

# **ANALYSE BI-POINTS ET MULTI-POINTS**

***(MIACGH - TP2)***

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# **DONNÉES FAMILIALES F8-MK16.DON**

*Qu'est ce que c'est ?*

**Fichier regroupant l'ensemble des liens de parentés ainsi que les génotypes, et ce pour chaque famille et marqueur associé.**

**Données disposées en colonnes**

*( fichier présenté sous format spécifique, nécessaire à sa lecture par le logiciel. )*

# DONNÉES FAMILIALES F8-MK16.DON

	A	B	C	D	E	F	G	H
1	famille	id	fath_id	moth_id	sex	D15S128	D15S10	D15S986
2	102	1	0	0	1	33	12	11
3	102	2	0	0	2	12	11	23
4	102	3	1	2	2	13	11	12
5	102	4	1	2	1	32	11	13
6	102	5	1	2	2	00	12	12
7	102	6	1	2	2	13	11	12
8	102	7	1	2	2	13	11	12
9	102	8	1	2	1	13	12	12
10	102	9	1	2	1	13	11	12
11	102	10	1	2	2	13	12	12
12	102	11	1	2	1	13	12	12
13	102	12	1	2	2	32	11	13
14	102	13	1	2	2	13	12	12
15	102	14	1	2	2	32	12	13
16	102	15	1	2	1	32	12	13
17	102	16	1	2	1	13	11	12

Numéro de l'individu

Numéro de la famille

Numéro des parents

1 = Homme  
2 = Femme

Génotype assigné à chaque marqueur

# FICHER “PARAMÈTRES”

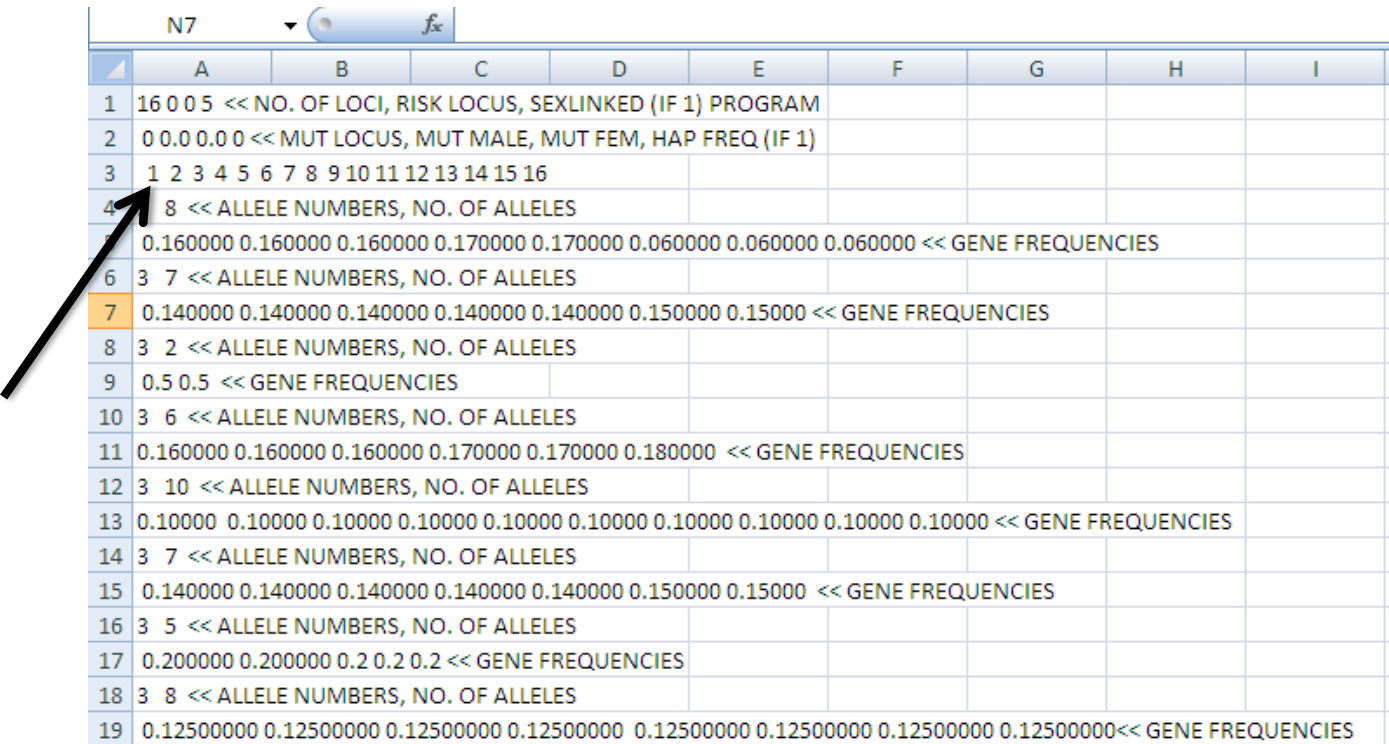
*Qu'est ce que c'est ?*

**Fichier regroupant les informations des marqueurs, nécessaires à une analyse de liaison par le logiciel LINKAGE**

**Données disposées en lignes**

# FICHER "PARAMÈTRES"

## Vue d'ensemble



	A	B	C	D	E	F	G	H	I
1	16 0 0 5 << NO. OF LOCI, RISK LOCUS, SEXLINKED (IF 1) PROGRAM								
2	0 0.0 0.0 0 << MUT LOCUS, MUT MALE, MUT FEM, HAP FREQ (IF 1)								
3	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16								
4	8 << ALLELE NUMBERS, NO. OF ALLELES								
	0.160000 0.160000 0.160000 0.170000 0.170000 0.060000 0.060000 0.060000 << GENE FREQUENCIES								
6	3 7 << ALLELE NUMBERS, NO. OF ALLELES								
7	0.140000 0.140000 0.140000 0.140000 0.140000 0.150000 0.150000 << GENE FREQUENCIES								
8	3 2 << ALLELE NUMBERS, NO. OF ALLELES								
9	0.5 0.5 << GENE FREQUENCIES								
10	3 6 << ALLELE NUMBERS, NO. OF ALLELES								
11	0.160000 0.160000 0.160000 0.170000 0.170000 0.180000 << GENE FREQUENCIES								
12	3 10 << ALLELE NUMBERS, NO. OF ALLELES								
13	0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 << GENE FREQUENCIES								
14	3 7 << ALLELE NUMBERS, NO. OF ALLELES								
15	0.140000 0.140000 0.140000 0.140000 0.140000 0.150000 0.150000 << GENE FREQUENCIES								
16	3 5 << ALLELE NUMBERS, NO. OF ALLELES								
17	0.200000 0.200000 0.2 0.2 0.2 << GENE FREQUENCIES								
18	3 8 << ALLELE NUMBERS, NO. OF ALLELES								
19	0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 << GENE FREQUENCIES								

Numéro des marqueurs .

Ici, il y'ena 16 étudiés.

# FICHER "PARAMÈTRES"

Nombre de marqueurs contenus dans le fichier familial

Nombre d'allèles du gène de maladie

Nombre de locus lié(s) au chromosome X

	A	B	C	D	E	F	G
1	16	0	0	5	<< NO. OF LOCI, RISK LOCUS, SEXLINKED (IF 1) PROGRAM		
2	0	0.0	0.0	0	<< MUT LOCUS, MUT MALE, MUT FEM, HAP FREQ (IF 1)		

Fréquence des haplotypes

Taux de mutation en fonction du sexe

Taux de mutation

# FICHER “PARAMÈTRES”

Précise que la ligne suivante concerne un marqueur (1 = locus maladie)

Nombre d'allèles

4	3	8	<< ALLELE NUMBERS, NO. OF ALLELES																	
5	0.160000	0.160000	0.160000	0.170000	0.170000	0.060000	0.060000	0.060000	<< GENE FREQUENCIES											

Fréquences de chaque allèle du marqueur

# FICHER "PARAMÈTRES"

Spécification d'une estimation du taux de recombinaison  
différente selon le sexe

Interférence

```
35 0.500000 0.500000 << GENE FREQUENCIES
36 0 0 << SEX DIFFERENCE, INTERFERENCE (IF 1 OR 2)
37 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 << RECOMBINATION VALUES
38 1 0.10000 0.45000 << REC VARIED, INCREMENT, FINISHING VALUE
```

*Variation d'un  
taux de  
recombinaison*

Valeur du pas

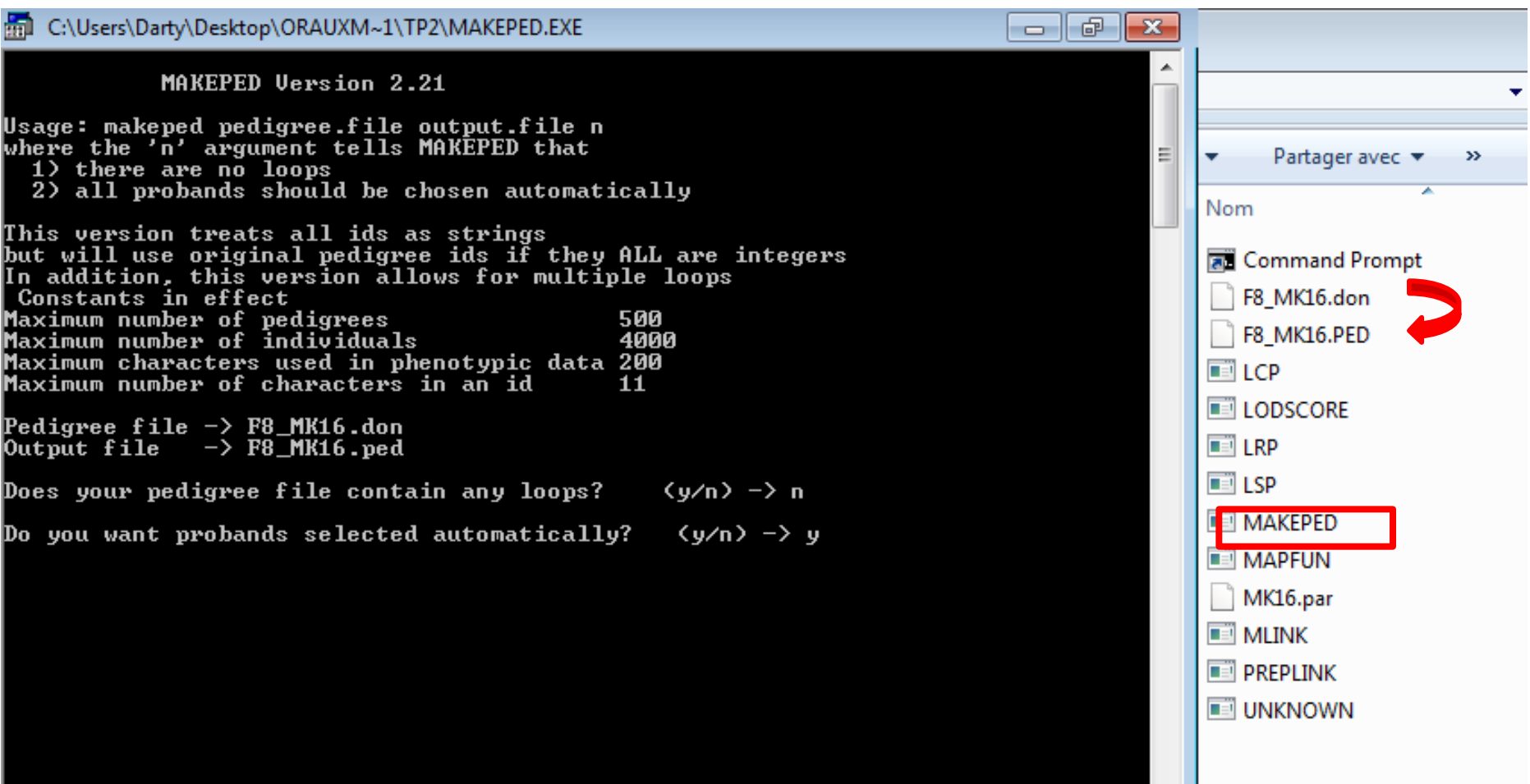
*Valeur final du  
taux de  
recombinaison*

Taux de  
recombinaison pour  
chaque marqueur



# MODIFICATION DU FICHER FAMILIAL

*En utilisant le programme MAKEPED, transformez le fichier F8\_MK16.don en F8\_MK16.ped*



The image shows a Windows desktop environment. On the left, a terminal window titled 'C:\Users\Darty\Desktop\ORAUXM~1\TP2\MAKEPED.EXE' displays the output of the MAKEPED program. The terminal text includes the version (2.21), usage instructions, and a list of constants. It also shows the user's input for the pedigree file (F8\_MK16.don) and output file (F8\_MK16.ped), and responses to two prompts: 'Does your pedigree file contain any loops?' (n) and 'Do you want probands selected automatically?' (y).

```
MAKEPED Version 2.21
Usage: makeped pedigree.file output.file n
where the 'n' argument tells MAKEPED that
 1) there are no loops
 2) all probands should be chosen automatically

This version treats all ids as strings
but will use original pedigree ids if they ALL are integers
In addition, this version allows for multiple loops
Constants in effect
Maximum number of pedigrees           500
Maximum number of individuals         4000
Maximum characters used in phenotypic data 200
Maximum number of characters in an id   11

Pedigree file -> F8_MK16.don
Output file   -> F8_MK16.ped

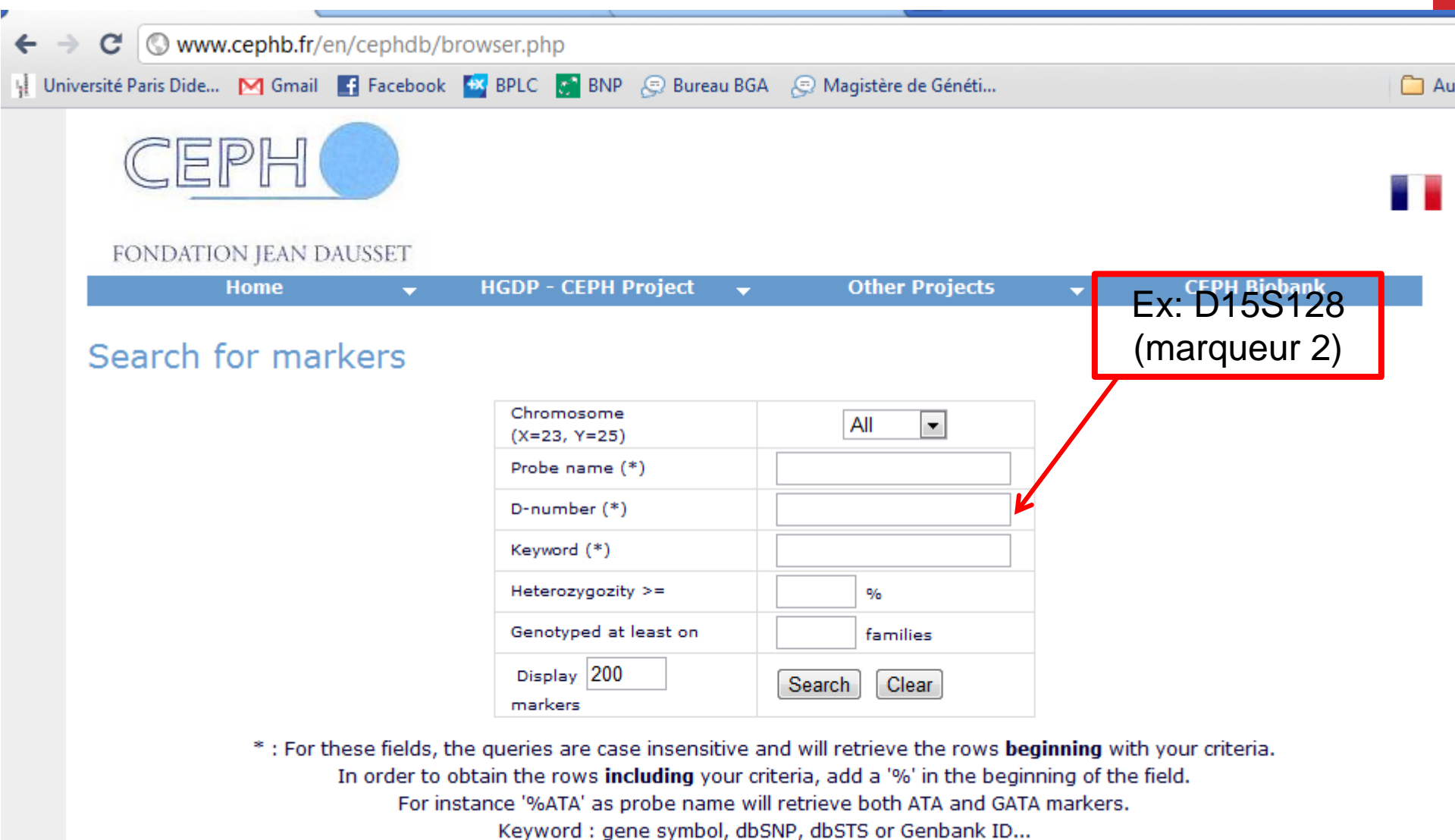
Does your pedigree file contain any loops?    <y/n> -> n
Do you want probands selected automatically?  <y/n> -> y
```

On the right, a file explorer window shows the contents of the directory 'C:\Users\Darty\Desktop\ORAUXM~1\TP2'. The files listed are: Command Prompt, F8\_MK16.don, F8\_MK16.PED, LCP, LODSCORE, LRP, LSP, MAKEPED, MAPFUN, MK16.par, MLINK, PRELINK, and UNKNOWN. The 'MAKEPED' file is highlighted with a red box, and a red arrow points from it to the 'F8\_MK16.PED' file.

# **MODIFICATION DU FICHIER PARAMÈTRE**

**Le fichier MK16.par contient des valeurs de fréquences allélique par défaut, il faut changer ses valeurs avec les valeurs données par le CEPH**

## Etape 1 : trouvez les fréquences alléliques sur le site du CEPH



The screenshot shows the CEPH website interface. At the top, there is a navigation bar with the CEPH logo and the text 'FONDATION JEAN DAUSSET'. Below this is a menu with options: 'Home', 'HGDP - CEPH Project', 'Other Projects', and 'CEPH Biobank'. The 'CEPH Biobank' option is highlighted in blue. Below the menu, there is a search section titled 'Search for markers'. This section contains a form with several input fields: 'Chromosome (X=23, Y=25)' with a dropdown menu set to 'All'; 'Probe name (\*)' with an empty text box; 'D-number (\*)' with an empty text box; 'Keyword (\*)' with an empty text box; 'Heterozygosity >=' with a text box and a '%' symbol; 'Genotyped at least on' with a text box and the word 'families'; and 'Display' with a text box containing '200' and the word 'markers' below it. There are 'Search' and 'Clear' buttons at the bottom of the form. A red box highlights the 'D-number (\*)' field, and a red arrow points from this box to the text 'Ex: D15S128 (marqueur 2)'. Below the form, there is a note explaining that queries are case insensitive and will retrieve rows beginning with the criteria. It also provides an example: '%ATA' as probe name will retrieve both ATA and GATA markers. The keyword field is defined as gene symbol, dbSNP, dbSTS or Genbank ID...

www.cephb.fr/en/cephdb/browser.php

CEPH

FONDATION JEAN DAUSSET

Home HGDP - CEPH Project Other Projects CEPH Biobank

Search for markers

Chromosome (X=23, Y=25)	All
Probe name (*)	<input type="text"/>
D-number (*)	<input type="text"/>
Keyword (*)	<input type="text"/>
Heterozygosity >=	<input type="text"/> %
Genotyped at least on	<input type="text"/> families
Display <input type="text" value="200"/> markers	<input type="button" value="Search"/> <input type="button" value="Clear"/>

\* : For these fields, the queries are case insensitive and will retrieve the rows **beginning** with your criteria.  
In order to obtain the rows **including** your criteria, add a '%' in the beginning of the field.  
For instance '%ATA' as probe name will retrieve both ATA and GATA markers.  
Keyword : gene symbol, dbSNP, dbSTS or Genbank ID...



FONDATION JEAN DAUSSET

Home

HGDP - CEPH Project

Other Projects

CEPH Biobank

## Matching systems

CEPH format



PC



Dump

Select all

Select to dump	Chr.	Probe/enzyme system	D-number	NCBI Entrez link	Heterozygosity	# of families
<input type="checkbox"/>	15	AFM273yf9 / (AC)n	D15S128	Z17197	80.77%	8

Number of systems matching your criteria : 1.

## Detail for system AFM273yf9/(AC)n system

<b>Chromosome</b>	15
<b>D-number</b>	<b>D15S128</b>
<b>Keyword</b>	<b>Z17197</b>
<b>Heterozygosity</b>	80.77%
<b>Collaborator 42</b>	Dr Jean WEISSENBACH Centre National de Séquençage 2, rue Gaston Crémieux - BP 191 91006 EVRY CEDEX, France Génoscope <a href="mailto:jsbach@genoscope.cns.fr">jsbach@genoscope.cns.fr</a> 33.(0) 1 60 87 25 02 33 (0)1 60 87 25 32

### List of markers close to AFM273yf9/(AC)n system

Families (# of genotyped individual)			
<b>102</b> (15)	<b>1331</b> (17)	<b>1332</b> (15)	<b>1347</b> (16)
<b>1362</b> (17)	<b>1413</b> (18)	<b>1416</b> (13)	<b>884</b> (16)

Fragment sizes		Allele frequencies	
Fragment	Size (Mb)	Allele	Frequency
1	0.207	1	0.115385
2	0.199	2	0.346154
3	0.201	3	0.211538
4	0.193	4	0.057692
5	0.205	5	0.153846
6	0.203	6	0.076923
7	0.209	7	0.038462

## Etape 2 : Remplacez ses valeurs dans le fichier MK16.par Exemple du marqueur 2

```
MK16 - Bloc-notes
Fichier Edition Format Affichage ?
16 0 0 5 << NO. OF LOCI, RISK LOCUS, SEXLINKED (IF 1) PROGRAM
0 0.0 0.0 0 << MUT LOCUS, MUT MALE, MUT FEM, HAP FREQ (IF 1)
  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
3   8 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.060000 0.060000 0.060000 << GENE FREQUENCIES
3   7 << ALLELE NUMBERS, NO. OF ALLELES
0.140000 0.140000 0.140000 0.140000 0.140000 0.150000 0.150000 << GENE FREQUENCIES
3   2 << ALLELE NUMBERS, NO. OF ALLELES
0.5 0.5 << GENE FREQUENCIES
3   6 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.180000 << GENE FREQUENCIES
3  10 << ALLELE NUMBERS, NO. OF ALLELES
0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 << GENE FREQUENCIES
3   7 << ALLELE NUMBERS, NO. OF ALLELES
0.140000 0.140000 0.140000 0.140000 0.140000 0.150000 0.150000 << GENE FREQUENCIES
3   5 << ALLELE NUMBERS, NO. OF ALLELES
0.200000 0.200000 0.2 0.2 0.2 << GENE FREQUENCIES
3   8 << ALLELE NUMBERS, NO. OF ALLELES
0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 << GENE FREQUENCIES
3   8 << ALLELE NUMBERS, NO. OF ALLELES
0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 << GENE FREQUENCIES
3   8 << ALLELE NUMBERS, NO. OF ALLELES
0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 << GENE FREQUENCIES
3   6 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.180000 << GENE FREQUENCIES
3   6 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.180000 << GENE FREQUENCIES
3   2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
3   2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
3   2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
3   2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
0 0 << SEX DIFFERENCE, INTERFERENCE (IF 1 OR 2)
0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000
0.1000 0.1000 << RECOMBINATION VALUES
1 0.10000 0.45000 << REC VARIED, INCREMENT, FINISHING VALUE
```

MK16 - Bloc-notes

Fichier Edition Format Affichage ?

```
16 0 0 5 << NO. OF LOCI, RISK LOCUS, SEXLINKED (IF 1) PROGRAM
0 0.0 0.0 0 << MUT LOCUS, MUT MALE, MUT FEM, HAP FREQ (IF 1)
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
3 8 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.060000 0.060000 0.060000 << GENE FREQUENCIES
3 7 << ALLELE NUMBERS, NO. OF ALLELES
0.115385 0.346154 0.211538 0.057692 0.153846 0.076923 0.038462 << GENE FREQUENCIES
3 2 << ALLELE NUMBERS, NO. OF ALLELES
0.5 0.5 << GENE FREQUENCIES
3 6 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.180000 << GENE FREQUENCIES
3 10 << ALLELE NUMBERS, NO. OF ALLELES
0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 0.10000 << GENE FREQUENCIES
3 7 << ALLELE NUMBERS, NO. OF ALLELES
0.140000 0.140000 0.140000 0.140000 0.140000 0.150000 0.150000 << GENE FREQUENCIES
3 5 << ALLELE NUMBERS, NO. OF ALLELES
0.200000 0.200000 0.2 0.2 0.2 << GENE FREQUENCIES
3 8 << ALLELE NUMBERS, NO. OF ALLELES
0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 << GENE FREQUENCIES
3 8 << ALLELE NUMBERS, NO. OF ALLELES
0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 << GENE FREQUENCIES
3 8 << ALLELE NUMBERS, NO. OF ALLELES
0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 << GENE FREQUENCIES
3 6 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.180000 << GENE FREQUENCIES
3 6 << ALLELE NUMBERS, NO. OF ALLELES
0.160000 0.160000 0.160000 0.170000 0.170000 0.180000 << GENE FREQUENCIES
3 2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
3 2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
3 2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
3 2 << ALLELE NUMBERS, NO. OF ALLELES
0.500000 0.500000 << GENE FREQUENCIES
0 0 << SEX DIFFERENCE, INTERFERENCE (IF 1 OR 2)
0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000 0.1000
0.1000 0.1000 << RECOMBINATION VALUES
1 0.10000 0.45000 << REC VARIED, INCREMENT, FINISHING VALUE
```

Fichier modifié!

# QUESTION 5 : INDIQUEZ À QUOI SERVENT SES TROIS ÉTAPES POUR EFFECTUER LES ANALYSES DE LIAISONS.

## *LCP, PEDIN, LRP*

**NB:** Sur un ordinateur personnel:

- Créer un répertoire de travail avec tous les fichiers
- Trouver le programme cmd.exe et le **COPIER** dans le répertoire de travail
- Trouver le programme config.nt, le **COPIER** dans le répertoire de travail
- Ouvrir config.nt avec le bloc note et modifié les dernières lignes pour avoir:

*dos=high, umb*

*device=%SystemRoot%\system32\himem.sys*

*device=%SystemRoot%\system32\ansi.sys*

*files=40*

-On peut commencer!

-Attention, certain programme fonctionne en anglais (en tout cas sur ordinateur personnel!) le clavier est donc en qwerty!

Ctrl+Z=Ctrl+W

\_ = majuscule +)



# UTILISATION DE LINKAGE

→ *L'emploi de ce logiciel nous permet de tester l'analyse de liaison entre 2 ou plusieurs marqueurs, par l'utilisation successive de 3 commandes:*

- **Linkage Control Program (LCP)**
  - **PEDIN**
- **Linkage Report Program (LRP)**

# LINKAGE CONTROL PROGRAM (LCP)

*Cette commande nous permet de créer un fichier de commande prenant en compte les informations décrites dans les fichiers familiales et paramètres*

```
LINKAGE CONTROL PROGRAM

Input Files

COMMAND file name [PEDIN.BAT] : PEDIN.BAT
LOG file name [FINAL.OUT] : FINAL.OUT
STREAM file name [STREAM.OUT] : STREAM.OUT
PEDIGREE file name [PEDIN.DAT] : PEDIN.DAT
PARAMETER file name [DATAIN.DAT] : DATAIN.DAT
Secondary PEDIGREE file name [] :
Secondary PARAMETER file name [] :

CTRL/A - Abort CTRL/H - Help CTRL/Z - Exit
```

Page down...

C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LCP

L I N K A G E   C O N T R O L   P R O G R A M

Pedigree Options

General pedigrees : <-  
Three-generation pedigrees :  
Experimental cross pedigrees :

CTRL/A - Abort   CTRL/H - Help   CTRL/Z - Exit

Page down...

```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LCP

LINKAGE CONTROL PROGRAM

General Pedigree Analysis Options
-----

LODScore : <-
ILINK    :
LINKMAP  :
MLINK    :

CTRL/A - Abort  CTRL/H - Help  CTRL/Z - Exit
```

Choisir le type d'analyse a effectuer et faire « entrer »

# Les types d'analyses vues en TP

## MKLINK

Locus order [] : 1 2 (*ordre des locus*)

Recombination fractions [.1] : 0 (*valeur initiale de  $\theta$* )

Recombination varied [1] : 1

*(variation d'un seul taux de recombinaison;  
plusieurs régions possibles quand plus de deux loci)*

Increment value [.1] : .1 (*valeur du pas*)

Stop value [.5] : .5 (*valeur finale de  $\theta$* )

*Calcul du lodscore entre les locus 1 et 2*

*Pour les valeurs de  $\theta$ : 0, 0.1, 0.2, 0.3, 0.4, 0.5*

## LODSCORE

First locus set [] : 1

Second locus set [] : 2

Male recombination fraction [.1] : .1

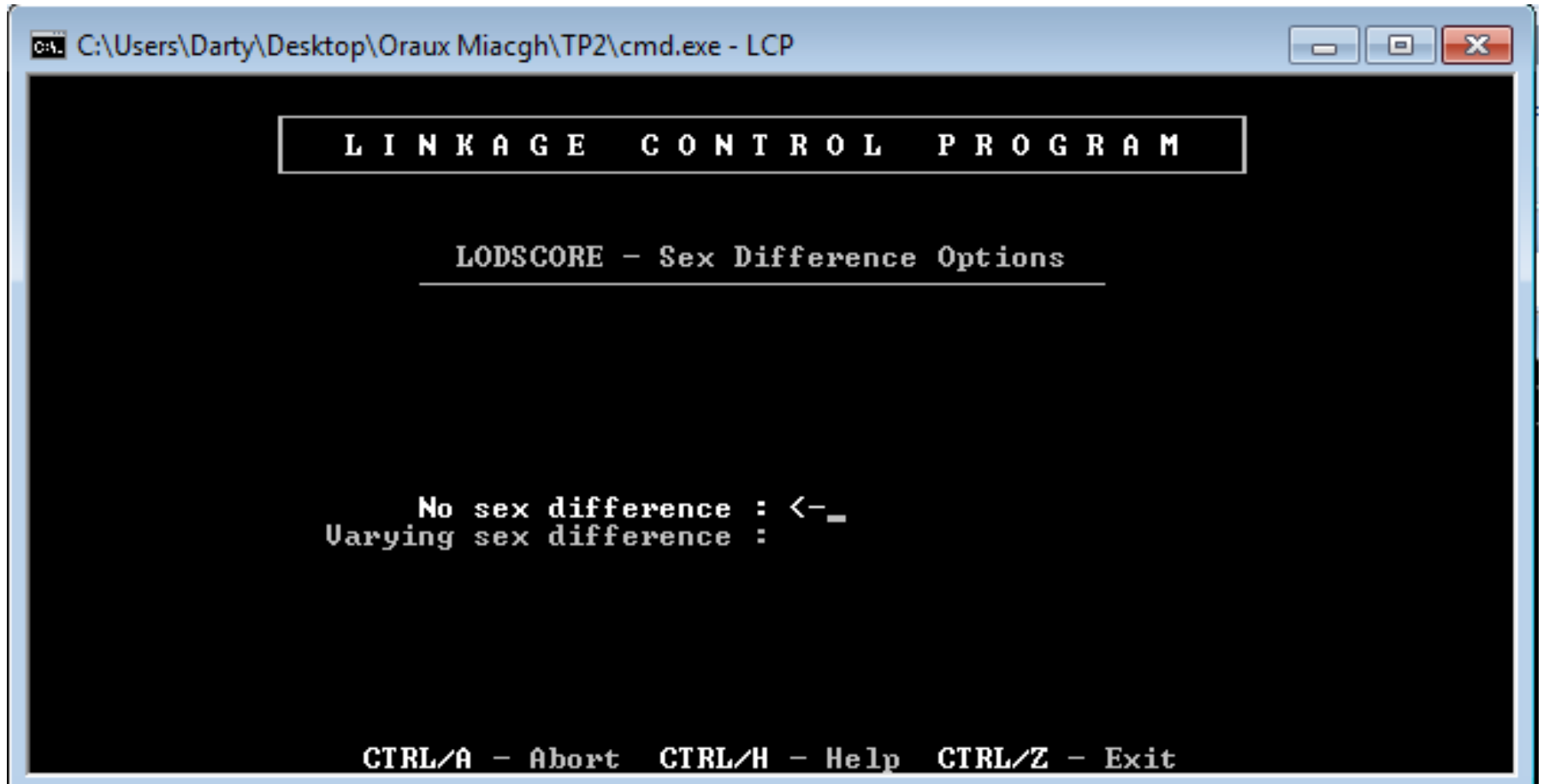
General Pedigrees

LOD SCORE

*Recherche de la valeur de  $\theta$  entre les locus 1 et 2*

*pour lequel le lodscore est maximum; valeur de ce lodscore*

# Analyse LODSCORE:



```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LCP

LINKAGE CONTROL PROGRAM

LODSCORE - Sex Difference Options

No sex difference : <-_
Varying sex difference :

CTRL/A - Abort CTRL/H - Help CTRL/Z - Exit
```

Page down...

```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LCP

LINKAGE CONTROL PROGRAM

LODScore - Locus Specification
-----
Command Screen

First locus set [] : 1
Second locus set [] : 2
Male recombination fraction [.1] : .1

CTRL/A - Abort CTRL/H - Help CTRL/Z - Exit
```

## LOD SCORE

*Recherche de la valeur de  $\theta$  entre les locus 1 et 2 pour lequel le lodscore est maximum*

*Ce programme donne la valeur de ce  $\theta$*

**Page down... ici on retourne a la page d'accueil, il faut sortir du programme Ctrl+Z**

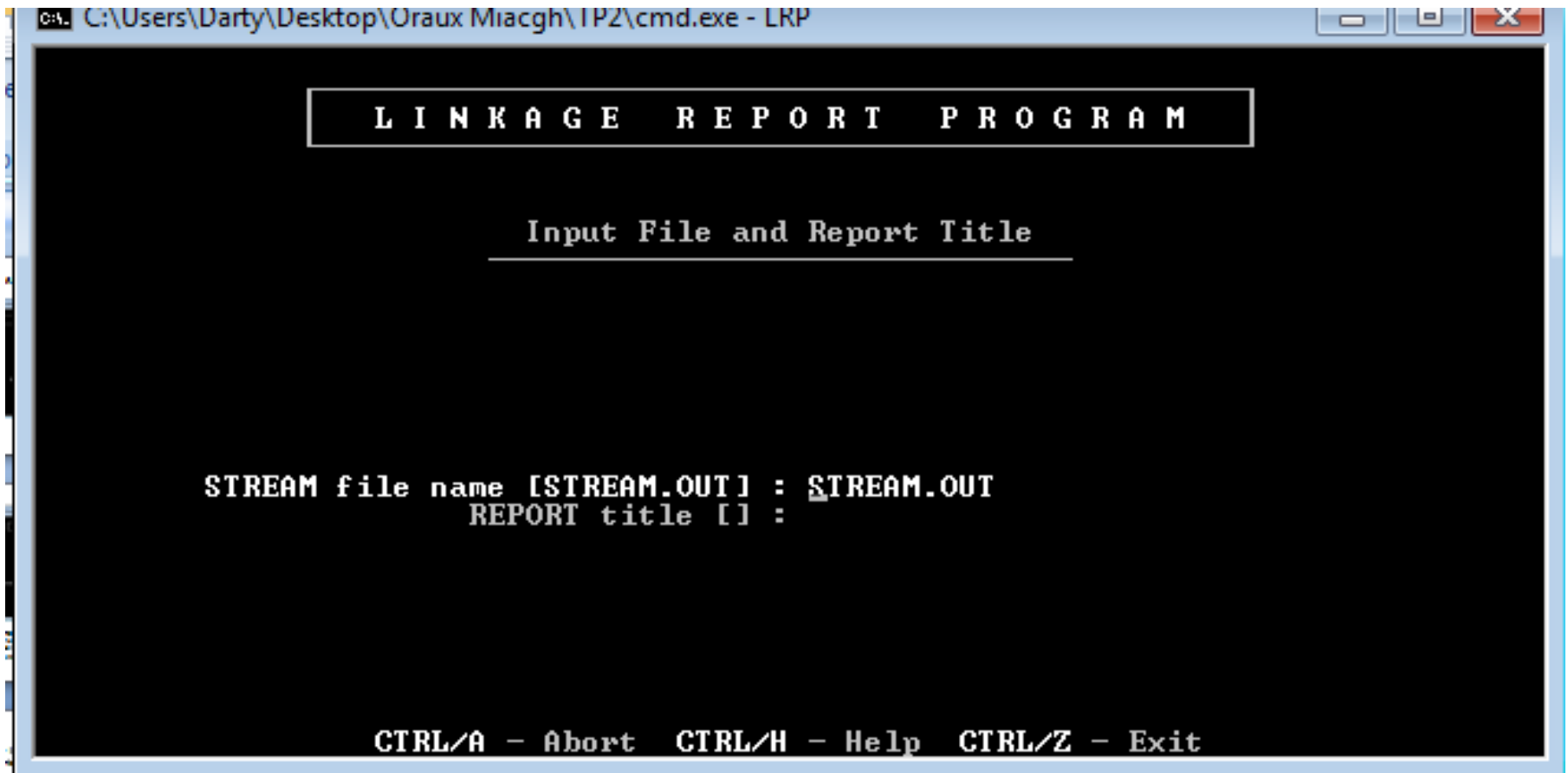
# PEDIN

***Cette commande est ce que l'on appelle un "fichier exécutable" qui va permettre de lancer les analyses créées par LCP***



# LINKAGE REPORT PROGRAM (LRP)

*Cette commande récupère l'ensemble des données obtenues par la commande PEDIN, puis les restitue sous une forme "lisible"*



```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LRP

LINKAGE REPORT PROGRAM

Input File and Report Title
-----

STREAM file name [STREAM.OUT] : STREAM.OUT
REPORT title [] :

CTRL/A - Abort CTRL/H - Help CTRL/Z - Exit
```

C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LRP

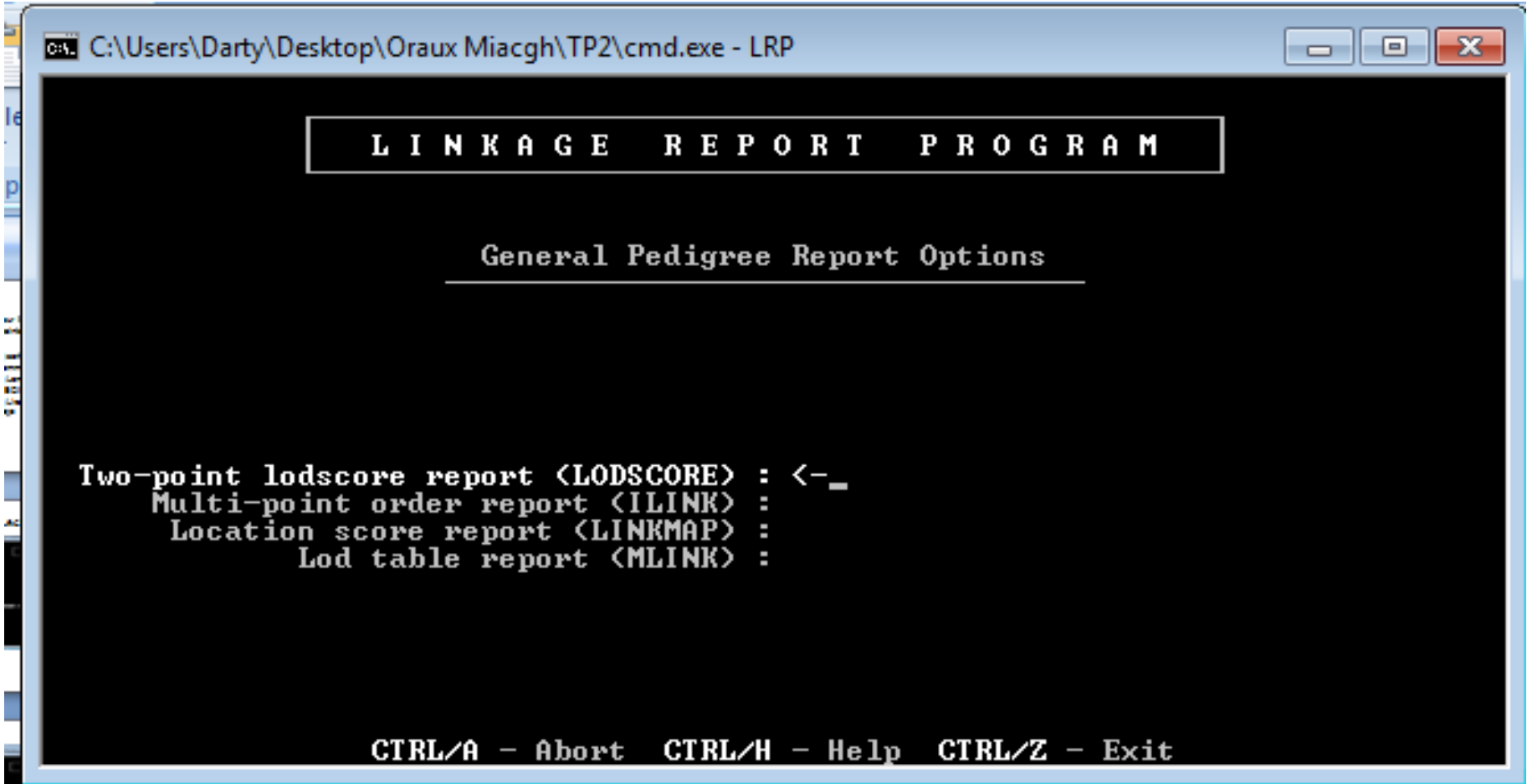
L I N K A G E   R E P O R T   P R O G R A M

Report Options

General pedigree reports : <-  
Three-generation pedigree reports :  
Experimental cross pedigree reports :  
Full stream file reports :

CTRL/A - Abort   CTRL/H - Help   CTRL/Z - Exit

Page down...



A cette étape on choisit les résultats que l'on veut visualiser grâce aux flèches de navigation et page down!

On choisi ici LODSCORE car c'est l'analyse que l'on a fait.

```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LRP

LINKAGE REPORT PROGRAM

Two-Point Lodscore Report <LODScore> Formats
-----

Table format : <-_
Full format :

CTRL/A - Abort CTRL/H - Help CTRL/Z - Exit
```

Page down...

```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LRP

LINKAGE REPORT PROGRAM

Report Output Options

Output report to the screen : <-
Output report to a file :

CTRL/A - Abort CTRL/H - Help CTRL/Z - Exit
```

Page down...

```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - LRP
TWO - POINT LODSCORE REPORT
File: STREAM.OUT                               Screen: 1 of 1
-----
Order      Recomb    Lodscore
-----
 2-12      0.2810    3.66
-----
Enter Command : _
CTRL/A - Abort  CTRL/H - Help  CTRL/Z - Exit  CTRL/R - Return
```

On a les résultats sur la fenêtre de commande on peut également le mettre dans un fichier.

**Retour : Ctrl+R**

Puis choisir « Output report to a file »

C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - lrp

L I N K A G E   R E P O R T   P R O G R A M

Report Output Options

Output report to the screen :  
Output report to a file : <\_

CTRL/A - Abort   CTRL/H - Help   CTRL/Z - Exit

Page down...

```
C:\Users\Darty\Desktop\Oraux Miacgh\TP2\cmd.exe - lrp

LINKAGE REPORT PROGRAM

Report File Options

REPORT file name [REPORT.TXT] : REPORT.TXT
REPORT page length [60] : 60
REPORT page width [80] : 80
Use form feeds [Yes] : Yes

CTRL/A - Abort CTRL/H - Help CTRL/Z - Exit
```




















Mettre le nom du fichier texte que l'on veut (ici report.txt)

**Page down...**

Retour à l'écran d'accueil!

Sortir du programme grâce à la commande Ctrl+Z



Nom	Modifié le	Type	Taille
 cmd	14/07/2009 03:14	Application	295 Ko
 F8_MK16.don	24/01/2006 17:41	Fichier DON	11 Ko
 F8_MK16.PED	14/03/2011 17:23	Fichier PED	16 Ko
 FINAL.bak	14/03/2011 17:30	Fichier BAK	1 Ko
 FINAL.OUT	14/03/2011 17:32	Fichier OUT	1 Ko
 LCP	24/01/2006 17:39	Application	159 Ko
 LODSCORE	24/01/2006 17:39	Application	141 Ko
 LRP	24/01/2006 17:40	Application	191 Ko
 LSP	24/01/2006 17:40	Application	268 Ko
 MAKEPED	24/01/2006 17:40	Application	43 Ko
 MAPFUN	24/01/2006 17:40	Application	24 Ko
 MK16	24/01/2006 17:41	Fichier PAR	3 Ko
 MLINK	24/01/2006 17:40	Application	115 Ko
 PEDIN	14/03/2011 17:32	Fichier de comma...	2 Ko
 PREPLINK	24/01/2006 17:40	Application	56 Ko
 REPORT	14/03/2011 17:39	Document texte	1 Ko
 STREAM.bak	14/03/2011 17:30	Fichier BAK	1 Ko
 STREAM.OUT	14/03/2011 17:32	Fichier OUT	1 Ko
 UNKNOWN	24/01/2006 17:41	Application	44 Ko

Le fichier est automatiquement créé dans le dossier !  
L'ouvrir et contempler votre œuvre!

T W O - P O I N T L O D S C O R E R E P O R T

Report Title :

Report File : REPORT.TXT

Report Date : 19-May-131 03:51:55

Stream File : STREAM.OUT

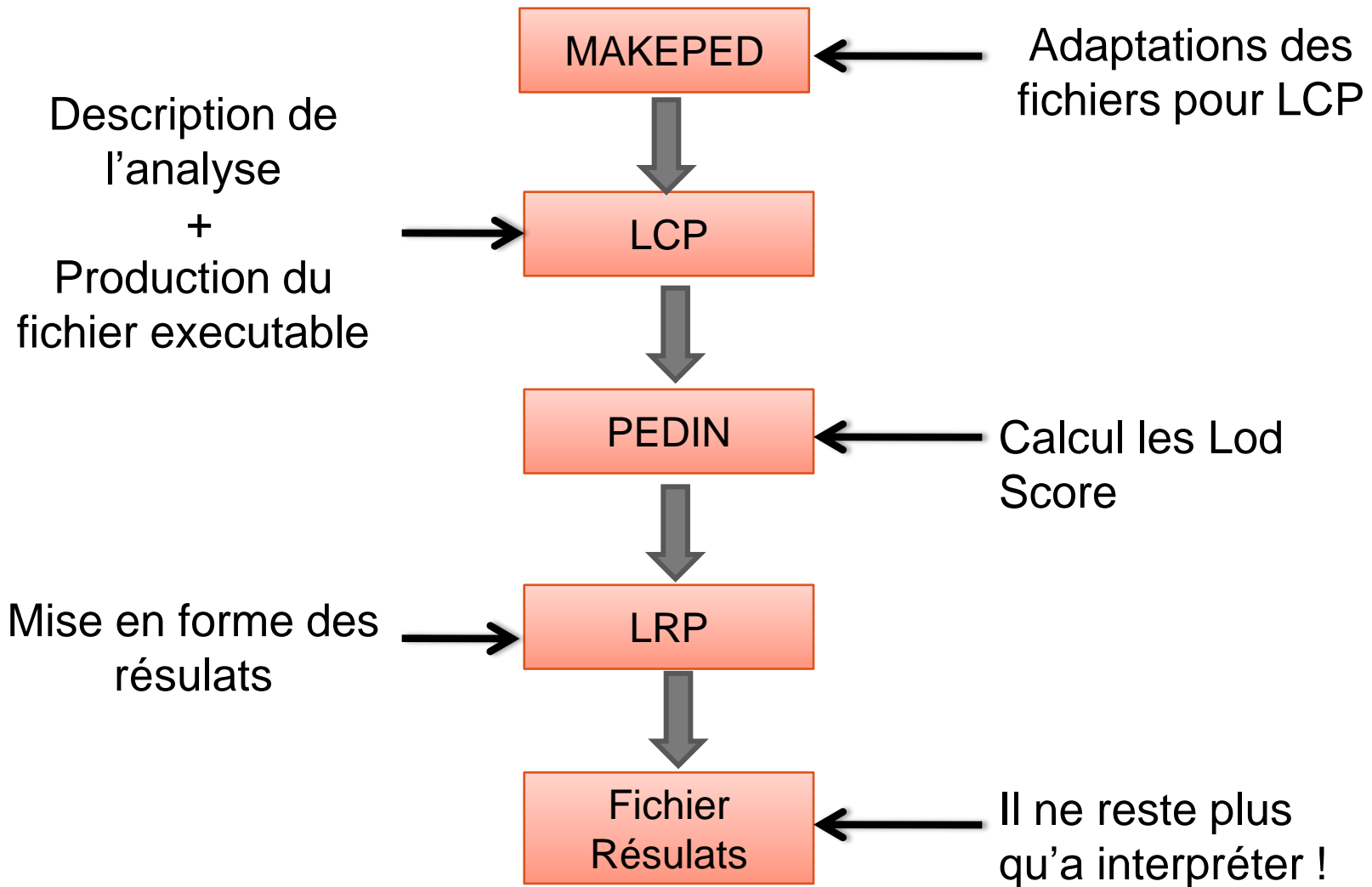
Stream Date : 19-May-131 03:45:57

T W O - P O I N T L O D S C O R E R E P O R T

Page: 2

Order	Recomb	Lodscore
2-12	0.2810	3.66

# CONCLUSION





**Merci de votre attention!!**