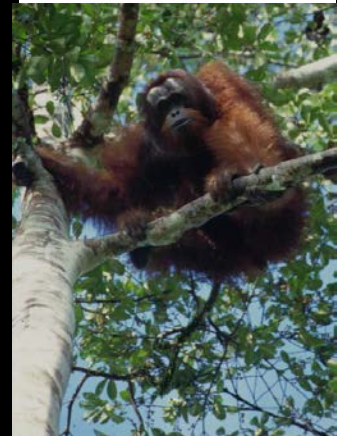




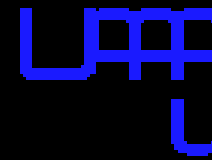
Very spatial indeed: trying to take (spatial) structure into account in population genetics inference



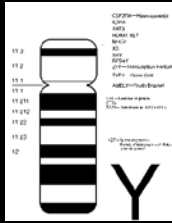
Laboratoire Evolution et Diversité Biologique, CNRS, Toulouse

Population and Conservation Genetics Group, IGC, Portugal

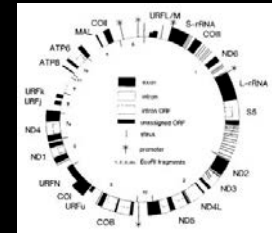
Toulouse INRA 2013 – 11 Mars 2013



POPULATION AND CONSERVATION GENETICS

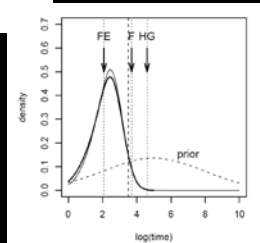


POPULATION GENETIC DATA
Y chromosome **mitochondrial DNA**
---CAGTCAGTCAGT---



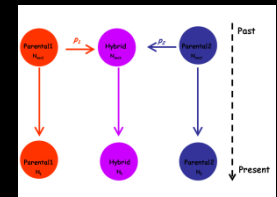
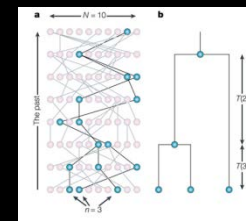
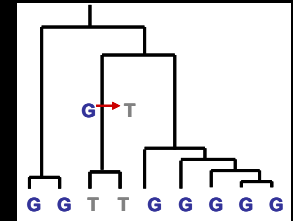
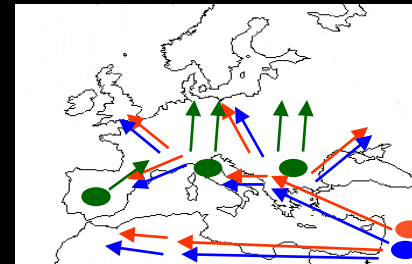
CONSERVATION GENETICS

- Habitat Fragmentation
- Population Decline
- Admixture in Domesticates



HUMAN PAST DEMOGRAPHY

- Neolithic Transition
- Admixture in Human Populations



NEW METHODS / SOFTWARE

OUTLINE

- A little reminder on population genetic diversity, bottlenecks (with some simulation results)
- Habitat loss and fragmentation in Madagascar
- Deforestation in Madagascar: humans or climate, who shaped the gene pool of the golden-crowned sifaka?



Master Students 2008-2009

Aubin Besolo

Density estimates



Emmanuel Rasolondraibe

Habitat and diet characterization





Students 2010

Mohamed Thani Ibouroi
morphological variation and density
estimates in mouse lemurs

Sam Viana
Optimus Alive! Grant 2010

Heriniaina Rakotoarisoa
Density estimates in crowned sifaka
(*Propithecus coronatus*)



**Volonteer 2010 /Field assistant 2011-2012:
Fabien Jan**





Students 2011-2012

Tantely RALANTOHARIJAONA
morphological variation and density
estimates in sportive lemurs

Célia Kun Rodrigues
Optimus Alive! Grant 2011-2012

Marion Carreira
Volunteer 2011-2012



PhD candidate: Jordi Salmona 2010-2014

**Said Ali Ousseni Durham
Masters student 2011-2012**



Some of the studies we develop in Madagascar

3 species of sifaka (genus *Propithecus*)

- *Propithecus tattersalli*
- *P. coquereli*
- *P. coronatus*



Density estimation

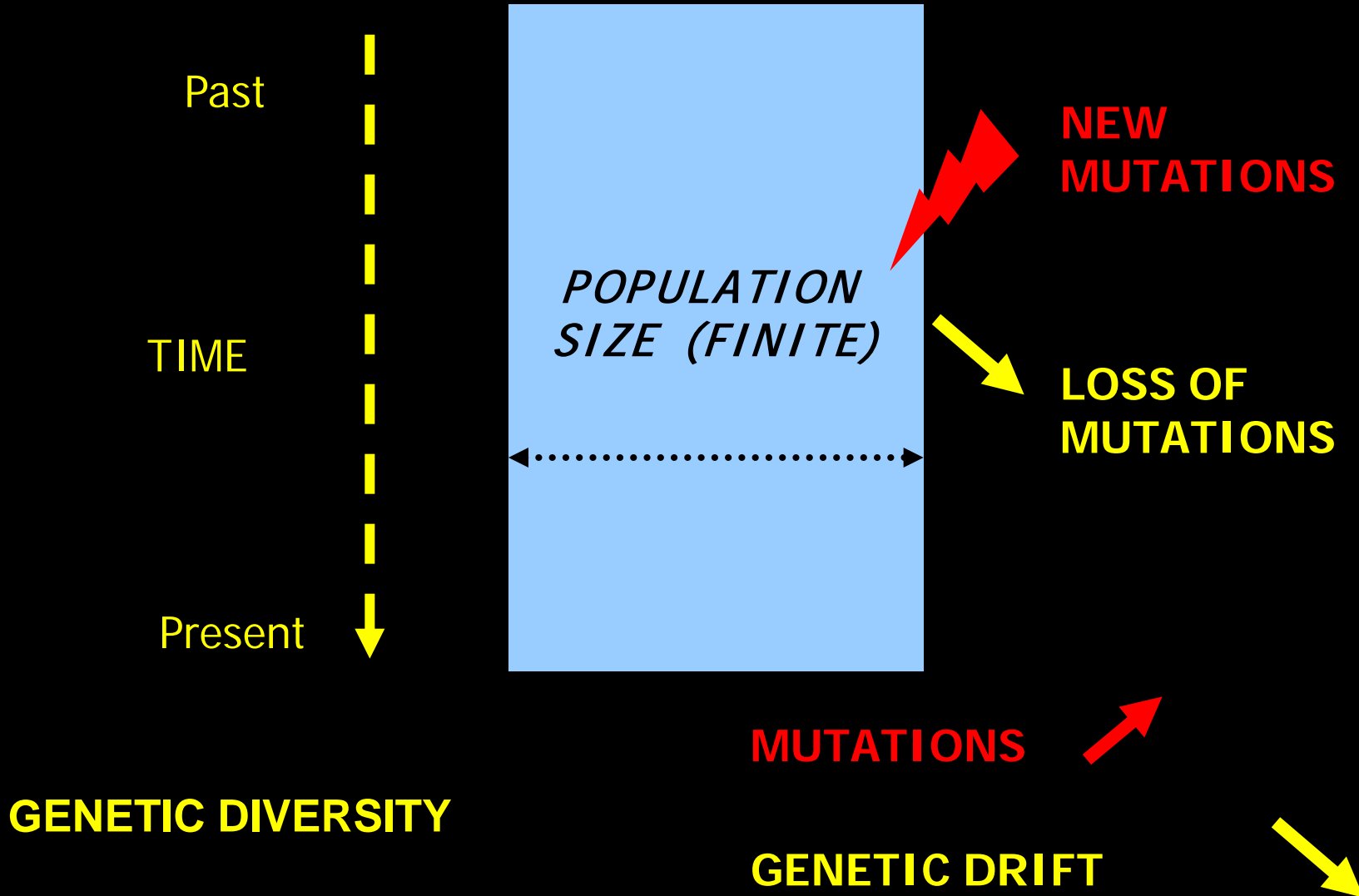
- Distance sampling
- Census

Non invasive sampling

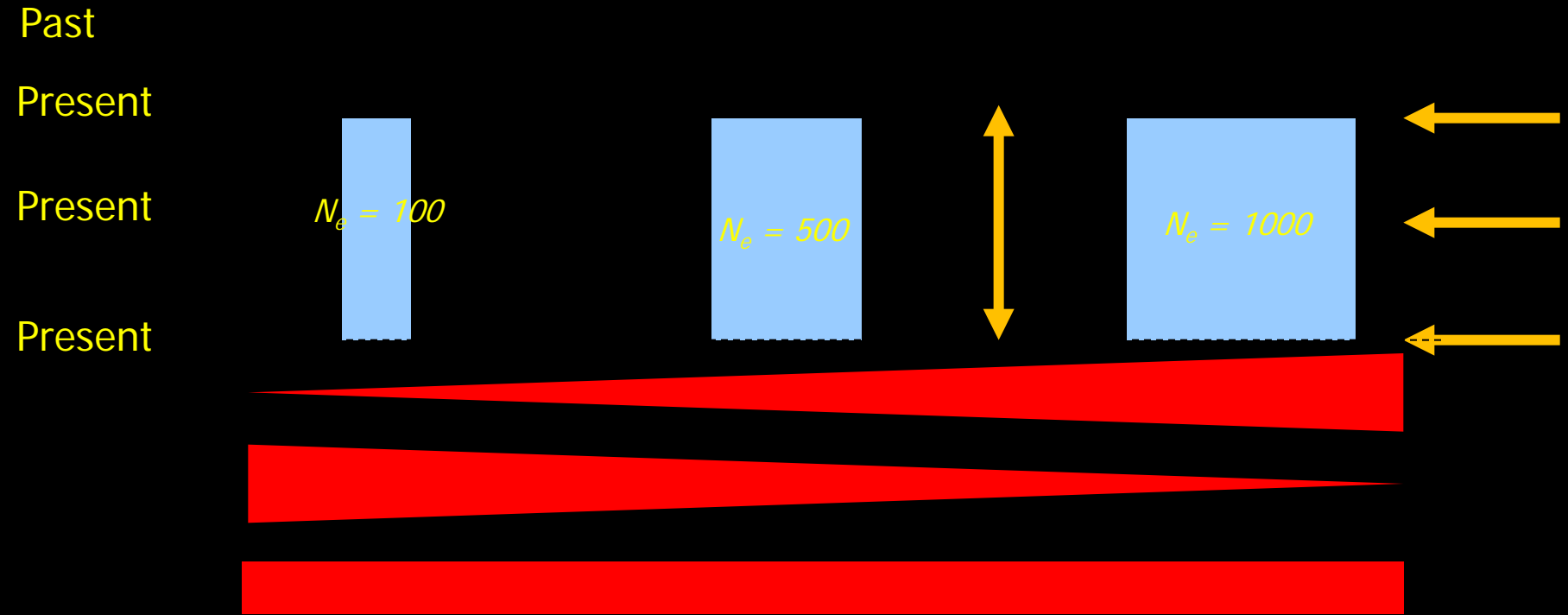
- Faeces



GENETIC DIVERSITY



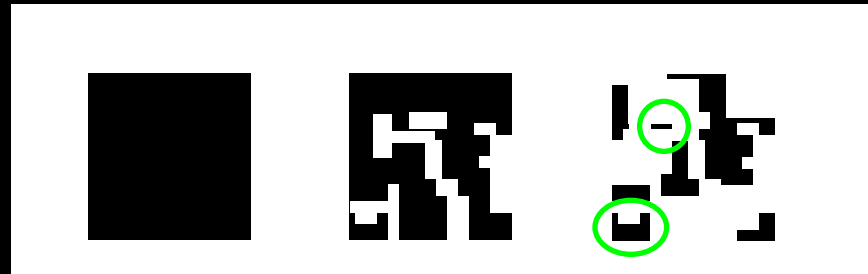
GENETIC DIVERSITY



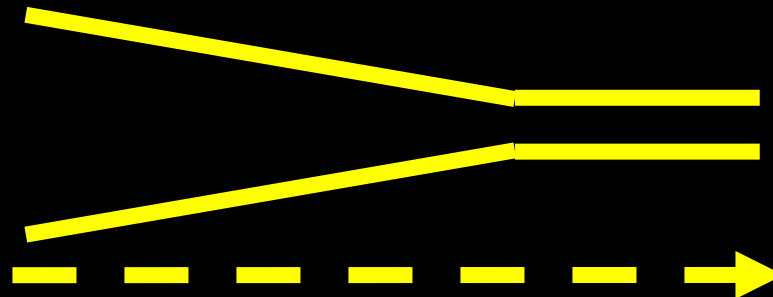
GENETIC DIVERSITY

Different demographic histories can produce similar or counter-intuitive results

Habitat fragmentation and loss as a temporal process

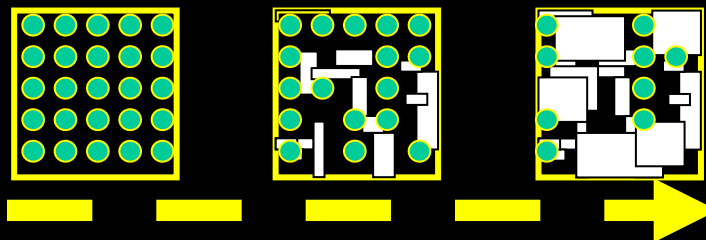


time



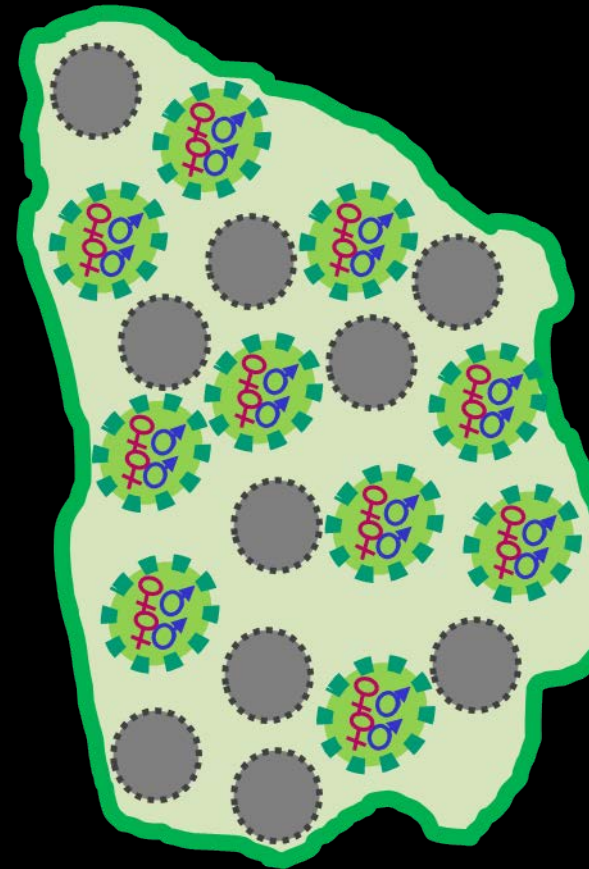
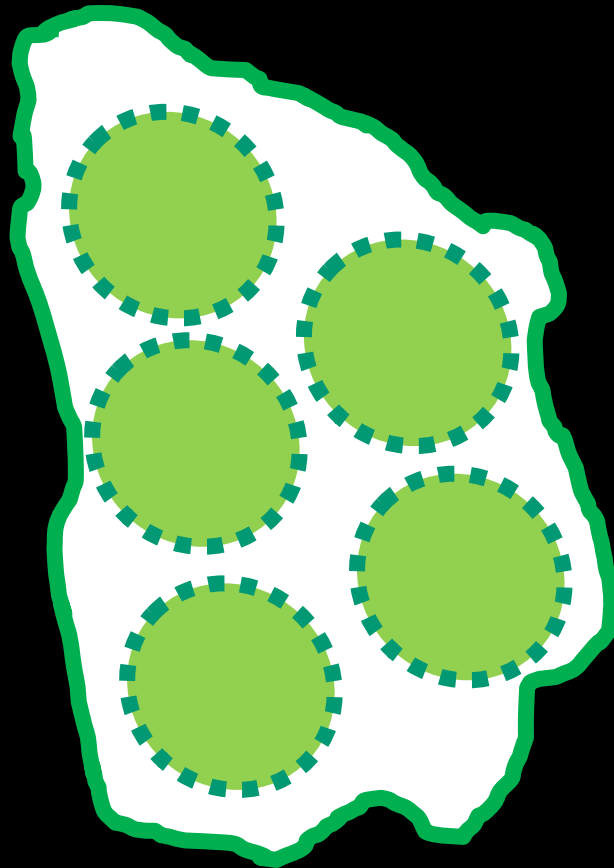
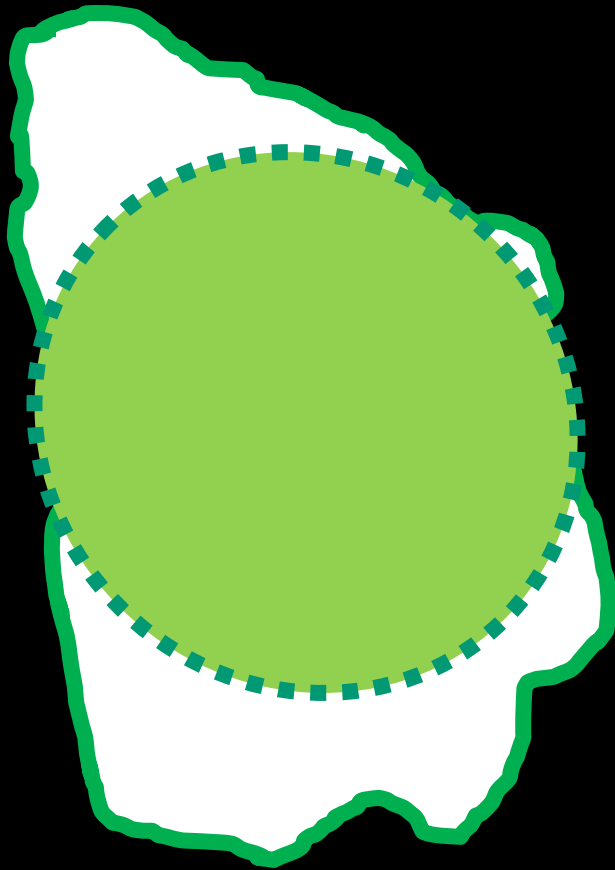
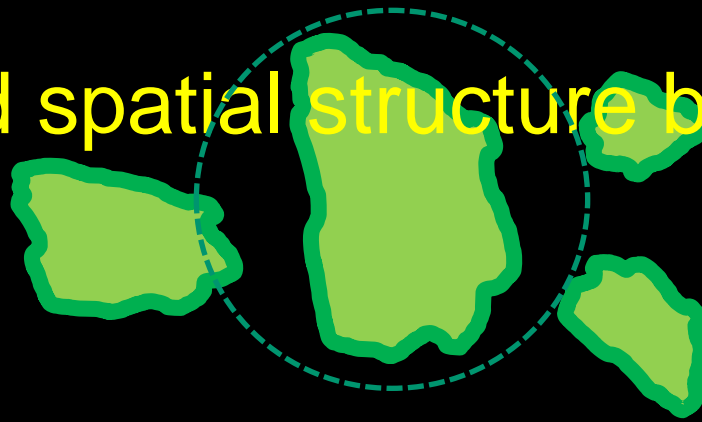
time

ALSO A SPATIAL PROCESS: population structure



time

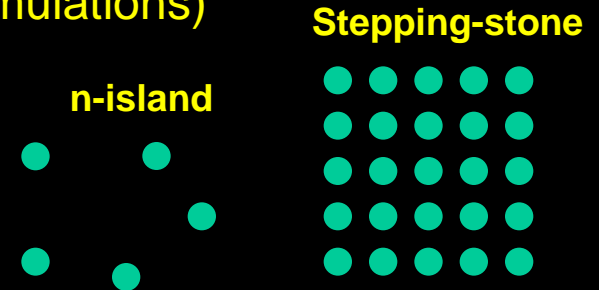
How should spatial structure be represented?



Effect of population structure on bottleneck signals

- Models of population structure (100 demes in all simulations)

- n-island model (100 islands)
- Stepping-stone (10 x 10) (toroidal)



- Parameters used

- Stepwise mutation model assumed to simulate data
- F_{ST} values used { 0.01 ; 0.05 ; 0.1 ; 0.25 }
- θ values used { 1 ; 10 }
- Number of loci { 5 ; 20 }
- 50 individuals sampled (100 genes)

Differentiation

Diversity

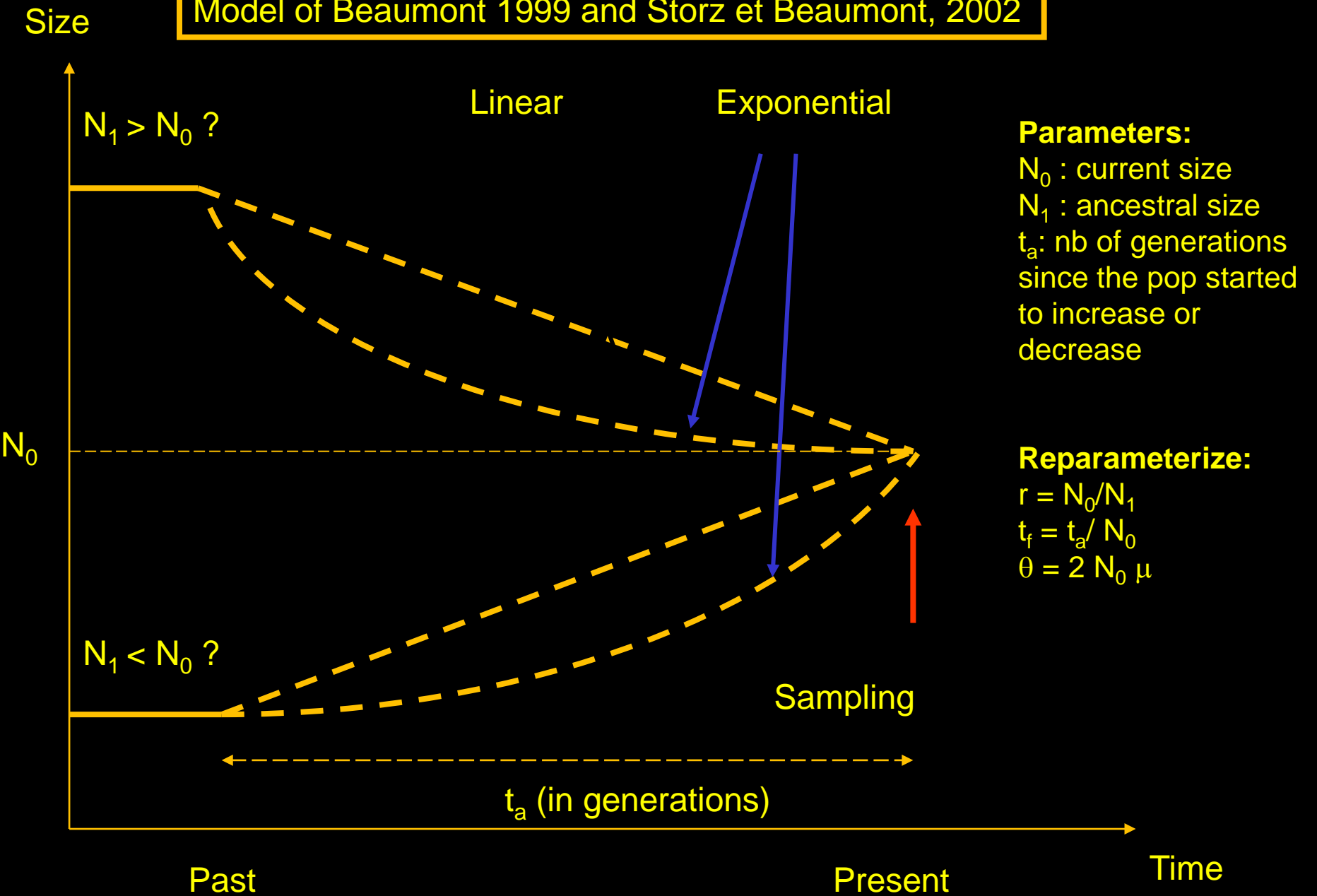
(mutation and pop size)

- Sampling schemes :

- n-islands model: samples from 1, 2, 10 and 50 demes
- Stepping stone model: samples from 1, 2 neighbouring and 2 distant demes

- 10 independent data sets for each parameter set (except 20 loci and 10 demes)

Model of Beaumont 1999 and Storz et Beaumont, 2002



Model of Beaumont 1999

Microsatellite
Data

Linear

Exponential

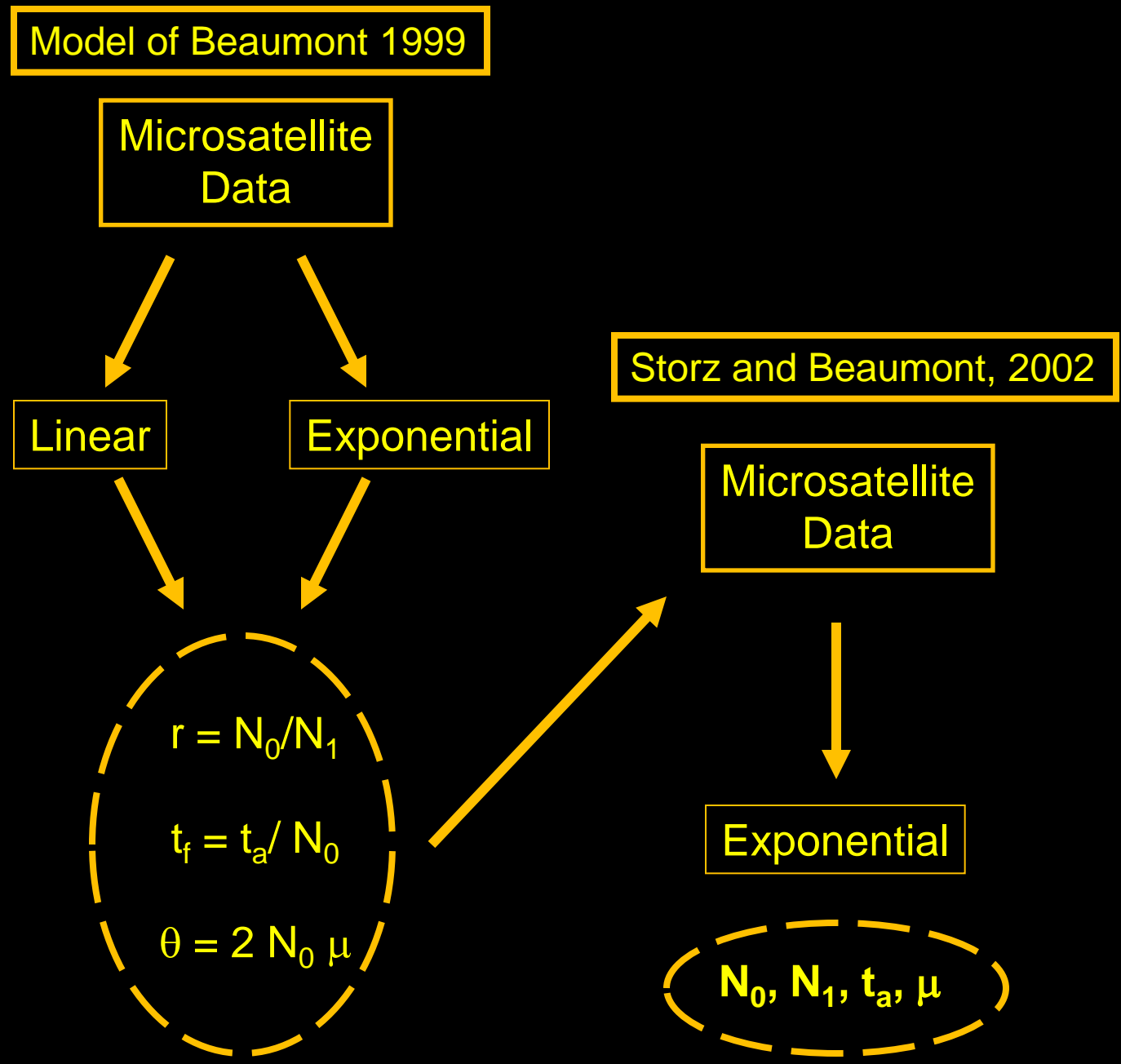
$$r = N_0/N_1$$
$$t_f = t_a / N_0$$
$$\theta = 2 N_0 \mu$$

Storz and Beaumont, 2002

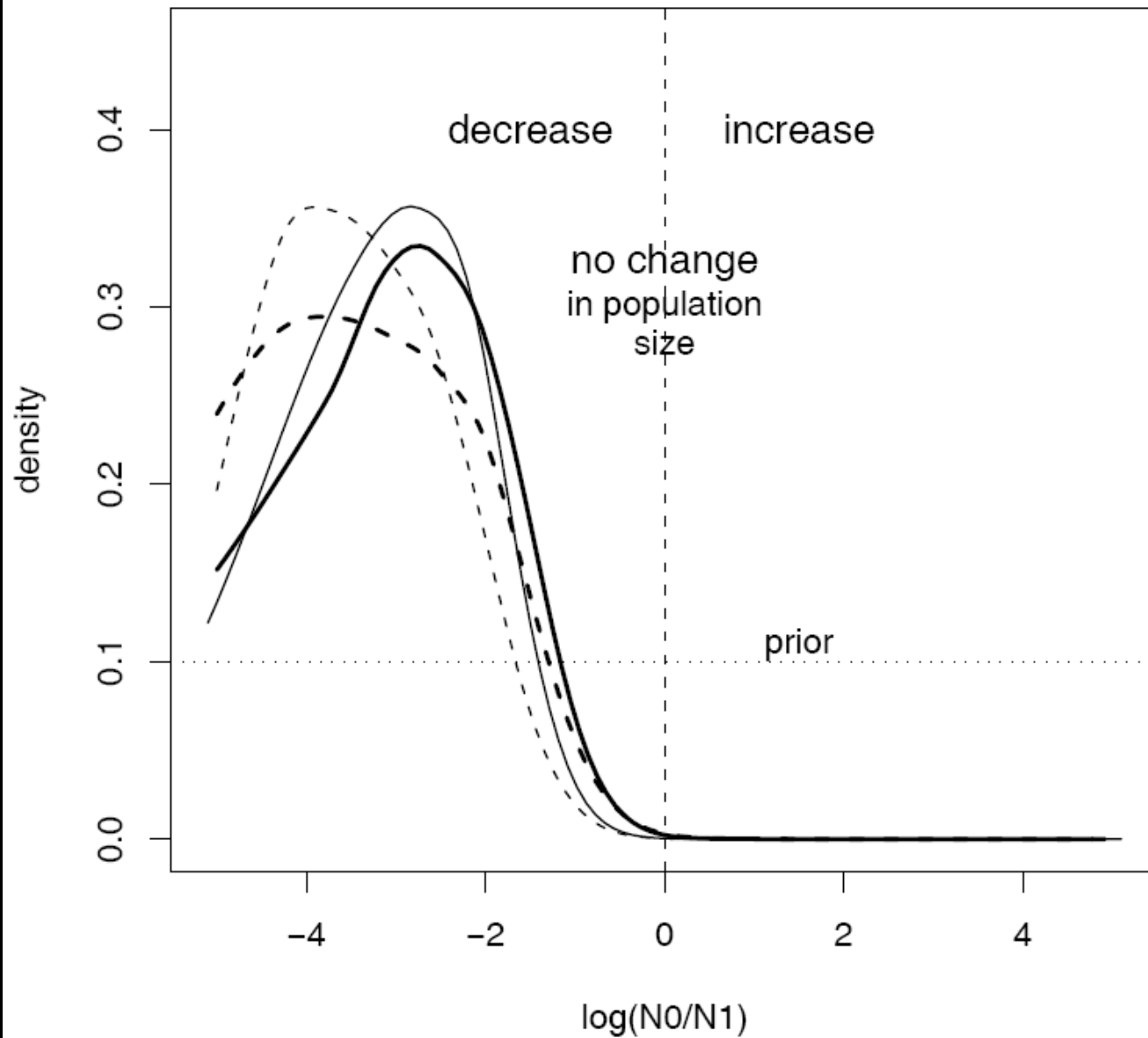
Microsatellite
Data

Exponential

N_0, N_1, t_a, μ

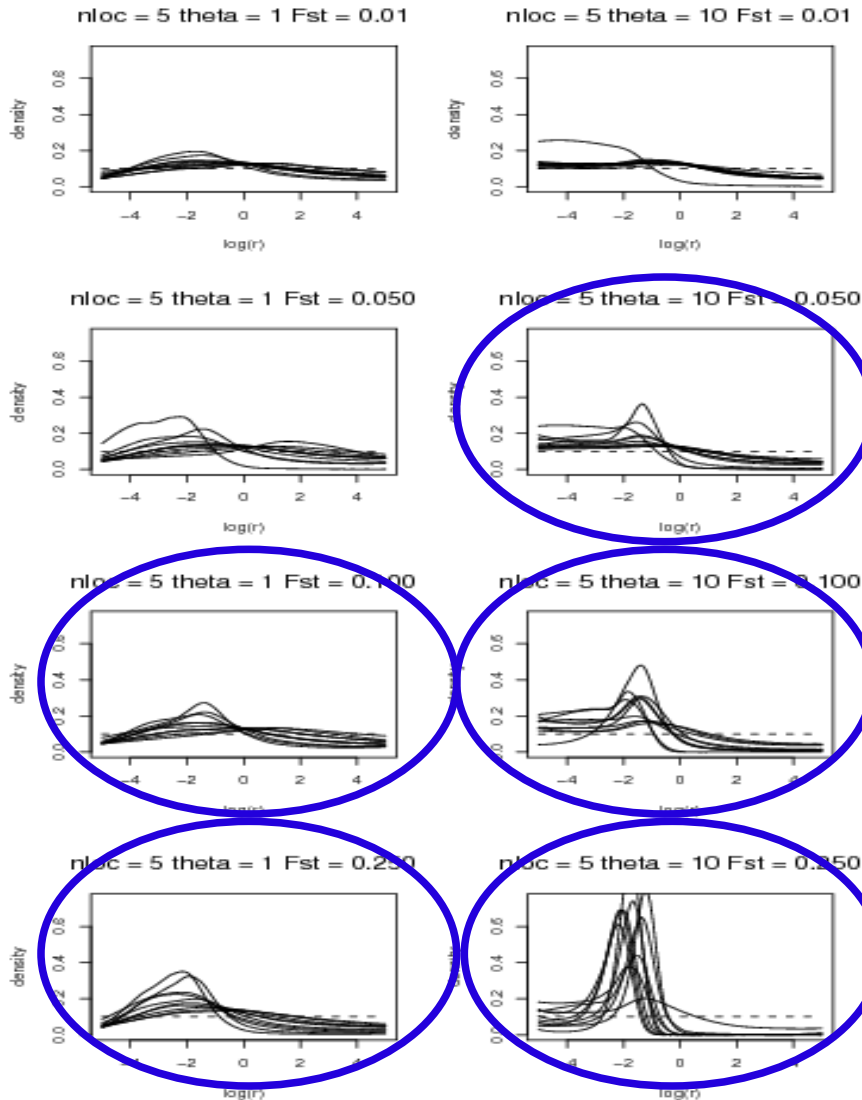


Population size change



Effect of population structure on bottleneck signals

Change in pop size (log r)
n-islands model
1 deme sampled



Can we separate population structure from population crash?

Bottleneck signals

PARTIAL CONCLUSION

1. Population structure can mimic bottleneck signals
2. The signal is particularly strong when
 1. Genetic differentiation is high (gene flow is limited)
 2. Genetic diversity is high
 3. The number of loci used is large
3. The effect is less important when more than one population is sampled

Genetics of recent habitat contraction and reduction in population size: does isolation by distance matter?

RAPHAEL LEBLOIS,^{*,††} ARNAUD ESTOUP[†] and REJANE STREIFF[†]
^{*}Laboratoire Génétique et Environnement, CNRS-UMR 5554, 34095 Montpellier, France, [†]Centre de Biologie et de Gestion des Populations, INRA, Campus International de Baillarguet, CS 30016, 34988 Montpellier sur Lez cedex, France

The Confounding Effects of Population Structure and the Sampling Scheme on the Detection and of Population Size Changes

Loumès Chikhi,^{*,†,‡,1} V. C. Sousa,^{‡,§} Pierre Luisi,^{*,††} Beno Mark A. Beaumont^{***}

Genetic Bottlenecks Driven by Population Disconnection

THOMAS BROQUET,^{*,††} SONIA ANGELONE,^{†‡} JULIE JAQUIERY,^{*,††} PIERRE JOUVEAU,[†] JEAN-PAUL LENA,[§] THIERRY LENGAGNE,[§] SANDRINE PLENET,[§] EMILIE PERRIN,[†] AND NICOLAS PERRIN^{*}

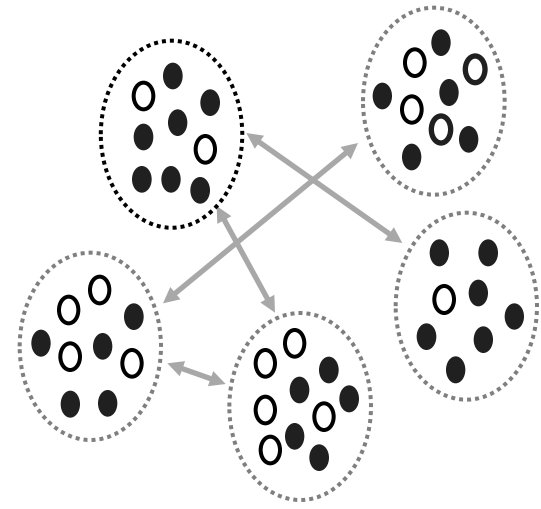
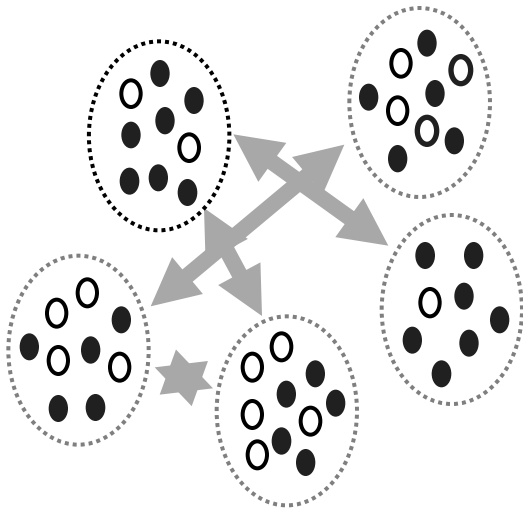
The Impact of Sampling Schemes on the Site Frequency Spectrum of a population subdivided by a Bayesian model choice

Thomas Städler,^{*,1} Bernhard Haubold,[†] Carlos Merino,[‡] Wolfgang Pfaffelhuber[§]

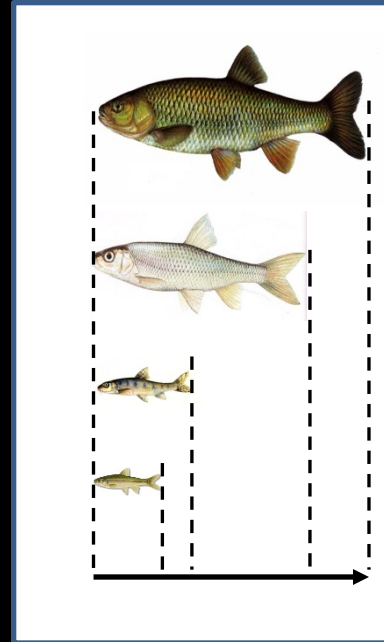
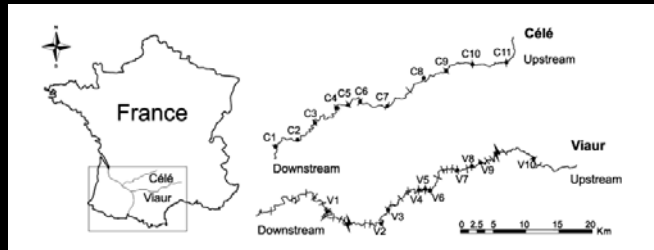
BENJAMIN M. PETER,^{*,†} DANIEL WEGMANN^{*1} and LAURENT EXCOFFIER^{††}
^{*}Computational and Molecular Population Genetics (CMPG), Institute of Ecology and Evolution, University of Bern, Baltzerstrasse 6, CH-3012 Bern, Switzerland, [†]Swiss Institute of Bioinformatics, 1015 Lausanne, Switzerland

Genetic Bottlenecks Driven by Population Disconnection

THOMAS BROQUET,^{*††} SONIA ANGELONE,^{†‡} JULIE JAQUIERY,^{*‡‡} PIERRE JOLY,[§]
JEAN-PAUL LENA,[§] THIERRY LENGAGNE,[§] SANDRINE PLENET,[§] EMILIE LUQUET,[§]
AND NICOLAS PERRIN^{*}



Do all models of population structure create genetic bottlenecks ?



Squalius cephalus

Leuciscus leuciscus

Gobio gobio

Phoxinus phoxinus

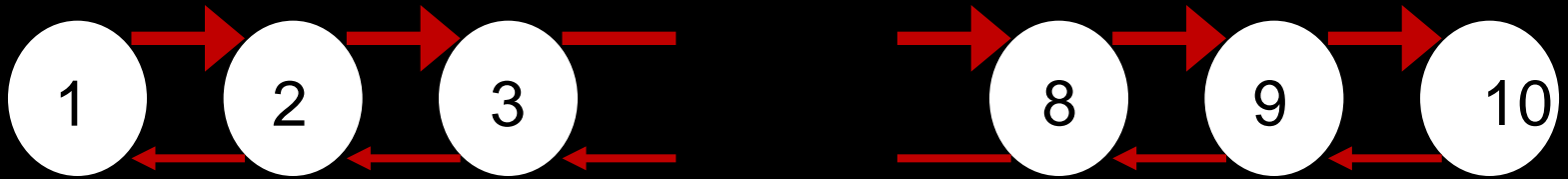
Simon Blanchet

Ivan Paz Géraldine Loot

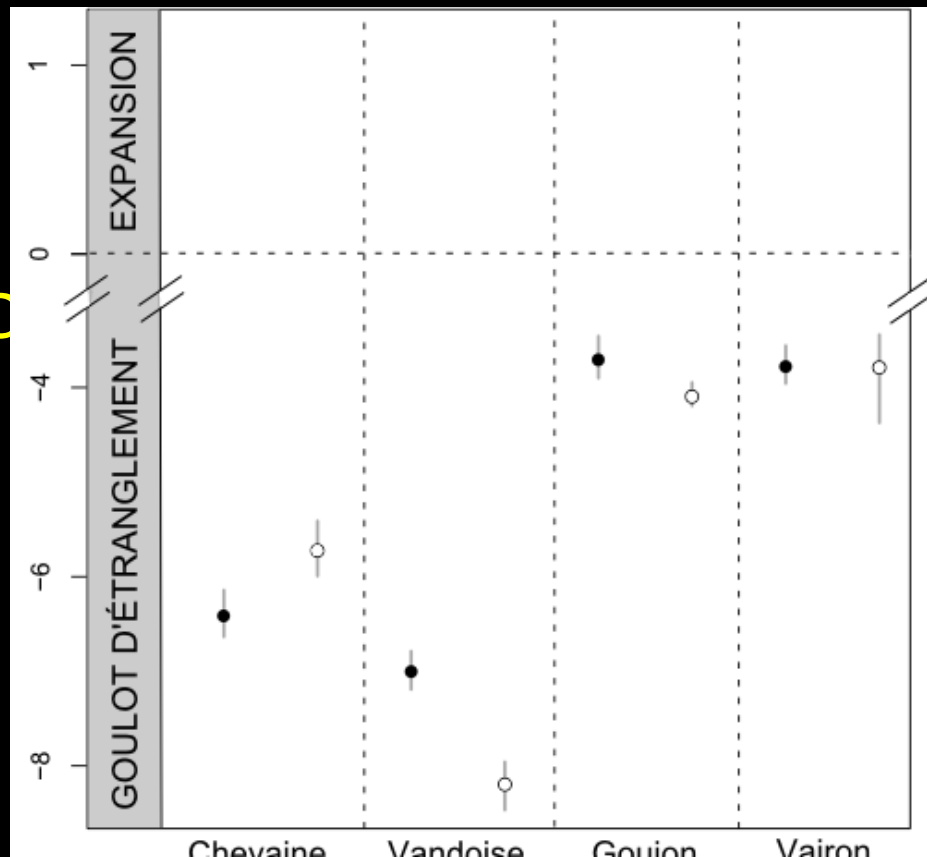


Asymmetrical gene flow

SOURCE



UPSTREAM



DOWNSTREAM

PARTIAL CONCLUSION

Need to

Develop methods that can separate these two kinds of scenarios (structure *versus* bottleneck)

Develop *ad hoc* ways to minimize the genetic structure effect is to spread sampling (one individual per “population”)

Rasmus Heller (post-doc): Skyline plots

Integrate information from other fields:

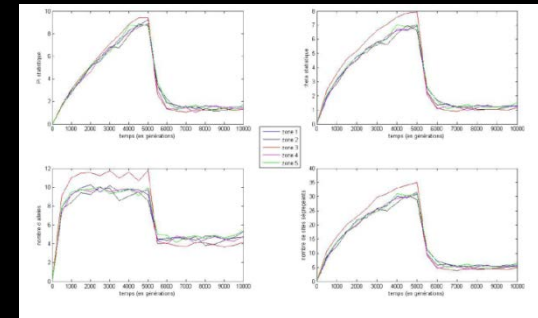
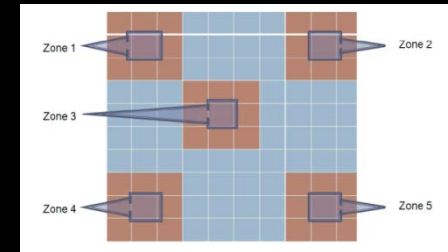
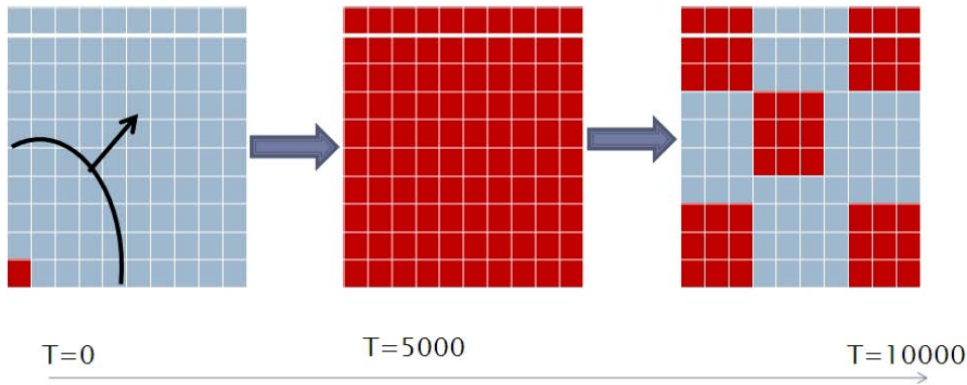
Geographic Information Systems → land cover over time

Ancient DNA

INTEGRATE SPACE AND TIME: SINS: (Simulating INdivivuals in Space)

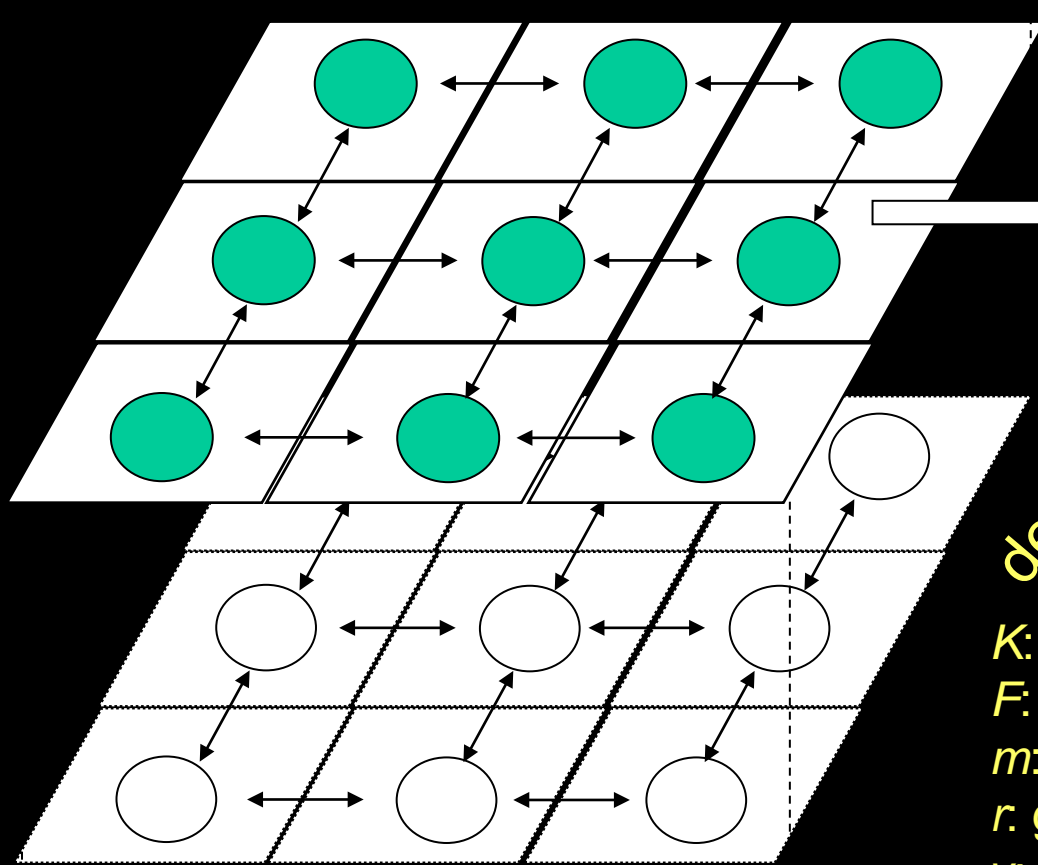
**EXPANSION
(Neolithic)**

FRAGMENTATION

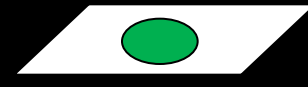
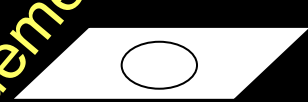
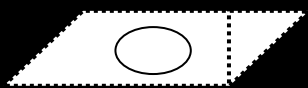
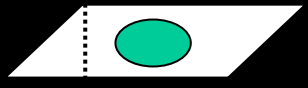


**Rita RASTEIRO
Pierre Antoine BOUTTIER
Damien MONIER
Vitor SOUSA**

Layer 1



Layer 2



cell

deme

K : carrying capacity

F : friction

m : migration rate

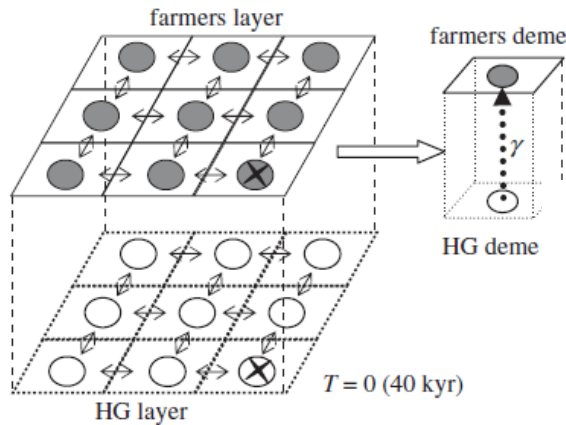
r : growth rate

γ : admixture

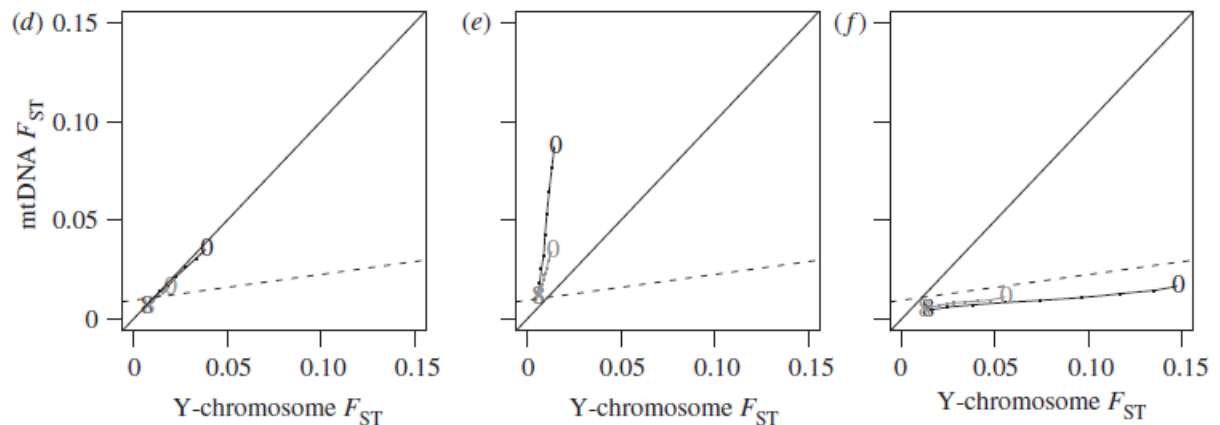
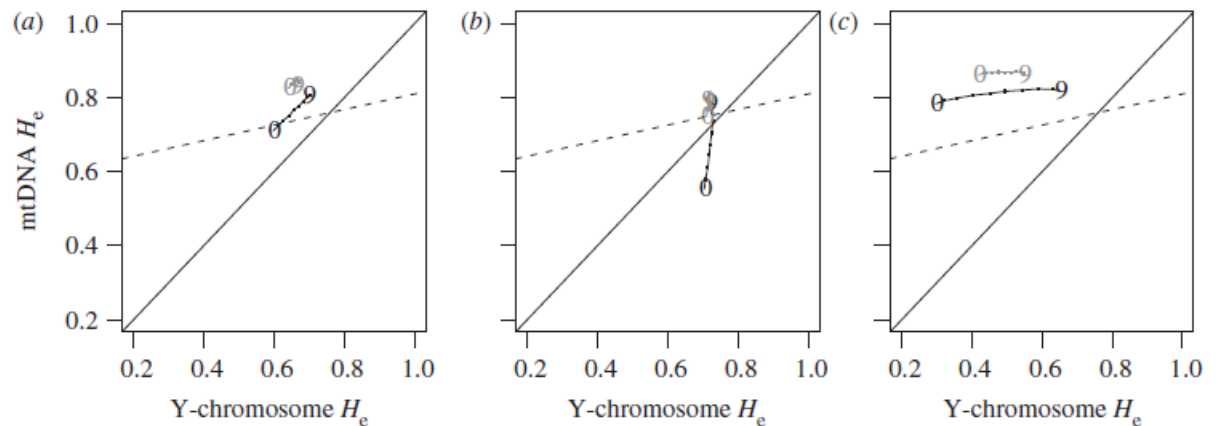
Genetic parameters: mutation rates, sequence length, etc

Investigating sex-biased migration during the Neolithic transition in Europe, using an explicit spatial simulation framework

Rita Rasteiro^{1,*}, Pierre-Antoine Bouttier^{1,‡}, Vítor C. Sousa^{1,§}
and Lounès Chikhi^{1,2,3,*}



bilocality **matrilocality** **patrilocality**

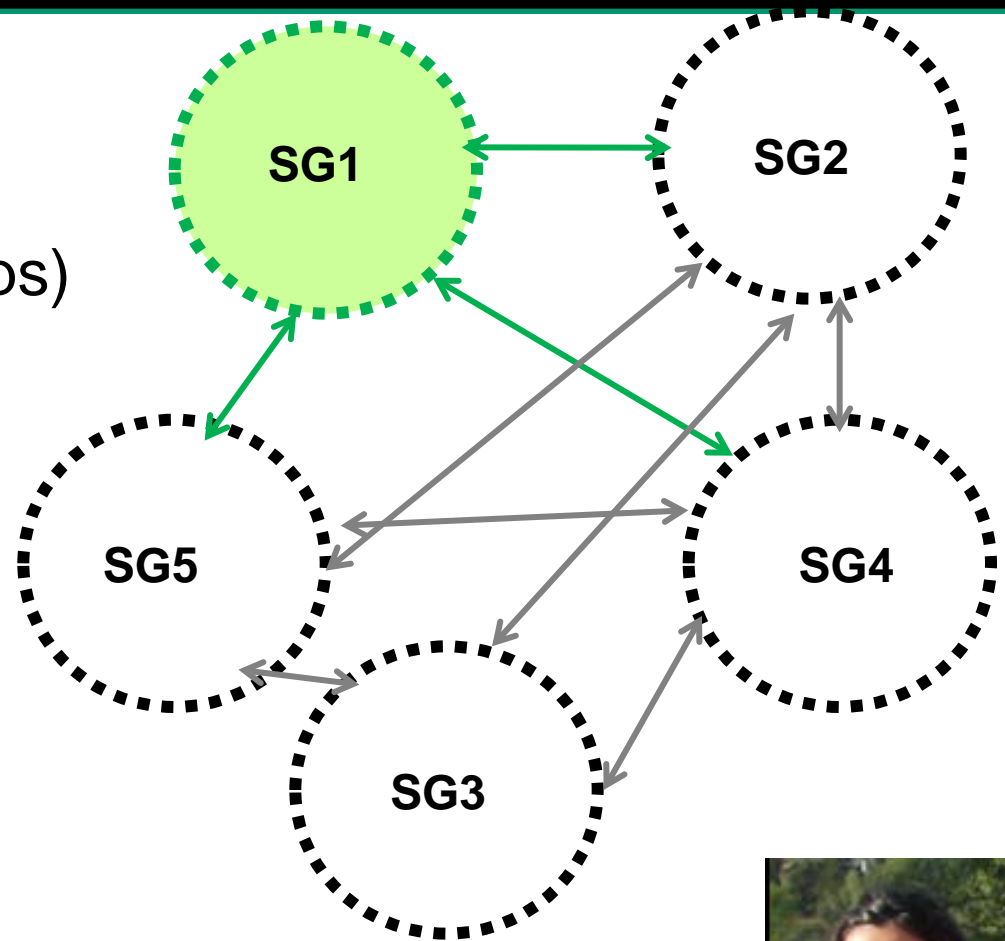


Modelling social structure (is it population structure ?)

MATRIX (ngroups*ngroups)

popstructure.txt

	S1	S2	S3	S4	S5
S1	0	1	0	1	1
S2	1	0	1	1	1
S3	0	1	0	1	1
S4	1	1	1	0	1
S4	1	1	1	1	0



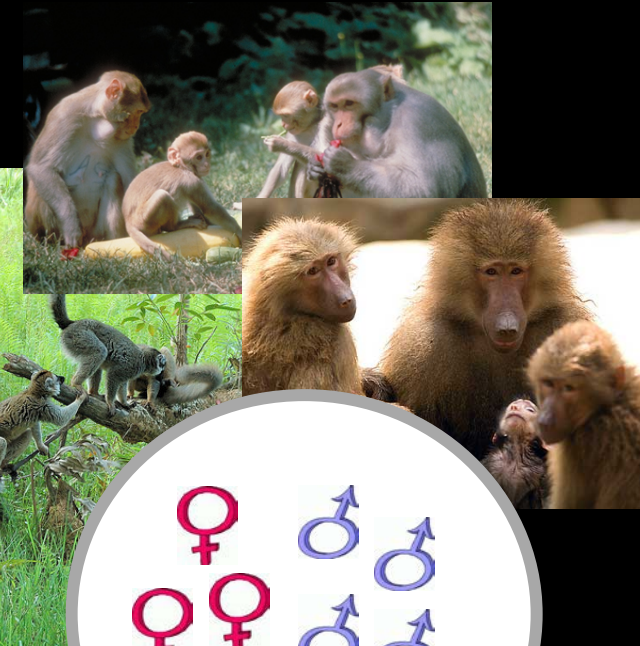
- SG1 is connected to pops 2, 4, 5
- SG3 is connected to pops 2, 4, 5
- SG2, SG4, SG5 are connected to all other SG's

B. Parreira

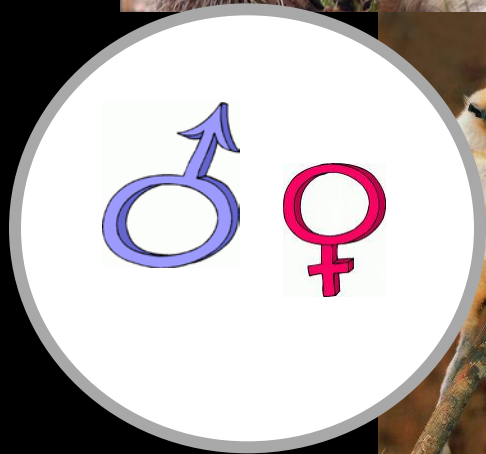


Types of mating system

Multi-males; multi-females



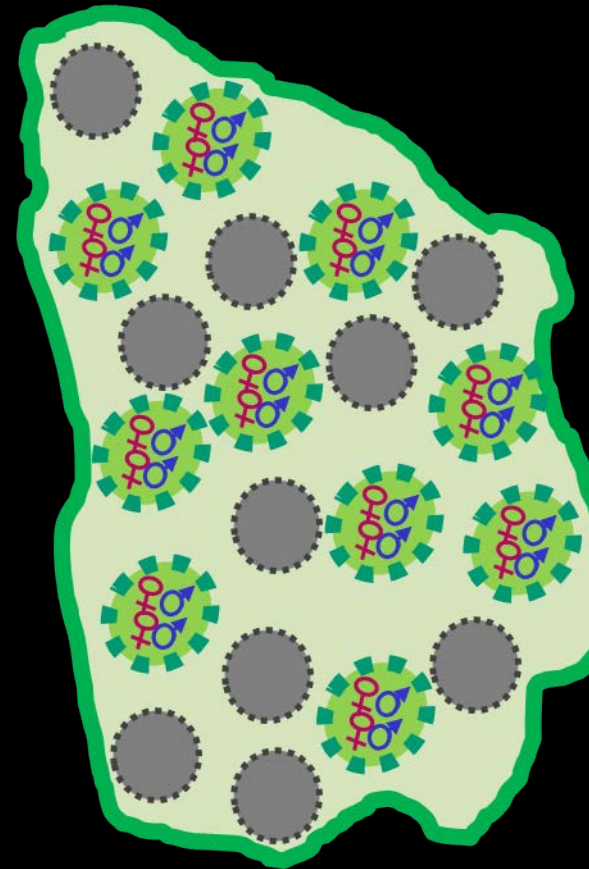
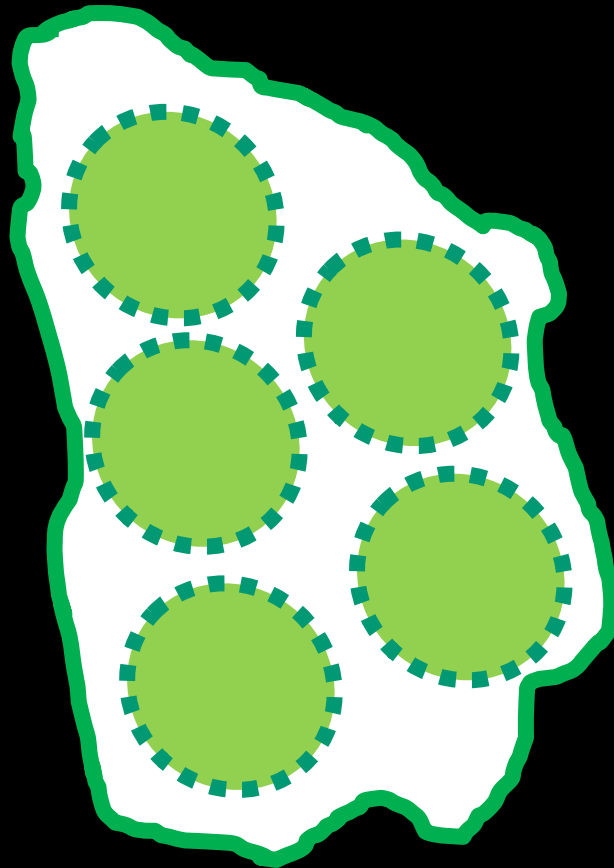
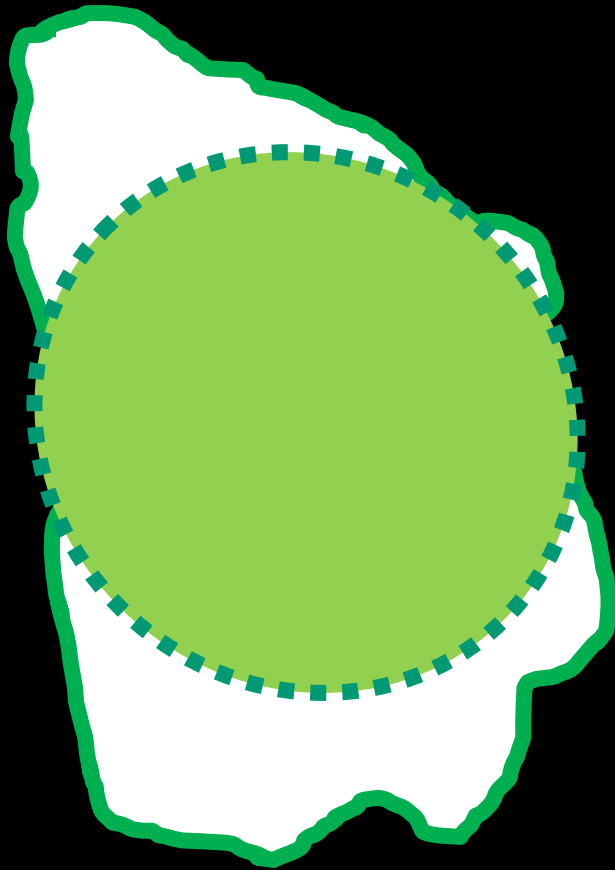
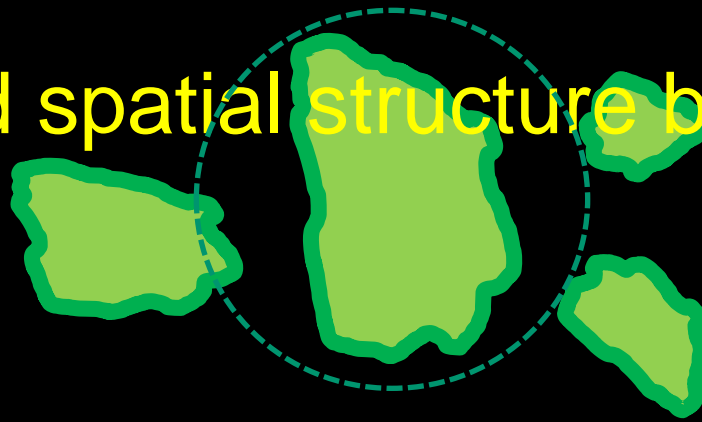
Monogamy



Dominance



How should spatial structure be represented?



PARTIAL CONCLUSION (again)

Collaborate with mathematicians/statisticians:

Ongoing work with

Simon Boitard (INRA)

Olivier Mazet (INSA, IMT)

Willy Rodriguez (PhD student)

Simona Grusea (INSA, IMT)

Mark Beaumont (Univ. Bristol)

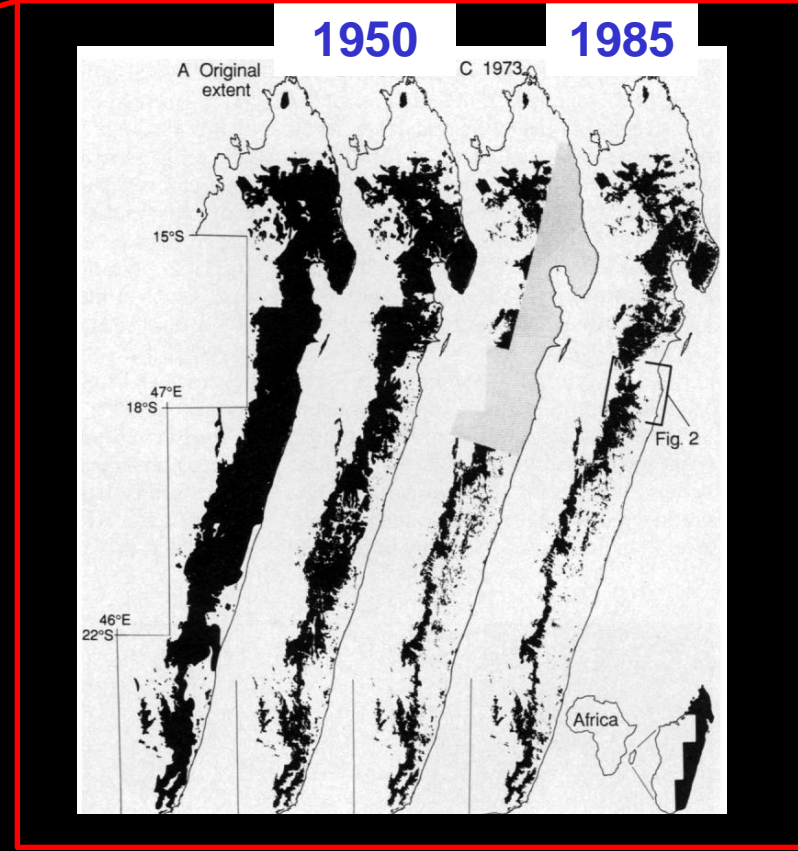
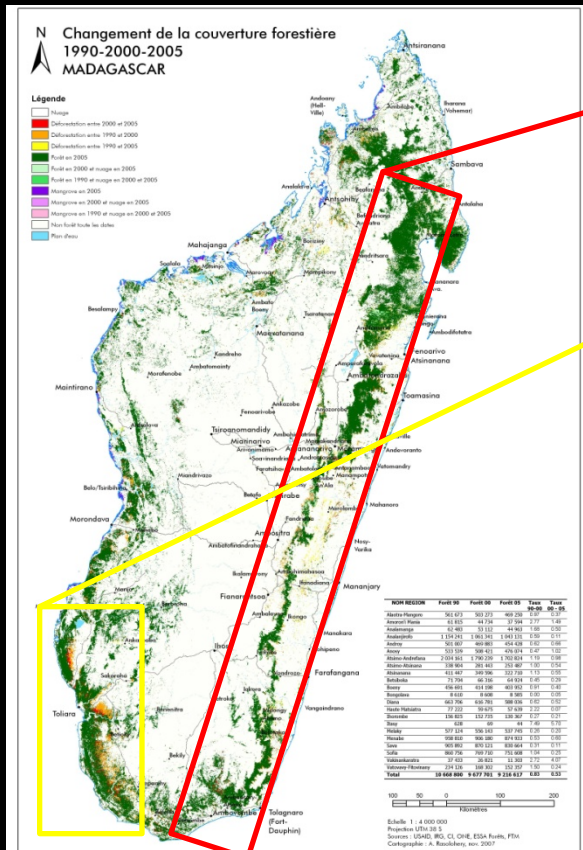
HABITAT LOSS AND FRAGMENTATION IN MADAGASCAR

FOREST HABITATS : 10-20 % TOTAL SURFACE

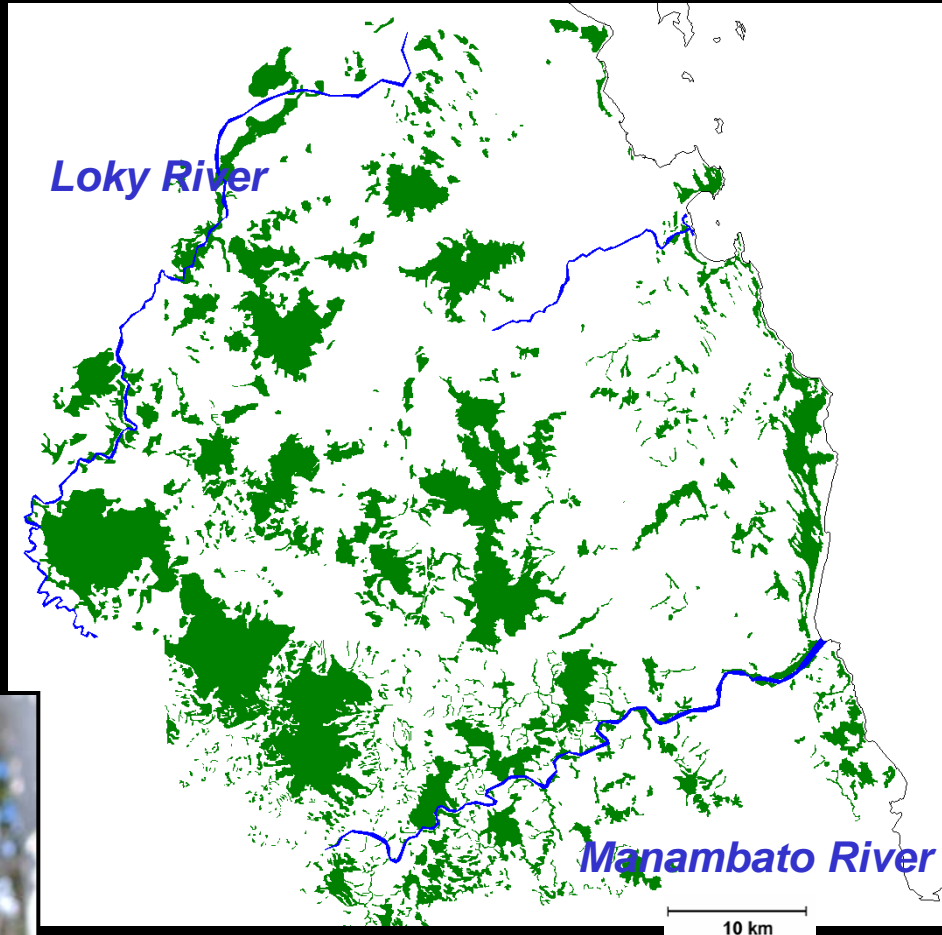
90% of vertebrates depend on forested habitats

Large size lemurs have disappeared

MOST present-day lemurs are threatened in Madagascar



HABITAT LOSS AND FRAGMENTATION AND SIFAKAS



Indian Ocean



Golden-crowned sifaka
Propithecus tattersalli



Erwan Quéméré

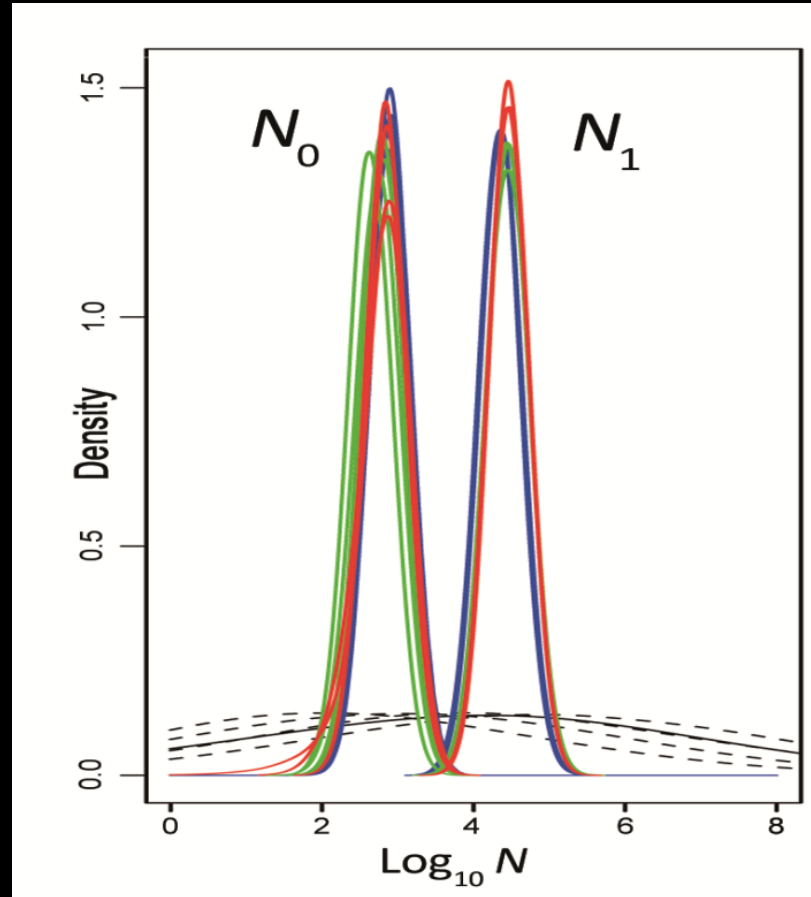
SIFAKAS (Propithecus)



IS HABITAT FRAGMENTATION DUE TO THE ARRIVAL OF HUMANS?

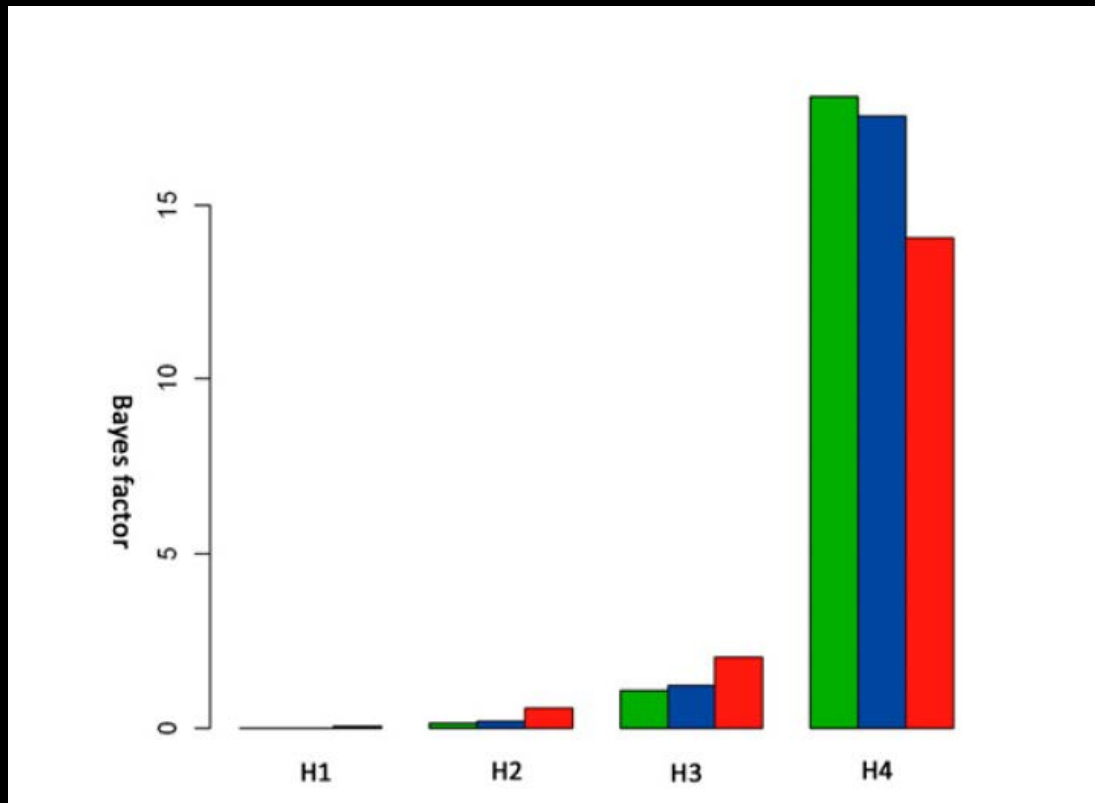
1. Is there a bottleneck signal in golden-crowned sifakas ?
2. When did it happen?
 - H1: in the last 100 years (recent pop increase)
 - H2: between 100 and 1000 years ago (first “real” demographic impact)
 - H3: 1000 - 2000 years ago (human arrival)
 - H4: 2,000 - 10,000 years (Holocene climatic)?

1. Is there a bottleneck signal in golden-crowned sifakas ?

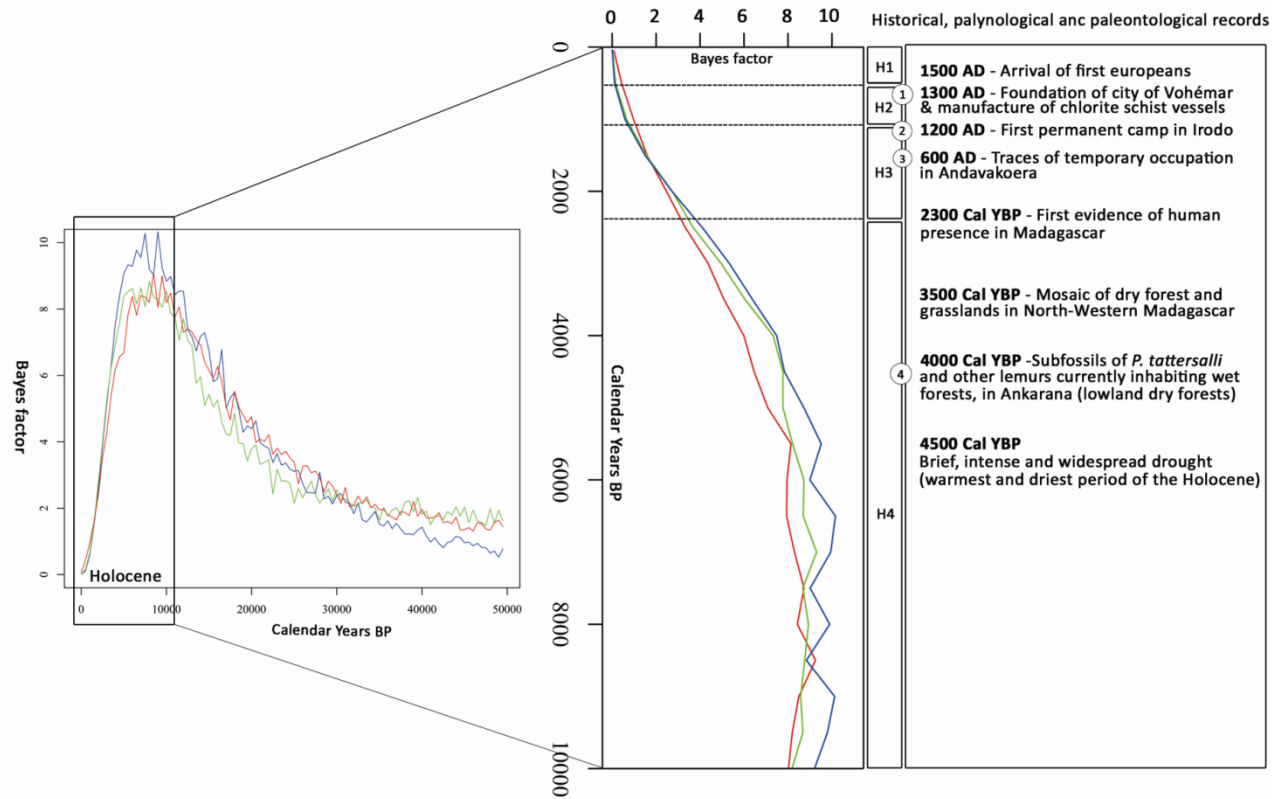


2. When did it happen?

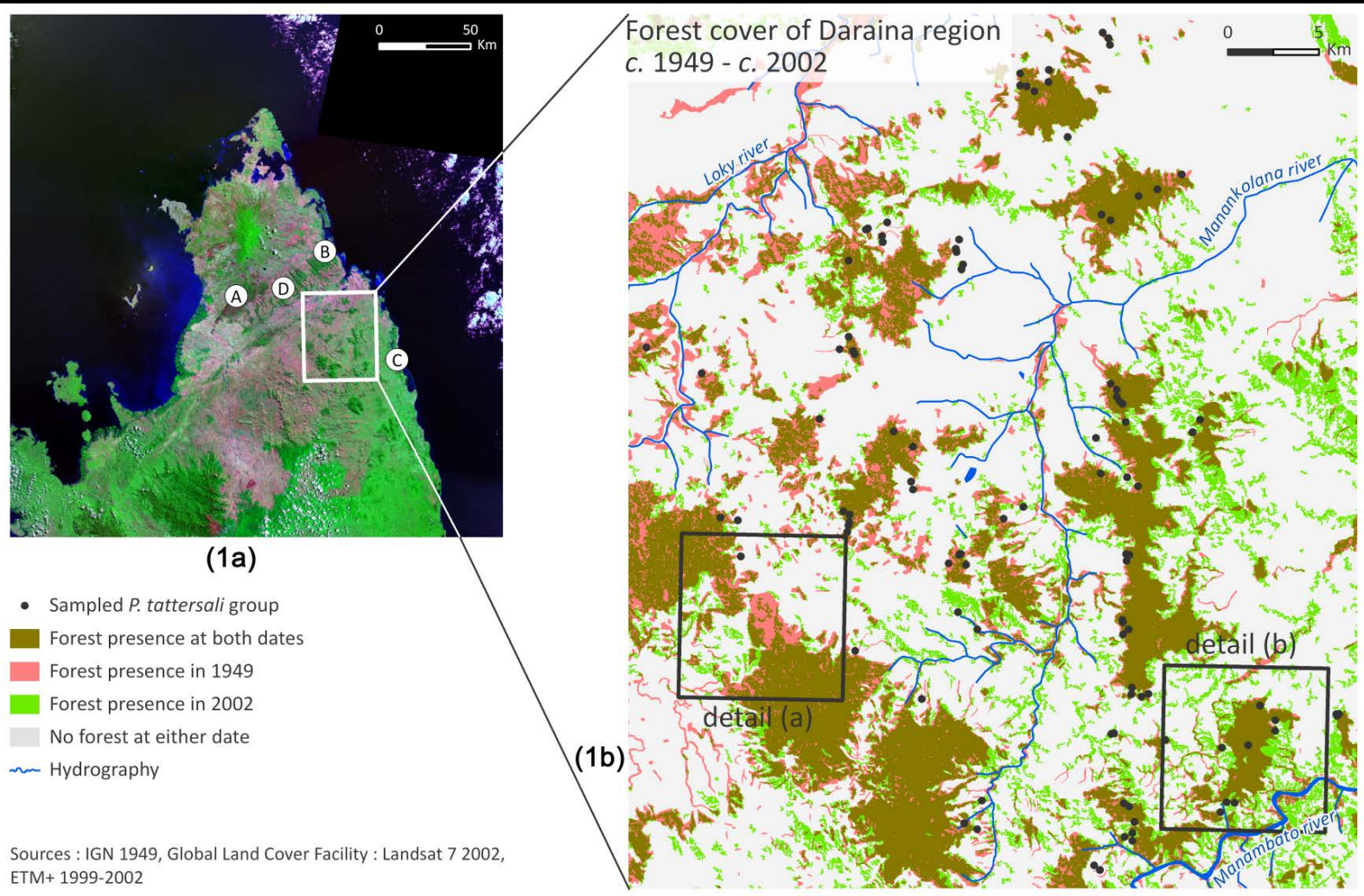
- H1: in the last 100 years (recent human pop increase)
- H2: 100 - 1000 years ago (first “real” demographic impact)
- H3: 1000 - 2000 years (human arrival)
- H4: 2000 - 10,000 years (Holocene droughts)?



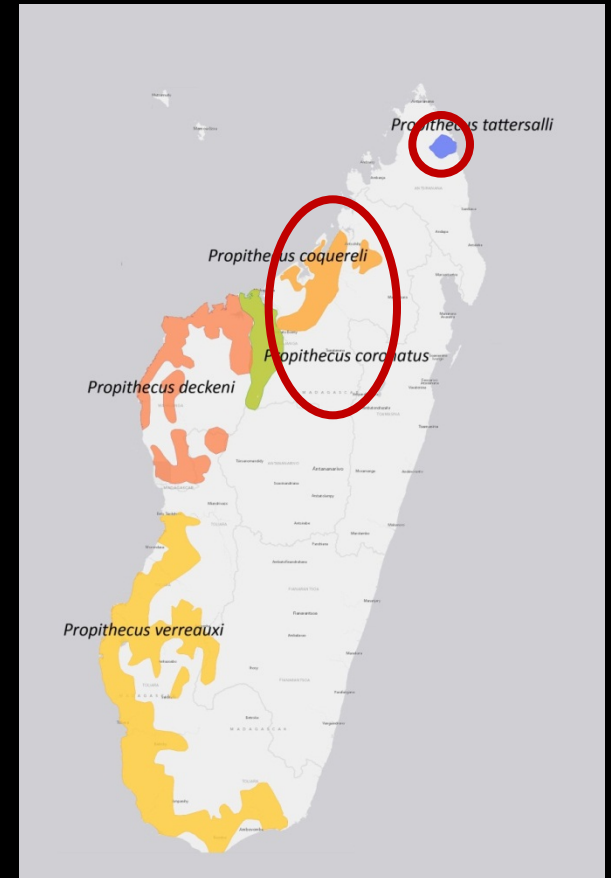
Most likely period for the start of the population decrease



EVOLUTION OF THE FOREST COVER IN DARAINA



Why is the golden-crowned sifaka so far away from its sister species ?



CONCLUSIONS AND PERSPECTIVES

- Statistical and simulation-based inference is an active research field.
- While population genetics tended to ignore space, spatial approaches originating in ecology tended to ignore time (and evolution)
- How other aspects of population structure (social, spatial, asymmetrical gene flow) should be integrated is less studied

CONCLUSIONS AND PERSPECTIVES

Madagascar is a particularly interesting region:

- Recent human colonisation
- “Independent” evolutionary replicates
- Comparative approaches





Mesopropithecus



Indri



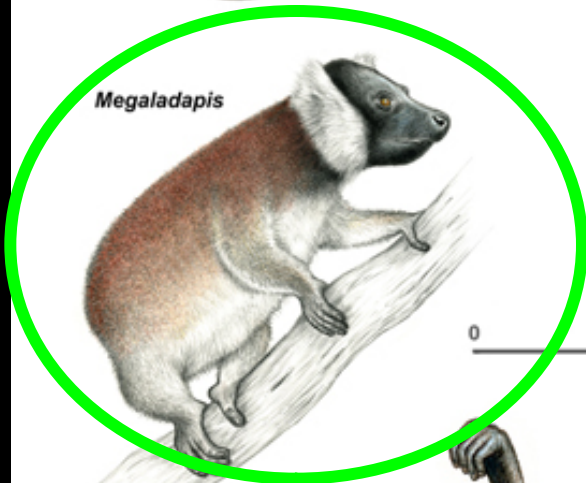
Pachylemur



Babakotia



Palaeopropithecus

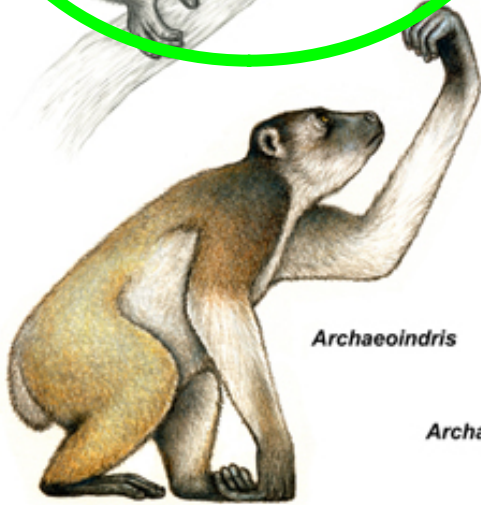


Megaladapis

0 50 cm



Hadropithecus



Archaeoindris

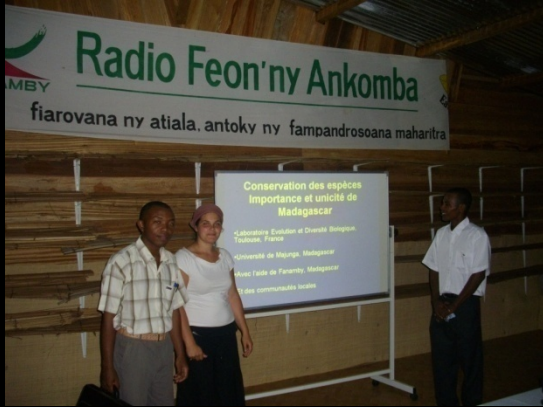


Archaeolemur



LEMUR REF

PRIMATE SPECIALIST GROUP
CONSERVATION PLANNING WORKSHOP 20
SPECIALIST GROUP, MARGOT MARSH BIODIVERSITY FOUNDATION,
IES CONSERVATION F... IN UNITE, CONSERVATION INTERNATIONAL MA



Anna Rozzi

**Mélanie Barnavon, Angelika Beck,
Barbara Le Pors, etc.**





THANK YOU

COME AGAIN

Brigitte Crouau-Roy Univ. Paul Sabatier, Toulouse, France

Lounes Chikhi CNRS and Univ. Paul Sabatier, Toulouse, France

Instituto Gulbenkian de Ciência, Oeiras, Portugal



Bárbara Parreira, Rita Rasteiro, Vitor Sousa Inst. Gulbenkian de Ciência, Portugal

Pierre Luisi, Pierre-Antoine Bouttier INSA, Toulouse, France



Benoît Goossens Cardiff Univ., UK – Sabah Wildlife Dept, Malaysia

Mark Beaumont: Reading Univ., UK

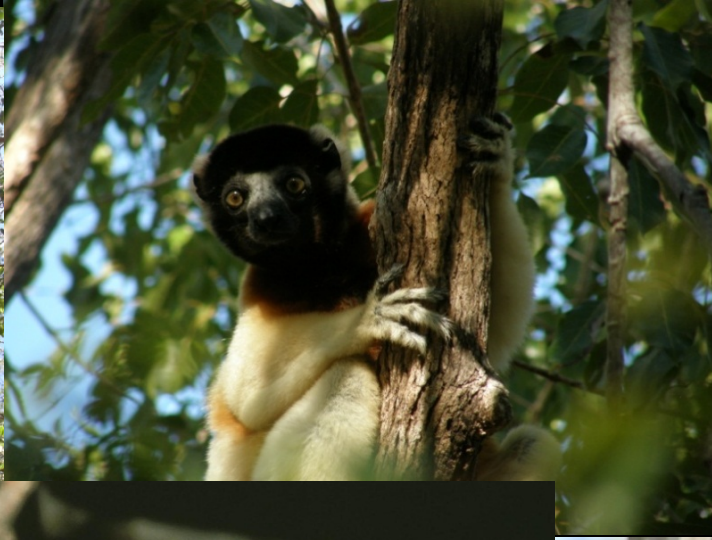


Erwan Quéméré: Univ. Paul Sabatier, Toulouse, France

Pedro Fernandes: Bioinformatics Unit, IGC

Ed Louis: Omaha Zoo

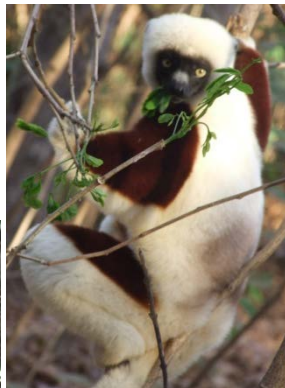




Related study species and corresponding distributions

3 species of sifaka

- *Propithecus tattersalli*
- *P. coquereli*
- *P. coronatus*



Habitat Fragmentation (and loss ?) in Daraina

44 000 ha of fragmented forest





Influence of forest fragmentation on an endangered large-bodied lemur in northwestern Madagascar

Mathias Craul^{a,*}, Lounes Chikhi^{b,c}, Vitor Sousa^c, Gillian L. Olivieri^a, Andriatahiana Rabesandratana^a, Elke Zimmermann^a, Ute Radespiel^a



Genetic structure and signature of population decrease in the critically endangered freshwater cyprinid *Chondrostoma lusitanicum*

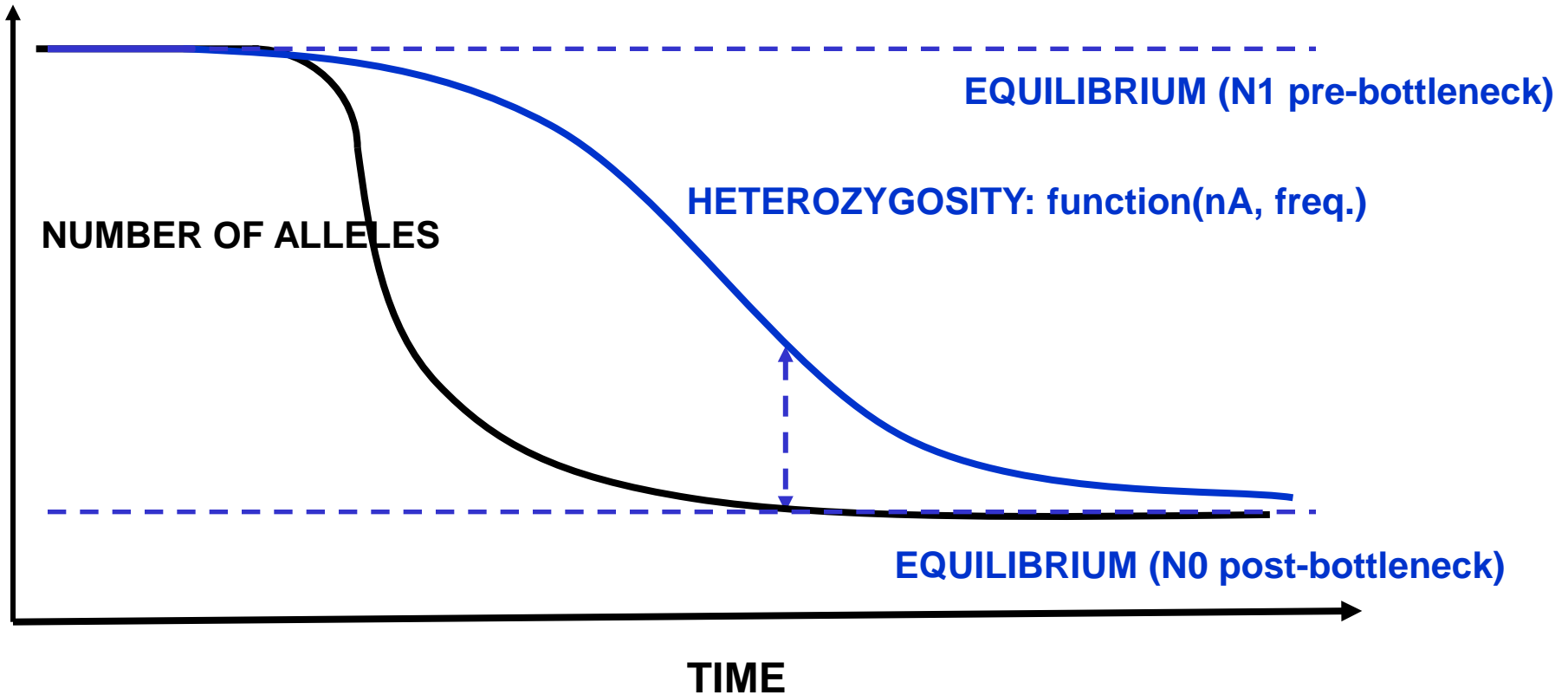
Vitor Sousa · Filipa Penha · Maria J. Collares-Pereira · Lounès Chikhi · Maria M. Coelho

From genetic diversity and structure to conservation: Genetic signature of recent population declines in three mouse lemur species (*Microcebus* spp.)

Gillian L. Olivieri^a, Vitor Sousa^{b,c}, Lounès Chikhi^{b,d}, Ute Radespiel^{a,*}



GENETIC DIVERSITY



DIFFERENT TEMPORAL DYNAMICS OF THE TWO MEASURES