

BONAPARTE DVI SYSTEM

MANUAL MATCHING USING THE WEB INTERFACE

BONAPARTE QUICK GUIDE

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How to Execute Manual Matches Using the Web Interface

WHAT YOU NEED

In order to proceed with the instructions provided in this manual, you need

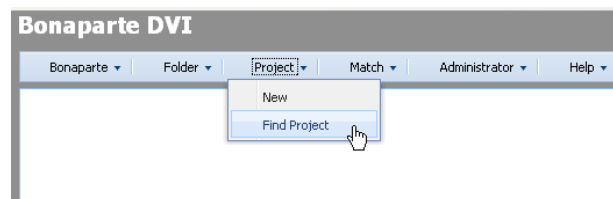
1. Firefox 3.0.xx web browser
2. Java 1.6 enabled
3. User ID and password for the Bonaparte System (after registration, your credentials will be emailed to you)

STEP BY STEP INSTRUCTIONS

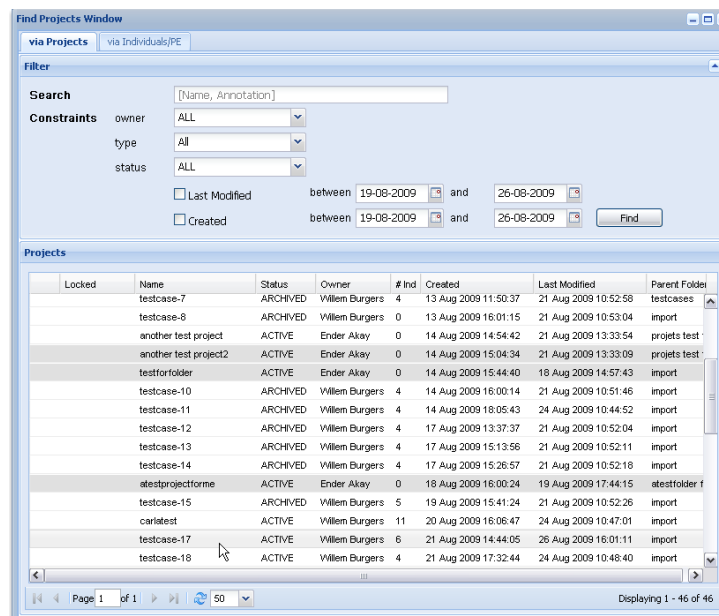
Start your browser and go to <https://bonaparte-dvi.nl:8282>. You need to log on using the credentials that were emailed to you.

1.

Open the project we created for you; go to the menu item “Project” → “Find Project”:



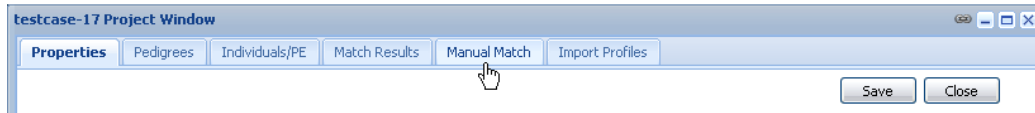
Then the ‘Find Projects Window’ opens:



Double click your project to open it.

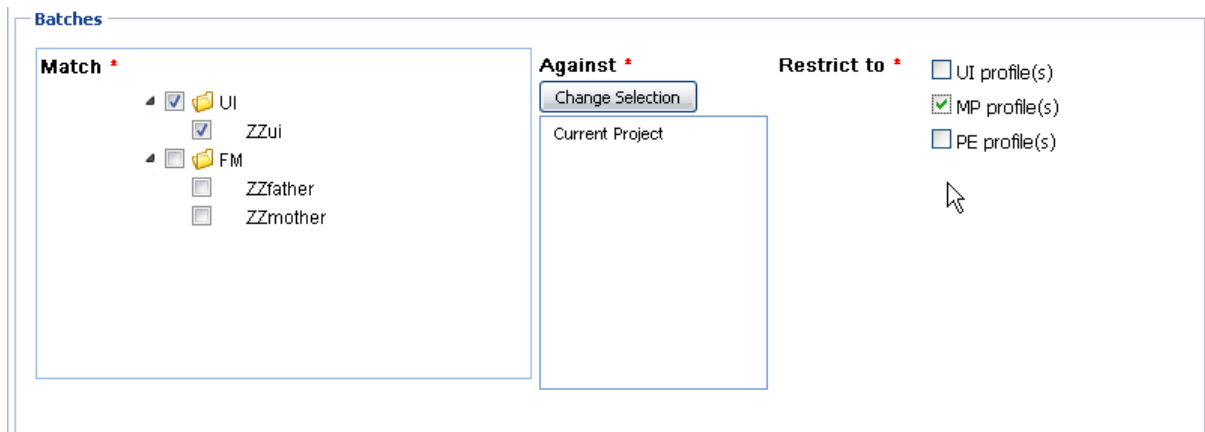
2.

Go to the 'Manual Match' tab:



3.

The left hand tree contains a list of all Unidentified Individuals (UI's) and Family Members in the current project. Select from this list the individuals you want to match. ("Change Selection" options is not available in the demo version) Next select the individual types to match the selected individuals against:



An UI against UI and UI against PE match is a 'direct' match, an UI against MP (Missing Person) uses pedigree information. The selection as displayed in the figure above indicates that all UI individuals are matched against all pedigrees; where both the UI's and pedigrees are coming from the current project.

4.

Now set the match parameters that you want to use:

Match Parameters

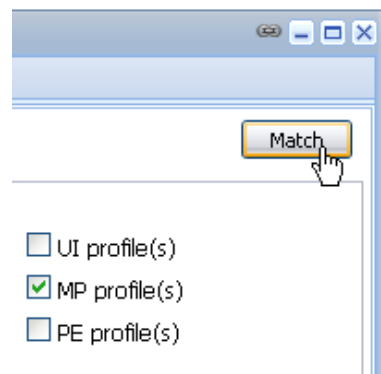
Population *	Caucasian	<input type="button" value="Default"/>
θ-correction *	0.00000	
Mutation model *	uniform(1.0E-3)	
Lambda Common *	3	
Lambda Rare *	1.5	
Lambda New *	0.7	

From the first drop list, select a suitable population for your problem. The populations in this list refer to the population statistics (probability distributions over alleles per loci) available in Bonaparte. These statistics can be viewed by choosing “Administration” → “Population Statistics” → [One of the available populations] from the Bonaparte main menu.

Next choose the mutation model. Currently only the uniform mutation¹ model with parameter μ is implemented. If you do not want mutation, select “uniform(0.0)” otherwise select one of the non-zero models.

The three lambda values (‘Common’, ‘Rare’ and ‘New’) bias the population statistics to account for unobserved alleles².

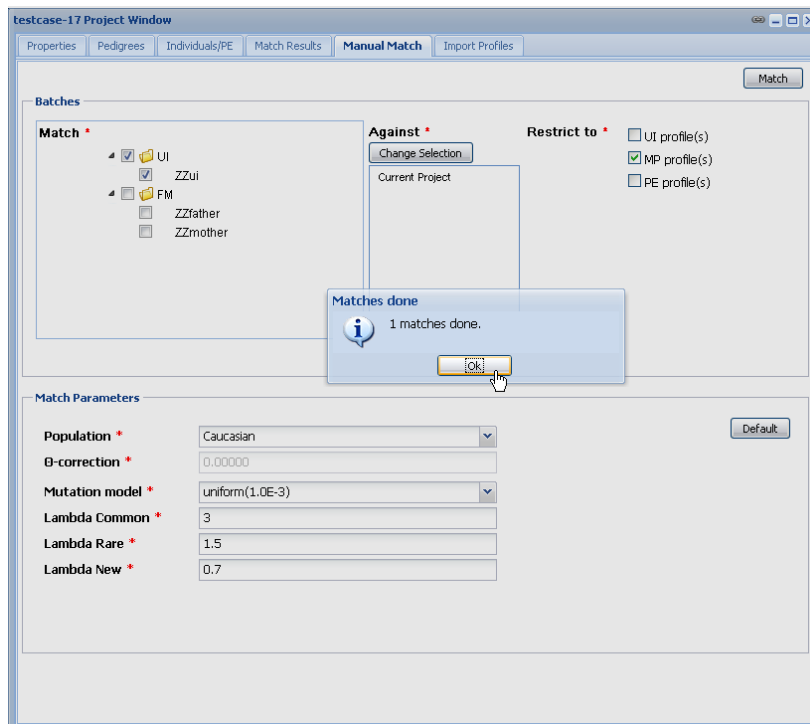
When all information is put in, click the “Match” button in the upper right corner:



This will start the match process. When the system has finished matching, a popup window is displayed with information about the number of matches performed:

¹ See “”

² See “Bonaparte ”

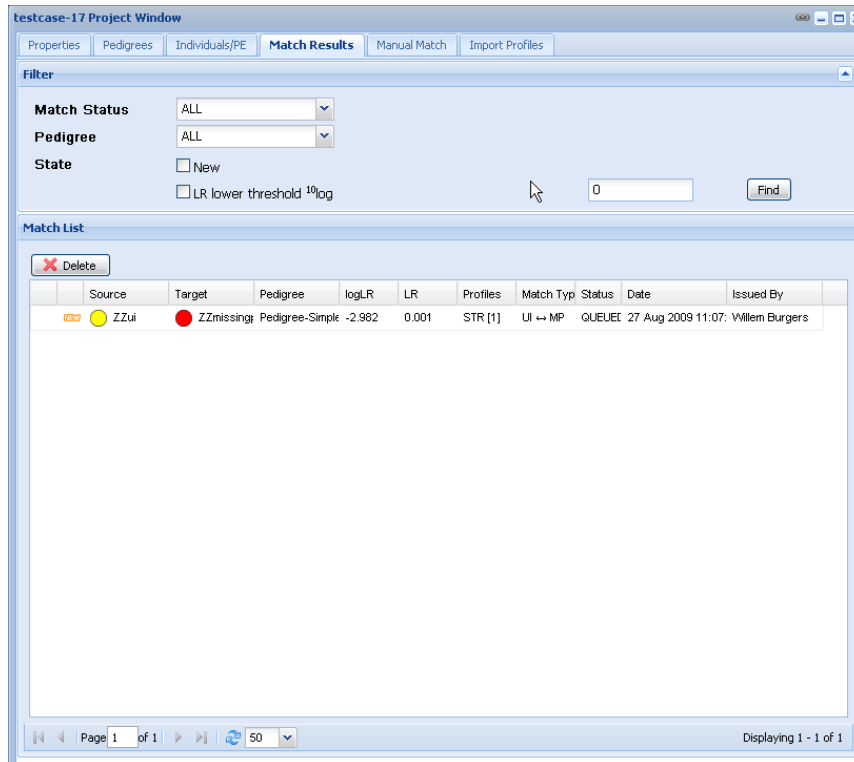


5.

To inspect the found matches, go to the “Match Results” tab:

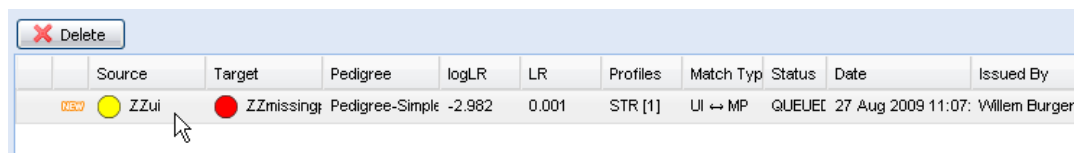


This will open a list of all matches for the current project (If the list is empty, **uncheck** the “LR lower threshold ¹⁰log” box and click “Find”):



The entry in the example above indicates that Unidentified Individual ‘ZZui’ is matched against ‘ZZmissingperson’ in pedigree ‘Pedigree-Simple’, that this match is done using STR profiles consisting on only one locus (“STR[1]”) and that the resulting likelihood ratio is 0.001.

Much more detail about the match can be viewed by double clicking the row:



this opens the match detail window where all information about your match is displayed.

Match Details Window

Date 27 Aug 2009 11:07:20 Issued by Willem Burgers Current Status QUEUED

ZZui

Project testcase-17 **In Folder** import

Profile ZZui

Type UI **Status** ACTIVE

Gender F

ZZmissingperson in Pedigree-Simple

Project testcase-17 **In Folder** import

Profile

Type MP **Status** ACTIVE

Gender F

Pedigree-Simple View

ZZmissingperson

Match Parameters Used for match

Population name Caucasian	Theta 0.000	Mutation Model uniform(1.0E-3)
Lambda Common 3.000	Lambda Rare 1.500	lambda New 0.700

Computation results

Locus	LR	¹⁰ log LR
VWA	0.001043182	-2.981640083
TOTAL	0.001043182	-2.981640083

Compute Posterior

 0 0