



The most textbook-cited example of natural selection is the shift in color patterns in the peppered moth *Biston betularia*. This moth has two genetically determined color patterns: a light, speckled ‘typica’ morph, and a dark, melanic ‘carbonaria’ morph. The color is determined by one gene with two alleles, with the dark allele dominant to the light (light morphs are all homozygous light). These moths are active at night, and spend their days resting on the bark of trees, where they are preyed upon by birds. Essentially defenseless against the birds, moths rely on *cryptic coloration* (camouflage) to hide from predators. On lichen covered tree bark light moths blend in, and dark moths stand out.

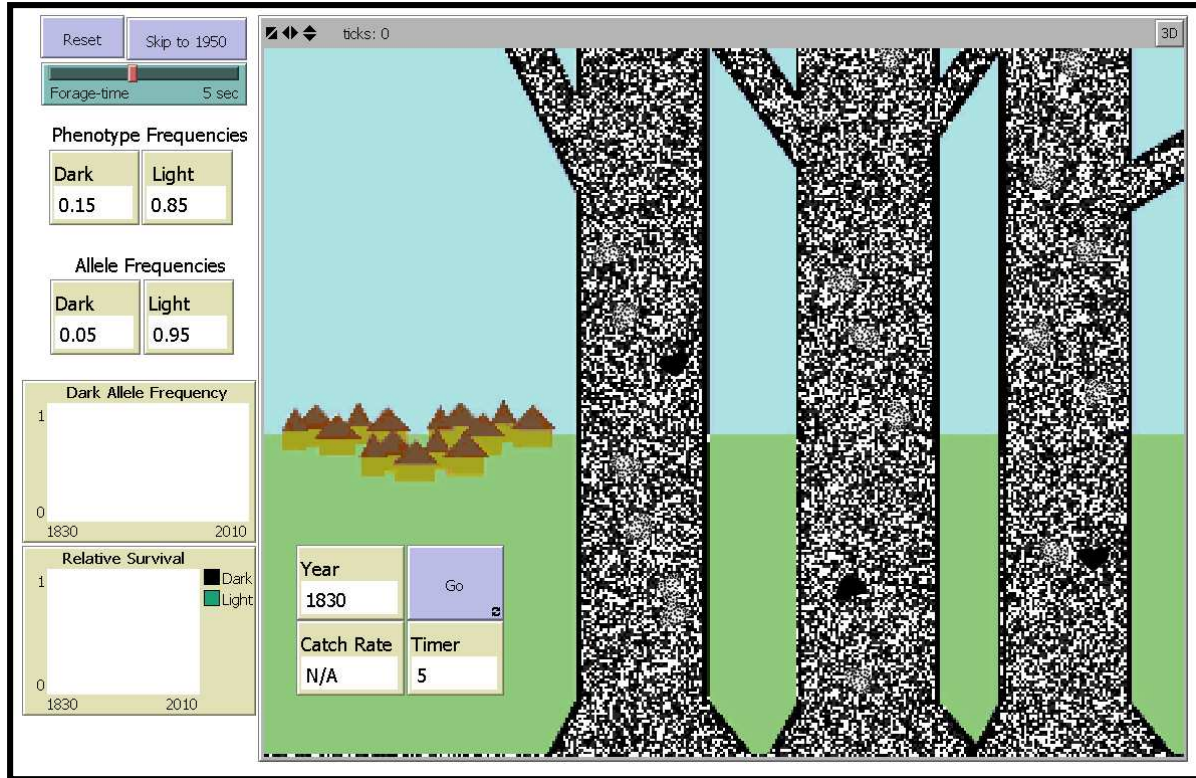
## Model Details

When the model opens, you will see three tree trunks with a total of 20 moths on them. The year is 1830 and the stand of trees is near a small, but growing, English village (Fig. 4). Being pre-industrial revolution, the trees are covered in lichen, and you may only be able to see the dark moths. You will also see several control buttons and sliders, along with various reporters and graphs. These controls and reporters are described in Table 1. The initial frequency of the dark allele is set at 0.05, which gives an average proportion of dark moths of 0.0975 (but this will vary because of randomness in the model).

To run the model, set the foraging time to 5 seconds, and click ‘Go’. A bird will appear in the world-view and follow the mouse cursor as the timer counts down from 5. While the timer is counting, move the bird around the trees and ‘eat’ moths by right-clicking the mouse over them. When five seconds have expired the bird will disappear. You can see how successful you were at catching moths by the ‘Catch Rate’ reporter, which gives a cumulative average of the number of moths caught per second. You can also read the phenotype and allele frequencies of the remaining moths. The dark allele frequency is graphed as a function of time, as are the proportions of each color morph surviving in each foraging bout. You can read specific values off of these graphs by scrolling over them.

When ‘Go’ is clicked again, the model creates 20 new moths with genotypes drawn from the current allele proportions. These new moths are randomly placed around the tree trunks. Also, the year is advanced by two. From 1835 on, the lichen begins to die off the trees until it is all gone. From 1955 on, the lichen begins to re-grow on the trees.

**Figure 1: Screen shot of ‘Industrial Melanism’ simulation**



**Table 1: Controls and reporters for ‘Industrial Melanism’ simulation**

Control	Action
Reset	Starts the simulation over at 1830
Forage-Time	Sets how long each foraging bout will last (1-10 sec)
Go	Brings in the bird, starts the timer, and allows foraging
Skip to 1950	Sets the year to 1950, just prior to pollution control measures
Reporter	Description
Year	The simulated year, which correlates with lichen growth
Timer	The number of seconds remaining in the foraging bout
Catch Rate	The mean number of moths caught per second
Phenotype Frequencies	The proportion of light and dark moths in the population
Allele Frequencies	The proportion of light and dark alleles in the population
Dark Allele Graph	Plots to proportion of the dark allele by year
Relative Survival Graph	Plots the proportion of each morph surviving predation