



Christian Albrechts University Kiel-Zoologisches Institut



République Tunisienne
Ministère de l'Agriculture
Direction Générale des
Forêts



Atelier de Formation Rhéhabilitation du cerf de Berbérie Tlemcen, 26-27 Décembre 2016

**Méthodes de Conservation et de Gestion du cerf de
Berbérie**

Dr.Sc. Ghayet El Mouna Hajji



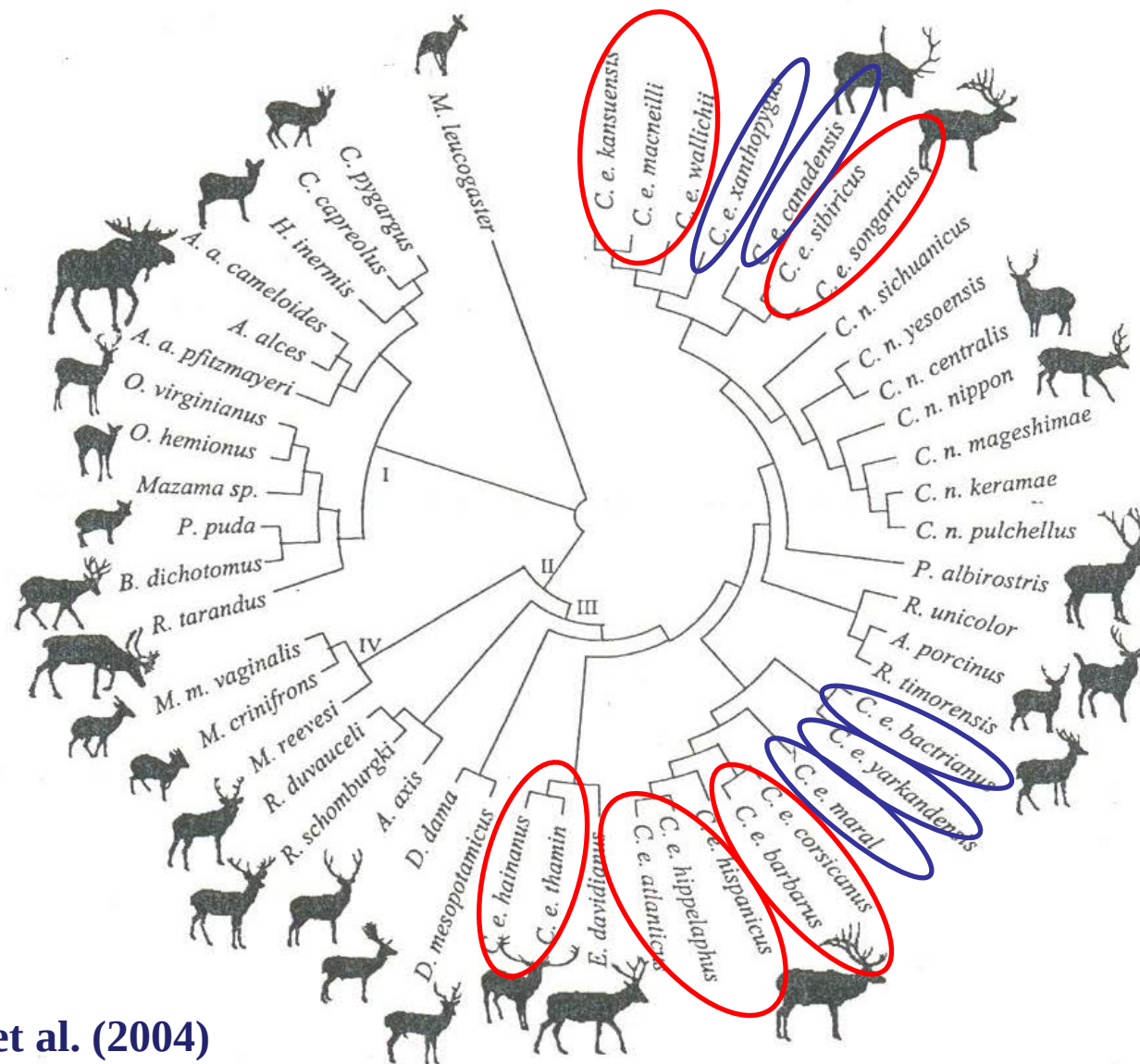
Cerf de Berbérie
Cervus elaphus



Afrique du Nord : LR / nt (1996: „Vulnerable“)

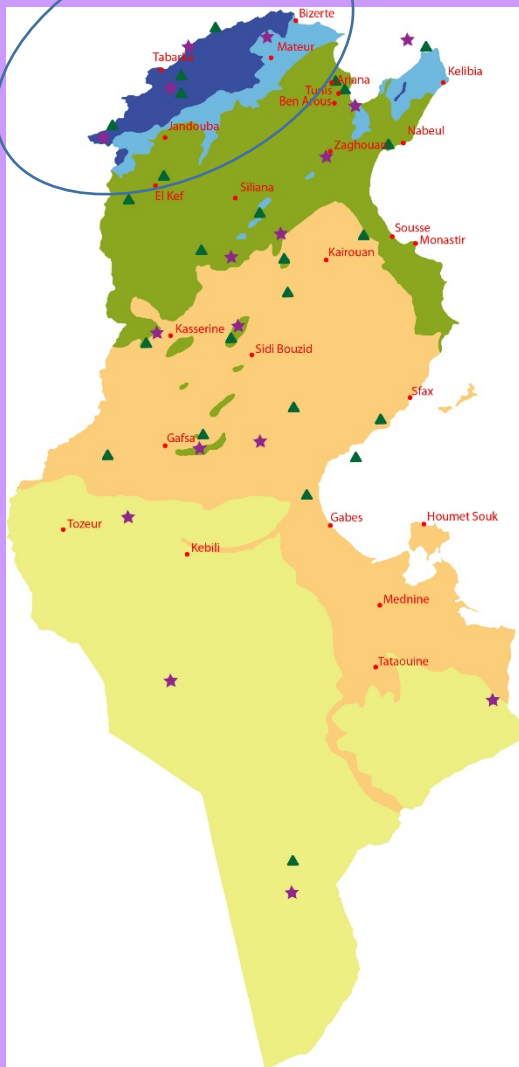
En Afrique du Nord

- Distribution: région frontalière tuniso-algérienne
- Statut de conservation: à faible risque d'extinction (1996); avant 1996: Vulnérable ???
- Annexe III , CITES
- Effectif: Tunisie = 800 (2000 effectif officiel)
Algérie = 500 (???)

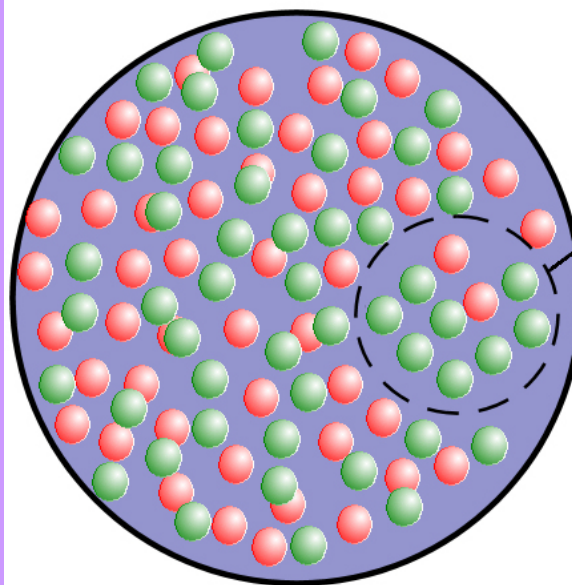


Pitra et al. (2004)

En 1960: 10 cerfs seulement!!!!!!!

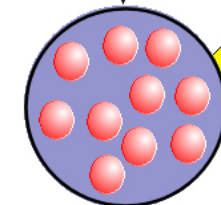
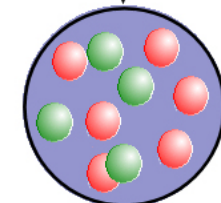
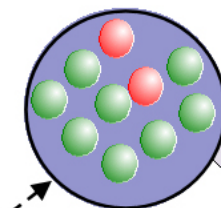


Originating population



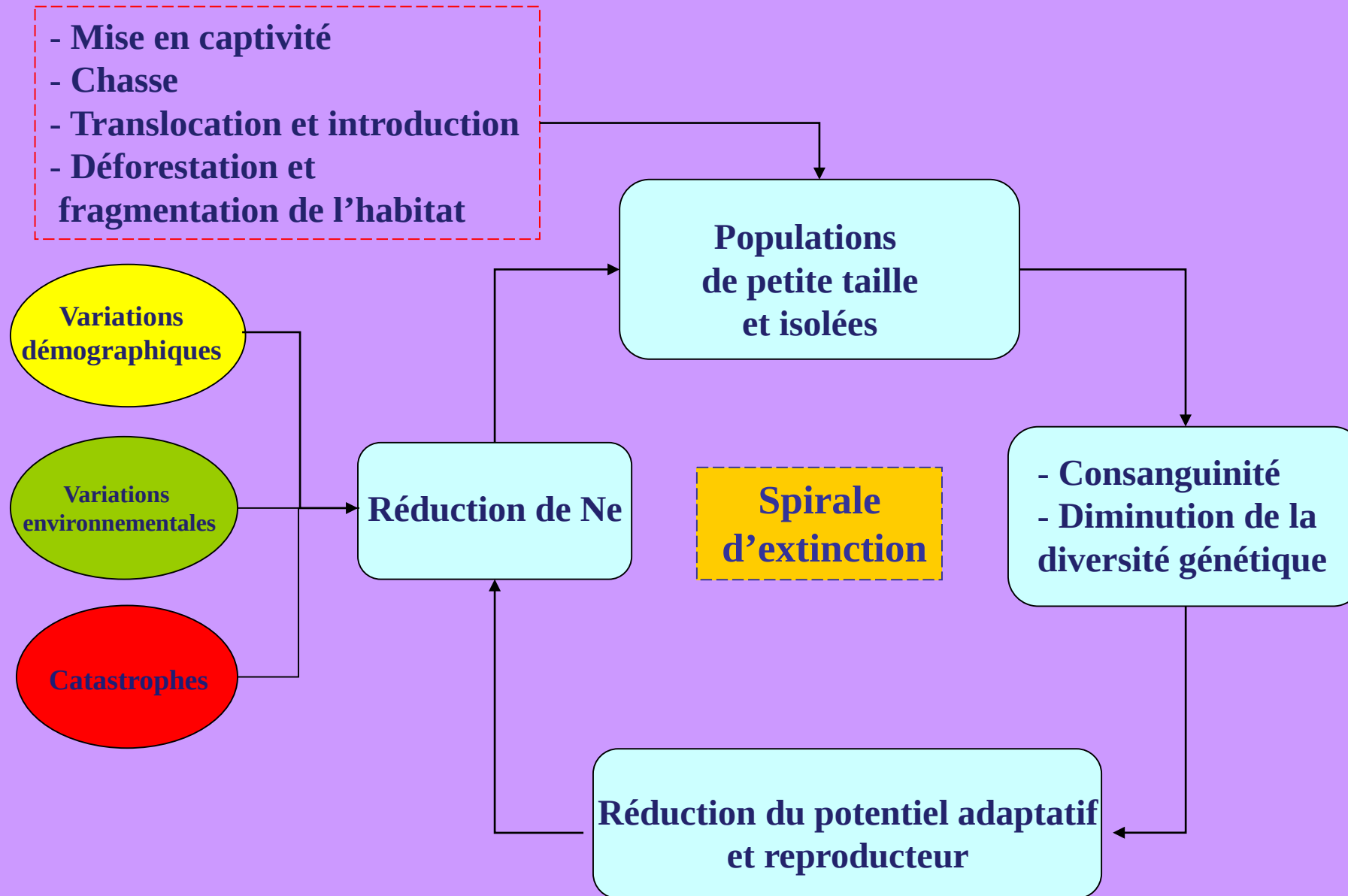
Ancestral population frequencies		
	Red	Green
Original	0.50	0.50

Founder population



Founder population frequencies		
	Red	Green
After split	0.20	0.80
Generation 1	0.40	0.60
Generation 2	0.50	0.50
Generation 3	0.60	0.40
Generation 4	0.90	0.10
Generation 5	1.00	0.00

Les menaces exercées sur les cerfs et leurs conséquences



1- Consanguinité et extinction

- Dépression de la consanguinité: effets délétères de la consanguinité sur la reproduction et la survie.
- Coef. de consanguinité: mesure de l'identité entre des allèles. Si > 0.8 : 80-95% de mortalité. (O. H. Frankel et M. E. Soulé, 1981)

1- Consanguinité et extinction

- Mortalité juvénile supérieure chez des individus consanguins. (K. Ralls et al., 1983)
- 90 % des individus consanguins ont des attributs plus pauvres / individus normaux. (P. Crnokrak et al., 1999)

2-Captivité et succès de la ré-introduction

- Captivité => population de petite taille => consanguinité.
- Si ignorance des facteurs génétiques, échec de la ré-introduction.
- Exemples: - poulets de l'Illinois

(R. L. Westemeier et al., 1998)

- Koalas australiens

(B.A. Houlden et al.,1996 ; A.M. Seymour et al., 2001)

Conséquences

- Consanguinité + ↘ de la diversité génétique => ↗ du risque d'extinction
- La consanguinité est néfaste pour les animaux en captivité et les animaux sauvages.
- Si les facteurs génétiques sont ignorés, une gestion correcte des ressources sera inutile.

Nécessité de conservation

Conservation génétique: étude des facteurs génétiques liés aux risques d'extinction et gestion de ces facteurs.

1- Inventorier et identifier les espèces menacées

2- Définir les unités de gestion

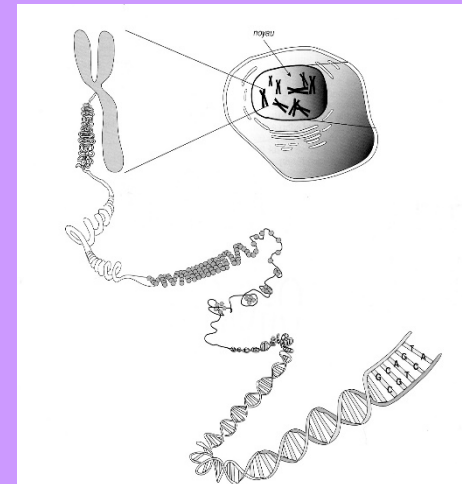
3- Conserver

4- Gérer

5- Connaître et évaluer les ressources génétiques



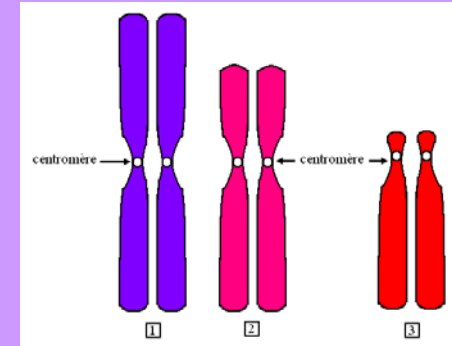
Marqueurs génétiques



Marqueurs génétiques: outils d'analyse en génétique de conservation

1- Polymorphisme chromosomique

- Nombre
- Forme (taille relative, position du centromère...)
- Bandes (quantité et distribution de chromatine)



2- Polymorphisme de l'ADNmt: région de contrôle (D-loop)

- Taux de mutation élevée
- Transmission maternelle
- Existence d'amorces universelles



3- Polymorphisme de l'ADN nucléaire: microsatellites

AGGTCTAGCACACACACACACACACAGGTCTTGAT
AGGTCTAGCACACACACACACACACACACACAGGTCTTGAT

- Nombreux
- Bien réparties dans le génome
- Polymorphe, neutres
- Faciles à isoler
- Détection de leur polymorphisme de façon automatique
- Standardisation des résultats au niveau international

Contexte: stratégie globale de conservation des ressources génétiques

↓ (Étude de génétique des populations)

Analyser :

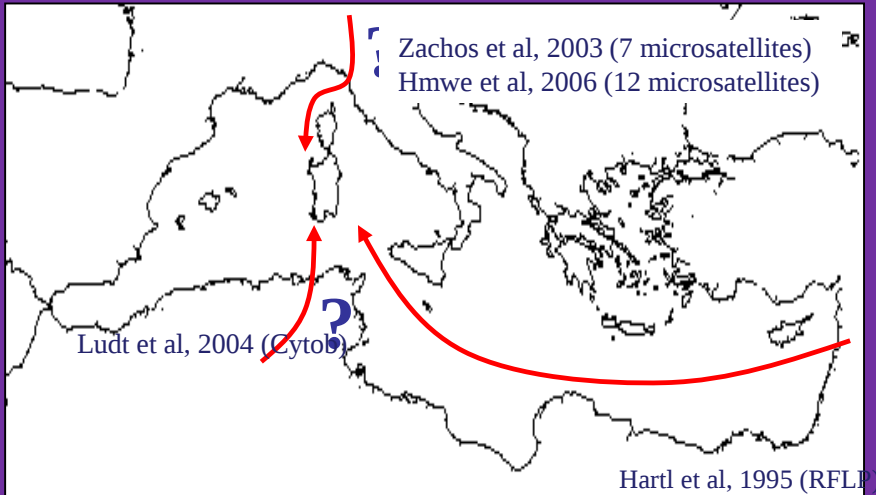
- la diversité génétique
- la structure génétique
- la relation génétique
- les processus d'évolution
- les processus de migration

↓ Populations locales

Optimiser les programmes de conservation
Intégrer les facteurs génétiques dans les programmes de gestion

Résultats de l'étude génétique de la population de cerf de Berbérie (Tunisie)

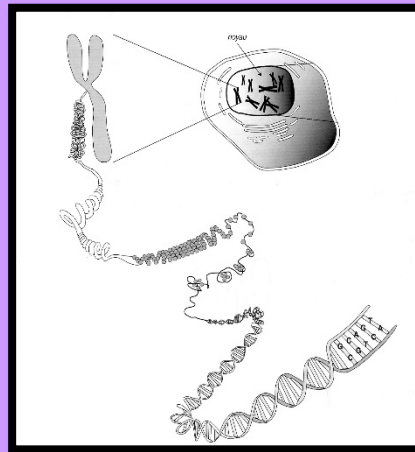
1. Variabilité génétique et mise en évidence d'un goulot d'étranglement dans la population tunisienne
2. Differentiation entre les sous-populations en Tunisia?
3. Origine phylogéographique de *C. e. corsicanus* et *C. e. barbarus*



Colonisation naturelle?
Introduction humaine?

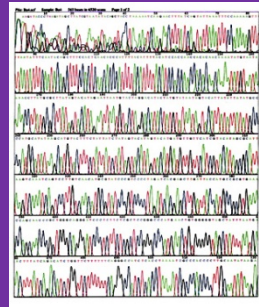
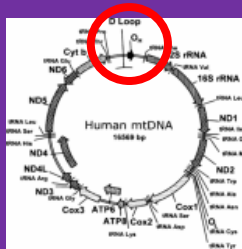


Echantillonnage non-invasif



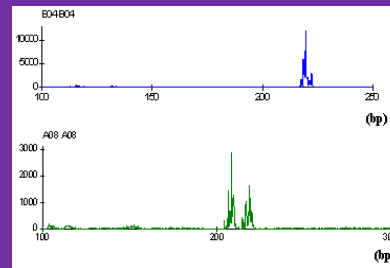
ADN

Marqueur génétique I: mtDNA control region (680 bp)

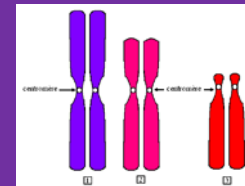
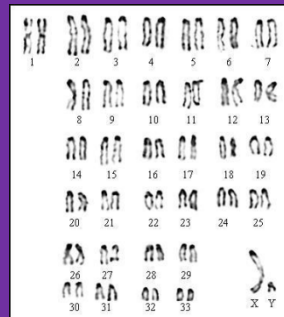
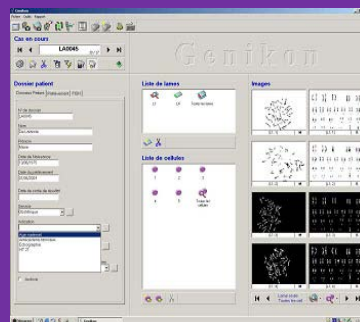


Marqueur génétique II: 13 (n = 19) / 8 (n = 30) microsatellite loci

GTCTAGCACACACACACACACACAGGTCTTGAT
GTCTAGCACACACACACACACACACACAGGTCT



Marqueur génétique III: Chromosomes (nombre, G, C et Nor Banding)



I- Analyse du polymorphisme mitochondrial: D-loop

Séquence : 680 pb pour 18 cerfs

Présence de deux haplotypes (16 transitions)

Diversité Haplotypique (DH) = 0.529

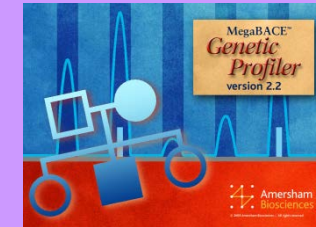
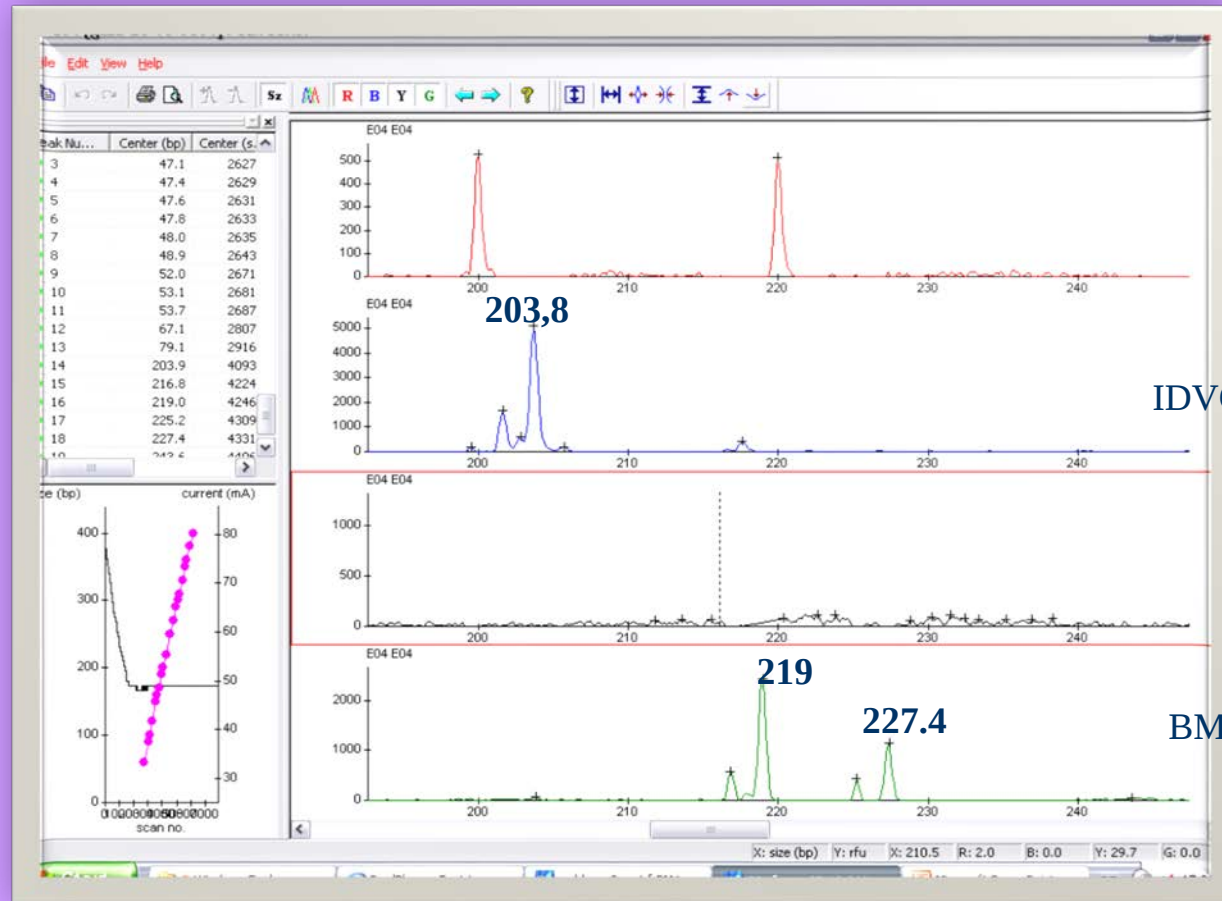
Diversité Nucléotidique (π) = 1.266%

Deux lignées maternelles très éloignées



- Goulot d'étranglement
- Effet fondateur

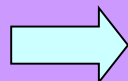
II- Analyse du polymorphisme des microsatellites



IDVGA55

BM203

13 loci/19 individus
8 loci/ 30 individus



335 génotypes

Paramètres de variabilité génétique des cerfs analysés

Locus	N	Ho	Ha	P(p= 0.0038)
INRA 121	9	0.63	0.82	0.0000
IDVGA 55	3	0.42	0.71	0.0874
BMC1009	5	0.68	0.76	0.1300
BM757	4	0.56	0.79	0.0049
BL42	5	0.47	0.80	0.0004
TGLA53	5	0.28	0.66	0.0028
BM203	4	0.21	0.74	0.0000
Oar VH110	4	0.53	0.73	0.0001
INRA11	6	0.47	0.77	0.0014
OarCP26	7	0.47	0.87	0.0000
OarFCB304	11	0.12	0.92	0.0000
BM888	7	0.61	0.83	0.0944
MAF109	6	0.47	0.80	0.0032
Ho=0.46 Ha= 0.78				

Diversité allélique= 5.6

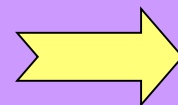
Test de structuration



F_{st} et $R_{st} \cong 0$

Test d'assignement: 36% correct: hasard

- Il s'agit d'une seule population
- Les déviations ne sont pas dues à la structuration de la population



Consanguinité élevée

Goulot d'étranglement

Le test «bottleneck » est significatif ($p=0.00018$)

- Le goulot d'étranglement a affecté la diversité haplotypique
- La variabilité génétique (marqueurs microsatellites) a été relativement moins affectée

Populations	H_O	H_E	DH	π [%]
Tunisie	0.46	0.78	0.529	1.266
Sardaigne	0.48	0.66	0.872	0.473
Mesola	0.51	0.62	0	0

- Les cerfs en Tunisie constituent une seule population homogène fragmentée en petites unités sans subir de différenciation

Action des facteurs anthropiques, écologiques et économiques

Fragmentation de l'habitat

Réduction de l'effectif efficace

Augmentation de la consanguinité

- Effet évident d'un goulot d'étranglement
- Faible variabilité génétique (pas très faible?): **migration des cerfs d'Algérie?**

Avant 1996: cerf de berbérie était classé comme une sous-espèce Vulnérable

A partir de 1996: Faible risque d'extinction: Low Risk/Near Threatened (1996)

Actions à court terme:

- **Restaurer la diversité génétique**
- **Diminuer la consanguinité**
- ✓ **Génotyper tous les cerfs vivant en captivité et les marquer**
- ✓ **Avoir au moins deux pools génétiques de cerfs**
- ✓ **Instaurer un programme d'échanges entre les différents pools**

Choix des cerfs

Nombre d'individus

Fréquence d'échanges

Perspectives

Analyser d'autres populations de cerf élaphe avec le même type de marqueurs moléculaire (microsatellites)

❑ Population algérienne: assurer la viabilité du cerf à une plus grande échelle

❑ Populations européennes: mieux comprendre la structuration de l'ensemble des populations européennes et établir une carte de répartition d'allèles microsatellites

Analyse de Viabilité des Populations

L'**analyse de viabilité des populations (AVP)** est une méthode d'évaluation des risques pour les espèces fréquemment utilisée en biologie de la conservation. Elle est traditionnellement définie comme le processus qui détermine la probabilité qu'une population s'éteigne dans un nombre d'années donné. Plus récemment, l'AVP a été décrit comme une union de l'écologie et des statistiques qui rassemble les caractéristiques des espèces et la variabilité de l'environnement afin de prévoir la santé de la population et son risque d'extinction. Chaque AVP est spécialement conçue pour une population cible ou une espèce, et par conséquent chaque AVP est unique. Le plus grand objectif de cette méthode est de s'assurer qu'une population donnée est viable sur le long terme¹.

Vortex 10

A stochastic simulation of the extinction process

Version 10.1.2.1



[Begin a New Project](#)

Open a Project: [Existing](#) | [Recent](#)

[Quit](#)

Vortex 10 - New Project - C:\Vortex10Projects\New Project\New Project.xml

File Simulation Help

Project Settings Simulation Input Text Output Project Report

Project Name:

Project Notes and Users

Special Options

- ☐ Do not show graphs during iterations
- ☐ Do not show messages during run
- ☐ Do not include last population in metapopulation tally
- ☐ Produce a file with the census for the first iterations
- ☐ Produce a file of all living animals at the end of the first iterations
- ☐ Produce a file of all animals created in each of the first iterations
- ☐ Produce a file with Gene Diversity by year and iteration
- ☐ Produce files with the first GSvars by year and iteration
- ☐ Produce files with the first PSvars by year and iteration
- ☐ Delay 1st year mortality until all annual mortality is done (rather than in Breed)
- ☐ Use "Harvest" to set to 0 ISvar:
- ☐ Prioritize breeding based on ISvar: (use negative for dynamic)
- ☐ Include extinct and extant runs in Genetic summary statistics
- ☐ Include extinct and extant runs in GSvar and PSvar summary statistics
- ☐ Sample EV from Beta distributions

☐ Use undocumented options:

Vortex 10 - Project name_ - C:\Vortex10Projects\New Project\New Project.xml

File Simulation **Pop**

Project Settings Simulation Input Text Output Project Report

Scenarios: Add Delete Reorder << >> Current: Basic - Test Basic - Test

Scenario Settings

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

Carrying Capacity

Harvest

Supplementation

Genetics

Copy input values from North this section to subsequent populations Copy

Scenario name Basic - Test **Am Ende: 1000**

Number of iterations 100

Number of years (timesteps) 100

Duration of each year in days 365

☐ Run as population-based model

Extinction definition ☐ Only 1 sex remains ☒ Total N < critical size 50

Number of populations 2 Reorder Populations (use with caution!)

	Population 1	Population 2
Name	North	South

Order of events in a Vortex year

EV
Breed
Mortality
Age
Disperse
Harvest
Supplement
rCalc
Ktruncation
UpdateVars
Census

Changing the sequence of events in the simulated year can have complex implications for your model. It is recommended that you become familiar with the standard Vortex model before you try changing the sequence.

Vortex 10 - Project name_ - C:\Vortex10Projects\New Project\New Project.xml

File Simulation Help

Project Settings Simulation Input Text Output Project Report

Scenarios: Add Delete Reorder << >> Current: Basic - Test Basic - Test

Scenario Settings

- Species Description
- State Variables
- Dispersal
- Reproductive System
- Reproductive Rates
- Mortality Rates
- Catastrophes
- Mate Monopolization
- Initial Population Size
- Carrying Capacity
- Harvest
- Supplementation
- Genetics

Species Description

☒ Inbreeding depression

Lethal equivalents 6,29

Percent due to recessive lethal alleles 50

Default value of 6.29 for Lethal Equivalents is the combined fecundity and first year survival reported by O'Grady et al. (2006, p. 42-51). Note that inbreeding can also affect later survival and other aspects of demography. To model effects on other demographic rates, enter rates as functions of inbreeding.

EV correlation between reproduction and survival 0,5

EV correlation among populations 0,5

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this section

to subsequent populations

Copy

levels of inbreeding depression (see page 23 ff.)
low: 0-3
medium 3-8
high 8-30

correlation of factors (see page 28 ff.)
no correlation: 0
total correlation: 1

File Simulation Help

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Project Settings Simulation Input Text Output Project Report

Scenarios: Add Delete Reorder << >> Current: Basic - Test

Basic - Test

Scenario Settings

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North

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to subsequent populations

Copy

State Variables

Global State Variables

Add

Delete

Variable	Label	Initialization function	Transition function
----------	-------	-------------------------	---------------------

Population State Variables

Add

Delete

which population you want to set functions:

North

Variable	Label	Initialization function	Transition function
----------	-------	-------------------------	---------------------

Individual State Variables

Add

Delete

Add Outbreak Vars

Add Spatial Vars

Variable	Label	Initialization function	Birth function	Transition function
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advanced users

Scenario Settings

Species Description

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Dispersal

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Dispersal Among Populations

Dispersing classes

Age range: Youngest

2

Oldest

10

Dispersing sex(es):



Males



Females

% Survival of dispersers

50

Dispersal modifier function (optional) *

☐ Don't allow dispersal into saturated populations☐ Use Dispersal to move a fixed number of individuals, rather than a percent

Import Rate Matrix

Apply multiplier of

2.0

Export Rate Matrix

Fill matrix with

1.0

* to „activate” dispersal if (and only if) K is reached (habitat saturation) use the following formula: $D \cdot (N \geq K)$.

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North

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to subsequent populations

Copy

Enter percents of individuals in each age-sex class that disperse between each pair of populations each year; Row = Source; Column = Recipient population

	North	South
North	90	10
South	33	67

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Reproductive System

☐ Monogamous ☒ Polygynous ☐ Hemaphroditic ☐ Long-term monogamy ☐ Long-term polygyny

(Note that "long-term" pairs can be separated under conditions entered in the Genetics input section.)

Age of first offspring females

2

Maximum age of female reproduction

10

Age of first offspring males

2

Maximum age of male reproduction

10

Maximum lifespan

10

Maximum number of broods per year

1

Maximum number of progeny per brood

2

Sex ratio at birth -- in % males

50

maximale Anzahl der Würfe pro Jahr
maximale Anzahl der Individuen in jedem Wurf

	North	South
Density dependent reproduction		☐
% Breeding at low density, P(0)	50	50
% Breeding at carrying capacity, P(K)	25	25
Allee parameter, A	1	1
Steepness parameter, L	2	2

advanced users

Section Notes

string

Scenario Settings

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Reproductive Rates

	North	South
% adult females breeding	80	80
SD in % breeding due to EV	8	8

Distribution of broods per year (enter as percents; last row filled automatically)

	North	South
0 Broods	10	10
1 Broods	90	90

Specify the distribution of number of offspring per female per brood

☒ Use normal distribution☐ Specify exact distribution (enter as perc

	North	South
Mean	1	1
Standard Dev	1	1

see Reproductive System:
maximum number of progeny per brood

North	South
0	
100	

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Mortality Rates

Mortality of females as %

	North	South
Mortality from age 0 to 1	50	50
SD in 0 to 1 mortality due to EV	10	10
Mortality from age 1 to 2	10	10
SD in 1 to 2 mortality due to EV	3	3
Annual mortality after age 2	10	10
SD in mortality after age 2	3	3

Mortality of males as %

Copy values from females

	North	South
Mortality from age 0 to 1	50	50
SD in 0 to 1 mortality due to EV	10	10
Mortality from age 1 to 2	10	10
SD in 1 to 2 mortality due to EV	3	3
Annual mortality after age 2	10	10
SD in mortality after age 2	3	3

Scenario Settings

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Catastrophes

Number of types of catastrophes

2

Select for which catastrophe you want to set rates:

Winter

Catastrophe Label Winter

Frequency and extent of occurrence

	North	South
Local	☐	☐
Frequency %	10	10

Severity (proportion of normal values)

	North	South
Reproduction	0.3	0.3
Survival	0.7	0.7

frequency

1: once every 100 years
5: once every 20 years
10: once every 10 years
50: once every 2 years
100: every year

0: total loss
1: no effect

The frequency and severity of catastrophes can be difficult to estimate. The review by Reed et al. (2003. The frequency and severity of catastrophic die-offs in vertebrates. *Animal Conservation* 6:109-114) indicates that severe die-offs (50% or greater decrease in population size) of vertebrate populations occur at a frequency of approximately 14% per generation.

Scenario Settings

Species Description

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Dispersal

Reproductive System

Reproductive Rates

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Genetics

Mate Monopolization

Degree of monopolization of breeding opportunities

	North	South
% Males in breeding pool	70	70

Calculate from % males siring offspring

Calculate from # mates / successful sire

The percent of adult males in the pool of potential breeders can be entered directly, or you can use the buttons below the table to have Vortex calculate it for you from either the % of males that successfully sire offspring (which will generally be greater than the percent in the breeding pool, because some are unlucky) or from the average number of females with which successful males are mated. Vortex makes these calculations based on the assumption that mating success by males is distributed according to a Poisson distribution.

Copy input values from

North

this section

to subsequent populations

Copy

Scenario Settings

Species Description

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Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

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Initial Population Size

Note: Stable age distribution may not be meaningful if some demographic rates are functions of other parameters. Also, initial population can be replaced by studbook population imported from a file.

To determine distribution:

☒ Use stable age distribution ☐ Use specified age distribution ☐ Enter proportional values for age distribution

	North	South
Initial Population Size	200	300

Female age distribution

	North	South
Age 1	15	26
Age 2	13	22
Age 3	12	20
Age 4	11	17
Age 5	10	15
Age 6	9	13
Age 7	9	11
Age 8	8	10
Age 9	7	9
Age 10	6	7

Male age distribution

	North	South
Age 1	15	
Age 2	13	
Age 3	12	
Age 4	11	
Age 5	10	
Age 6	9	
Age 7	9	
Age 8	8	
Age 9	7	
Age 10	6	

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

Carrying Capacity

Harvest

Supplementation

Genetics

Carrying Capacity

	North	South
Carrying Capacity (K)	500	600
SD in K due to EV	50	60

check that $K > N$

EV in K can be a tricky concept, because K is usually defined as the population size that can be sustained in the habitat over the long term. You can use it to impose fluctuations in habitat quality or extent, but be careful not to double-count EV that is affecting mortality.

	North	South
Future change in K?	☒	☐
Over how many years?	50	
% Annual increase or decrease	-1	

decrease is linear
calculate area!

Copy input values from

North

this section

to subsequent populations

Copy

☐ Implement K based on a limit on some population variable other than N

Population variable to be tested against K

=N

☐ During K truncation, remove only individuals meeting criteria:

1

☐ Prioritize K truncation based on ISvar:

0

(use negative for dynamic; 0 for none)

Caution: If you define K as a limit on something other than N, that will have implications for any functions which use K.

Caution: Prioritized K truncation can be very slow, especially if dynamic.

Scenario Settings

Species Description

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Reproductive Rates

Mortality Rates

Catastrophes

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Supplementation

Genetics

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Harvest

☐ Implement as Translocation?

Percent survival during Translocation

100

	North	South
Population harvested?	☒	☐
First year of harvest	1	0
Last year of harvest	100	0
Interval between harvests	1	0
Optional criteria for harvest	0	1
Optional criteria for individuals	0	1

Specify the years and condi

Number of females of each age to be harvested

	North	South
Harvest from age 1 to 2	20	0
Harvest from after age 2	30	0

Number of males of each age to be harvested

	North	South
Harvest from age 1 to 2	10	0
Harvest from after age 2	20	0

Scenarios: Add Delete Reorder << >> Current: Basic - Test

Basic - Test

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

Carrying Capacity

Harvest

Supplementation

Genetics

Supplementation

☐ Implement as Translocation? if: 1

Percent survival during Translocation 100

Optional criteria for individuals to be released

	North	South
Population supplemented?	☒	☐
First year of supplement	1	0
Last year of supplement	50	0
Interval between supplements	5	0
Optional criteria for supplements	1	1

Specify

Number of females of each age to be supplemented

	North	South
Supplement from age 1 to 2	2	0
Supplement from after age 2	4	0

Copy input values from

North

this section

to subsequent populations

Copy

Number of males of each age to be supplemented

	North	South
Supplement from age 1 to 2	2	0
Supplement from after age 2	4	0

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

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Harvest

Supplementation

Genetic

Copy input values from

North

this section

to subsequent populations

Copy

Genetics

Genetic Input

☐ Read initial population(s) from studbook file: ☐ Append studbook to initial population, rather than replacing initial NNumber of neutral loci to be modeled Loci included in summary statistics: ☒ Locus 1 only ☐ All loci only ☐ All lociNumber of loci to be subject to mutation with ☐ Read initial allele frequencies from file:

Genetic Management

Select a population to manage: North

Apply to All Populations

(Optional) Criteria for Genetic Management of population ☐ Breed to maintain the population at K☐ Pair according to mean kinships☐ Use a dynamic MK list ☒ Use a static MK list

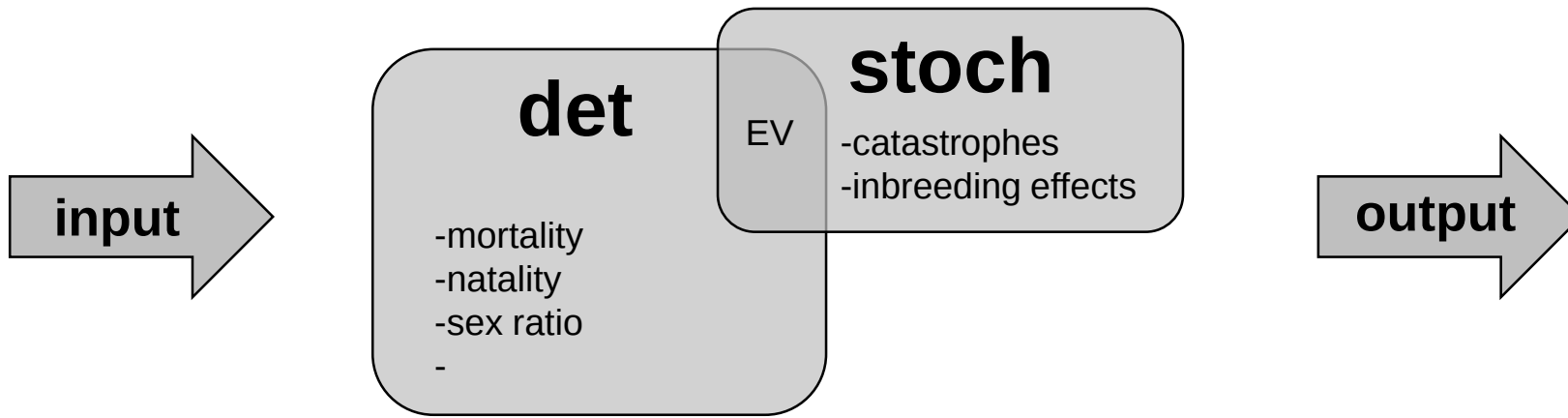
The following options can model either management by humans, or natural breeding constraints:

☐ Prevent matings with kinships (inbreeding) greater than Start population with all inbreeding and kinships set to: Maximum number of female mates (blank or 0 for no limit) (Optional) Criteria for acceptable mates Number of times to try to find a mate (Optional) Criteria for separating a long-term pair

Genetic Output

☐ Produce a file in GenePop format at the end of each iteration☐ Produce a file of allele frequencies and probabilities of persistence

advanced users



Vortex 10 - Project name_ - C:\Vortex10Projects\New Project\New Project.xml

File Simulation Help

Det. ST

Project Settings Simulation Input Text Output Project Report

Scenarios: Add Delete Reorder << >> Current: Basic - Test Basic - Test

Scenario Settings

- Species Description
- State Variables
- Dispersal
- Reproductive System
- Reproductive Rates
- Mortality Rates
- Catastrophes
- Mate Monopolization
- Initial Population Size
- Carrying Capacity
- Harvest
- Supplementation

Deterministic Rates

Deterministic rates for current values in scenario: Basic - Test

	North	South
r	-0,0454	0,0031
lambda	0,9556	1,0031
R0	0,7874	1,0161
Female Generation Time	5,26	5,10
Male Generation Time	5,26	5,10
Mean Generation Time	5,26	5,10

see page 132
The Dynamics of Small Populations

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

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Harvest

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Genetics

Copy input values from

North

this section

to subsequent populations

Copy

Scenario Settings

Scenario name Basic - Test

Number of iterations 100

Number of years (timesteps) 100

Duration of each year in days 365

☐ Run as population-based model

Extinction definition

☐ Only 1 sex remains☒ Total N < critical size

50

Number of populations 2

Reorder Popu

	Population 1	Population 2
Name	North	South

Order of events in a Vortex year

EV
Breed
Mortality
Age
Disperse
Harvest
Supplement
rCalc
Ktruncation
UpdateVars
Census

Add

Delete

Up

Down

Changing the sequence
have complex implicatio
that you become familia
before you try changing the sequence.

Section Notes

Choose

Select a scenario to use as a base:

Basic - Test

Cancel

OK

Scenarios: Add Delete Reorder << >> Current: Basic - Test

Basic - Test

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

Carrying Capacity

Harvest

Supplementation

Genetics

Copy input values from

North

this section

to subsequent populations

Copy

Scenario Settings

Scenario name Basic - Test

Number of iterations 100

Number of years (timesteps) 100

Duration of each year in days 365

☐ Run as population-based modelExtinction definition ☐ Only 1 sex remains☒ Total N < critical size 50

Number of populations 2

Reorder

	Population 1	Population 2
Name	North	South

Order of events in a Vortex year

EV
Breed
Mortality
Age
Disperse
Harvest
Supplement
rCalc
Truncation
UpdateVars
Census

Add

Delete

Up

Down

Section Notes

Number of Copies

How many copies of Basic - Test would you like to make?

3

Cancel

OK

Changing the sequence of events in the simulated year can have complex implications for your model. It is recommended that you become familiar with the standard Vortex model before you try changing the sequence.

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

Carrying Capacity

Harvest

Supplementation

Genetics

Copy input values from

North

this section

to subsequent populations

Copy

Scenario Settings

Scenario name

Low inbreeding

Number of iterations

100

Number of years (timesteps)

100

Duration of each year in days

365

☐ Run as population-based model

Extinction definition

☐ Only 1 sex remains☒ Total N < critical size

50

Number of populations

2

Reorder Populations (use with caution!)

	Population 1	Population 2
Name	North	South

Order of events in a Vortex year

EV
Breed
Mortality
Age
Disperse
Harvest
Supplement
rCalc
Ktruncation
UpdateVars
Census

Add

Delete

Up

Down

Section Notes

Changing the sequence of events in the simulated year can have complex implications for your model. It is recommended that you become familiar with the standard Vortex model before you try changing the sequence.

Vortex 10 - Project name_ - C:\Vortex10Projects\New Project\New Project.xml

File Simulation Help

ST

Project

Scenario: Low inbreeding Basic - Test Low inbreeding Basic - Test-Copy2 Basic - Test-Copy3

first save, then run

Scenario Settings

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

Carrying Capacity

Harvest

Supplementation

Genetics

Copy input values from
North
this section
to subsequent populations
Copy

Scenario name: Low inbreeding

Number of iterations: 100

Number of years (timesteps): 100

Duration of each year in days: 365

☐ Run as population-based model

Extinction definition:
☐ Only 1 sex remains
☒ Total N < critical size 50

Number of populations: 2
Reorder Populations (use with caution!)

	Population 1	Population 2
Name	North	South

Order of events in a Vortex year

EV
Breed
Mortality
Age
Disperse
Harvest
Supplement
rCalc
Ktruncation
UpdateVars
Census

Add Delete Up Down

Changing the sequence of events in the simulated year can have complex implications for your model. It is recommended that you become familiar with the standard Vortex model before you try changing the sequence.

Section Notes

Scenario Settings

Species Description

State Variables

Dispersal

Reproductive System

Reproductive Rates

Mortality Rates

Catastrophes

Mate Monopolization

Initial Population Size

Carrying Capacity

Harvest

Supplementation

Genetics

Copy input values from

North

this section

to subsequent populations

Copy

Scen

Scenario n

Number of

Number of

Duration of

☐ Run as

Extinction

Number of

Name

Order of e

EV

Breed

Mortality

Age

Disperse

Harvest

Supplem

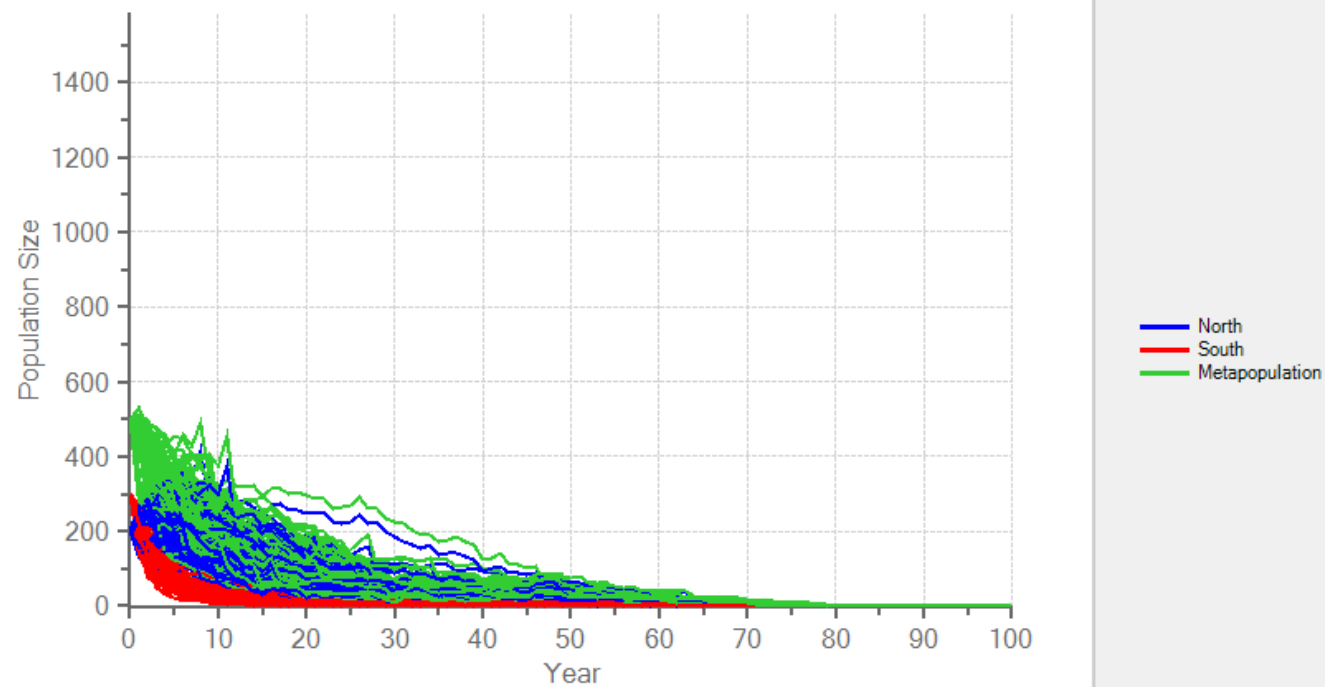
rCalc

Ktruncati

UpdateV

Census

Basic - Test-Copy3

Results: $r = -0,076$; $SD(r) = 0,149$; Pr.Extinction = 1,00; N = 0; GeneDiv = 0

Print Graph

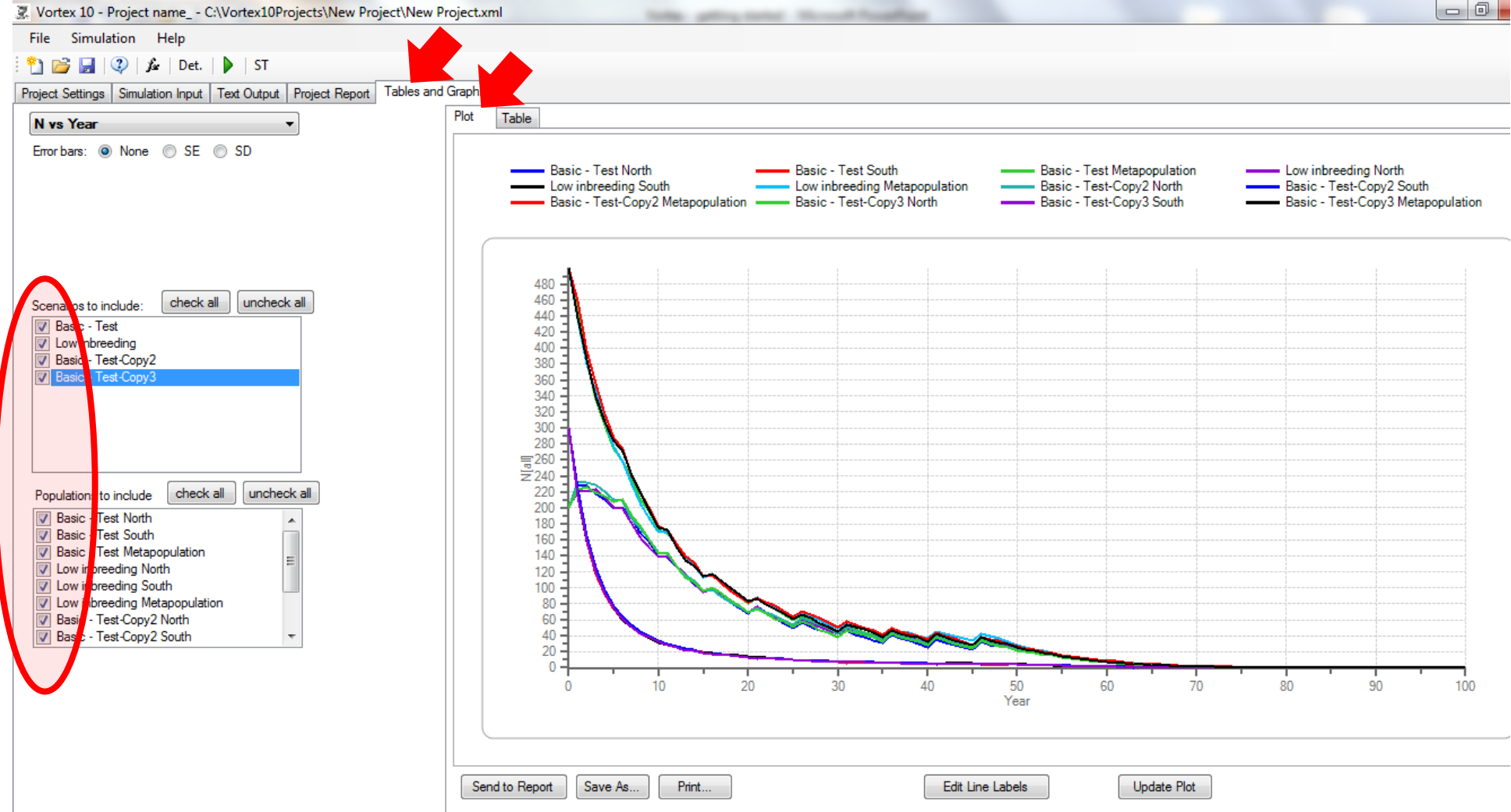
Save Graph

Add

Delete

Up

Down



Vortex 10 - Project name_ - C:\Vortex10Projects\New Project\New Project.xml

File Simulation Help

Project Settings Simulation Input Text Output Project Report **Tables and Graphs**

N vs Year

Error bars: ☒ None ☐ SE ☐ SD

Scenarios to include:

- ☒ Basic - Test
- ☒ Low inbreeding
- ☒ Basic - Test-Copy2
- ☒ Basic - Test-Copy3

Populations to include:

- ☒ Basic - Test North
- ☒ Basic - Test South
- ☒ Basic - Test Metapopulation
- ☒ Low inbreeding North
- ☒ Low inbreeding South
- ☒ Low inbreeding Metapopulation
- ☒ Basic - Test-Copy2 North
- ☒ Basic - Test-Copy2 South

Plot Table

	Year																
Populations	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Basic - Test North	200	227.98	227.79	217.76	210.69	199.46	198.46	187.66	168.29	157.38	139.54	138.8	127.46	115.46	105.12	94.7	99.4
Basic - Test South	300	217.91	157.64	117.73	92.33	74.01	60.2	50.3	42.38	37.7	33.31	29.77	26.16	23.45	21.36	19.26	17.6
Basic - Test Metapopulation	500	445.89	385.43	335.49	303.02	273.47	258.66	237.96	210.67	195.08	172.85	168.57	153.62	138.91	126.48	113.96	117
Low inbreeding North	200	220.85	220.84	223.87	213.4	201.16	199	180.31	162.09	149.86	137.84	140.47	127.12	116.64	105.81	93.97	98.83
Low inbreeding South	300	215.24	158.43	121.93	95.65	75.02	59.98	50.62	43.16	36.09	31.27	28.56	26.33	22.95	21.24	18.78	17.79
Low inbreeding Metapopulation	500	436.09	379.27	345.8	309.05	276.18	258.98	230.93	205.25	185.95	169.11	169.03	153.45	139.59	127.05	112.75	116.62
Basic - Test-Copy2 North	200	233.69	231.64	229.1	220.82	210.98	209.15	185.86	173.92	159.65	143.47	142.26	127.67	116.17	109.17	95.44	98.08
Basic - Test-Copy2 South	300	225.02	165.31	126.41	97.21	77.63	64.22	53.59	45.41	39.07	33.75	29.36	27.08	24.08	22.05	18.84	17.46
Basic - Test-Copy2 Metapopulation	500	458.71	396.95	355.51	318.03	288.61	273.37	239.45	219.33	198.72	177.22	171.62	154.75	140.25	131.22	114.28	115.54
Basic - Test-Copy3 North	200	223.79	226.23	218.94	214.1	208.01	210.33	190.46	176.16	159.17	142.5	143.79	126.89	112.91	107.17	95.92	100.66
Basic - Test-Copy3 South	300	214.34	159.24	120.33	93.28	75.35	61.41	50.97	42.95	37.63	32.18	28.03	24.83	21.85	20.58	18.42	16.73
Basic - Test-Copy3 Metapopulation	500	438.13	385.47	339.27	307.38	283.36	271.74	241.43	219.11	196.8	174.68	171.82	151.72	134.76	127.75	114.34	117.39

Send to Report Save As... Print... Update Table

Material & Method

Species Description

Parameter	Values	Comments	Source
Inbreeding (Lethal Equivalents)	6,29/ 50%		

Dispersal

Parameter	Values	Comments	Source
Youngest / Oldest			
Males / Females			
% survival of dispersers			

Reproductive System

Parameter	Values	Comments	Source
Monogamous, Polygonous, etc			
Females first offspring last year			
Males first offspring last year			
Maximum lifespan			
Broods per year			
Progeny per brood			
Sex ratio at birth			
Density dependence?			

Reproductive Rates

Parameter	Values	Comments	Source
% females breeding			
0 broods, 1 brood, etc			

Mortality Rates

Parameter	Values	Comments	Source
Females Mortality age class 1 age class 2			

...			
Males Mortality age class 1 age class 2			
...			

Catastrophes

Parameter	Values	Comments	Source
Number of catastrophes			
Local/global			
Severity to reproduction to survival	0=total loss 1=no effect		

Mate Monopolization

Parameter	Values	Comments	Source
% males in breeding pool			

Initial Population Size

Parameter	Values	Comments	Source

Carrying Capacity

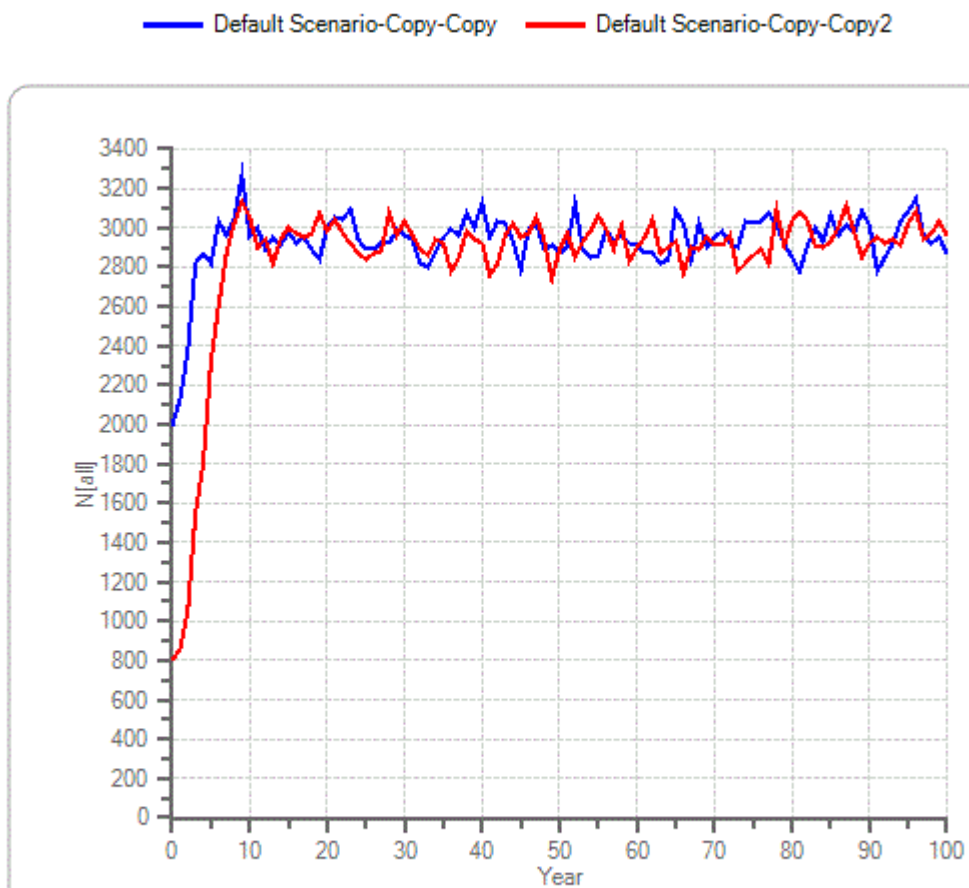
Parameter	Values	Comments	Source

Harvest, Supplementation

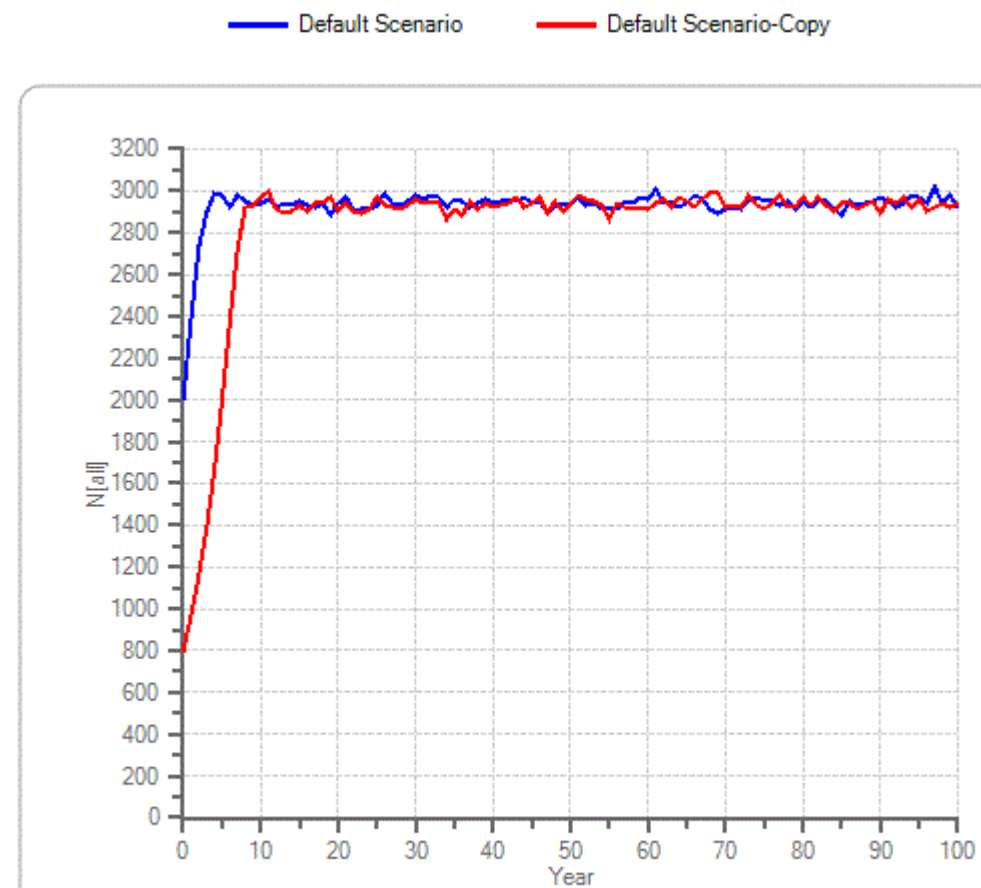
Analyse de Viabilité de la population de cerf de Berbérie en Tunisie

Paramètres	Valeurs	Comments	Source
Système de reproduction	polygenique		
Âge 1ere reproduction-femelle	3 ans		
Âge max de reproduction-femelle	15 ans		
Âge 1ere reproduction mâle	8 ans		
Âge max de reproduction	14 ans		
Longévité	18/mâles-19/femelles		
Nombre max de portée/an	1		
Nombre max de / portée	1		
Sex ratio/naissance	50		
% de reproduction	70%		
% femelles reproductrices			
Distribution de portée/ an			
Taux de mortalité/femelles/mâles			
0-1 an			
1-2ans			
Après 3 ans			
Effectif de la population	800/2000		
Capacité de charge	3000		
catastrophes	2/3	Incendie / braconnage/maladie	

Scénario avec catastrophe: maladie -30%

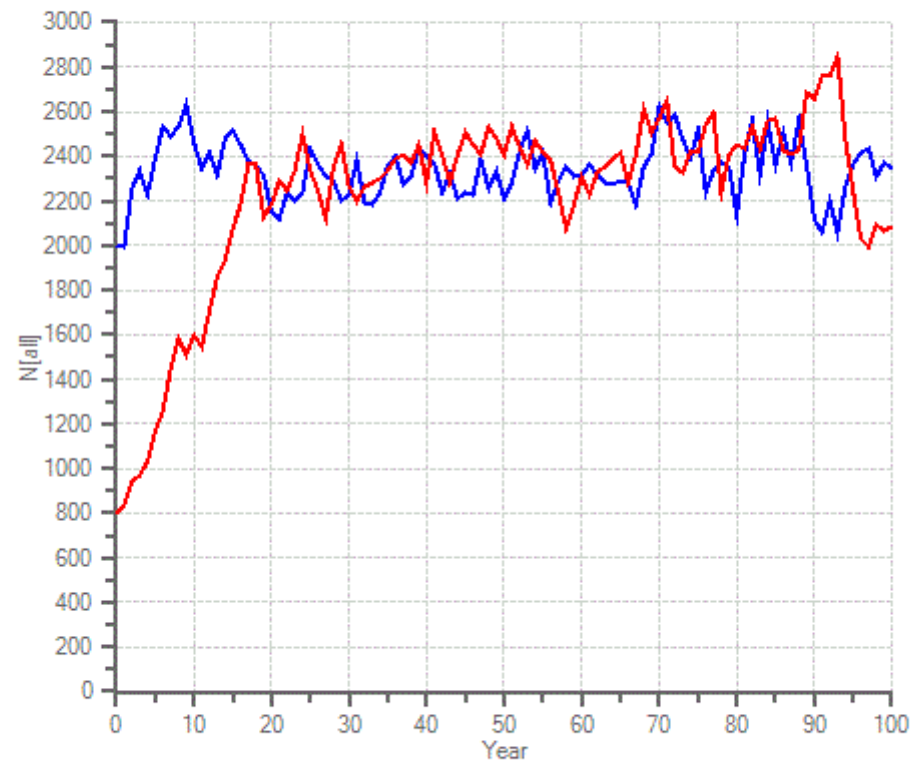


Scénario sans catastrophes



Deux catastrophes 30%

— Default Scenario-Copy2-Copy2-Copy — Default Scenario-Copy2-Copy2-Copy-Copy



2catas10%

— Default Scenario-Copy2-Copy2 — Default Scenario-Copy2-Copy2-Copy

