

A bisexual bidimensional branching process in a genetic context

M. González¹, D. Hull², R. Martínez³ and M. Mota⁴.

It is well known that the sex of human or animal individuals is controlled by a pair of chromosomes X and Y . Individuals having chromosomes XX will be females (F) whereas those having chromosomes XY will be males (M). Some genes related to certain characters are carried by chromosome X , chromosome Y or both of them. In this paper, we study the case in which a character associated to a gene with a pair of alleles R or r is linked to chromosome Y .

The evolution of such a character within a population can be modelled through an extension of the Bisexual Galton-Watson Branching Process (BBP) with mating fidelity (see [1]). We will denote MR a male with allele R and Mr a male with allele r . Females haven't got the gene so they will be denoted only by F . In order to mate, females will prefer MR males better than Mr males. This priority has been already considered by Hull in other context (see [2]). Therefore we have two types of mating units denoted by FMR and FMr , respectively. Fidelity in the mating means that each individual only forms one mating unit.

The mathematical definition of such a model is given by a sequence

¹Departamento de Matemáticas, Universidad de Extremadura, Avda. Elvas s/n, 06071 Badajoz, Spain (e-mail: mvelasco@unex.es).

²Department of Mathematics and Computer Science, Valparaiso University, Valparaiso, Indiana 46383, United States (e-mail: david.hull@valpo.edu).

³Departamento de Matemáticas, Universidad de Extremadura, Avda. Elvas s/n, 06071 Badajoz, Spain (e-mail: rmartinez@unex.es).

⁴Departamento de Matemáticas, Universidad de Extremadura, Avda. Elvas s/n, 06071 Badajoz, Spain (e-mail: mota@unex.es).

$\{(ZR_n, Zr_n)\}_{n \geq 0}$, where ZR_n , (Zr_n) denotes the number of FMR (FMr) mating units in the n -th generation, being:

$$(ZR_0, Zr_0) = (i, j), \quad i, j \in \mathbb{Z}^+$$

and for $n \geq 0$

$$(F_{n+1}, MR_{n+1}, Mr_{n+1}) = \left(\sum_{l=1}^{ZR_n} FR_{nl} + \sum_{l=1}^{Zr_n} Fr_{nl}, \sum_{l=1}^{ZR_n} MR_{nl}, \sum_{l=1}^{Zr_n} Mr_{nl} \right) \quad (1)$$

Good

with $\sum_{l=1}^0 = 0$, $\{(FR_{nl}, MR_{nl})\}_{n \geq 0, l \geq 1}$, $\{(Fr_{nl}, Mr_{nl})\}_{n \geq 0, l \geq 1}$ independent sequences of i.i.d. non-negative integer-valued bivariate random variables and $L(\cdot)$ the mating function, where:

$$L(F_n, MR_n, Mr_n) = (\min\{F_n, MR_n\}, \max\{0, \min\{F_n - MR_n, Mr_n\}\})$$

Notice that (FR_{01}, MR_{01}) and (Fr_{01}, Mr_{01}) may have different distributions. If these random vectors had the same distribution then $\{Z_n\}_{n \geq 0}$, with $Z_n = ZR_n + Zr_n$, would be a BBP with mating fidelity.

This work is devoted to study some interesting events for the model (1). In the main results, we provide sufficient conditions for the almost sure extinction of alleles R and r , as well as for having positive probability that these alleles survive. Moreover, some simulated examples are given.

References

- [1] D.J. Daley. Extinction conditions for certain bisexual Galton-Watson branching processes. *Z. Wahrscheinlichkeitstheorie verw. Geb.*, 1968, 9, 315-322.
- [2] D.M. Hull. A reconsideration of Galton's problem (using a two-sex population). *Theoretical Population Biology*, 1998, 54, 105-116.