

Simulator[7]'s screen for exhibition (example)

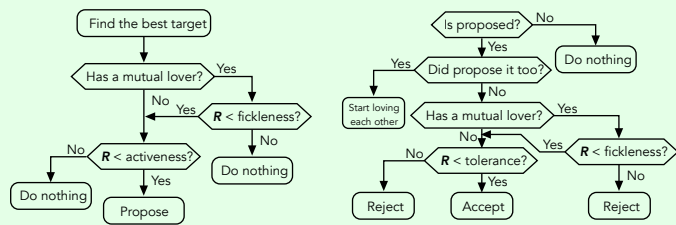
Motivation

Let's do ALIFE researches that contribute Humanities, by *Human Life As-It-Could-Be!*
ex. for better understanding of sexual orientation from a viewpoint of evolutionary psychology [2] in a context of nature-culture interaction.

Model

Sexual orientation = behavioral relation between two individuals as a result of mutual attraction.

-- based on hereditary (partially) sex-influenced traits of appearance and preference (2 out of 4 elements are sex-influenced).
Human-like life cycle: birth, grown-up, love, proposal, birth of baby, separation and death.



Mating algorithm

Simulation

Starting from 4,000 random agents for 4,000 years (96,000 steps) of evolution for ancestry species, then more 4,000 years for

1. Restricting partnerships to opposite sex,
 2. Continuing no suppression on partnership selection, and
 3. 2,000 years of suppression then sudden relaxation of restriction.
- Taking the average over 20 independent processes for each settings.
 - Sexual dimorphism → Gene distance between sex-influenced genes.
 - Speciation → Cluster tendency by Hopkins statistic [3].

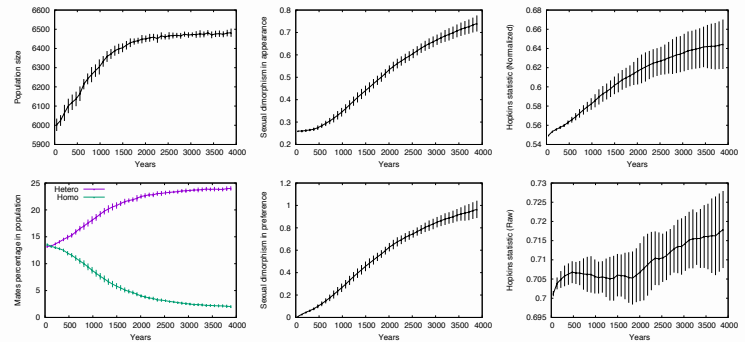
Result

Main observations:

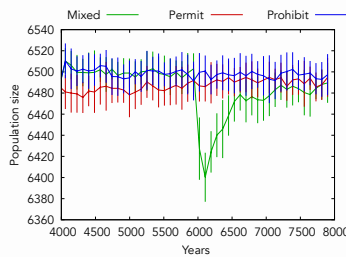
1. Restricting partnerships to opposite sex resulted in a relatively higher reproduction rate.
 2. Imposing no suppression on partnership selection promoted both sexual dimorphism and speciation.
- No suppression → phenotypic separation between sexes.
 - Suppression → gradually breaks the dimorphism.
 - This suggests an ironical fact that the suppression promotes the wider diversity of sexual orientation in terms of who prefers who.

What's next

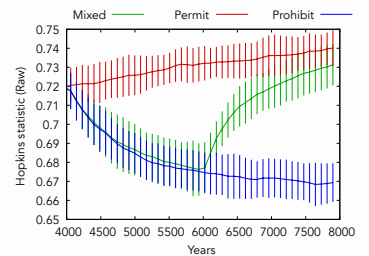
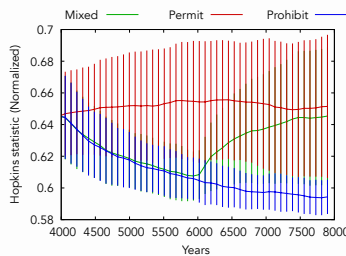
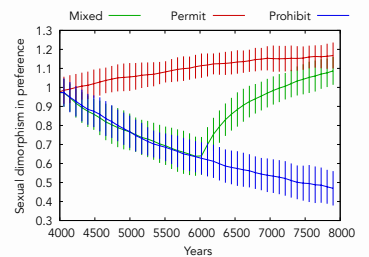
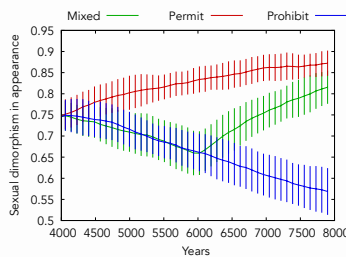
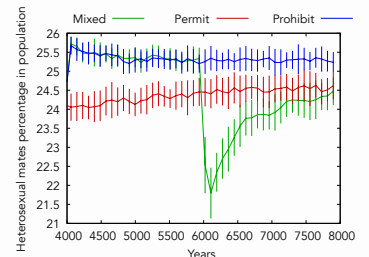
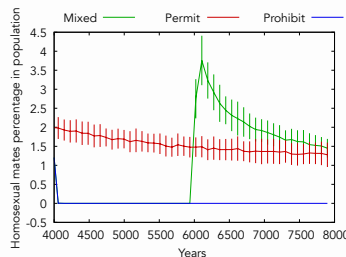
- Introduction of the diploid and sex chromosome for genetics, resource possession and sharing for economics, and others.
- Application for another issue, such as incest avoidance, multiple vs single mates, origin of aesthetics, ethics on faithfulness, etc.



Early 4,000 years for ancestry species starting from random genes.



The web site URL of the parent project.



References

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