”



The screenshot displays a web-based file management interface for a folder named "ABSENCE_CELLS_FROM_AQUAMAPS_ID_f2a875fc-2bd6-4d7c-8f69-87c82fc664f6". The interface includes a search bar, a toolbar with various actions (New Folder, Upload, Refresh, Delete, Rename, Copy, Paste, Download, Preview, Open, Get Link, Public Link, Upload Archive), and a main content area showing a file and two folders: "Input Data Sets" and "Output Data Sets".

A context menu is open over the "ABSENCE_CELLS_FROM_AQUAMAPS_ID_f2a875fc-2bd6-4d7c-8f69-87c82fc664f6" folder, with the "Share" option selected. An arrow points from the "Share" option to a "Share folder" dialog box.

The "Share folder" dialog box shows the following details:

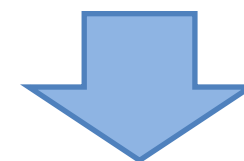
- Folder Name: ABSENCE_CELLS_FROM_AQUAMAPS_ID_f2a875fc-2bd6-4d7c-8f69-87c82fc664f6
- Owner: Gianpaolo Coro
- Share with users: Donatella Castelli
- Add more: Choose Contacts
- Description: An algorithm producing cells and features (HCAF) for a species containing absence points taken by an Aquamaps Distribution
- Permissions: Read Only, Write Own, Write Any

At the bottom of the interface, there is a footer: "EGI Conference 2016, 6-8 April 2016, Amsterdam".

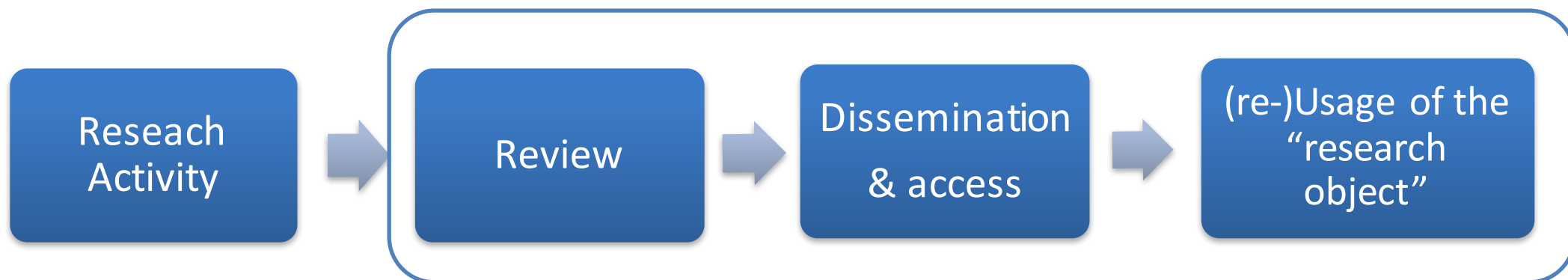
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