

LAMARCKIAN EVOLUTION SIMULATION BASED ON INTELLIGENT SPECIES

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1. Why have we decided to make this model? (General)

Most of the evolutionary simulations represent Darwinian/Wrightian mode of evolution in which random mutations are maintained and/or eliminated for the influence of the environment (selection) or genetic drift. However, such simulations quite rarely (as for us) refer to a Lamarckian mode that lies in acquired inheritance, which is indeed a remarkably interesting phenomenon, albeit it's not as ubiquitous Darwinian/Wrightian mode. So (initially) our goal was to develop an illustrative simulation referring to the molecular model of Lamarck [it will be discussed in the next, more precise version of our simulation] in prebiotic (maybe RNA-world) times proposed by our colleagues (in unpublished materials). Although the final model is still Lamarckian, it doesn't correspond well our initial aim, so it has been decided to save this simulation as a demo-version with more simplistic Lamarckian scheme for testing out some environmental parameters and neural networks, and, after all, it's fun!

2. Lamarckian evolution (Biology)

This evolutionary idea proposed by Jean-Baptiste Lamarck at the beginning of the 19th century had been the first mechanistic explanation of how evolution works. In his theory, species had an "urge to change" (explained by the natural flow of fluids in the organism's body) which drove them to adapt and thus evolve and adaptive traits were passed to the next generations (gained inheritance), so the changes were intentional (remember a picture of giraffes stretching their necks). However, Lamarck's theory of acquired heredity had been proven to be incorrect [The evolutionary theorist August Weismann argued that inheritance only takes place by means of germ cells and that germ cells cannot be affected by anything somatic cells of the body acquire during their lifetime]. Later more realistic theories based on much more precise observations were proposed (natural selection, modern synthesis, and so on). Although Lamarck has been "doomed" for a long time, in the last two decades scientist have reviewed their paradigm with the discovery of mechanisms of adaptive immunity such as CRISPR-Cas and many others that resemble Lamarckian mode. For example, bacteria insert viral DNA in the special region of their genomes and then transcribe into special RNA that guides viral DNA destruction. This locus is passed to the following generations, and thus they gain adaptive immunity. There are way more mechanisms for different purposes, but they all share the feature of inserting alien DNA (usually for one's destruction). Also, quasi-Lamarckian mechanisms are known, where mutations themselves are random, but they are initiated intentionally, for example, in stress-induced mutagenesis (in plants and bacteria): organism induces rapid accumulation of

mutation to find variants of proteins that will be fitting best to the changing environment (bacteria in the presence of antibiotic).

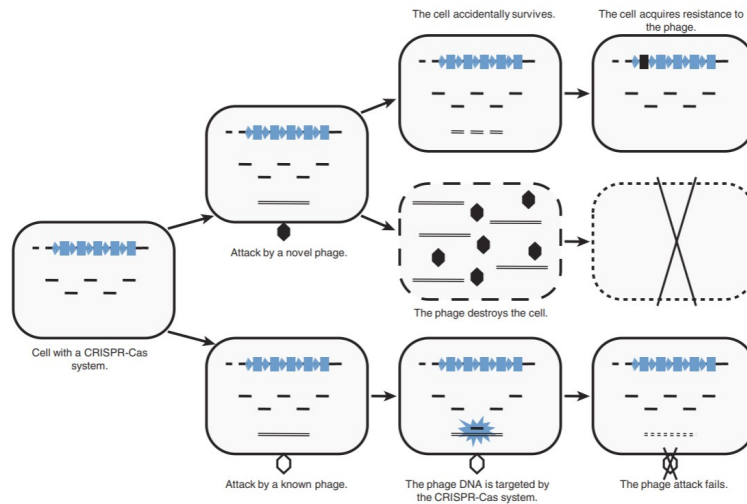


Figure 9-2 The CRISPR-Cas system and its mechanism of action: the showcase of Lamarckian evolution. Adapted from Koonin and Wolf, 2009b.

And thus we might figure out a general scheme for Lamarckian mode based on our knowledge of genetics: change in environment causes non-random change in the genome, adaptation is got and it's inherited by descendants.

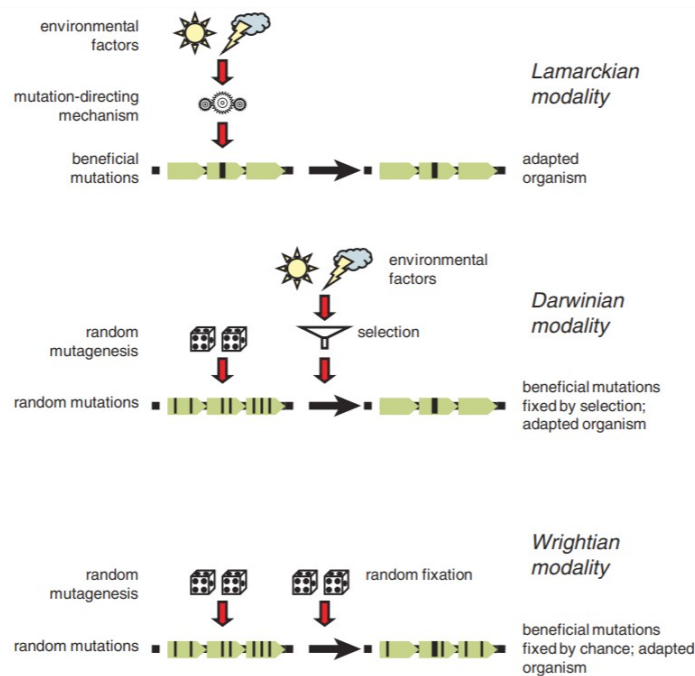


Figure 9-1 The Darwinian, Lamarckian, and Wrightian modalities of evolution. Adapted from Koonin and Wolf, 2009b.

Whereas it looks quite obvious that Lamarckian evolution would be very effective, it's rather an exception than the rule. The question is: why? Basically, there are two main reasons. Firstly, the mechanism of direct phenotypic changes' transmission to

the genome would be unimaginably complex and (maybe) improbable to evolve. Secondly, in multicellular organisms traits should have been somehow transmitted to germ cells, which is also undoubtedly a problem. To summarize, we've got two great obstacles on the way of developing a more general Lamarckian mechanism: genotype-phenotype and soma-germ differentiation. The existing mechanisms bypass this trouble by using alien DNA. However, it's obvious that those mechanisms have developed in a Darwinian mode (but actually can Lamarck exist without Darwin?). Also, these mechanisms hardly constitute the mainstream of genome evolution, perhaps due to the selection against genomic instability. In contrast, the mechanisms denoted quasi-Lamarckian are ubiquitous. These mechanisms seem to be no less remarkable than the genuine Lamarckian scenario: The quasi-Lamarckian processes translate random mutations into specific, adaptive responses to environmental changes.

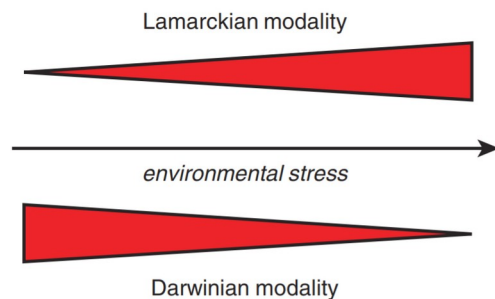


Figure 9-3 Environmental pressure and the transition from the Darwinian to the (quasi) Lamarckian modality. Adapted from (Koonin and Wolf, 2009b).

So it turns out that most universal Lamarckian mechanisms would develop and be useful in the stressful, highly changeable environment since most of the existing mechanisms evolved for a response to stressful situations, such as viral invasion (environment would change faster than organism's generations) and would have no genotype-phenotype differentiation. Therefore the best place (and time) for developing and existing of universal Lamarckian mode is RNA-world in the environment more changeable than one that was present on Earth 4 billion years ago.

[For further reading on Lamarckian evolution topic we really recommend the book "Logic of chance" by biologist Eugene Koonin (chapter 9 specifically).]

3. Description of the model (General)

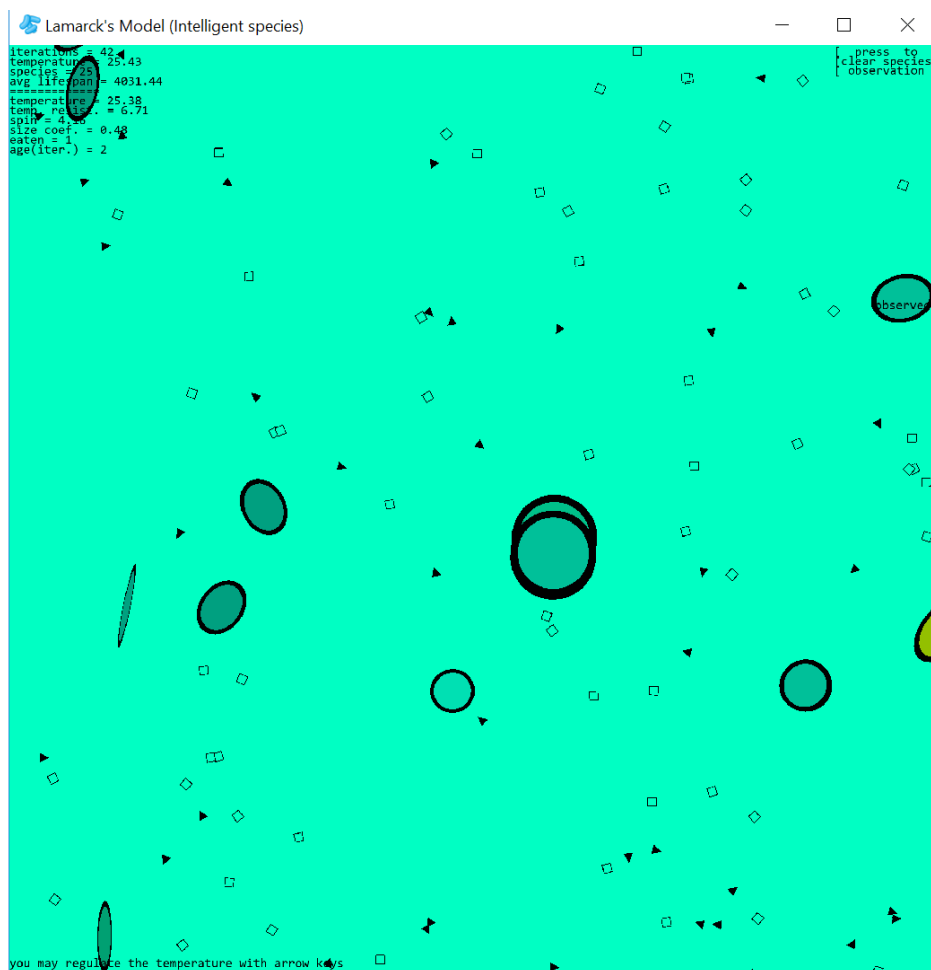
In this model, our organisms are represented with ellipse-like objects living in an environment with shifting temperature. Temperature affects organisms' and other objects' velocity (it also depends on the object's size). Temperature of the environment and objects can fluctuate from 0 to 50 points, in our representation we also added colors to illustrate it (0 is violet-blue, whereas 50 is orange). Organisms have a parameter of temperature resistance, and they can gain heat by spinning

and eating. Species' colors become darker if they live for several breeding iterations.

So-called modifiers are also presented here, triangle-shaped structures, which can alter some parameters of the organism after interacting with it. Organisms have the ability to adapt to fluctuating temperatures (this trait may be modified throughout life).

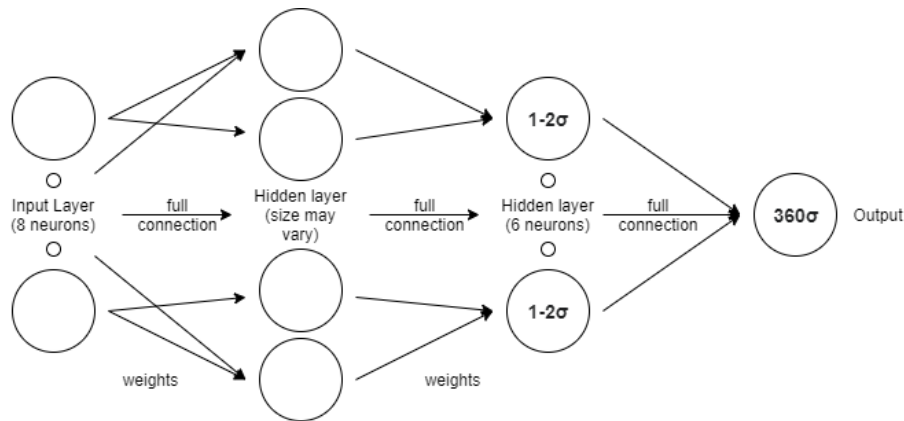
Furthermore, organisms show some primitive kind of orientation (some of them take into account the location of food and their neighbors while moving). Intelligence can also be modified and inherited. Organisms need food to maintain their lives, they feed on square-like food particles or their smaller neighbors. When it comes to reproduction, organisms spawn basically their copies that inherit traits acquired by parent through life.

And that's why model is actually Lamarckian. Organisms adapt to environmental triggers (temperature fluctuation) and pass changes to their descendants. Although we biased somewhat from initial model, we tried to maintain continual geno-phenotype (which means without strict genotype-phenotype differentiation; organism is a continuum of changing geno-phenotype) Lamarckian concept.



4. The AI behind (Tech & Math)

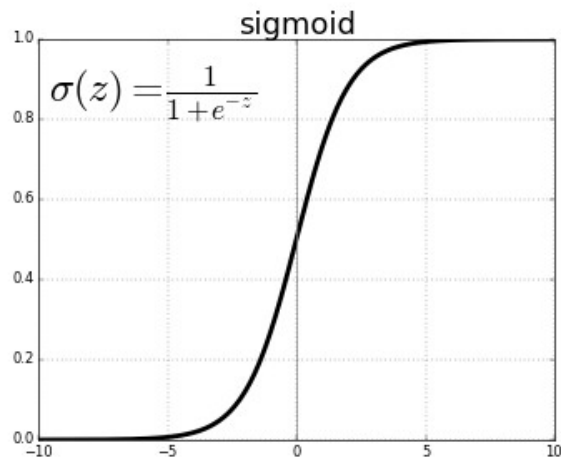
Each organism has a neural network in it, a primitive and untrained AI (Artificial Intelligence) that allows our species to choose a direction of their movement based on their surroundings. Our NN has fully-connected multiple layer structure.



It has 8 values as its input:

1. Ratio between sizes of the species (the owner and the closest one to it)
2. Direction to the closest food instance
3. Direction to the closest modifier instance
4. Direction to the closest alive instance
5. Distance to the closest food instance
6. Distance to the closest modifier instance
7. Distance to the closest alive instance
8. Environment temperature

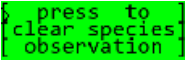
The first hidden layer's size can be adjusted with a ".config" file [see **6. "settings.config" and death logs** part] but it is 32 by default, the second one always has 6 neurons in it. This structure was chosen due to the features of our activation function on the output layer, the sigmoid function. Here is the graph of it:



When the argument is 6 or larger, the function outputs a value close to 1, and same for -6 and 0. Since we want our output to be a direction from 0 to 360, we will multiply the sigmoid by 360, and since we need an input being a value from -6 to 6, we put a hidden layer of 6 neurons, each with a sigmoid activation function returning a value from -1 to 1, before the last neuron, so that the maximum sum of all the outputs of this layer is 6 and the minimum is -6. Remember, the sum of this layer's outputs is the last neuron's input and there are no weights between these. Speaking of weights, they are located on both sides of the first hidden layer, and are values adjustable by modifiers and inheritable by children.

5. GUI and controls (General)

Our simulation has a simple Graphic User Interface (GUI). At the top-left corner of the window you may see some basic information about what is happening. If you place your mouse pointer on an organism, it becomes observed and you are shown some data about it a few lines lower the general info. You may stop observation by

clicking on the top-right corner: . Moreover, the temperature can be manually controlled by pressing arrow keys on your keyboard (Up and Down keys).

6. "settings.config" and death logs (Tech)

We created a possibility to change some global constants of environment and the simulation in general with a configuration file. It is located in "C:\Users\%username%\AppData\Roaming\NearlyLamarcksModel" and is created with these values by default:

```
1  neural network size:
2  32
3  learning rate:
4  1.5
5  iteration(sec):
6  60
7  particles number:
8  100
9  cannibal coef.:
10 1.5
11 food needed to survive:
12 1
13 alive size <min/max>: <
14   0.019
15   0.3
16 >
17 survivable temperature <min/max>: <
18   5
19   45
20 >
21 temperature change speed <max>(sec): <
22   30
23 >
24 spin <max>: <
25   6
26 >
```

This file may be opened in any text editor and changed (please, change only the numbers, any syntax changes are considered dangerous).

Tips for your experiments:

- Maximum temperature change speed should be less than iteration duration for the evolution to be Lamarckian
- Cannibal coefficient is how different two species should be for one of them eating another
- Particles number is a number of food and modifier instances together
- Learning rate is a coefficient of all weights changes in neural networks
- Neural network size is a number of neurons in the first hidden layer (consider larger numbers slow the calculations up, yet at times make species move more smoothly)

Death logs have been removed in the last edition (7/20/2020) and can be turned on only from the Game Maker: Studio 2 project, in the `death_log_add.gml` script. The idea of death logs was to register every death of species in details, however it created lots of unnecessary files.