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TRITIPOL

Gestion étendue de séquences de triticées et analyse de polymorphismes



A “How to” manual Version α



EAGLE

Ecological & Association Genetics in LEgumes

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Questions, feed back, etc. about this manual?

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First Things first

How to get a user account?

Q How to get an account on the Tritipol Database

A Send a small email to Jacques David (Jacques.Davis@ensam.inra.fr)

Q How to get an account on the Eagle Database

A Send a small email to Thomas Bataillon (tbata@daimi.au.dk)

You will get an email notifying you that your account has been created and some basic info on how to log in.

Connecting to the database

From an INRA computer you can simply point your favorite Web browser to one of the address above.

<http://bioweb.ensam.inra.fr/tritipol>

<http://bioweb.ensam.inra.fr/eagle>

If you are using a computer which is NOT an INRA computer you must either
Get a VPN client from INRA.

Have your IP address registered as a friendly and known user. To do so find out what is your machine IP number and send us an email (5/3/2006 this option may not work right now because of the current security settings on the Bioweb.ensam.fr server hosting the databases).

You should see a page looking like that

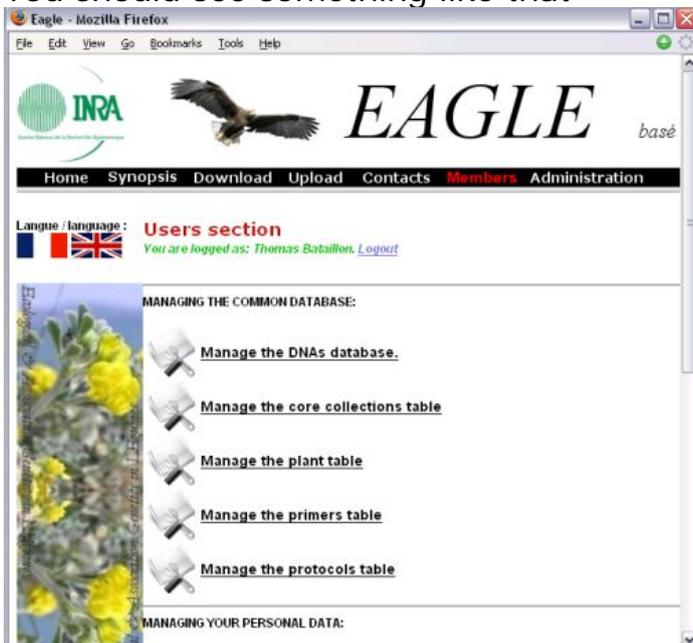


Managing your password.

After you first login it is a good idea to replace the default password you got by one you can actually remember! Click **Members** on the upper banner. You should see something like that



Enter your User Name and password and click the button confirm user. You should see something like that



[Managing your user settings on Eagle](#)

Scroll down and go to the section

A. How to retrieve data from the database in three easy steps?

Step 1. To do so click on the **Download** button on the banner and you should see something like that.



To get raw sequence data (.ab1 files) or info on protocols, primers, genotypes, etc. click Query by criteria  and you will get the following



Step 2. Choose the kind of data you want to download.

Note that the data categories are displayed in French (oh bugger!), but you should be able to figure out what is what:

To get raw sequences data (.abi .ab1 files) choose **Sequences**,

To get Fasta like sequences choose **F-Sequences**, Etc.

Refer to the summary table for an exact description of each type of data

Just click on of the categories displayed above and the screen will be automatically "refreshed" to look like that

Home Synopsis **Download** Upload Contacts Members Administration

Langue / language : **Downloading platform**
 You are logged as: Thomas Bataillon [Logout](#)

Query interface for files
[Reset Query](#) [aide](#)

Searching for: ADN Core collections Plantes Primers Protocoles Séquences Alignments F.Séquences

Search options for sequences :

numseq: chemiseq:
 nomadn nomprotocole
 nomprimer propriétaire:
 groupe: dateupload:
 codeposts: numcapitale:
 qualiteL: qualiteR:
 trimL: trimR:
 TPAR: ipupload:

Search using approximate values
 Repeat column headings every results (0 = inactive)

Step 3. Filter out the data you want

You want to retrieve say sequence data obtained for a specific fragment amplified with a given primer say MTU something you can enter "MTU04" in the nomprimer field and click the "SEARCH" button

A hint: You should always tick the option "search using approximate values" first

Based on your result you can always narrow the search later by iteratively refining your entries before clicking again search

You should get something like that

qualiteL: qualiteR:
 trimL: trimR:
 TPAR: ipupload:

Search using approximate values
 Repeat column headings every results (0 = inactive)

[Options enabled. Current status of request: SELECT DISTINCT 'sequences',' FROM 'sequences' WHERE 'sequences'.nomprimer LIKE "%MTU04%"]

<input checked="" type="checkbox"/>	numseq	chemiseq	nomadn	nomprotocole	nomprimer	propriétaire				
<input checked="" type="checkbox"/>	1208	uploaded/sequences22.3.2006-17.36.40/L0514C	MTUC5A	MTU04F	G06	001.ab1	L0514C	MTUC5A	MTU04F	27
<input checked="" type="checkbox"/>	1209	uploaded/sequences22.3.2006-17.36.40/Champ	MTUC5A	MTU04F	F12	001.ab1	Champ	MTUC5A	MTU04F	27
<input checked="" type="checkbox"/>	1210	uploaded/sequences22.3.2006-17.36.40/L0049B	MTUC5A	MTU04F	B01	001.ab1	L0049B	MTUC5A	MTU04F	27
<input checked="" type="checkbox"/>	1211	uploaded/sequences22.3.2006-17.36.40/L0122C	MTUC5A	MTU04F	C01	001.ab1	L0122C	MTUC5A	MTU04F	27
<input checked="" type="checkbox"/>	1212	uploaded/sequences22.3.2006-17.36.40/L0144B	MTUC5A	MTU04F	D01	001.ab1	L0144B	MTUC5A	MTU04F	27

And the list possibly goes on and on..

You can tick the sequences you want to download and if you scroll all the

way down the page you will get some options marked by a to export your data as a more manageable zip file or to create a Staden database if you use that package.

B. How to make more complex queries using the SQL language.

Go to the download section by clicking **Download** in the banner

Choose  to operate you direct SQL queries. You get an interface looking like that



Hint 1 If you have never used SQL queries try to browse the [EXAMPLES](#) available in this page

Hint 2 Try to do some queries by criteria using the examples outlined above and notice that one you have pressed search the SQL translation of your query is displayed before the list of entries matching your query

Hint 3 Try to google the web for a gentle introduction to SQL
Try for instance <http://www.geocities.com/SiliconValley/Vista/2207/sql1.html>

How to upload data

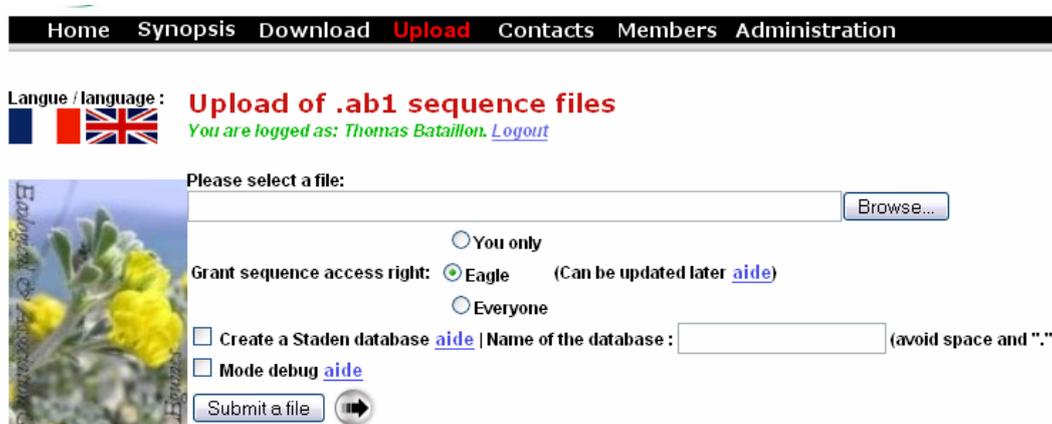
Upload of sequence data in four easy steps!

Step 0 Prepare your data.

Your sequence data should consist in a .zip file, say XXX.zip, containing a series of .ab1 files. Realistically the XXX.zip file should not exceed 10 Mbytes or the upload will be very slow and most likely will not be completed.

- ⚠ The filename XXX.zip must not contain spaces or dots. So "something.zip" "something_like_that.zip" is legal but "something like.zip" is NOT.

Step 1 Click on **Upload** in the upper banner to go the uploading web page.



The screenshot shows a web page with a navigation bar at the top containing links: Home, Synopsis, Download, Upload, Contacts, Members, and Administration. Below the navigation bar, there is a language selection section with flags for French, English, and another language, and the text "Langue / language : Upload of .ab1 sequence files". Below this, it says "You are logged as: Thomas Bataillon. Logout". The main content area is titled "Please select a file:" and features a "Browse..." button. Below the file selection, there are radio buttons for "You only", "Eagle" (selected), and "Everyone". The "Eagle" option has a note "(Can be updated later aide)". There are also checkboxes for "Create a Staden database aide" and "Mode debug aide". A "Name of the database:" field is present with a note "(avoid space and \".")". At the bottom of the form is a "Submit a file" button with a right-pointing arrow.

Step 2 Select the location of your xxx.zip file using the "Browse..." button.

Step 3 Choose whether the sequence can be viewed by you only, any EAGLE/Tritipol authorized user or everyone.

Step 4 Click the "Upload file" button next to

You are (almost) done!

... Just be patient as the upload can typically take a few minutes...

Upon completion you will get a confirmation web page and an Email automatically sent to the email address associated with you user account.