Executive Summary — SCUDEM Fall 2018, Problem A: Patrilineal Clans

Introduction

Research into genetic history shows a bottleneck in genetic diversity in the Y-chromosome from 7000 BCE to 5000 BCE, but not in maternally-inherited mtDNA. Previous hypotheses suggest that this is due to formation of patrilineal clans and conflict between them. The model made by Zeng, Aw & Feldman (2018) accounts for this conflict, but assumes a uniform population of females instead of distinguishing between females in various clans. We present a system of differential equations which models male and female members of clans and their conflict and intermarriage dynamics.

Assumptions: Our key assumptions are as follows:

- The populations of the clans will tend toward a carrying capacity with a 50:50 gender ratio.
- The rate of increase for the population will be proportional to their sizes.
- Females are associated with a clan but can choose to switch clans. Females will have some preference to stay in their own clan or to seek better mating opportunities.
- Males will die from conflict at a rate proportional to the size of the male population in both clans. Females do not die in conflict.
- The clans will have the same population dynamics, carrying capacity, and conflict morbidity rates.
- Clans will have different intermarriage rates.

Model: A model of two clans is as follows:

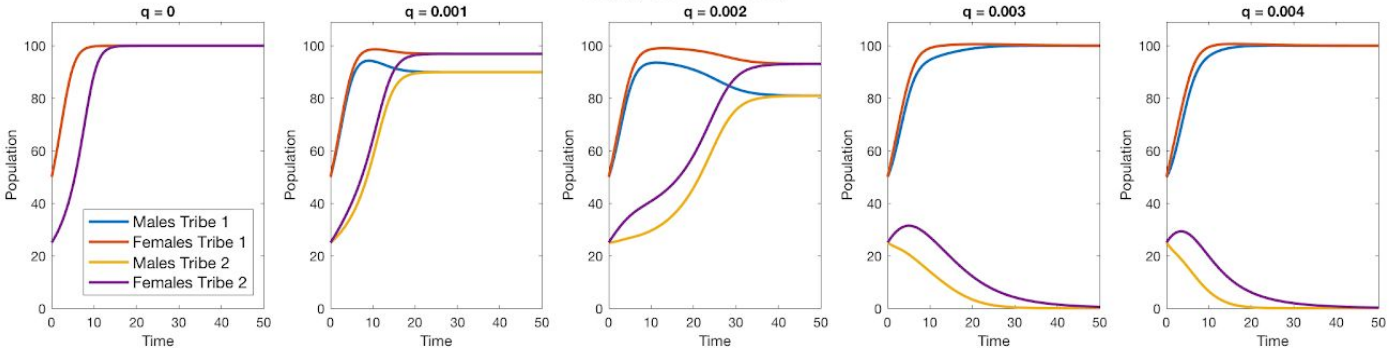
$$\frac{dF_1}{dt} = r_1 F_1 M_1 \left(1 - \frac{F_1}{K - M_1}\right) - r_2 F_1^2 - c_1 F_1 M_2 + c_2 F_2 M_1 \qquad \frac{dM_1}{dt} = r_1 F_1 M_1 \left(1 - \frac{M_1}{K - F_1}\right) - r_2 M_1^2 - q\, M_1 M_2$$

$$\frac{dF_2}{dt} = r_1 F_2 M_2 \left(1 - \frac{F_2}{K - M_2}\right) - r_2 F_2^2 - c_2 F_2 M_1 + c_1 F_1 M_2 \qquad \frac{dM_2}{dt} = r_1 F_2 M_2 \left(1 - \frac{M_2}{K - F_2}\right) - r_2 M_2^2 - q\, M_1 M_2$$

The variables in our model are F_i and M_i where i refers to the clan and F and M respectively refer to the population of females and males in that clan. The parameters in our model include growth rates r_1 and turnover rate r_2, carrying capacity parameter *K*, conflict morbidity rate *q*, and intermarriage rates c_i, where a higher c_i indicates lower clan attachment for females in clan *i*. All parameters are nonnegative, and variables are defined only for nonnegative values.

Solution & Analysis:

Varying morbidity of conflict: We kept all parameters the same but varied the conflict parameter *q* from 0 to 0.004, to show the effect of conflict morbidity on clan outcomes. High *q* is higher conflict morbidity.

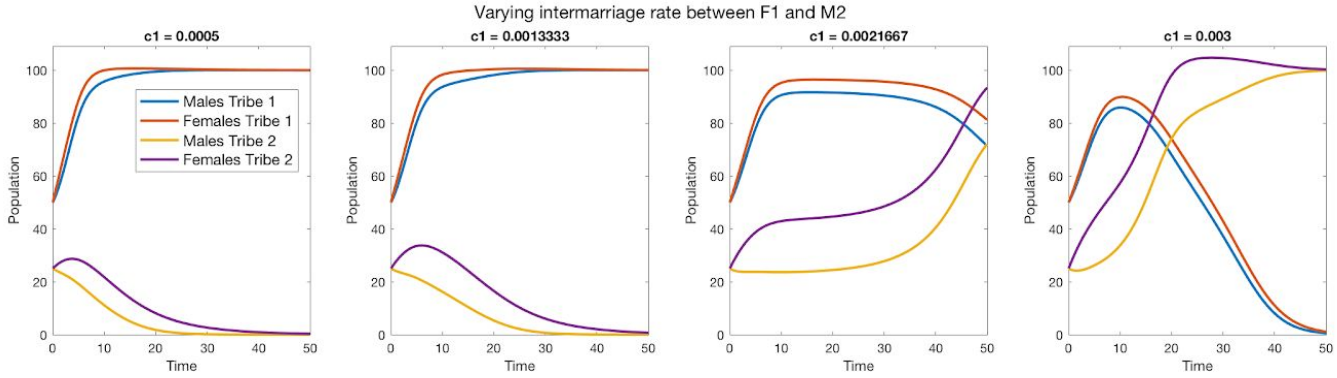


Our model suggests that:

1. Without deaths from conflict (q = 0), the male and female populations arrive at a gender ratio 50:50 and grow to approach the carrying capacity.

2. With low conflict morbidity (q <0.002), both clan populations will ultimately equilibrate, but the gender ratio will not be 50:50. This is due to the effect of ongoing war killing males but not females. In this case, there will be no Y-chromosome loss.
3. With higher conflict morbidity (q > 0.003), the smaller clan will not be able to recover the population. This leads to a permanent loss of this clan's Y-chromosome.

Varying intermarriage rates: When we vary the intermarriage rate for the smaller clan, keeping conflict rate *q* at 0.003 and the other clan's intermarriage rate (c_2) at 0.001, the smaller clan can be rescued by a high intermarriage rate.



In this analysis, clan 2 starts with a smaller population, and the parameter describing the rate of intermarriage between females of clan 1 and males of clan 2 is c_1, which we vary. As c_1 increases, clan 2 can survive despite smaller initial size, and ultimately clan 1 dies out as females move from clan 1 to clan 2.

Limitations & Extensions: Many factors may contribute to the survival or extinction of human genetic lineages which are not represented by our model. In particular, we have not accounted for group fusion or fission except as it occurs in intermarriage. We have also not accounted for potential variability in parameters between groups. For example, in a real-world scenario, we would likely see different growth rates, intermarriage rates, conflict morbidity rates, and/or carrying capacities among different groups.

Our analysis focuses on two clans, but our model can be extended to more. If there are *n* clans total, the *i*th clan would be modeled as follows:

$$\frac{dF_i}{dt} = r_1 F_i M_i \left(1 - \frac{F_i}{K - M_i}\right) - r_2 F_i^2 - \sum_{k=1,\, k\neq i}^{n} c_i F_i M_k + \sum_{k=1,\, k\neq i}^{n} c_k F_k M_i$$

$$\frac{dM_i}{dt} = r_1 F_i M_i \left(1 - \frac{M_i}{K_i - F_i}\right) - r_2 M_1^2 - \sum_{k=1}^{n} q\, M_i M_k$$

This accounts for interactions between all clans with respect to both marriage and conflict.

Conclusion: For our model to be consistent with the Y-chromosome bottleneck in the genomic record, the parameters must be such that one population of males among competing clans will die out. This requires conflict morbidity rates to be sufficiently high. Intermarriage rates help determine which clan will survive, even when conflict morbidity rates suggest that the smaller clan would otherwise die out.

References

Oota, H., Settheetham-Ishida, W., Tiwawech, D., Ishida, T., & Stoneking, M. (2001). Human mtDNA and Y-chromosome variation is correlated with matrilocal versus patrilocal residence. *Nature Genetics*, *29*(1), 20.

Zeng, T. C., Aw, A. J., & Feldman, M. W. (2018). Cultural hitchhiking and competition between patrilineal kin groups explain the post-Neolithic Y-chromosome bottleneck. *Nature Communications*, *9*(1), 2077. https://doi.org/10.1038/s41467-018-04375-6