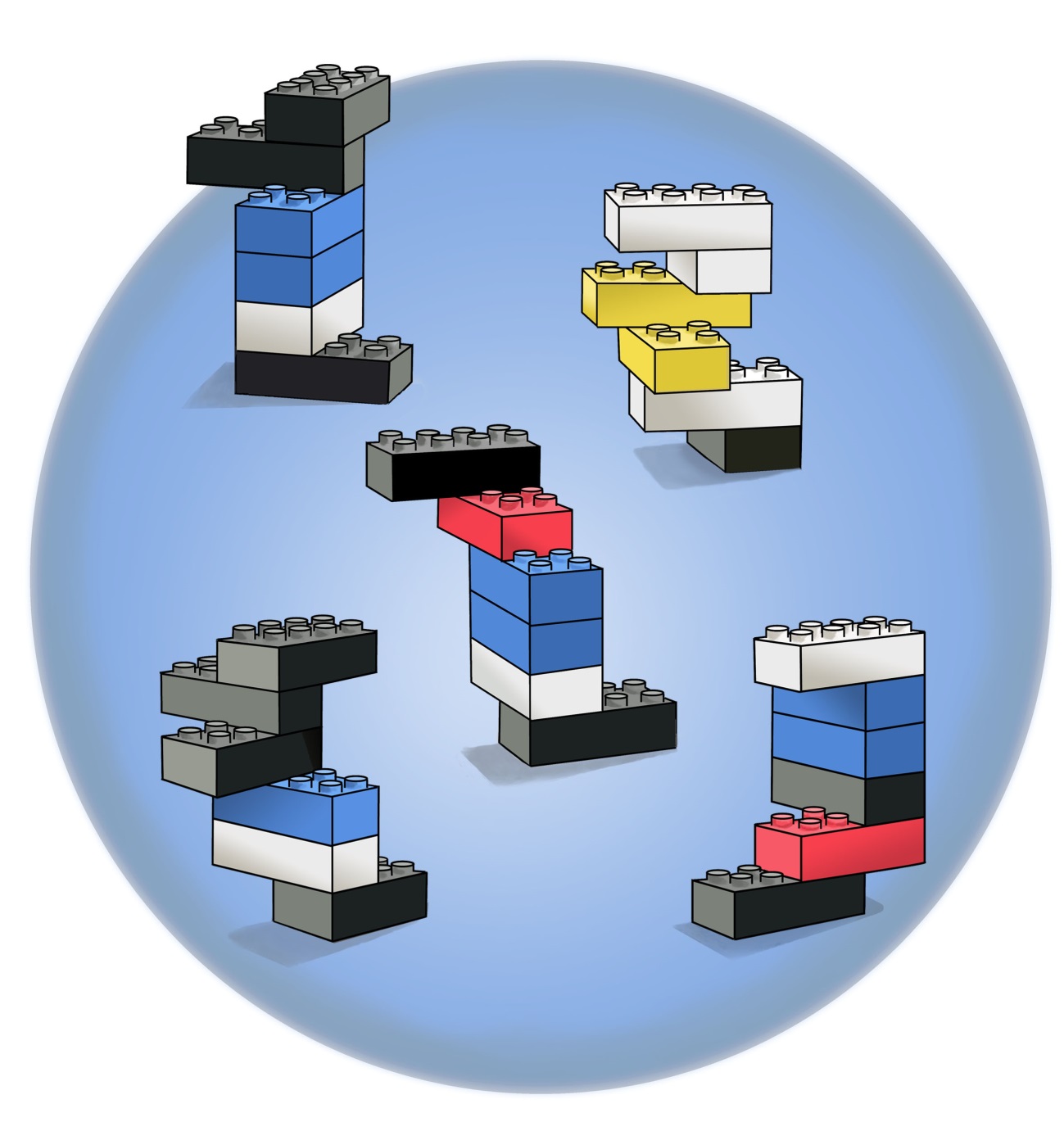
**Evolution of Legorgs: a physical simulation of adaptation by natural selection**

This activity illustrates adaptation by natural selection for a trait, in this case motility of animals with genetically specified morphology, assembled from six Lego® bricks. The animals are called Legorgs, (short for leg-organisms) since they only consist of a leg.

The individual Legorgs are constructed by random draw from the gene pool of five 8x2 Lego® bricks, each representing a body segment. Each of the bricks can have five colours (alleles), and each colour specifies a morphogenetic rule. The morphogenetic rule specifies how to place the brick on the previous brick (therefore, it is necessary to specify a foot segment, which we by convention always select as black. The motility of the animal is the distance it can move under controlled conditions (see below). We assume that fitness is proportional to the motility, and that individuals transmit genes to the next generation proportional to their fitness. The experiment is to measure the fitness of animals and their descendants through five generations. Our prediction is that in general, fitness should increase with generation.



**Fig. 1 Fifth-generation Legorgs, with on average 30 mm motility**

**Scoring fitness.**

Legorgs are built from five genes, specifying five segments placed on a foot (Figure 1). The animals are drawn randomly from the gene pools, described below. Each allele (colour) corresponds to a morphogenetic rule, specifying how to place the brick on the previous one, as detailed in the “Morphogenetic rules for assembly of Legorgs.” Therefore, the genetic structure will build Legorgs with different morphology. Fitness is scored by assembling the Legorgs (segment 1 is placed on the black foot-segment) and righting them on the foot. When released, the animal may tip and fall, and when righted again it will have moved a certain distance on the surface. The distance moved by a corner of the foot is marked and measured. The average of five measurements is the fitness of the Legorg and is entered in the “Generation of Legorgs” table. For best results let the Legorgs move on a hard, smooth surface such as a glass or whiteboard plate. Here, it is convenient to mark the corner of the foot segment with a whiteboard marker.

**First generation**

For the first generation Legorgs, use the “Generation of Legorgs” table to record the alleles for each Legorg. Each Legorg consists of five genes (bricks) placed on a foot; each of the genes can be one of five alleles (colours).

* Five opaque plastic bags are filled with 5 bricks (1 of each colour in each bag). Each of these bags simulates the gene pool for one of the five genes (in the following generations it is desirable to have 100 bricks in each bag, but it is not necessary in the first generation with equal distribution of alleles).
* Shake bags to ensure randomised draw. Draw a brick from each bag (the sequence is important). Note the sequence of colours drawn on the “Generation of Legorgs” table. When bricks from the five bags are drawn, the animal is specified genetically. Do not construct the animal now, so put the bricks back into the bags (NB!) and select again for the next Legorg.
* Repeat this until you have the genetic structure of 10-20 Legorgs noted on the “Generation of Legorgs” table.
* Now build the Legorgs using the “Morphogenetic rules for assembly of Legorgs,” score their fitness and enter fitness value in the final column of the “Generation of Legorgs” table. Calculate and enter the sum and average for fitness for the Legorgs.

Next, the contribution of each individual gene (position of brick with respect to foot) to the overall fitness of the Legorg can be calculated. Each gene is detailed on a copy of the “Gene pool table” – one per gene per generation, i.e. there will be five “Gene pool tables” for the first generation.

* The allele of each Legorg is weighed by their fitness. This is done by entering the fitness of the Legorg (obtained previously) in the table at the position of the allele (colour) for that gene (particular position of the segment relative to the foot).
* Calculate the sum of fitness (Σ fitness) for all Legorgs and the sum of fitness for each allele (Σ colour weight).
* Calculate fitness for each allele relative to the total fitness in percent (rounded to nearest whole number), using the formula
* The percentage of each allele is simply the number of bricks of each colour needed to fill the gene pool (assuming 100 bricks for the next generation gene pool bag).

**Second to fifth generation**

* Fill the opaque bags with coloured bricks, according to the calculation from the last generation gene pool table.
* Mutations can be simulated by changing one brick in each of the bags with a brick of another (randomly chosen) colour. This corresponds to an unnaturally high mutation rate, (0,01 against normally 10-4 to 10-7), but can probably show effects of mutations during the few generations used here.

As previously, draw the genetic structure of 10 or 20 Legorgs, build, determine fitness and note them in the “Generation of Legorgs” table. After determining fitness of all the Legorgs, transfer the values to the corresponding “Gene pool table” and calculate the next generation gene pools, as performed previously.

**Morphogenetic rules for assembly of Legorgs**

The morphogenetic rules for assembly of Legorgs are shown below. Legorgs are assembled from segment 1, “counter-clockwise” i.e. the previous segment (grey) is turned counter-clockwise to orient it up-down as in the figures. Segment 1 is placed on the foot that is always black.

|  |  |  |
| --- | --- | --- |
| **Allele/Colour** | **Description** |  |
| **Red** | **Staggered, ahead** | lego-red1 |
| **Blue** | **Just on top** | lego-blue1 |
| **White** | **Traverse, right** | lego-white |
| **Black** | **Traverse, left** | lego-black |
| **Yellow** | **Traverse, middle** | lego-yellow1 |

**Generation of Legorgs**

|  |  |  |  |
| --- | --- | --- | --- |
| **Generation No.** | |  | |
| **Legorg no.** | *Note allele (colour) for each of the 5 genes in the Legorg and measure fitness* | | | | | | | |
| **Gene 1** | | **Gene 2** | | **Gene 3** | **Gene 4** | **Gene 5** | **Fitness** |
| 1 |  | |  | |  |  |  |  |
| 2 |  | |  | |  |  |  |  |
| 3 |  | |  | |  |  |  |  |
| 4 |  | |  | |  |  |  |  |
| 5 |  | |  | |  |  |  |  |
| 6 |  | |  | |  |  |  |  |
| 7 |  | |  | |  |  |  |  |
| 8 |  | |  | |  |  |  |  |
| 9 |  | |  | |  |  |  |  |
| 10 |  | |  | |  |  |  |  |
| 11 |  | |  | |  |  |  |  |
| 12 |  | |  | |  |  |  |  |
| 13 |  | |  | |  |  |  |  |
| 14 |  | |  | |  |  |  |  |
| 15 |  | |  | |  |  |  |  |
| 16 |  | |  | |  |  |  |  |
| 17 |  | |  | |  |  |  |  |
| 18 |  | |  | |  |  |  |  |
| 19 |  | |  | |  |  |  |  |
| 20 |  | |  | |  |  |  |  |
| **Sum of fitness:** | |  |
| **Average fitness:** | |  |

**Gene pool table**

Each individual Legorg can be described within a gene pool table, as shown below. There should be one table per gene per generation.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Generation No.** |  | **Alleles** | | | | |
| **Gene No.** |  | Note Legorg’s fitness in column of the animal’s allele (colour) | | | | |
| Legorg No. | Fitness | Yellow | Red | Black | Blue | White |
| 1 |  |  |  |  |  |  |
| 2 |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |
| 5 |  |  |  |  |  |  |
| 6 |  |  |  |  |  |  |
| 7 |  |  |  |  |  |  |
| 8 |  |  |  |  |  |  |
| 9 |  |  |  |  |  |  |
| 10 |  |  |  |  |  |  |
| 11 |  |  |  |  |  |  |
| 12 |  |  |  |  |  |  |
| 13 |  |  |  |  |  |  |
| 14 |  |  |  |  |  |  |
| 15 |  |  |  |  |  |  |
| 16 |  |  |  |  |  |  |
| 17 |  |  |  |  |  |  |
| 18 |  |  |  |  |  |  |
| 19 |  |  |  |  |  |  |
| 20 |  |  |  |  |  |  |
| **Σ fitness** |  | Σ yellow weight | Σ red weight | Σ black weight | Σ blue weight | Σ white weight |
| **Relative fitness**  **% of each allele** | |  |  |  |  |  |

**Note:** The sum of fitness () is calculated from the total fitness values, regardless of colour of the allele. The sum of the weight for each colour () is calculated from the sum of each of the entries for that colour’s column



**Step 1: Calculating next generation gene pools**

**Step 2: Gene pools 1-5 filled with correct allele ratios**

**Step 3: Drawing Legorgs**

**Step 4: Building Legorgs according to morphogenetic rules**

**Step 5: Scoring fitness**

**Questions**

1. Sketch the average fitness results in the diagram below:



1. What do your results show?
2. Which elements of the simulation are realistic and which are unrealistic from a biological perspective?
3. Is motility a good measure for fitness?
4. Describe some biological adaptations.
5. How does natural selection affect genetic variation in a population, and when is it beneficial to have large genetic variation instead of “optimised” adaptation?
6. How would a population of e.g. 100 individuals have influenced your gene pools?
7. Why does natural selection not optimise organisms completely?
8. Which optimisations are improbable by the mechanism of natural selections (hint: think of changes in body plan, like extra sets of appendages)?
9. Why can you see an evolution in just 5 generations in this activity, when we only see evolution happening over many generations?

|  |  |  |
| --- | --- | --- |
| **Genetic drift**  In November 2010 there was an international meeting on tigers in St. Petersburg, Russia. The purpose was to make a plan for saving the wild tigers. It is estimated that there are about 3000 wild tigers left in the world. Of these approximately 1000 of them are females capable of giving birth to new tigers.  Try to describe what can happen to the genetic variation among wild tigers, when there is such a small population for breeding. |  | |
| **Natural selection**  Take a look on the four animals in the figure. Give an explanation on how there can be so many different animal species on Earth |  | |
| **Fitness**  The peppered moth has two variations, a light and a dark. In England approx. 97% of all peppered moths were of the light variation before the industrial revolution. After this the picture turned and the ratio turned to having approx. 97% of the dark variant. After the introduction of smoke cleaning and particle filters the population has turned once again so there is again approx. 97% of the light variant and 3% of the dark. Try to give an explanation of this using your knowledge of genetics | |  |