How to use GeneClass2 ?

Standard disclaimer: This program is provided "as-is". The authors and providers disclaim all warranties, expressed or implied, regarding the performance of this software. You may distribute this program freely in any format, so long as the following conditions are met: the program remains intact without modification, the help file is included without modification, no fee of any kind is charged.

Please cite this reference if you use GeneClass2:

> Piry S, Alapetite A, Cornuet, J.-M., Paetkau D, Baudouin, L., Estoup, A. (2004) GeneClass2: A Software for Genetic Assignment and First-Generation Migrant Detection. *Journal of Heredity* **95**:536-539.

WARNING: For reasons of international compatibility, the decimal separator used in GeneClass2 is a dot ".".

In order to use GeneClass2, your dataset(s) must be in a recognizable format. The file formats that are

recognized are: GenePop (alleles coded with 2 or 3 digits, or haploid) (Raymond & Rousset, 1995; see also "Genepop on the web"), FStat (Goudet, 1995), Genetix (Belkhir *et al.*), plus a XML (eXtended Markup Language) based format and an internally-used format (CIRAD-PRN). Please consult these references for detailed information on the file formats.
Note that it is preferable that the datafile contains as few missing data as possible (see Piry *et al.*, 2004 for missing data management).

The language (French or English) can be choosen with the "Language" menu of GeneClass2.

It is worth noting that for most options chosen in the program a reference is indicated in a window: it is recomended to consult such references when detailed information are needed.

The following links provide more detailed instructions on the use of GeneClass2.

1. Detection of migrants
2. Assignment of individuals (or groups of individuals)
3. Data file conversion and description of population diversity

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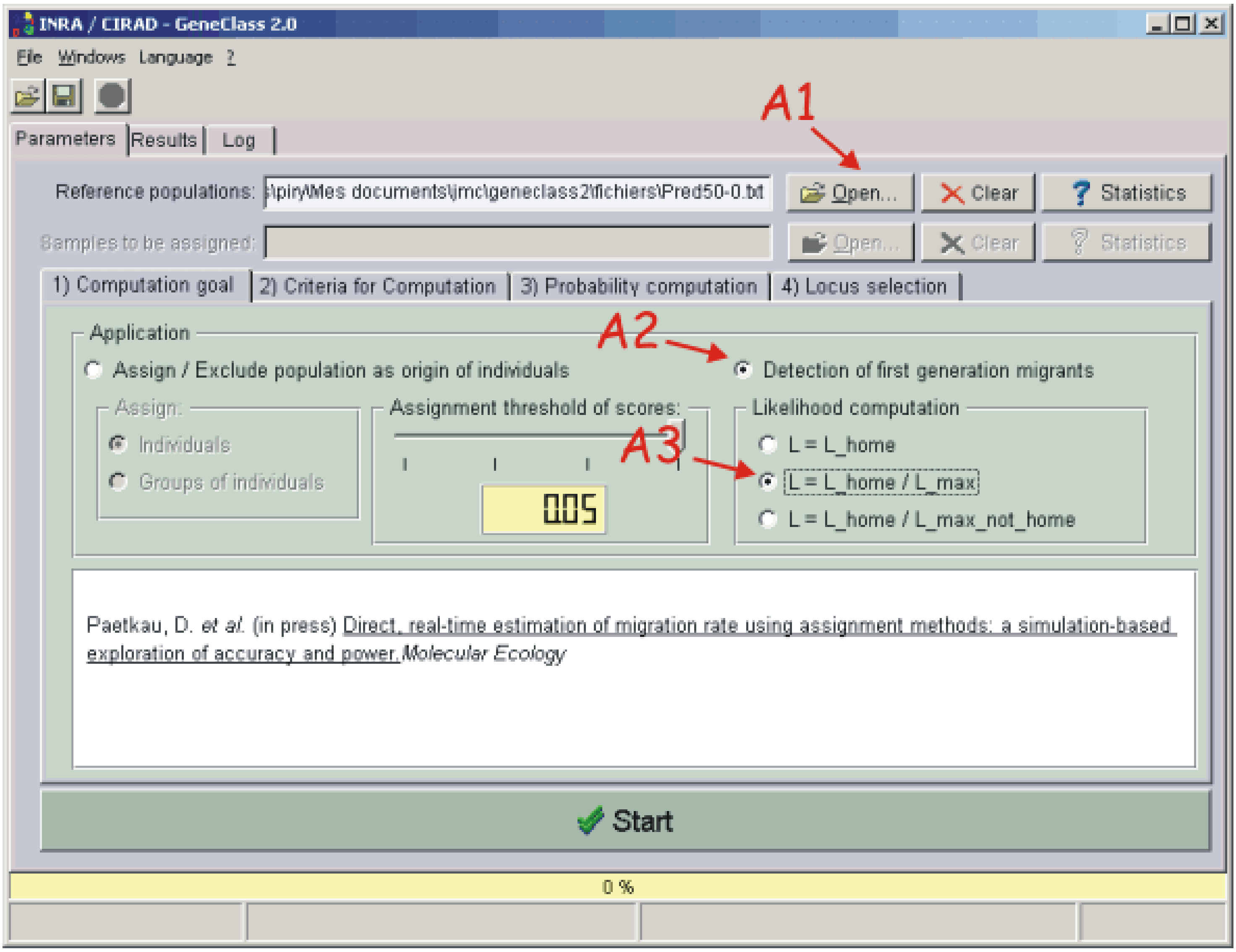
- CBGP Website
- CBGP software Website

1) Detection of first generation migrants

Migrant detection needs a single data file that includes both the populations for which migrants will be seeked and the potential source populations for migrants.

Start GeneClass2 from your "Start" menu, folder "CBGP". The splash-screen appears, followed by the main window of GeneClass2.

Load a datafile by clicking on the "Open" button and choose a datafile in the selector [**A1**].
Choose the "Detection of first generation migrants" option in the first tab of the main window [**A2**].
Select the type of likelihood computation to use for migrant detection. For instance select "L = L_home / L_max" which is the ratio of the likelihood computed from the population where the individual was sampled (L_home) over the highest likelihood value among all population samples including the population where the individual was sampled (L_max) [**A3**] (see Paetkau *et al.* 2004).



Reference populations: \piry\Mes documents\jmc\geneclass2\fichiers\Pred50-0.txt

○ Assign / Exclude population as origin of individuals
● Detection of first generation migrants

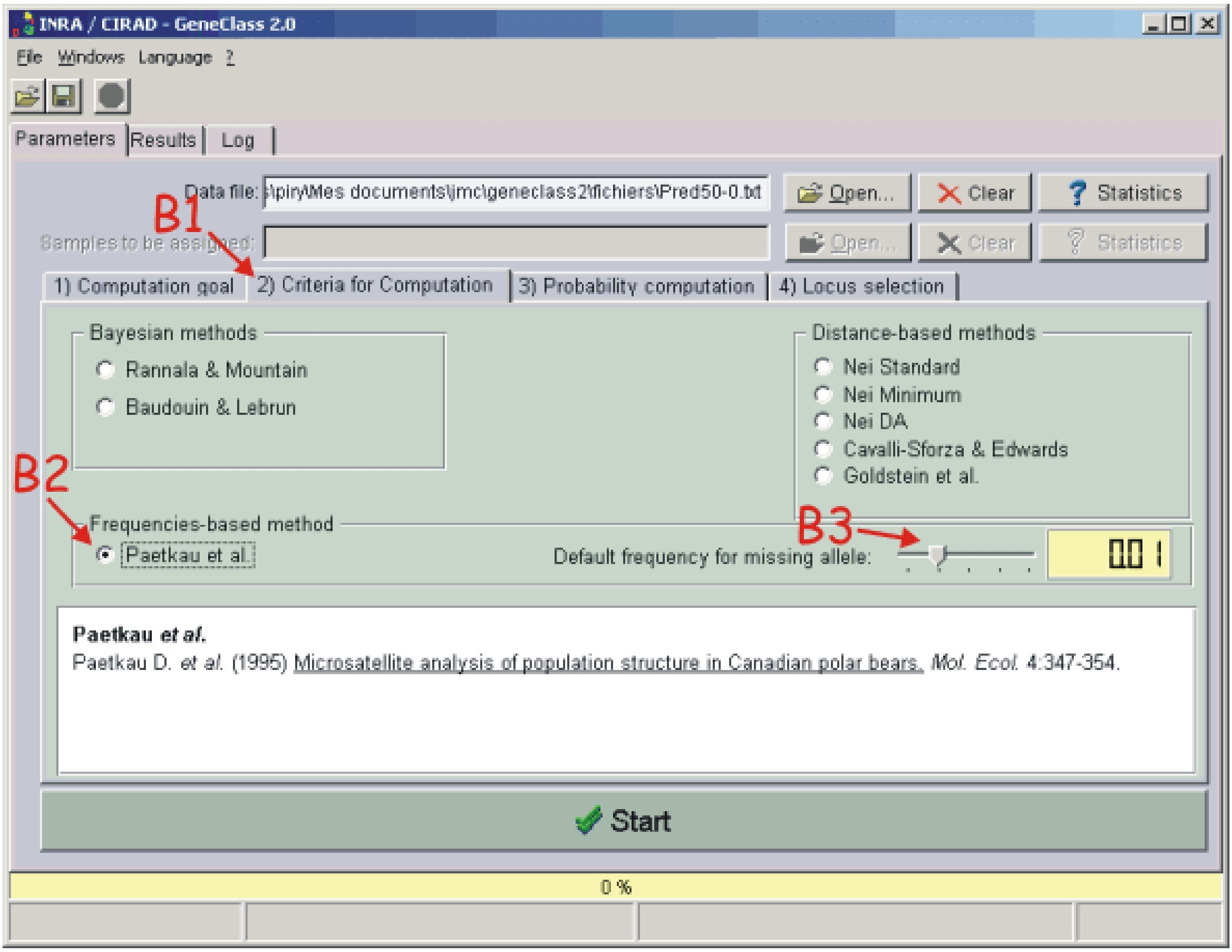
Assignment threshold of scores: 0.05

Likelihood computation:
○ L = L_home
● L = L_home / L_max
○ L = L_home / L_max_not_home

Paetkau, D. *et al.* (in press) Direct, real-time estimation of migration rate using assignment methods: a simulation-based exploration of accuracy and power. *Molecular Ecology*

0 %

By clicking on the "2) Criteria for Computation" tab [**B1**] you can now select the criterion that will be used for likelihood computations. Bayesian and Frequencies-based methods appears to be better than distance-based methods (see Cornuet *et al.* 1999 for a comparative study). Let's for instance select Paetkau *et al.* (1995)'s criterion [**B2**]. This criterion needs a specific parameter which is the default frequency in the case of missing allele (Paetkau *et al.* 2004). You can slide the cursor [**B3**] to define this default value (eg. 0.01).



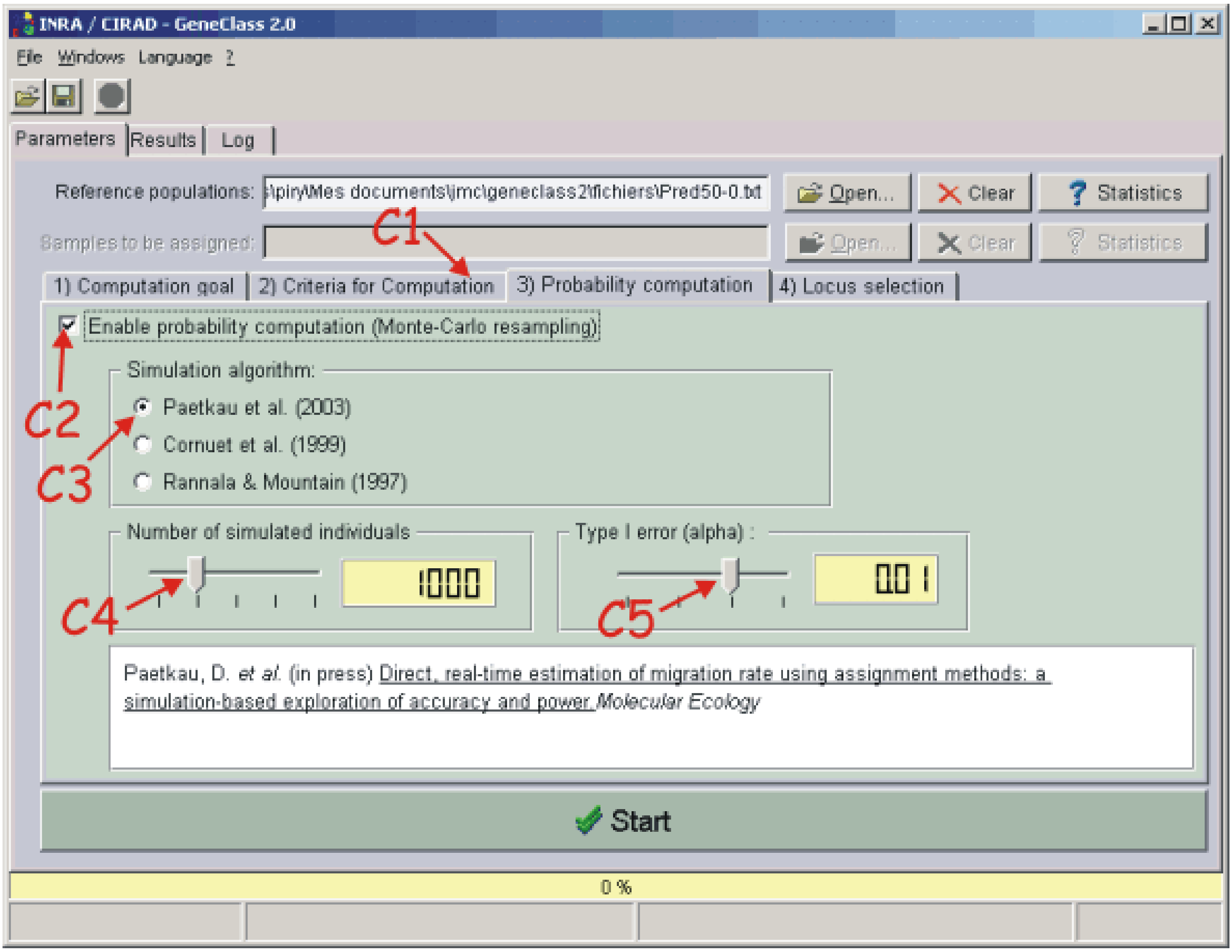
Data file: :\piry\Mes documents\jmc\geneclass2\fichiers\Pred50-0.txt

● Paetkau et al.

Default frequency for missing allele: 0.01

Paetkau *et al.*
Paetkau D. *et al.* (1995) Microsatellite analysis of population structure in Canadian polar bears. *Mol. Ecol.* 4:347-354.

If you want to compute the probability that an individual is a resident (i.e. not a first generation migrant), click on the "3) Probability computation" tab [**C1**], and then check the "Enable probability computation (Monte-Carlo resampling)" box [**C2**].
You can now choose a resampling algorithm [**C3**] (eg. Paetkau *et al.* 2004; recommended for first generation migrants detection, but see Rannala & Mountain (1997) and Cornuet *et al.* (1999)). Slide the cursors to define the minimum number of simulated individuals [**C4**] (eg. 1000, default value or 10000 leading to a ten times longer but more precise computation), and the "Type I error (alpha)" cursor [**C5**] (eg. 0.01, default value, see Cornuet *et al.* (1999); Paetkau *et al.* (2004)):



Reference populations: s\piry\Mes documents\jmc\geneclass2\fichiers\Pred50-0.txt

☑ Enable probability computation (Monte-Carlo resampling)

Simulation algorithm:

- ● Paetkau et al. (2003)
- ○ Cornuet et al. (1999)
- ○ Rannala & Mountain (1997)

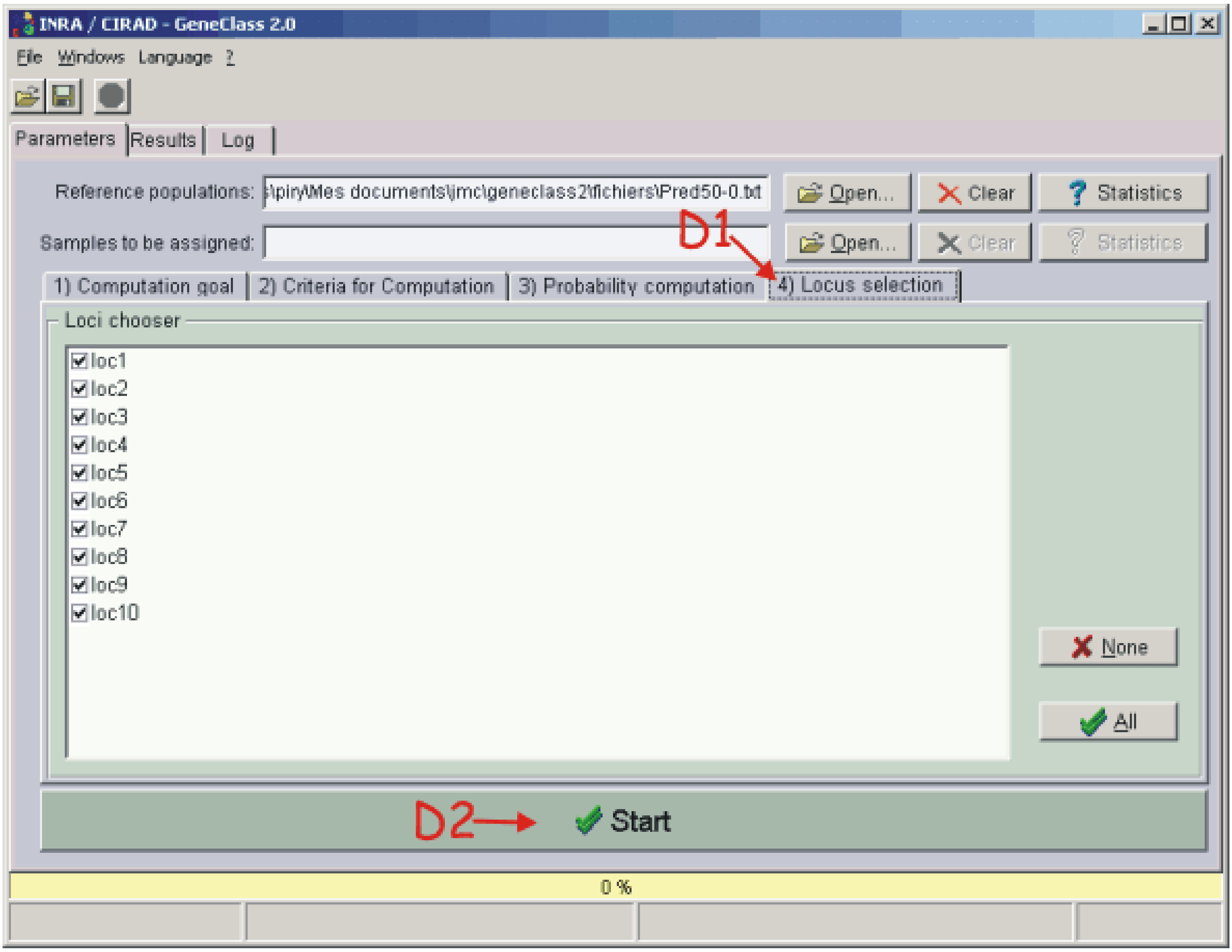
Number of simulated individuals: 1000

Type I error (alpha) : 0.01

Paetkau, D. *et al.* (in press) Direct, real-time estimation of migration rate using assignment methods: a simulation-based exploration of accuracy and power. *Molecular Ecology*

0 %

If needed, you can deselect some loci in the "Loci selection" tab [**D1**]. Deselected loci will be ignored during calculations.
Finally, click on the "Start" button [**D2**] to run the computation.

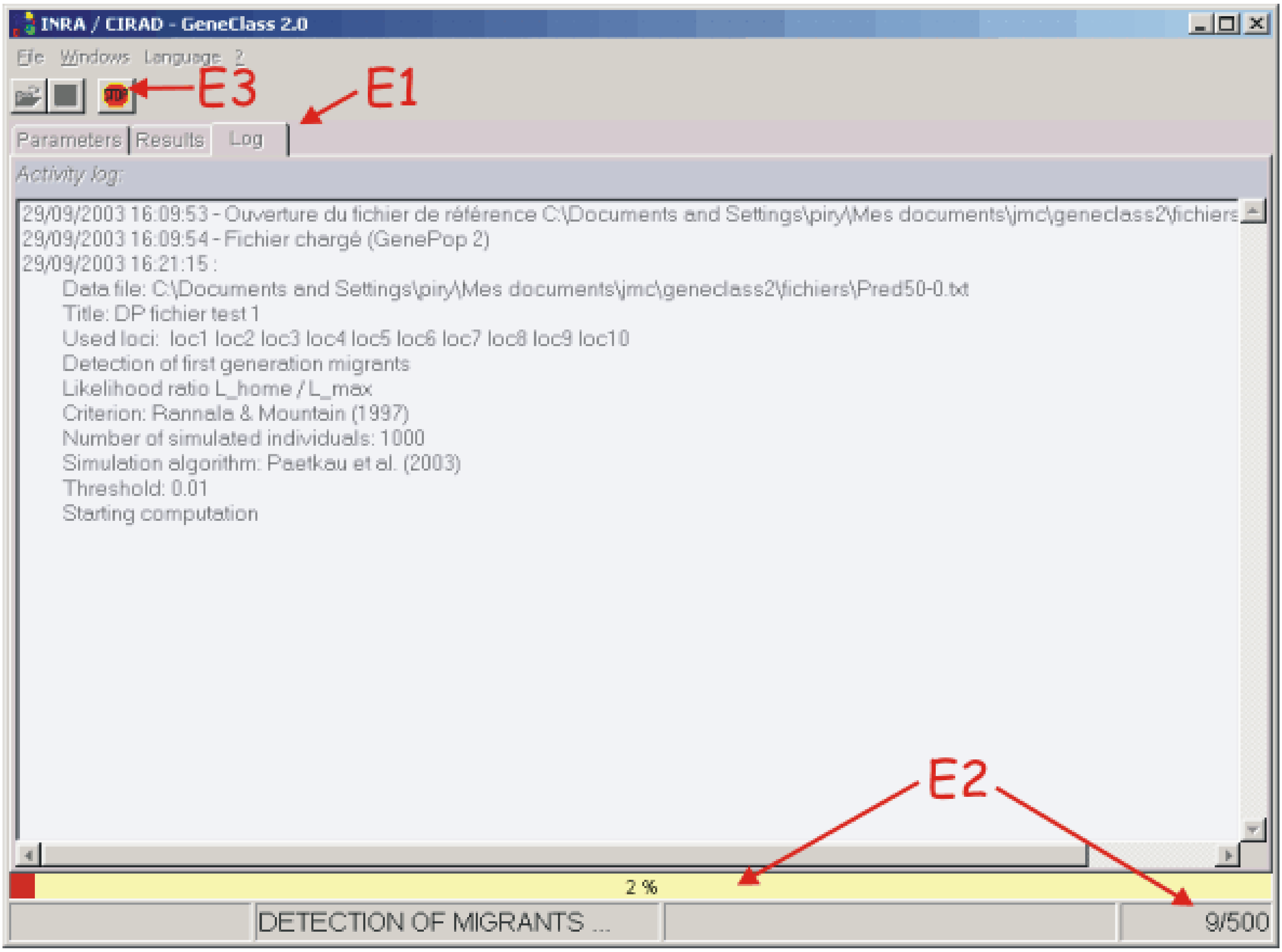


Reference populations: s\piry\Mes documents\jmc\geneclass2\fichiers\Pred50-0.txt

Samples to be assigned:

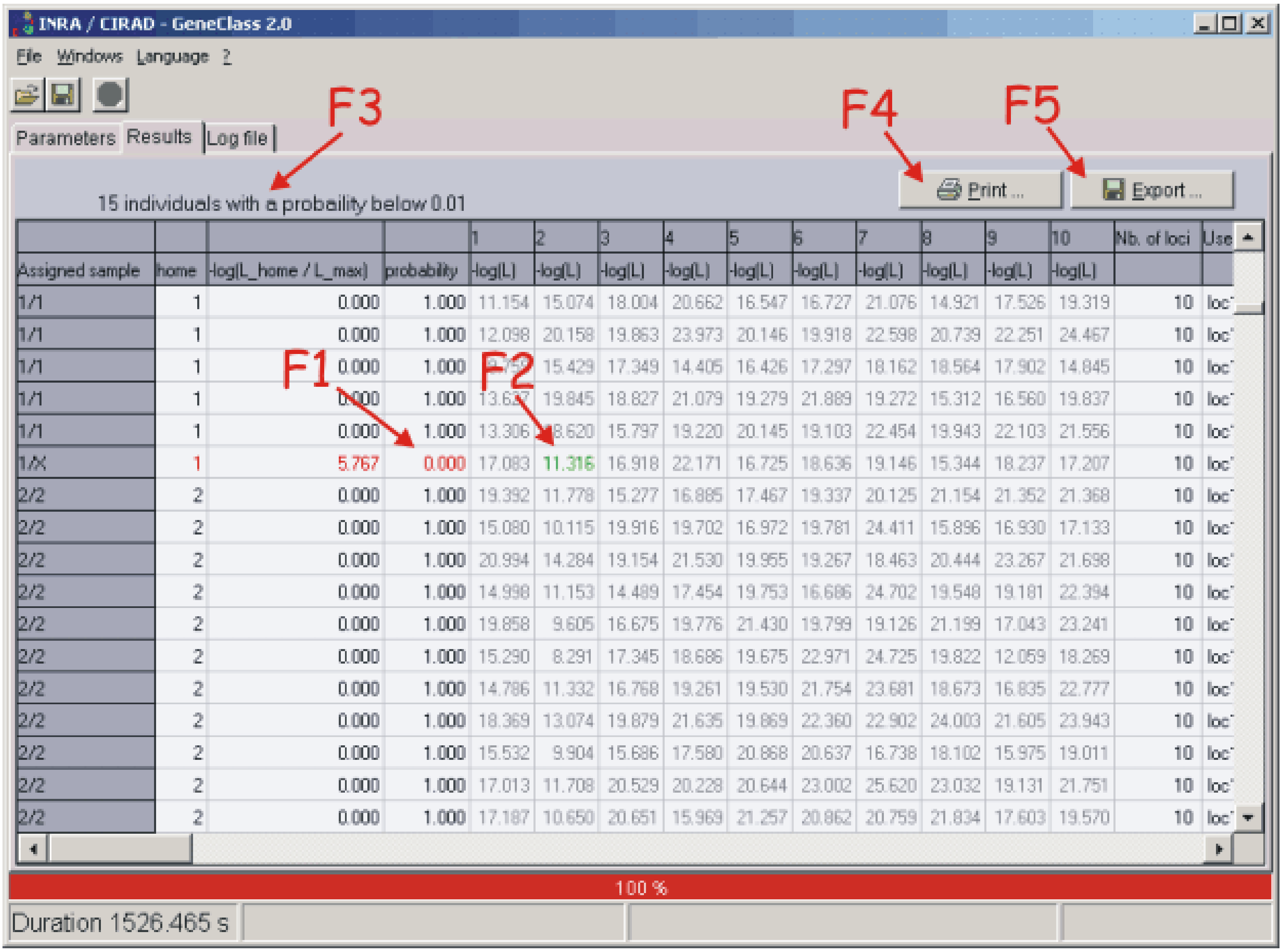
☑ loc1
☑ loc2
☑ loc3
☑ loc4
☑ loc5
☑ loc6
☑ loc7
☑ loc8
☑ loc9
☑ loc10

The program displays the "Log file" [**E1**] that displays the running parameters.
The progress bar and a counter shows the state of the computation [**E2**].
The "Stop" button [**E3**] allows the computation to be aborted.



```
29/09/2003 16:09:53 - Ouverture du fichier de référence C:\Documents and Settings\piry\Mes documents\jmc\geneclass2\fichiers
29/09/2003 16:09:54 - Fichier chargé (GenePop 2)
29/09/2003 16:21:15 :
        Data file: C:\Documents and Settings\piry\Mes documents\jmc\geneclass2\fichiers\Pred50-0.txt
        Title: DP fichier test 1
        Used loci:  loc1 loc2 loc3 loc4 loc5 loc6 loc7 loc8 loc9 loc10
        Detection of first generation migrants
        Likelihood ratio L_home / L_max
        Criterion: Rannala & Mountain (1997)
        Number of simulated individuals: 1000
        Simulation algorithm: Paetkau et al. (2003)
        Threshold: 0.01
        Starting computation
```

Once computations are finished, the results are displayed in a grid where potential F0 migrants (Paetkau *et al.*, 2004) are labelled in red (p < threshold) [**F1**] and the most likely population in green [**F2**]. The number of individuals with a probability below the threshold value is also indicated [**F3**].
Results can be printed ("Print" button [**F4**]) or exported in csv format ("Export" button [**F5**]).



15 individuals with a probaility below 0.01

				1	2	3	4	5	6	7	8	9	10	Nb. of loci	Use
Assigned sample	home	-log(L_home / L_max)	probability	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)		
1/1	1	0.000	1.000	11.154	15.074	18.004	20.662	16.547	16.727	21.076	14.921	17.526	19.319	10	loc
1/1	1	0.000	1.000	12.098	20.158	19.863	23.973	20.146	19.918	22.598	20.739	22.251	24.467	10	loc
1/1	1	0.000	1.000	9.759	15.429	17.349	14.405	16.426	17.297	18.162	18.564	17.902	14.845	10	loc
1/1	1	0.000	1.000	13.627	19.845	18.827	21.079	19.279	21.889	19.272	15.312	16.560	19.837	10	loc
1/1	1	0.000	1.000	13.306	18.620	15.797	19.220	20.145	19.103	22.454	19.943	22.103	21.556	10	loc
1/X	1	5.767	0.000	17.083	11.316	16.918	22.171	16.725	18.636	19.146	15.344	18.237	17.207	10	loc
2/2	2	0.000	1.000	19.392	11.778	15.277	16.885	17.467	19.337	20.125	21.154	21.352	21.368	10	loc
2/2	2	0.000	1.000	15.080	10.115	19.916	19.702	16.972	19.781	24.411	15.896	16.930	17.133	10	loc
2/2	2	0.000	1.000	20.994	14.284	19.154	21.530	19.955	19.267	18.463	20.444	23.267	21.698	10	loc
2/2	2	0.000	1.000	14.998	11.153	14.489	17.454	19.753	16.686	24.702	19.548	19.181	22.394	10	loc
2/2	2	0.000	1.000	19.858	9.605	16.675	19.776	21.430	19.799	19.126	21.199	17.043	23.241	10	loc
2/2	2	0.000	1.000	15.290	8.291	17.345	18.686	19.675	22.971	24.725	19.822	12.059	18.269	10	loc
2/2	2	0.000	1.000	14.786	11.332	16.768	19.261	19.530	21.754	23.681	18.673	16.835	22.777	10	loc
2/2	2	0.000	1.000	18.369	13.074	19.879	21.635	19.869	22.360	22.902	24.003	21.605	23.943	10	loc
2/2	2	0.000	1.000	15.532	9.904	15.686	17.580	20.868	20.637	16.738	18.102	15.975	19.011	10	loc
2/2	2	0.000	1.000	17.013	11.708	20.529	20.228	20.644	23.002	25.620	23.032	19.131	21.751	10	loc
2/2	2	0.000	1.000	17.187	10.650	20.651	15.969	21.257	20.862	20.759	21.834	17.603	19.570	10	loc

Duration 1526.465 s

To main page

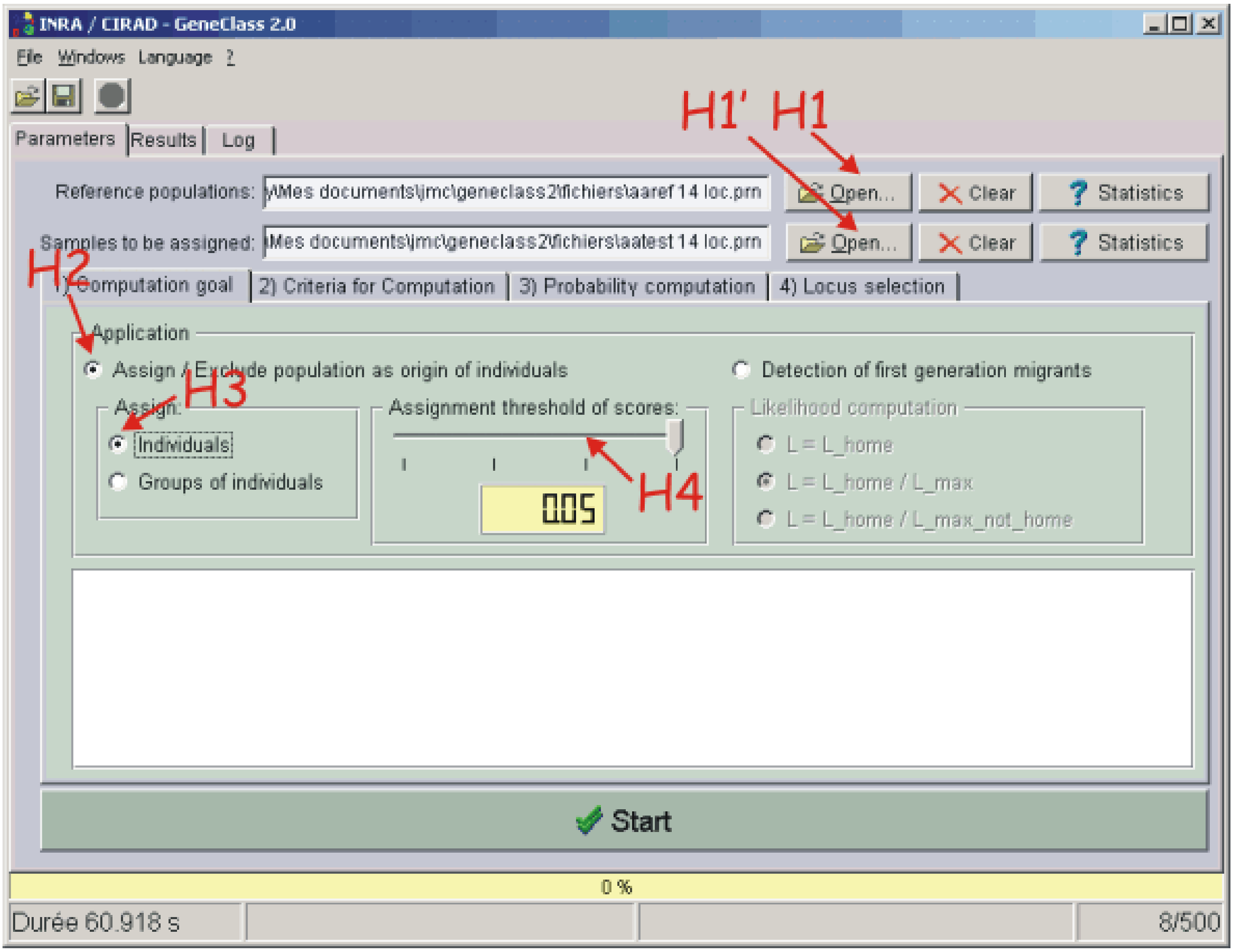
2) Assignment or exclusion of individuals (or groups of individuals)

Start GeneClass2 from your "Start" menu, folder "CBGP". The splash-screen appears, then the main window of GeneClass2.

Load a reference datafile by clicking on the upper "Open" button [**H1**] and choose the datafile in the selector.
Load a to-be-assigned individuals datafile by clicking on the lower "Open" button [**H1'**] and choose the datafile in the selector.
Note that for self-assignment purposes only a single file is needed (i.e. the reference file [**H1**]) .

Choose "Assignment" [**H2**] in the first tab of the main window and "Individuals" [**H3**] in the "Assign:" box. Note that assignment statistics can be also computed for groups of individuals rather than individual genotypes (Baudouin & Lebrun, 2000). Groups of individuals must be coded as populations in the samples file.

The assignment threshold (without probability computation) can be set by sliding the "Assignment threshold of scores" cursor [**H4**] (see computations without associated probabilities section for a definition of scores).



Reference populations: \Mes documents\jmc\geneclass2\fichiers\aaref14loc.prn

Samples to be assigned: \Mes documents\jmc\geneclass2\fichiers\aatest14loc.prn

● Assign / Exclude population as origin of individuals

Assign: ● Individuals

Assignment threshold of scores: 0.05

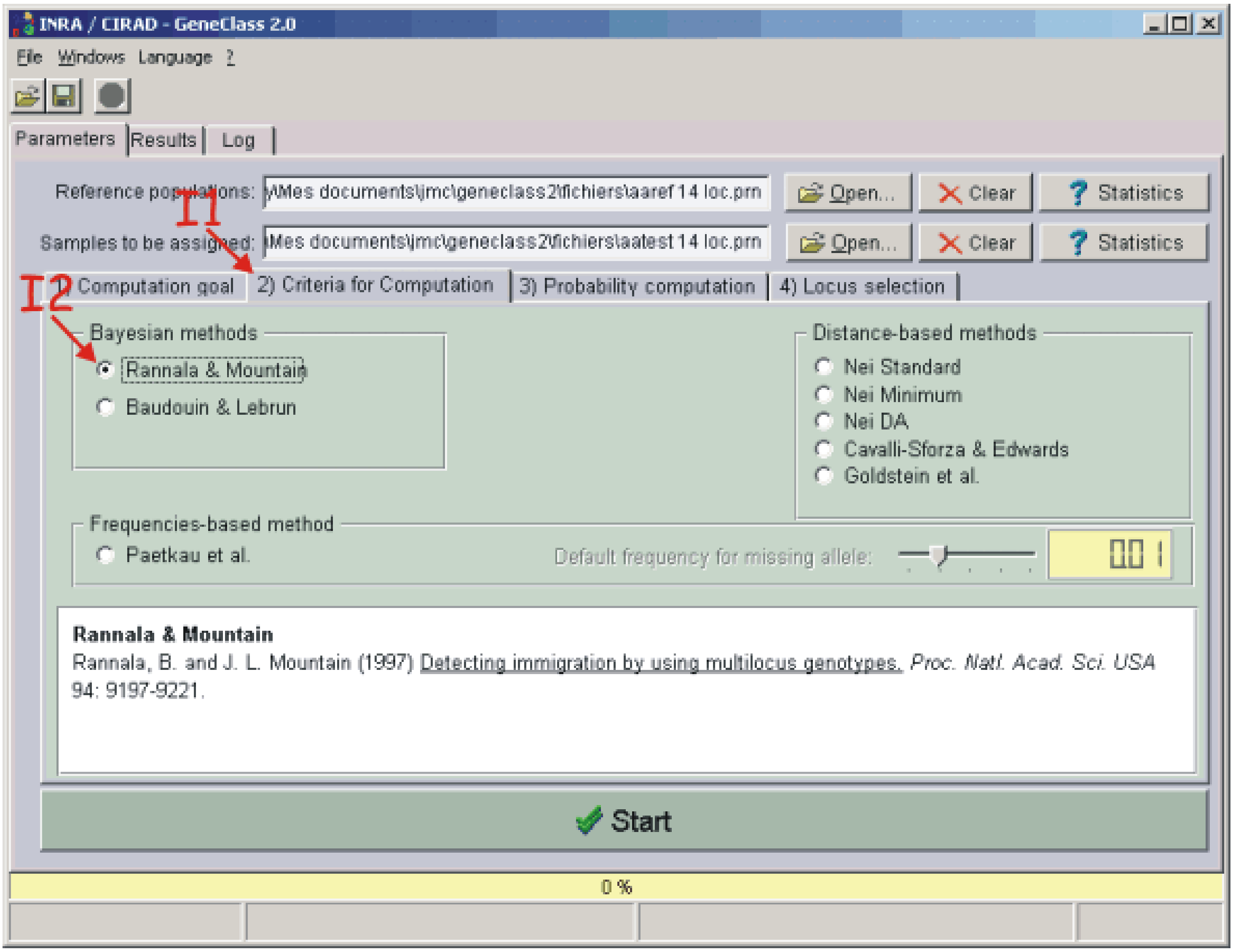
Likelihood computation: ● L = L_home / L_max

0 %

Durée 60.918 s

8/500

Click on the "2) Criteria for Computation" [**I1**] tab and choose the desired criterion (e.g. "Rannala & Mountain" [**I2**], see Rannala & Mountain, 1997 and Cornuet *et al.*, 1999). Bayesian and Frequencies-based methods appears to be better than distance-based methods (see Cornuet *et al.* 1999 for a comparative study).



Reference populations: \Mes documents\jmc\geneclass2\fichiers\aaref14loc.prn

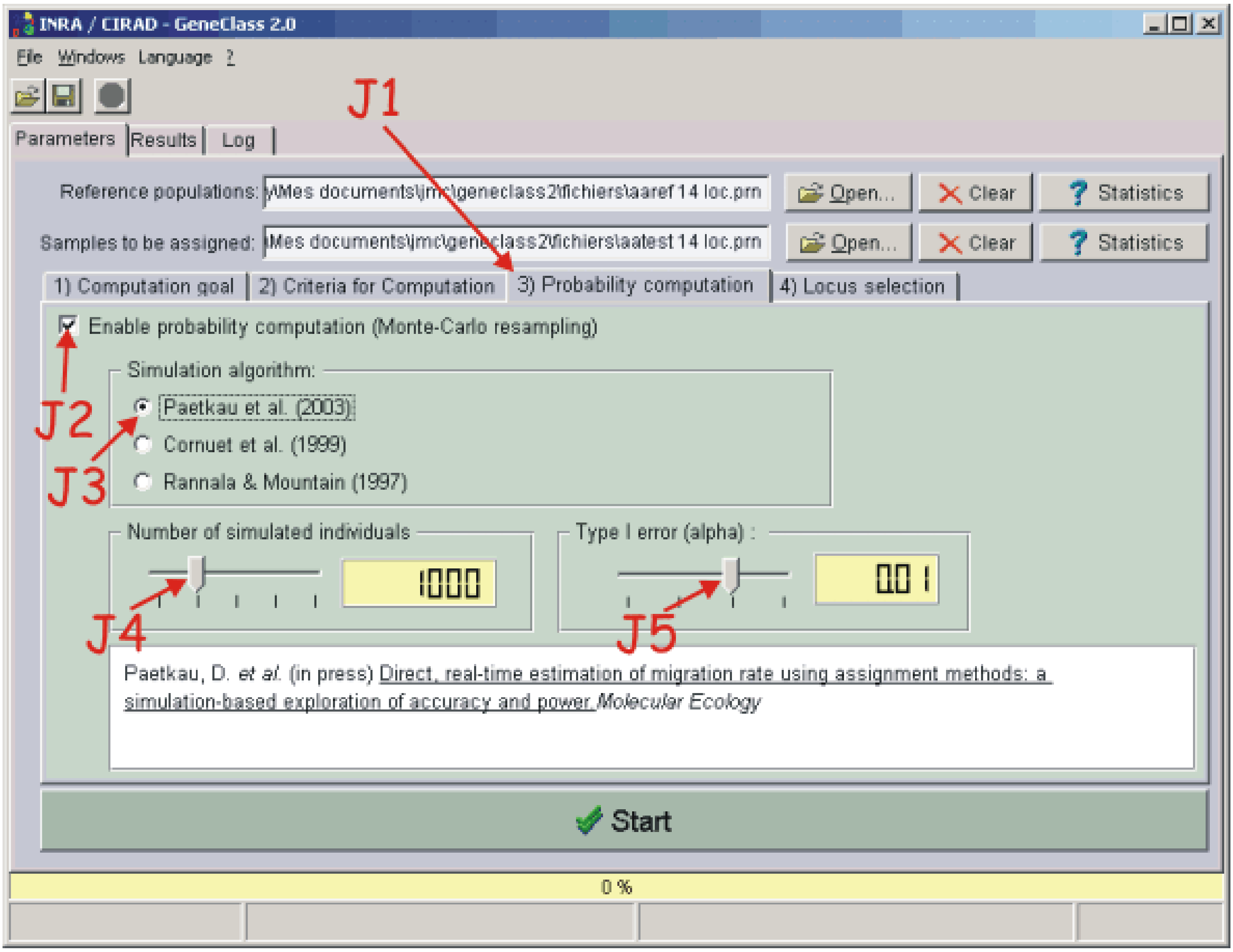
Samples to be assigned: \Mes documents\jmc\geneclass2\fichiers\aatest14loc.prn

● Rannala & Mountain

Rannala & Mountain
Rannala, B. and J. L. Mountain (1997) Detecting immigration by using multilocus genotypes. *Proc. Natl. Acad. Sci. USA* 94: 9197-9221.

If you want to compute the probability that an individual belongs to each reference population, click on the "3) Probability computation" tab [**J1**], and then check the "Enable probability computation (Monte-Carlo resampling)" box [**J2**].

You can now choose a resampling algorithm [**J3**], eg. Paetkau *et al.* (2004) (recommended, but see Rannala & Mountain 1997 and Cornuet *et al.* 1999). Slide the cursor [**J4**] to define the minimum number of simulated individuals (eg. 1000, default value or 10000, leading to ten times longer but more precise computation), and the cursor [**J5**] setting the type one error eg. 0.01, default value (see Cornuet *et al.* 1999; Paetkau *et al.* 2004).



Reference populations: \Mes documents\jmc\geneclass2\fichiers\aaref14loc.prn

Samples to be assigned: \Mes documents\jmc\geneclass2\fichiers\aatest14loc.prn

☑ Enable probability computation (Monte-Carlo resampling)

Simulation algorithm:

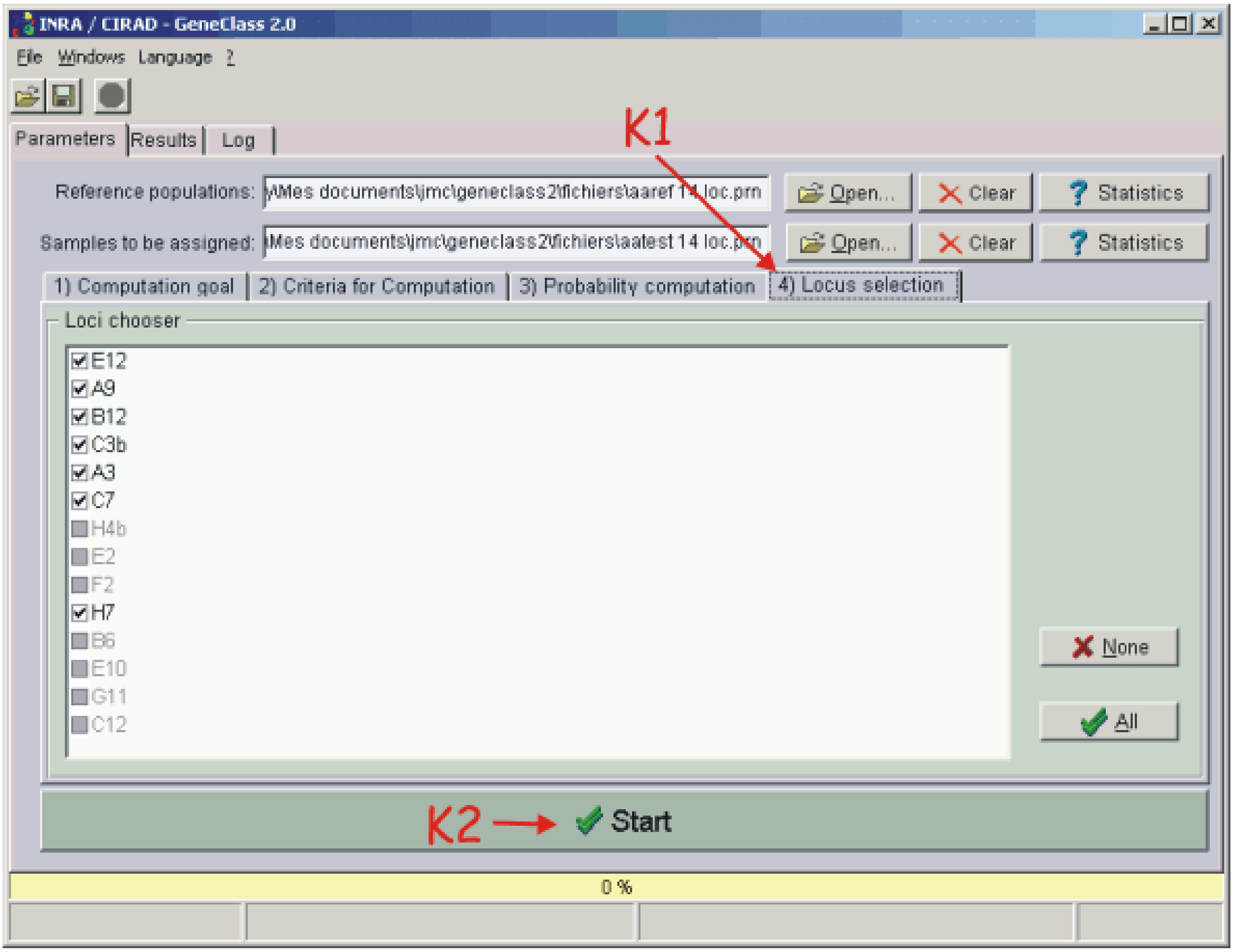
- ● Paetkau et al. (2003)
- ○ Cornuet et al. (1999)
- ○ Rannala & Mountain (1997)

Number of simulated individuals: 1000

Type I error (alpha) : 0.01

Paetkau, D. *et al.* (in press) Direct, real-time estimation of migration rate using assignment methods: a simulation-based exploration of accuracy and power. *Molecular Ecology*

If needed, you can deselect some loci in the "Loci selection" tab [**K1**]. Deselected loci will be ignored during calculations.
Finally, click on the "Start" button [**K2**] to run the computation.



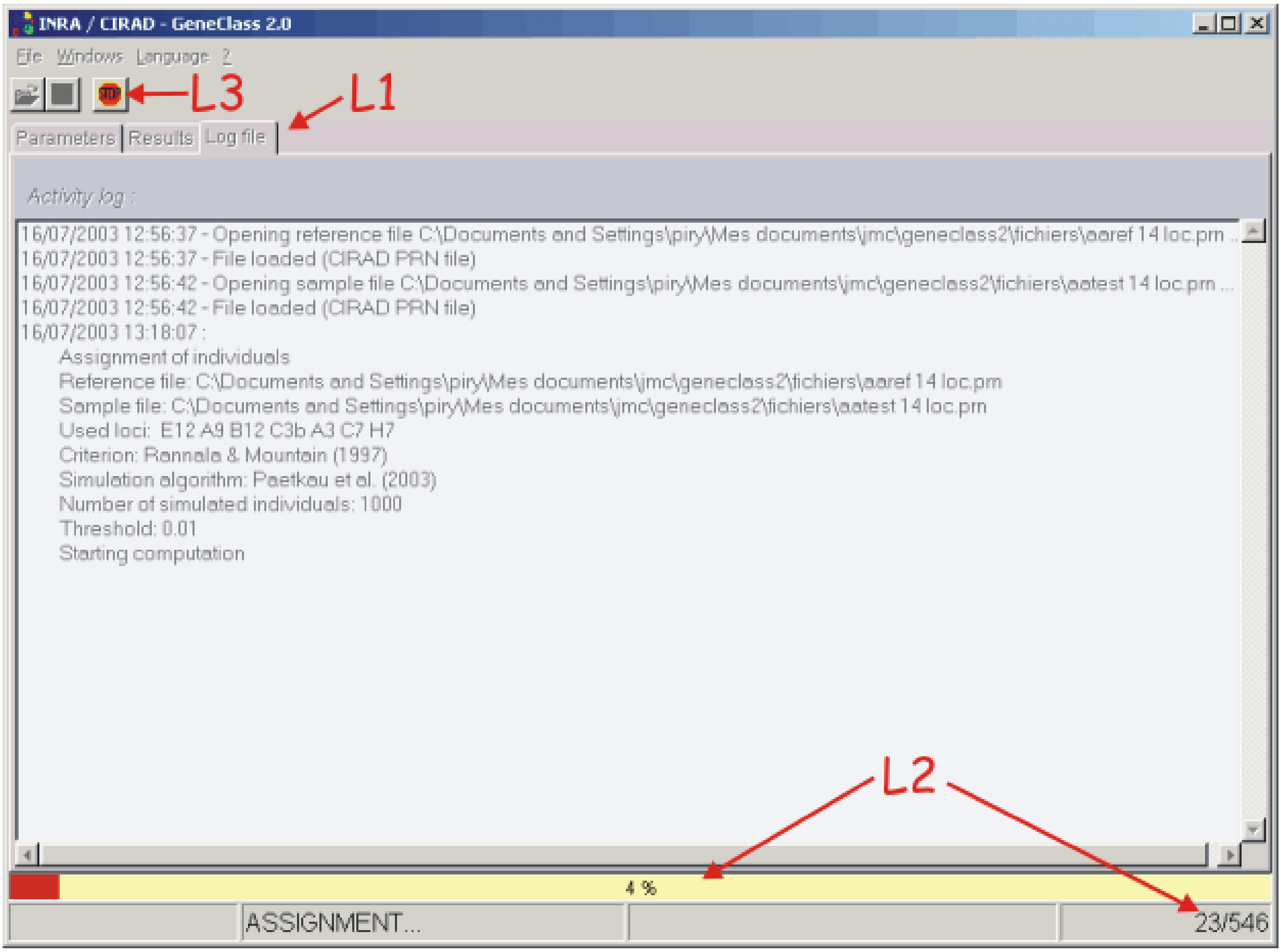
Reference populations: \Mes documents\jmc\geneclass2\fichiers\aaref 14 loc.prn

Samples to be assigned: \Mes documents\jmc\geneclass2\fichiers\aatest 14 loc.prn

☑ E12
☑ A9
☑ B12
☑ C3b
☑ A3
☑ C7
☐ H4b
☐ E2
☐ F2
☑ H7
☐ B6
☐ E10
☐ G11
☐ C12

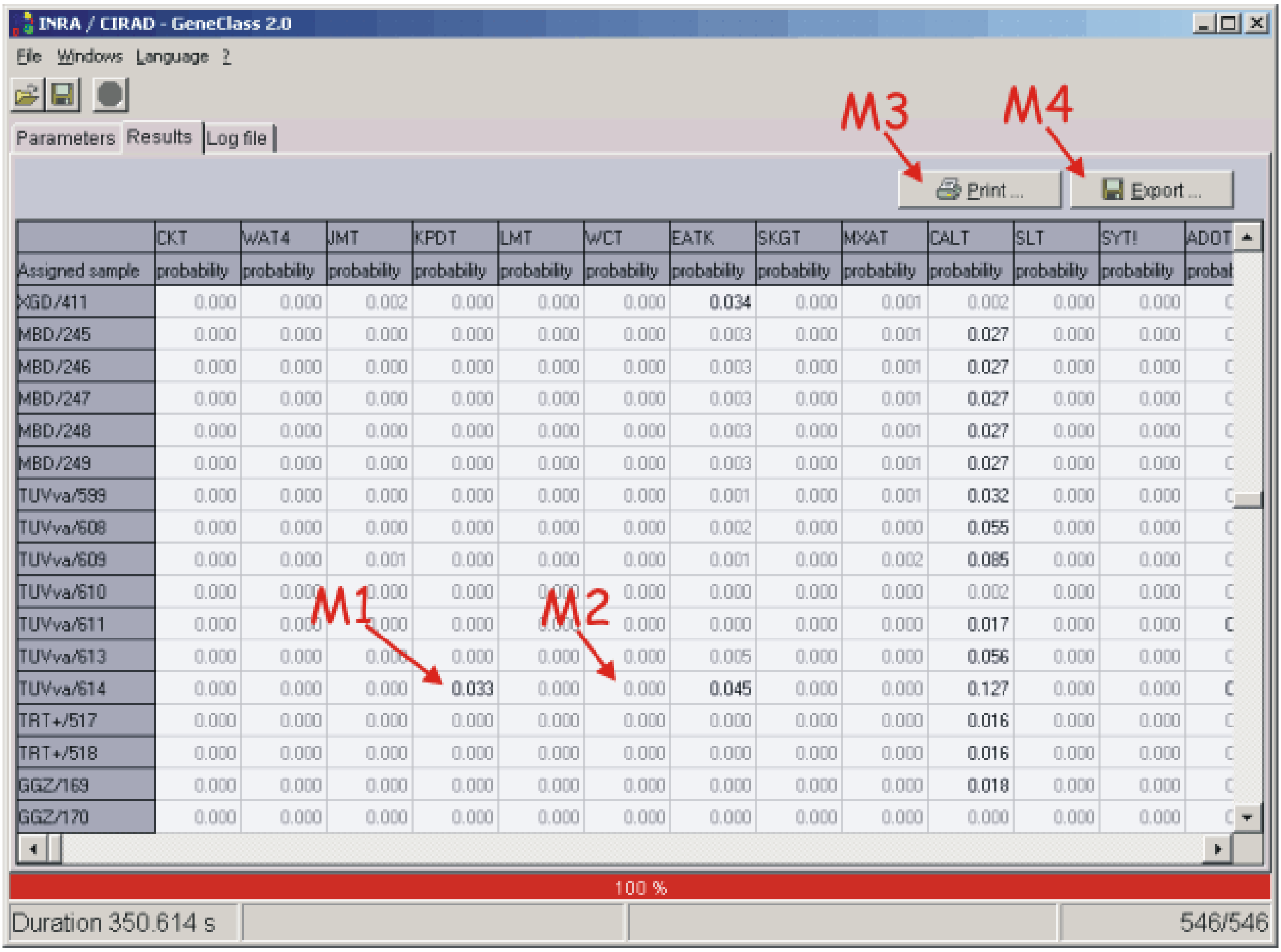
0 %

The program displays the "Log file" [**L1**] that displays the running parameters.
The progress bar and a counter shows the state of the computation [**L2**].
The "Stop" button [**L3**] allows the computation to be aborted.



```
16/07/2003 12:56:37 - Opening reference file C:\Documents and Settings\piry\Mes documents\jmc\geneclass2\fichiers\aaref 14 loc.prn ...
16/07/2003 12:56:37 - File loaded (CIRAD PRN file)
16/07/2003 12:56:42 - Opening sample file C:\Documents and Settings\piry\Mes documents\jmc\geneclass2\fichiers\aatest 14 loc.prn ...
16/07/2003 12:56:42 - File loaded (CIRAD PRN file)
16/07/2003 13:18:07 :
        Assignment of individuals
        Reference file: C:\Documents and Settings\piry\Mes documents\jmc\geneclass2\fichiers\aaref 14 loc.prn
        Sample file: C:\Documents and Settings\piry\Mes documents\jmc\geneclass2\fichiers\aatest 14 loc.prn
        Used loci:  E12 A9 B12 C3b A3 C7 H7
        Criterion: Rannala & Mountain (1997)
        Simulation algorithm: Paetkau et al. (2003)
        Number of simulated individuals: 1000
        Threshold: 0.01
        Starting computation
```

Once computations are finished, the results are displayed in a grid in which the probability for each individual belonging to each reference population is displayed [**M1**] (Cornuet *et al.*, 1999). If a given individual's probability in a given reference population is lower than the previously defined threshold, the value is greyed [**M2**].
Results can be printed ("Print" button [**M3**]) or exported in csv format ("Export" button [**M4**]).



	CKT	WAT4	JMT	KPDT	LMT	WCT	EATK	SKGT	MXAT	CALT	SLT	SYT!	ADOT
Assigned sample	probability	probability	probability	probability	probability	probability	probability	probability	probability	probability	probability	probability	probab
XGD/411	0.000	0.000	0.002	0.000	0.000	0.000	0.034	0.000	0.001	0.002	0.000	0.000	
MBD/245	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.001	0.027	0.000	0.000	
MBD/246	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.001	0.027	0.000	0.000	
MBD/247	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.001	0.027	0.000	0.000	
MBD/248	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.001	0.027	0.000	0.000	
MBD/249	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.001	0.027	0.000	0.000	
TUVva/599	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.001	0.032	0.000	0.000	
TUVva/608	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.055	0.000	0.000	
TUVva/609	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.002	0.085	0.000	0.000	
TUVva/610	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.000	
TUVva/611	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	
TUVva/613	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.056	0.000	0.000	
TUVva/614	0.000	0.000	0.000	0.033	0.000	0.000	0.045	0.000	0.000	0.127	0.000	0.000	
TRT+/517	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016	0.000	0.000	
TRT+/518	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016	0.000	0.000	
GGZ/169	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018	0.000	0.000	
GGZ/170	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

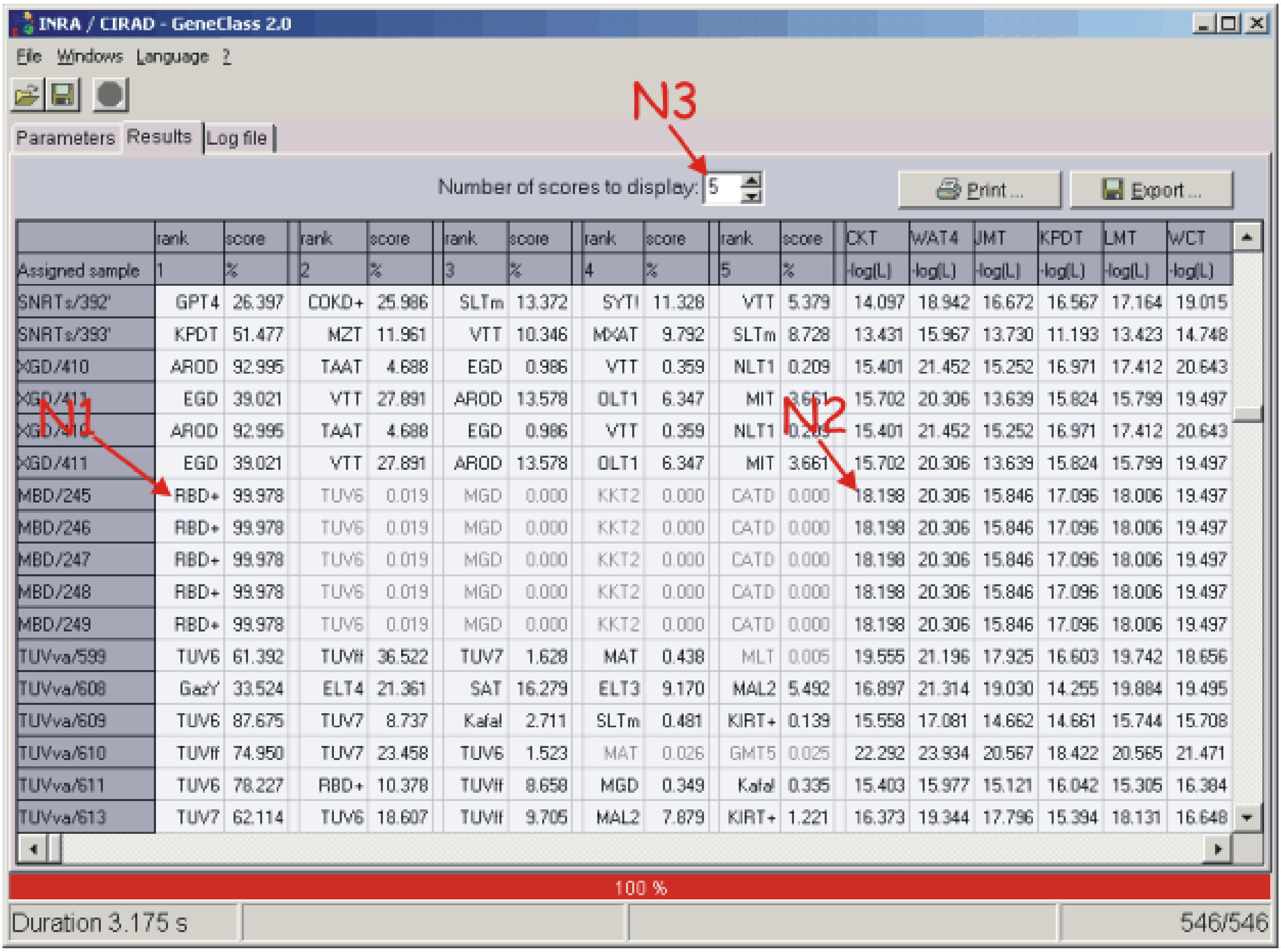
Duration 350.614 s

546/546

Computations without associated probabilities:

If you did not check the "Enable probability computation (Monte-Carlo resampling)" box [**J2**] the results are displayed as follows: The five first pairs of columns show, for each individual, the most likely populations and their relatives scores (*cf.* note below) in decreasing order [**N1**]. The right part of the grid displays -log values of the likelihoods [**N2**].
The number of displayed scores can be changed with the spin edit area [**N3**].

> **Note:** In a reference file with k populations the score of an individual i in a population l is computed as follow:
>
> $$score_{i,l} = \frac{L_{i,l}}{\sum_{j=1}^{k} L_{i,j}},$$
>
> with $L_{i,l}$ the likelihood value of the individual i in the population l.



Number of scores to display: 5

	rank	score	rank	score	rank	score	rank	score	rank	score	CKT	WAT4	JMT	KPDT	LMT	WCT
Assigned sample	1	%	2	%	3	%	4	%	5	%	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)	-log(L)
SNRTs/392'	GPT4	26.397	COKD+	25.986	SLTm	13.372	SYT!	11.328	VTT	5.379	14.097	18.942	16.672	16.567	17.164	19.015
SNRTs/393'	KPDT	51.477	MZT	11.961	VTT	10.346	MXAT	9.792	SLTm	8.728	13.431	15.967	13.730	11.193	13.423	14.748
XGD/410	AROD	92.995	TAAT	4.688	EGD	0.986	VTT	0.359	NLT1	0.209	15.401	21.452	15.252	16.971	17.412	20.643
XGD/411	EGD	39.021	VTT	27.891	AROD	13.578	OLT1	6.347	MIT	3.661	15.702	20.306	13.639	15.824	15.799	19.497
XGD/410	AROD	92.995	TAAT	4.688	EGD	0.986	VTT	0.359	NLT1	0.2[illegible]	15.401	21.452	15.252	16.971	17.412	20.643
XGD/411	EGD	39.021	VTT	27.891	AROD	13.578	OLT1	6.347	MIT	3.661	15.702	20.306	13.639	15.824	15.799	19.497
MBD/245	RBD+	99.978	TUV6	0.019	MGD	0.000	KKT2	0.000	CATD	0.000	18.198	20.306	15.846	17.096	18.006	19.497
MBD/246	RBD+	99.978	TUV6	0.019	MGD	0.000	KKT2	0.000	CATD	0.000	18.198	20.306	15.846	17.096	18.006	19.497
MBD/247	RBD+	99.978	TUV6	0.019	MGD	0.000	KKT2	0.000	CATD	0.000	18.198	20.306	15.846	17.096	18.006	19.497
MBD/248	RBD+	99.978	TUV6	0.019	MGD	0.000	KKT2	0.000	CATD	0.000	18.198	20.306	15.846	17.096	18.006	19.497
MBD/249	RBD+	99.978	TUV6	0.019	MGD	0.000	KKT2	0.000	CATD	0.000	18.198	20.306	15.846	17.096	18.006	19.497
TUVva/599	TUV6	61.392	TUVff	36.522	TUV7	1.628	MAT	0.438	MLT	0.005	19.555	21.196	17.925	16.603	19.742	18.656
TUVva/608	GazY	33.524	ELT4	21.361	SAT	16.279	ELT3	9.170	MAL2	5.492	16.897	21.314	19.030	14.255	19.884	19.495
TUVva/609	TUV6	87.675	TUV7	8.737	Kafal	2.711	SLTm	0.481	KIRT+	0.139	15.558	17.081	14.662	14.661	15.744	15.708
TUVva/610	TUVff	74.950	TUV7	23.458	TUV6	1.523	MAT	0.026	GMT5	0.025	22.292	23.934	20.567	18.422	20.565	21.471
TUVva/611	TUV6	78.227	RBD+	10.378	TUVff	8.658	MGD	0.349	Kafal	0.335	15.403	15.977	15.121	16.042	15.305	16.384
TUVva/613	TUV7	62.114	TUV6	18.607	TUVff	9.705	MAL2	7.879	KIRT+	1.221	16.373	19.344	17.796	15.394	18.131	16.648

100 %

Duration 3.175 s

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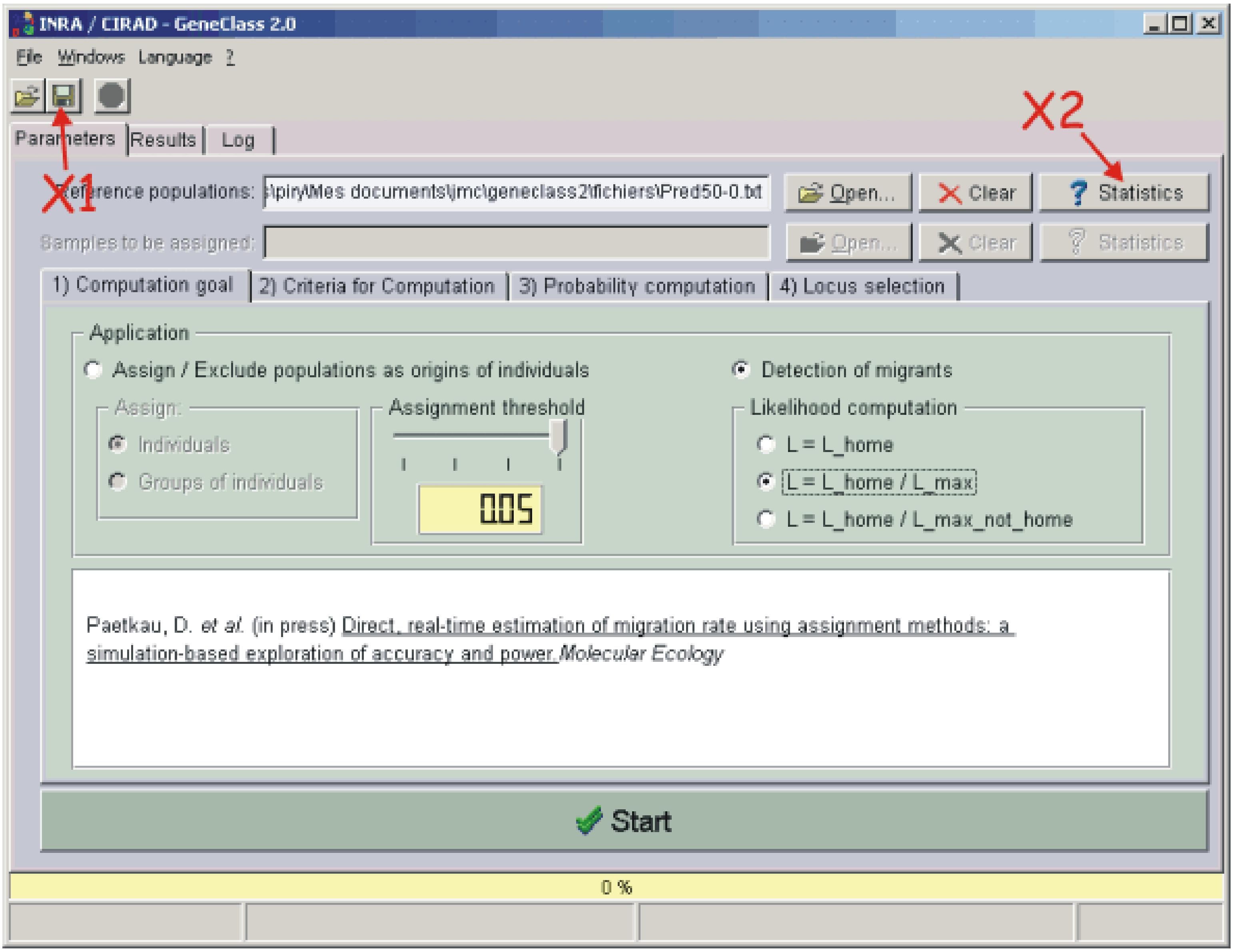
3) Data file conversion and description of population diversity

Datafiles can be exported into another format using the "Floppy" button [**X1**] in the upper bar, or with the "Save reference file as..." item in the "File" menu. GeneClass2 can therefore be used as a file-format converter between applications.

A preview of the usual statistics describing the diversity of populations can be obtained before or after any computation from the "Statistics" button [**X2**] in the main window.



Reference populations: :\piry\Mes documents\jmc\geneclass2\fichiers\Pred50-0.txt

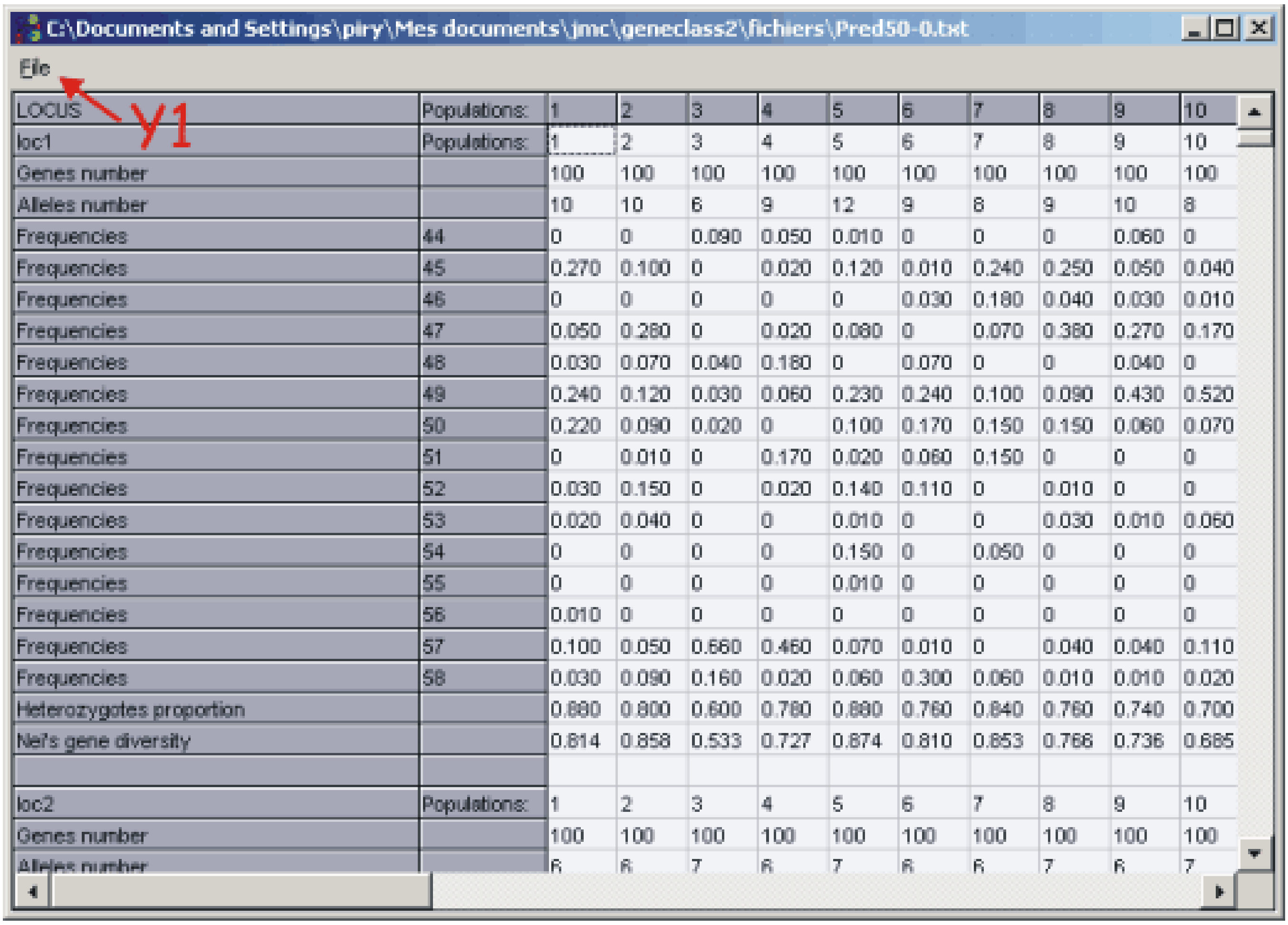
● Detection of migrants

Assignment threshold: 0.05

● L = L_home / L_max

Paetkau, D. *et al.* (in press) Direct, real-time estimation of migration rate using assignment methods: a simulation-based exploration of accuracy and power. *Molecular Ecology*

The result is a window with a grid containing allele frequencies, for each locus and for each population, heterozygotes proportion and Nei's gene diversity (Heterozygozity *sensu* Nei, 1987).
This grid can be printed or exported in csv format from the "File" menu [**Y1**].



LOCUS	Populations:	1	2	3	4	5	6	7	8	9	10
loc1	Populations:	1	2	3	4	5	6	7	8	9	10
Genes number		100	100	100	100	100	100	100	100	100	100
Alleles number		10	10	6	9	12	9	8	9	10	8
Frequencies	44	0	0	0.090	0.050	0.010	0	0	0	0.060	0
Frequencies	45	0.270	0.100	0	0.020	0.120	0.010	0.240	0.250	0.050	0.040
Frequencies	46	0	0	0	0	0	0.030	0.180	0.040	0.030	0.010
Frequencies	47	0.050	0.280	0	0.020	0.080	0	0.070	0.380	0.270	0.170
Frequencies	48	0.030	0.070	0.040	0.180	0	0.070	0	0	0.040	0
Frequencies	49	0.240	0.120	0.030	0.060	0.230	0.240	0.100	0.090	0.430	0.520
Frequencies	50	0.220	0.090	0.020	0	0.100	0.170	0.150	0.150	0.060	0.070
Frequencies	51	0	0.010	0	0.170	0.020	0.060	0.150	0	0	0
Frequencies	52	0.030	0.150	0	0.020	0.140	0.110	0	0.010	0	0
Frequencies	53	0.020	0.040	0	0	0.010	0	0	0.030	0.010	0.060
Frequencies	54	0	0	0	0	0.150	0	0.050	0	0	0
Frequencies	55	0	0	0	0	0.010	0	0	0	0	0
Frequencies	56	0.010	0	0	0	0	0	0	0	0	0
Frequencies	57	0.100	0.050	0.660	0.460	0.070	0.010	0	0.040	0.040	0.110
Frequencies	58	0.030	0.090	0.160	0.020	0.060	0.300	0.060	0.010	0.010	0.020
Heterozygotes proportion		0.880	0.800	0.600	0.780	0.880	0.760	0.840	0.760	0.740	0.700
Nei's gene diversity		0.814	0.858	0.533	0.727	0.874	0.810	0.853	0.766	0.736	0.685
loc2	Populations:	1	2	3	4	5	6	7	8	9	10
Genes number		100	100	100	100	100	100	100	100	100	100
Alleles number		6	6	7	6	7	6	6	7	6	7

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