Code summaries

November 21, 2016

0.1 Statement of purpose

This document was written to describe the methods taken to answer questions in the Phenology project, as well as point out how to use the code. This is intended as an internal document, although may be useful for methods or supplements in any future publications.

1 Underlying model

In order to examine the evolution of multiple-trait cueing decisions, we constructed a general mathematical model. Each day, an organism can calculate their emergence value:

$$E = 100 \frac{cue_1}{trait_1} + 100 \frac{cue_2}{trait_2} \dots$$

When the emergence value E is greater than or equal to 100, the organism decides to emerge. Note that we use E=100 because we liked larger numbers - there's no reason that E couldn't equal 1. We multiply by our threshhold E value (here 100) so that the interpretation of each trait value is simple. If an organism has a $trait_1 = X$, then that means that this organism would emerge when $cue_1 = X$ if other cues remained at zero.

Organisms actually emerge *lag* days after deciding to emerge (default 1), which both increases biological realism and allows to remove this potential source of autocorrelation. They then collect fitness for *duration* days (default 10), and their total fitness is the sum of the daily fitness they collected.