

The files here correspond to the project described in the paper titled “Natural selection subsumes and unites multiple theories of perceptual compression”, which is authored by Victor Quintanar-Zilinskas. All references below to tables, figures, and paper sections correspond to parts of the paper.

Latest revision to:

Code: Jan 2019

Paper (as posted on bioRxiv): Jan 2019

All “.m” files were generated and run using Matlab.

Simul.m performs the simulations described in “Methods, Interface allele competition”. The data generated are saved in “.mat” files that are labeled with a letter and a number that respectively correspond to the simulation condition (as defined in Table 1) and to the replicate.

X#.mat (“X” represents a single letter) file rows each represent a simulated generation. Odd columns can be ignored; column 2 (4, 6) corresponds to the population in which 90% (50%, 20%) of the population is reproductive from one generation to the next. The numerical values in these columns indicate the number of simulated organisms carrying the “optimal” allele.

qlook.m extracts and organizes data from the “.mat” files and performs the statistical tests reported in Table 1.

Pan_x_Jan19 (“x” represents a, b, or c) files generate the data and graphs shown in Fig. 2; data generation is described in “Methods, Expected utility computation”.

SuppEqSolutions.nb is a Wolfram Mathematica notebook that serves this project as a workbench for manipulating and simplifying mathematical expressions. Section labels correspond to subsections of the “Supplementary Equations” (SE) paper section, and the expressions manipulated are presented in order of their appearance in SE.

SuppEqSolutions.pdf is provided for those without access to Wolfram Mathematica.

IGNORE

Pan_a through **Pan_e** files correspond to Fig. 2 in the Dec 2018 version of the paper