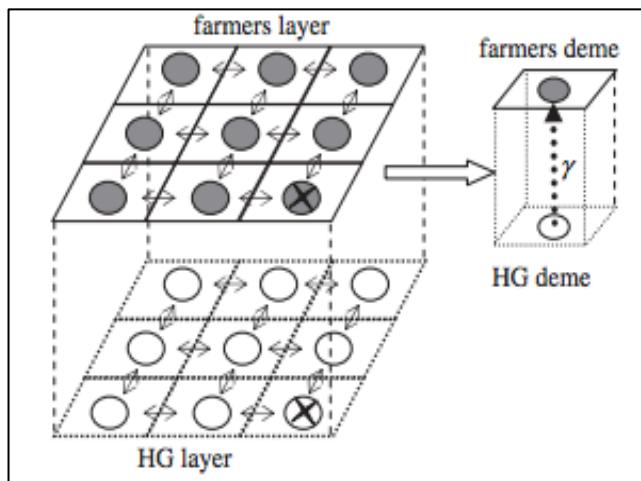


Simulating populations in space: Practicals with SINS software

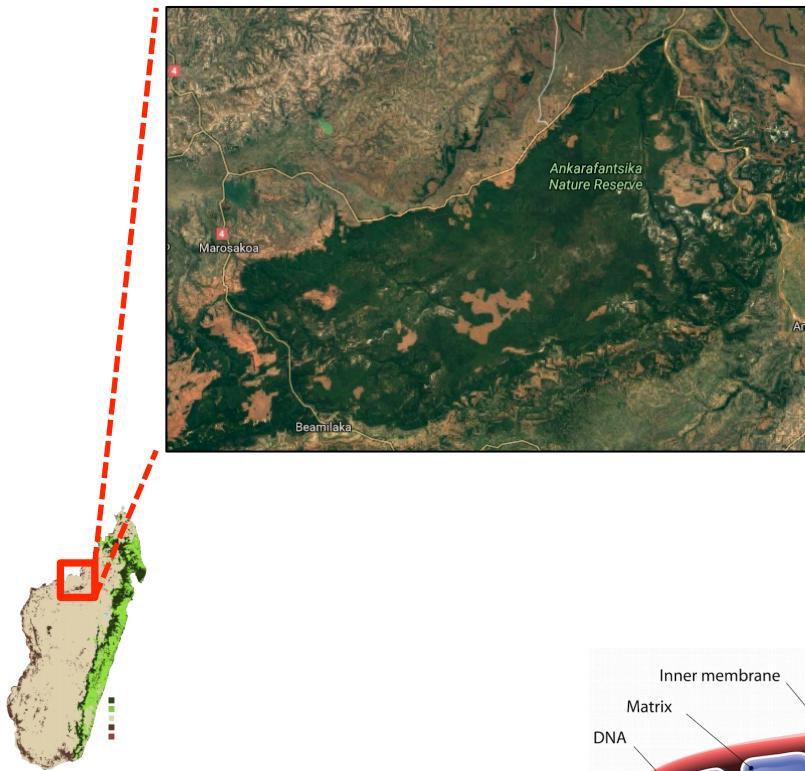
Investigating sex-biased migration during the Neolithic transition in Europe, using an explicit spatial simulation framework

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

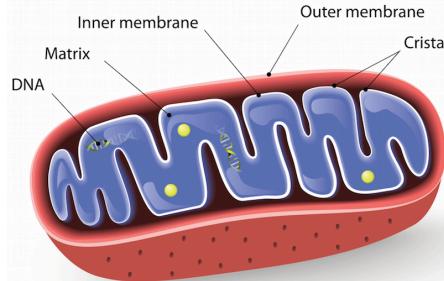


They tested different scenarios to identify **which social organization** would **best explain** present genetic data.

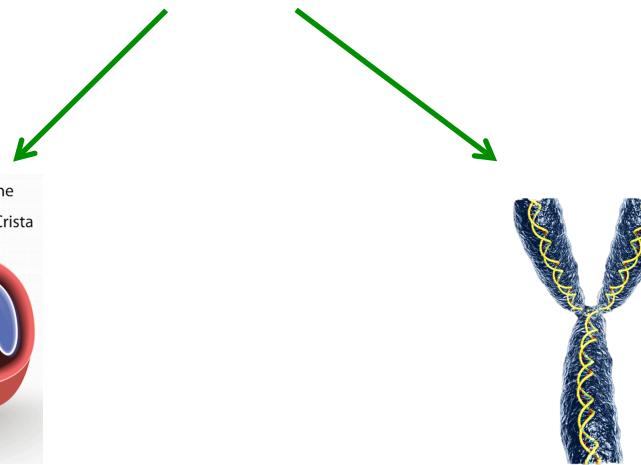
Fieldwork: genetic sampling



500 bp sequence
from non-
recombinant DNA



mtDNA



Y chromosome

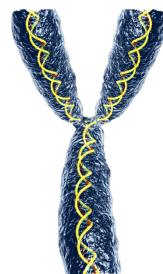


mtDNA

**Maternally
inherited**



Proxy of female
demography



Y chromosome

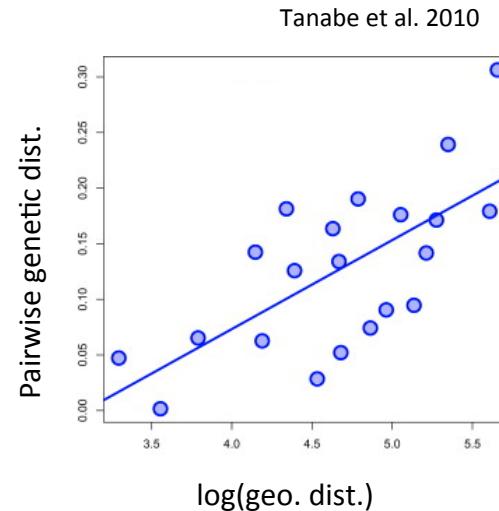
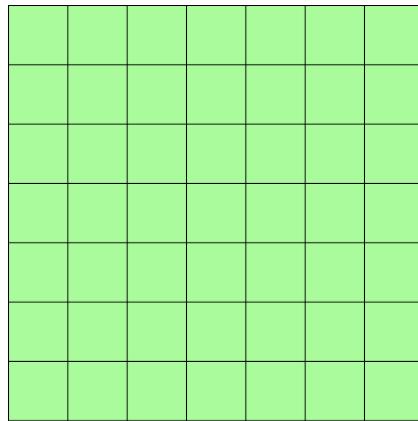
**Paternally
inherited**



Proxy of male
demography

Isolation by distance (IBD)

Dispersal is localized in space, which means that individuals geographically close to each other are more likely to mate.

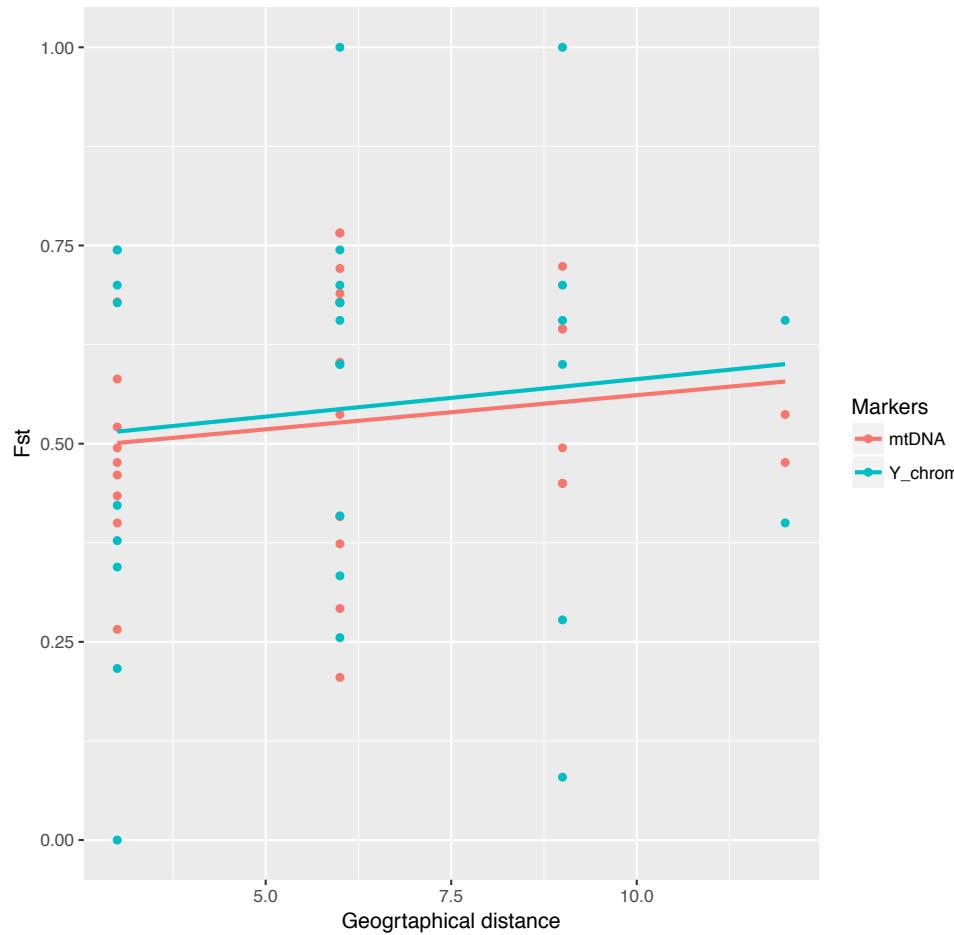


Main assumptions on the landscape:

- Continuous
- Homogenous (e.g. all sub-populations have same size)

The slope of the regression may be used to estimate $1/(4 \cdot N \cdot \pi \cdot m)$

How would you explain the observed pattern?

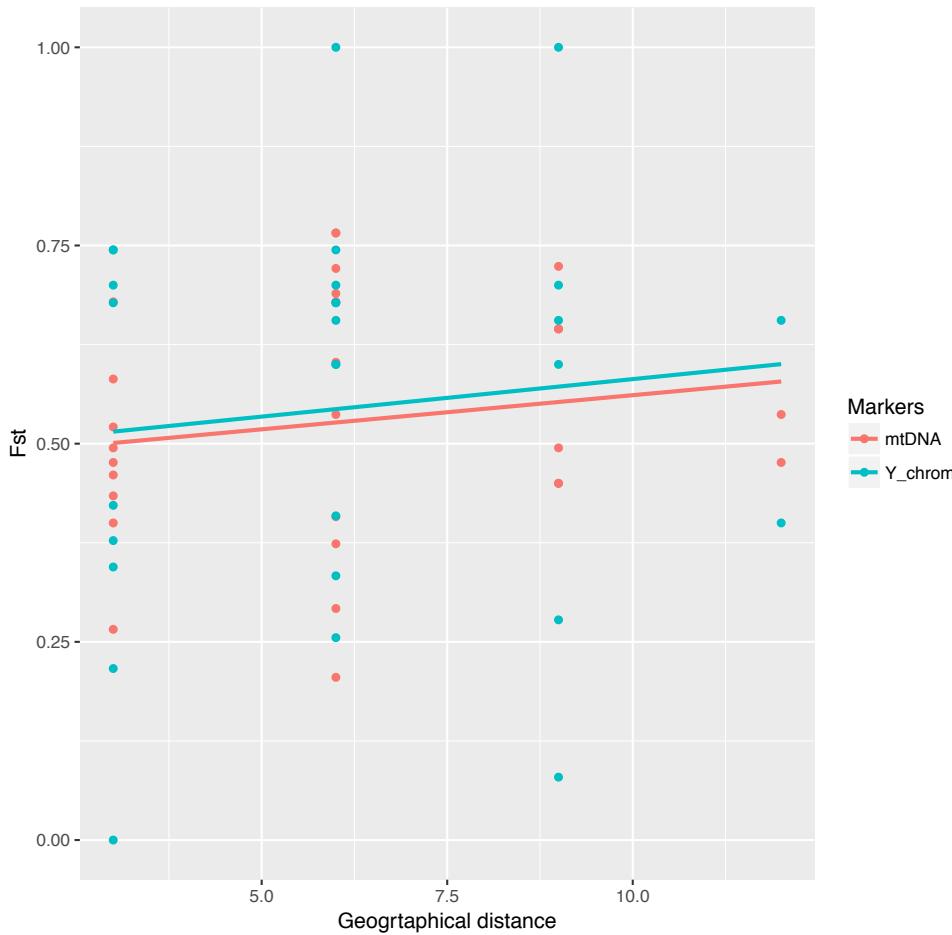


Behavioural ecologists



Male reproductive success: 10%

How would you explain the observed pattern?



Male
reproductive
success: 10%

Starting simulations of populations in space

General settings:

Starting: whole world is filled

Population density: 100 ind. / deme

Difficulty to cross (F) : 0.01

Growth rate (r) : 0.8

Time of the simulation: 18.000 generations

Start Recording data: at generation 12000

Record genetic data every: 100 generations

Record demographic data every: 100 generations

Genetic marker settings:

Y chromosome:

Marker type: sequence

N° base-pairs: 500 bp

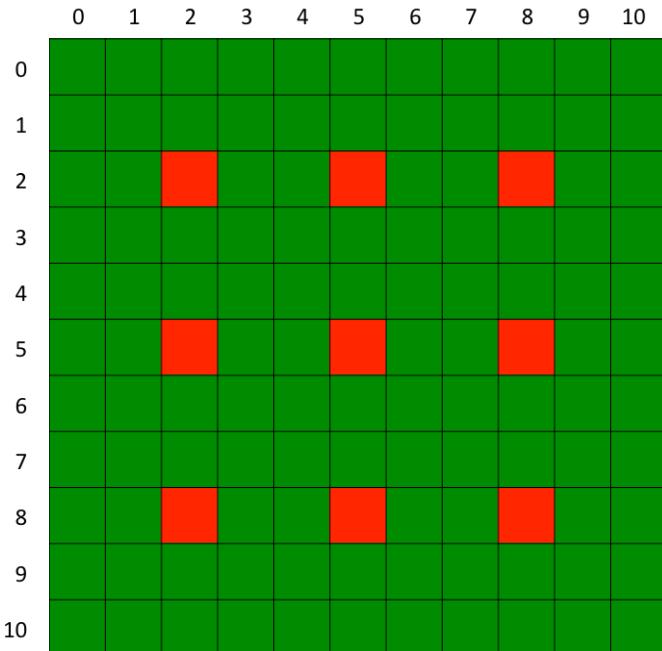
Mutation rate: 3×10^{-8} per base-pair/ generation

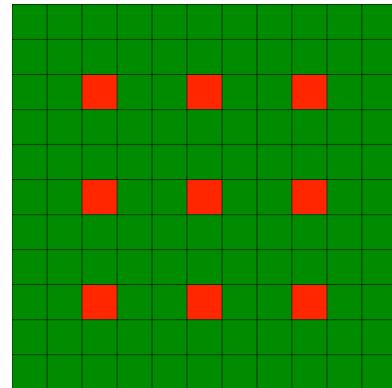
Mitochondrial DNA:

Marker type: sequence

N° base-pairs: 500 bp

Mutation rate: 3×10^{-8} per base-pair/ generation





Bilocal
&
migr. rate 0.1

- reprodMale: 1
- reprodFemale: 1
- migrationRate: 0.1
- msR 0.5

?

Bilocal
&
migr. rate 0.01

- reprodMale: 1
- reprodFemale: 1
- migrationRate: 0.01
- msR 0.5

?

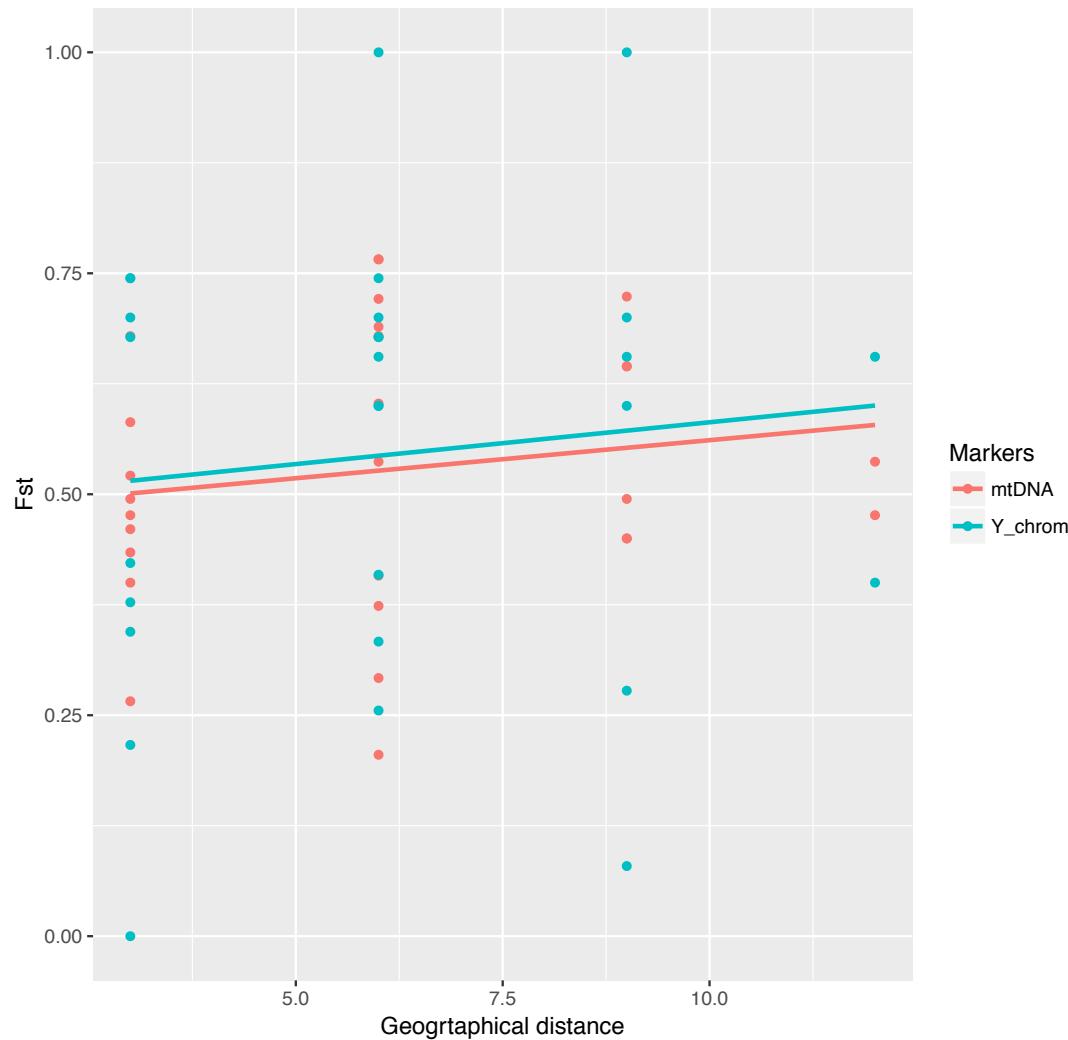
Female philopatry
&
Male Reproductive success

- reprodMale: 0.1
- reprodFemale: 1
- migrationRate: 0.1
- msR 0.1

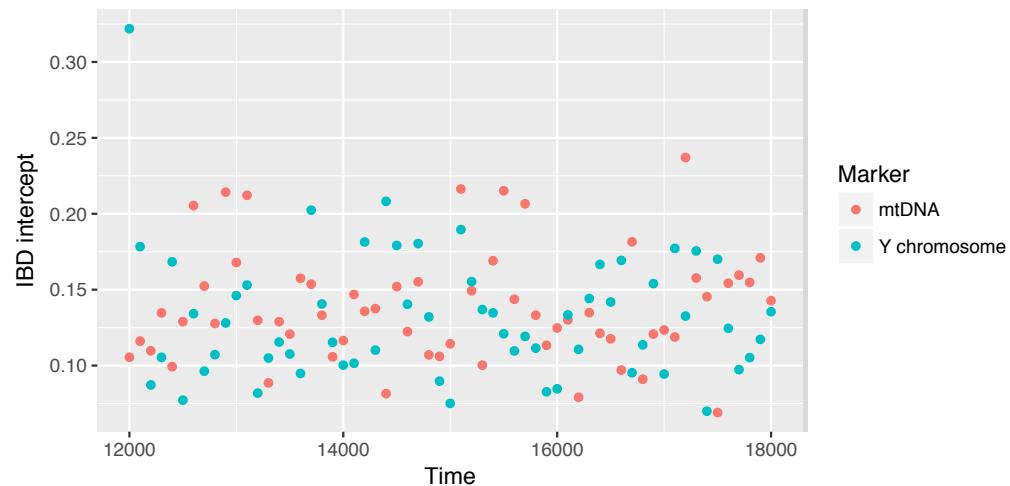
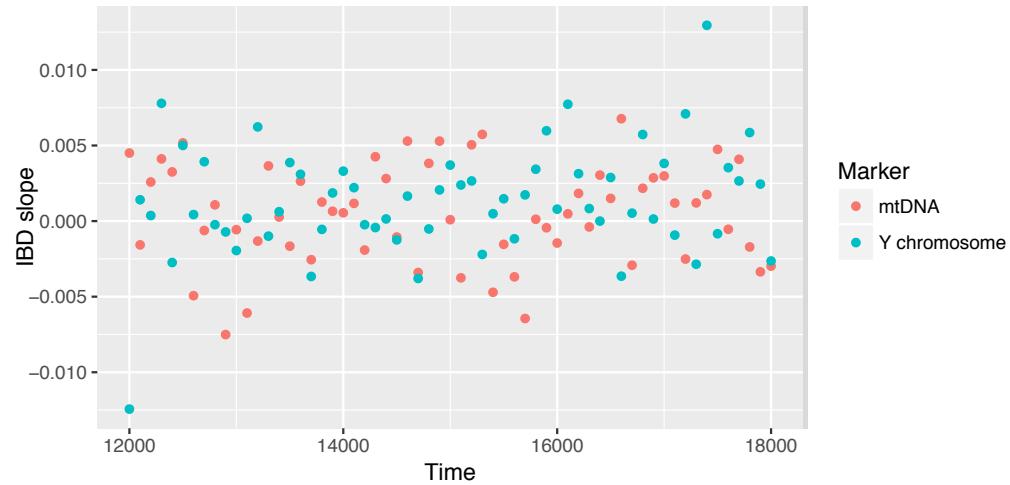
?

Results & Discussion

How would you explain the observed pattern?

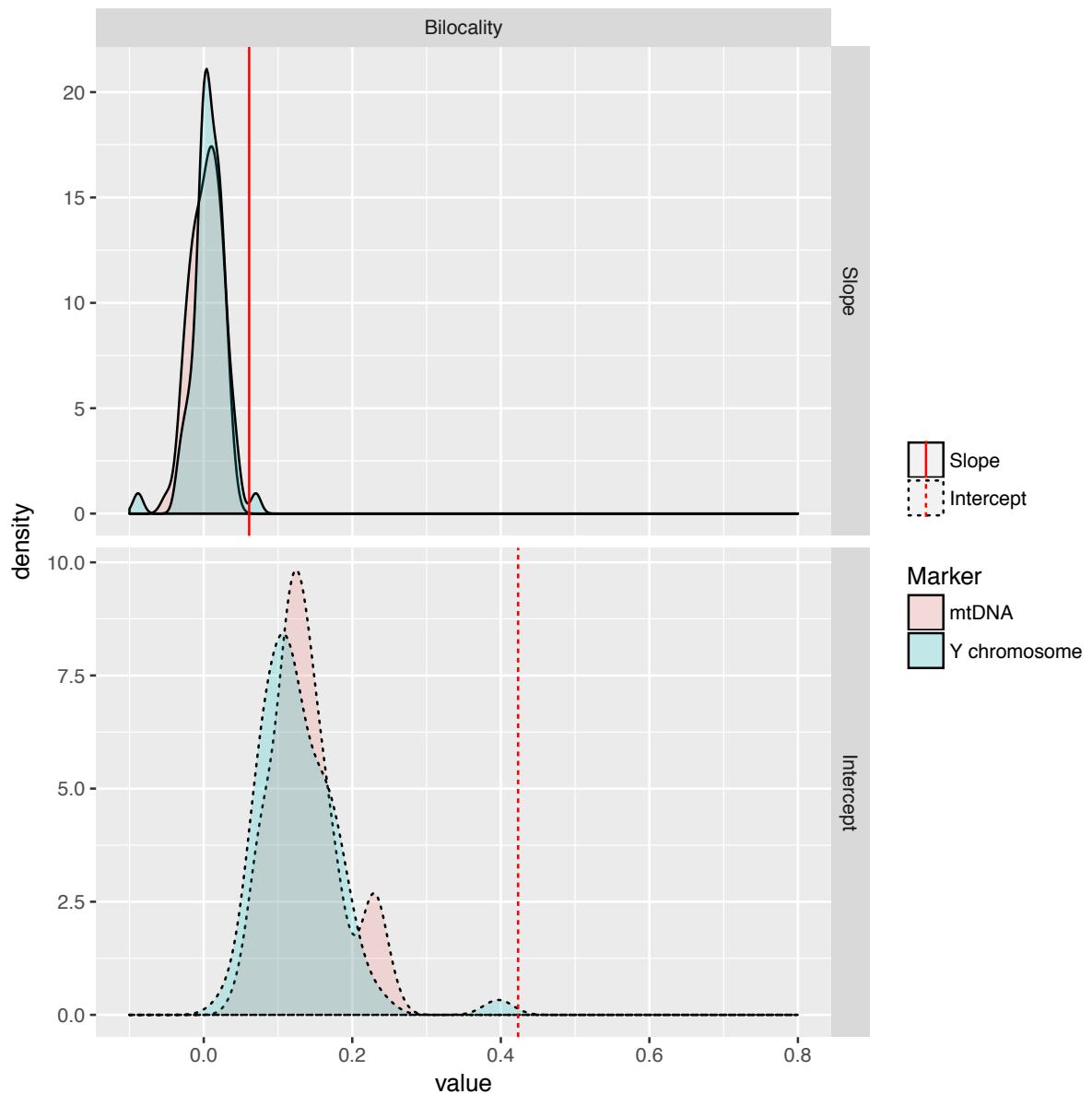


IBD slope and intercept over time



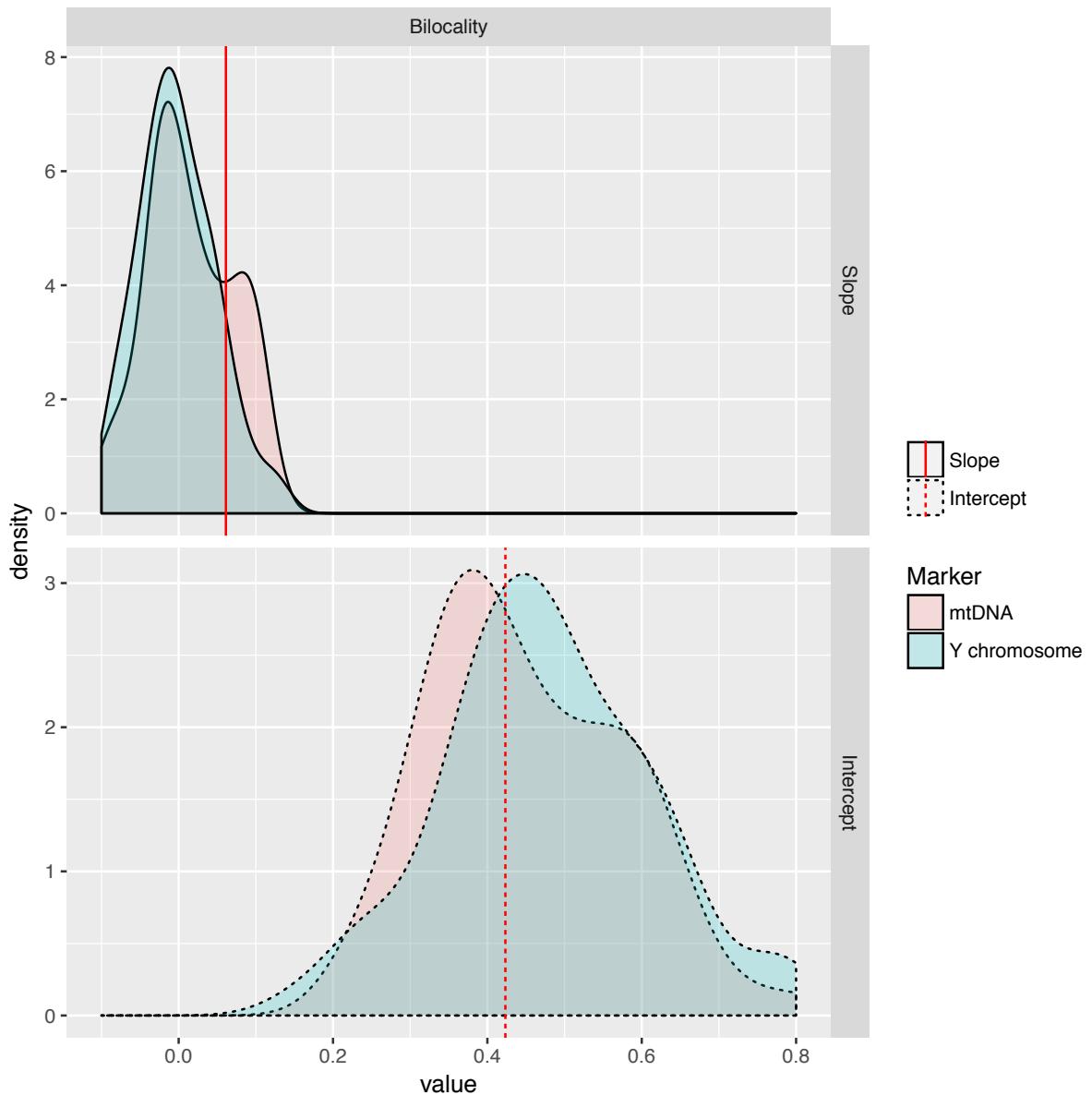
Bilocal
&
migr. rate 0.1

migr. rate: 0.1



*Bilocal
&
migr. rate 0.01*

migr. rate: 0.01

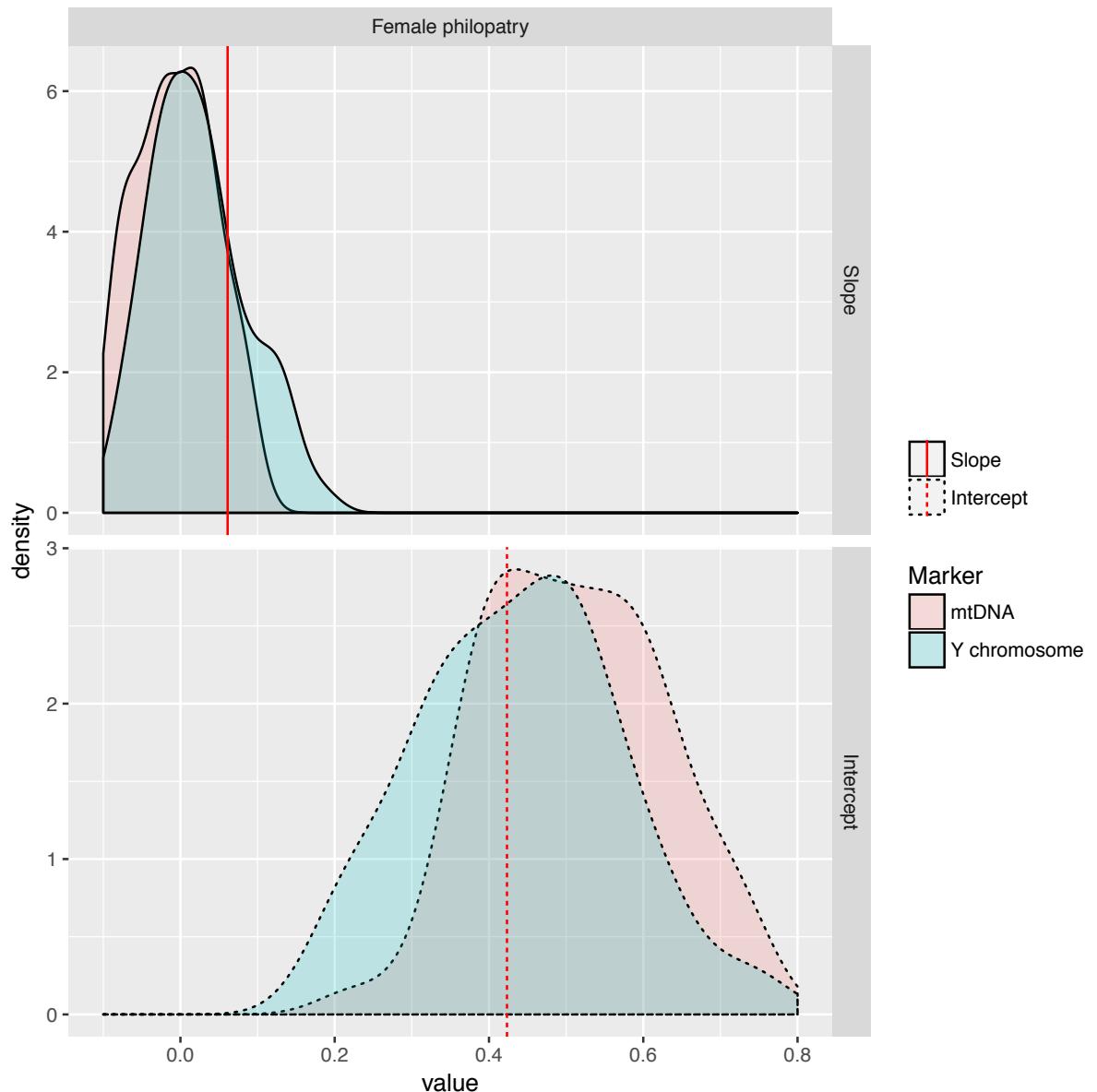


*Female philopatry
&*

Male Reproductive success

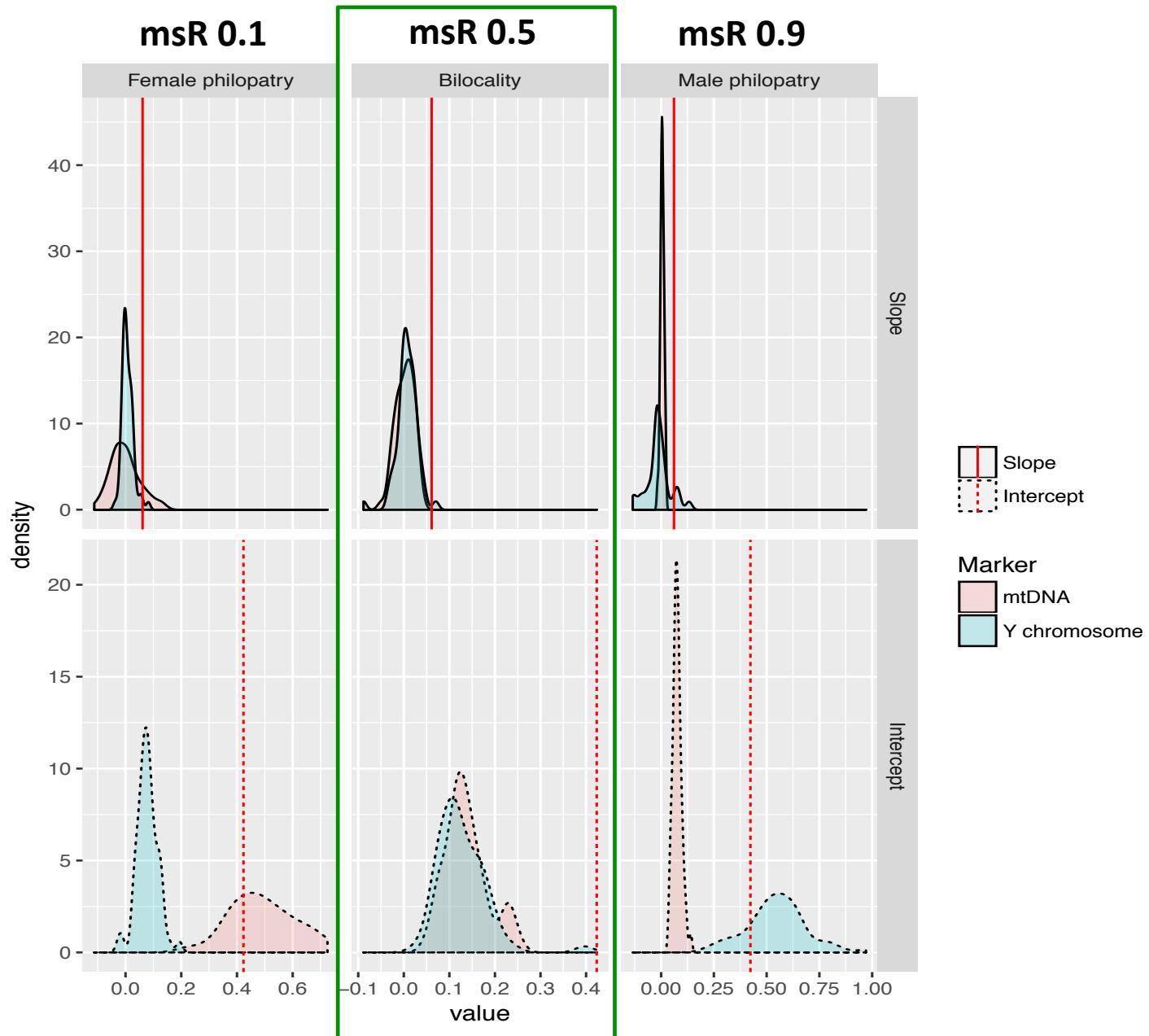
migr. rate: **0.1**

**Male reproductive
success:**
0.1



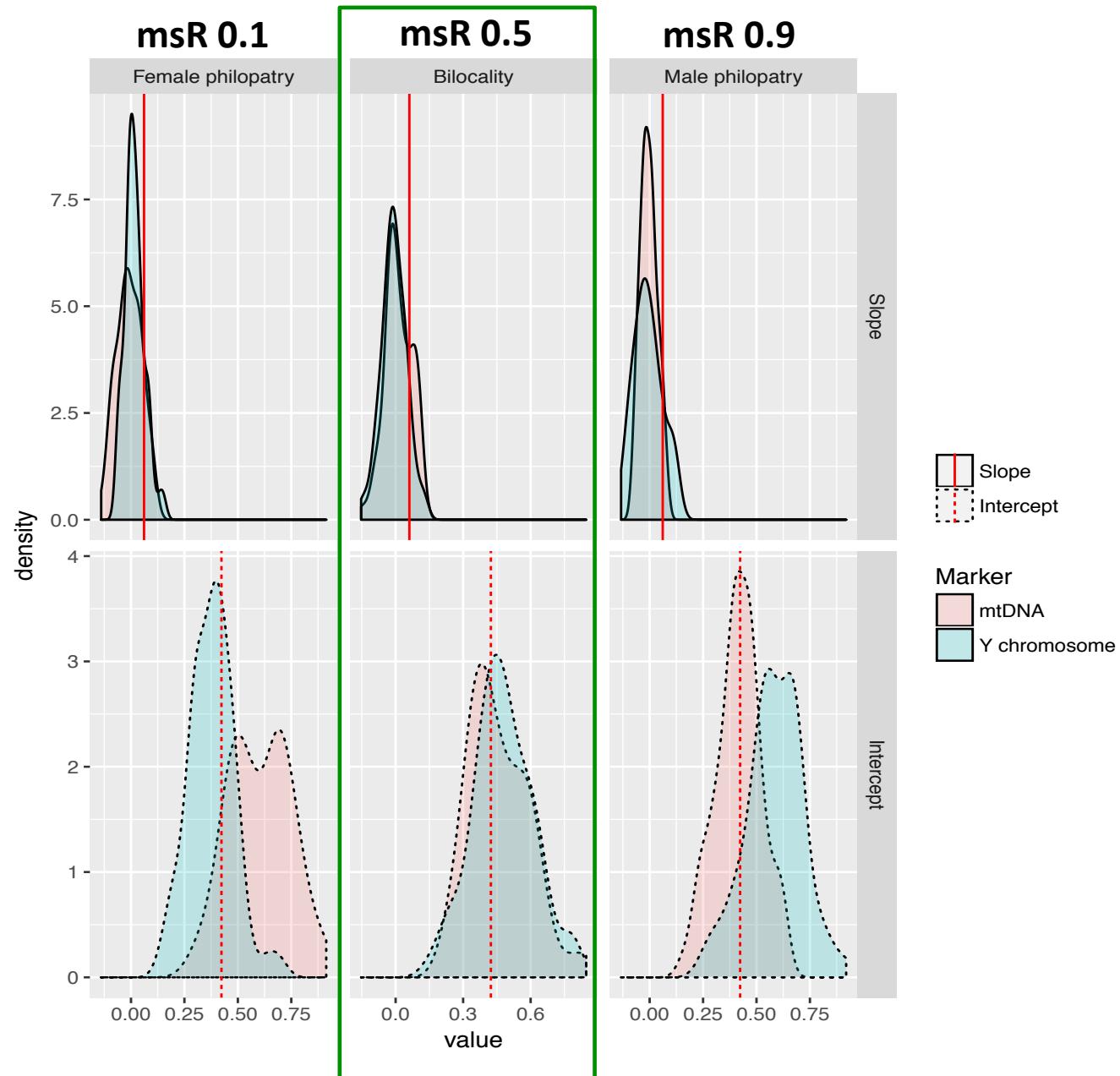
Bilocal
&
migr. rate 0.1

migr. rate: 0.1



Bilocal
&
migr. rate 0.01

migr. rate: 0.01

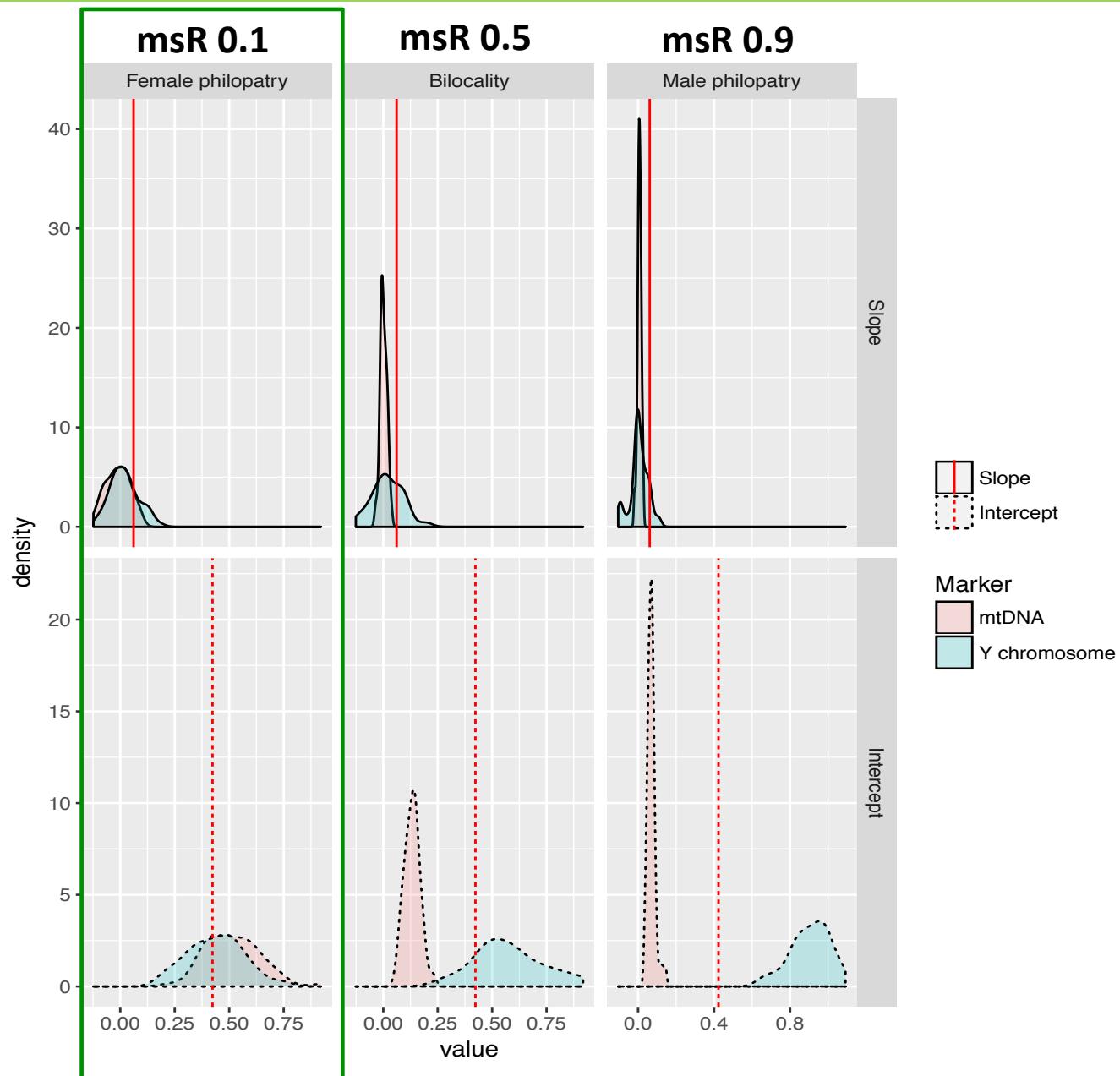


Female philopatry
&

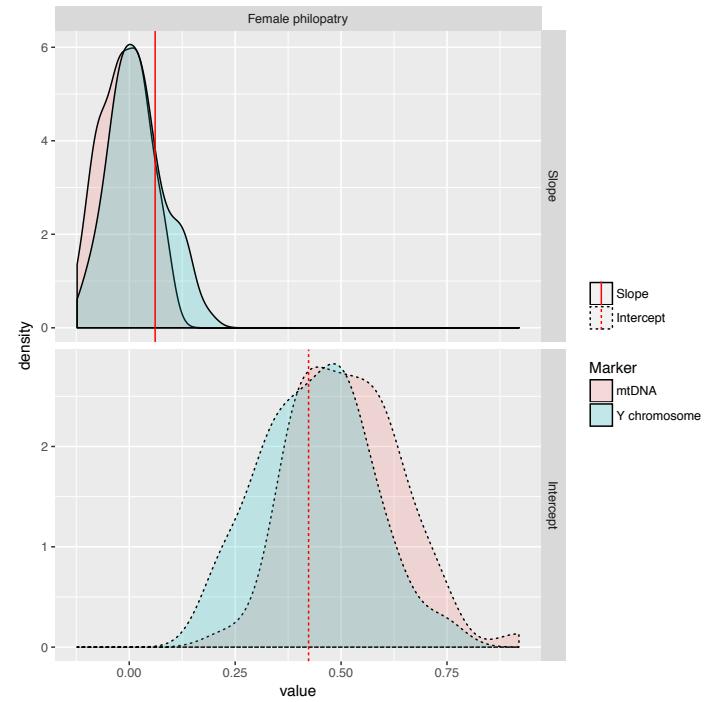
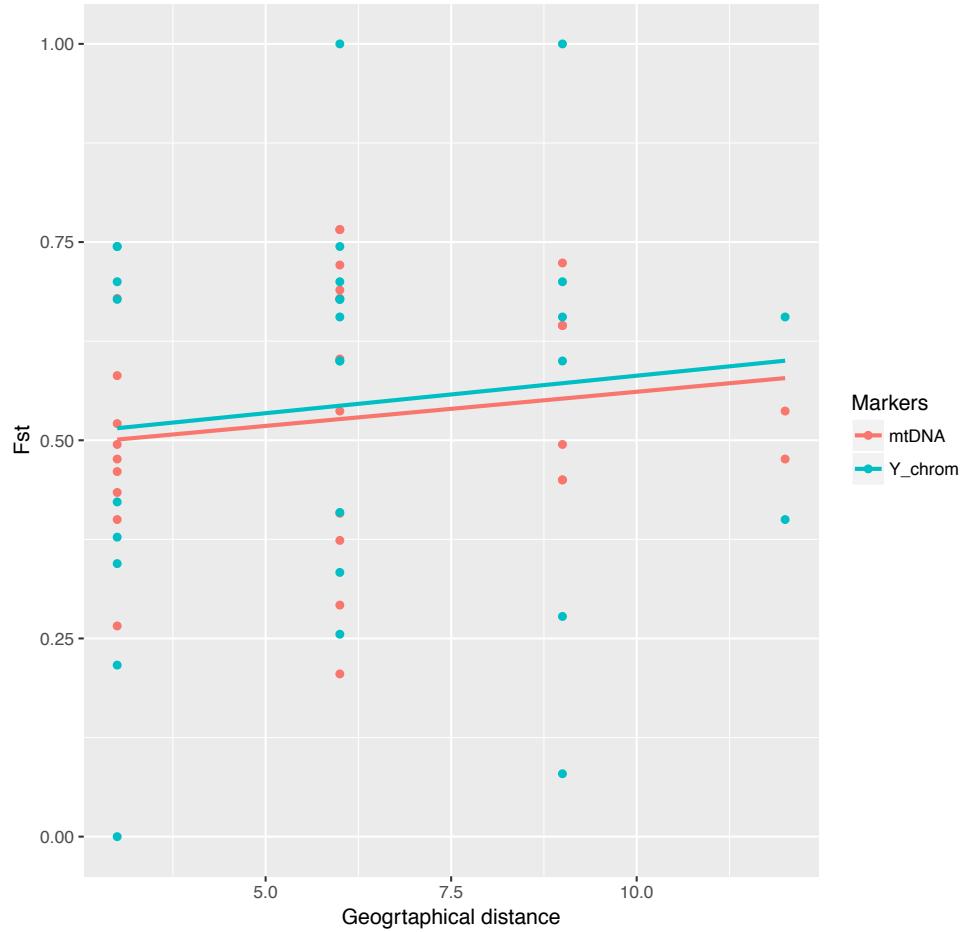
Male Reproductive success

migr. rate: **0.1**

**Male reproductive
success:**
0.1



That pattern was obtained by simulating a population with migr. rate 0.1 & male reproductive success 0.1



Conclusions