"The Blind Watchmaker" Revisited | how Richard Dawkins misinterprets Genetic Algorithms

by Henry Dalcke, January 2018
independent.academia.edu/henrydalcke

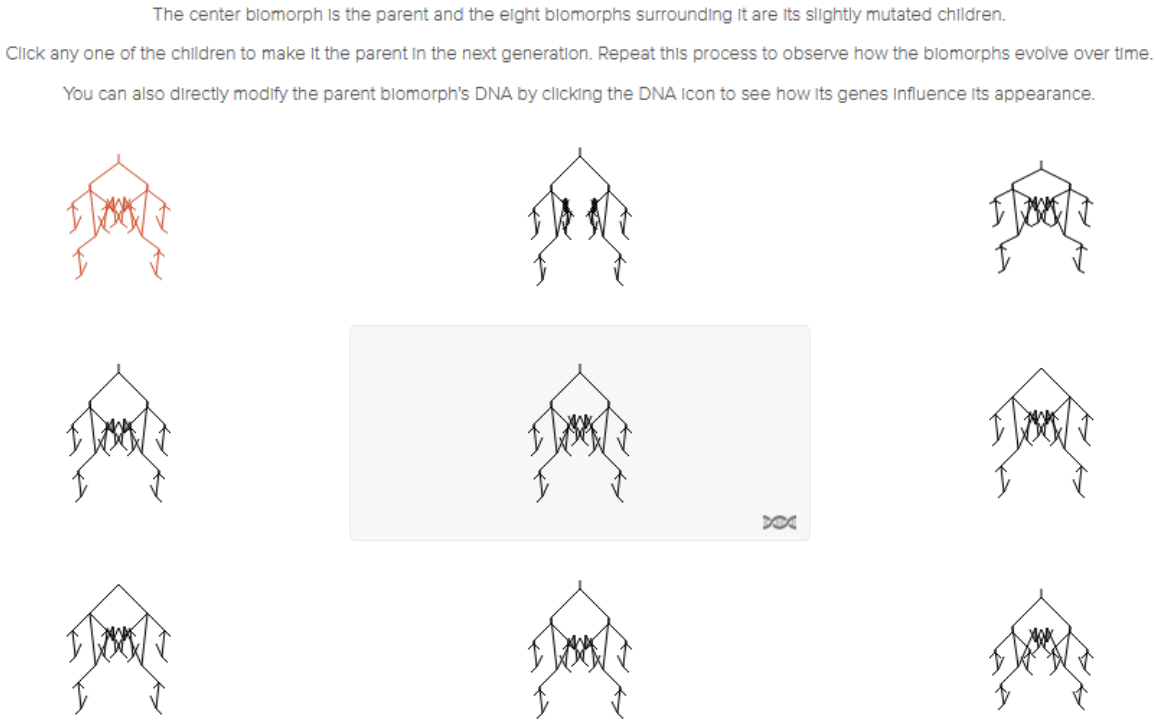
Synopsis

It is a widely known *objection against the Teleological Argument* that creationists commit a *category mistake*, if they *compare technical things to biological organisms*. Yet, in his book "The Blind Watchmaker", Richard Dawkins tries to show that evolution is a button-up process *using a technical thing* he programmed in a top-down fashion, leading me to the conclusion that one can indeed compare technical things to organisms - with all the resulting implications.
This paper is offering a closer look at the computer programs he used to make his case and why, by using them, he is actually making a point for creation and intelligent design - not evolution!

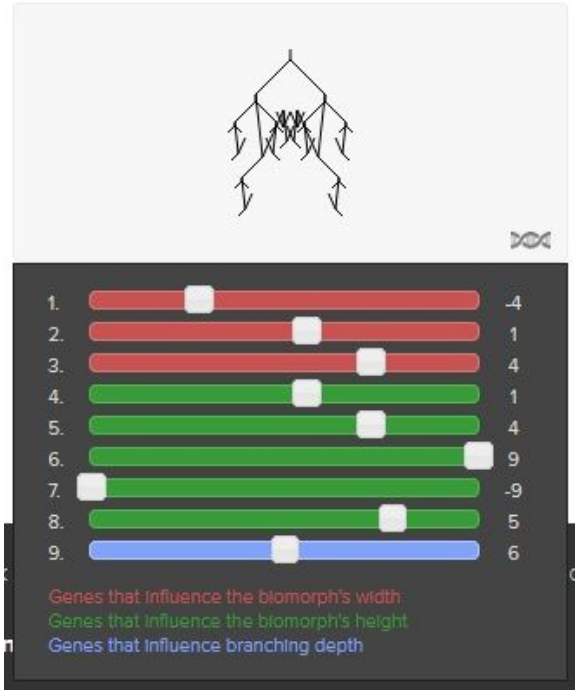
Biomorphs

The graphical structures below are Richard Dawkins' "Biomorphs".
These are being generated by a genetic algorithm that randomly changes integer values which each resemble a parametric "gene" that changes parts of the graphical appearance of the Biomorphs. In order to evolve the Biomorphs, the genetic algorithm is presenting 8 randomly generated Biomorphs to the user, out of which the user is now asked to select an individual Biomorph by clicking on it. The now selected Biomorph is then replicating 8 times and in a next step all 8 new individuals are being altered by slightly changing one or more parametric "genes" respectively, resulting in Biomorphs that are all slightly different than their parent Biomorph. By repeating this procedure, the user will soon notice that the Biomorphs are being forced to take shape according to the selection criterion of the user.
Using the Biomorphs, Richard Dawkins wants to demonstrate the power of selection, but he doesn't mention what actually is the >subject< that selection is acting on.
What evolutionists need selection to act on are the phenotypic results of random mutations, while the creationist position would already be sufficiently substantiated by selection acting on the phenotypic results of re-combination according to the Mendelian Laws Of Inheritance established by Gregor Mendel in the mid 1800s.
In this paper I'll prove that Richard Dawkins is actually making a point in favor for the creationist perspective, as his programs are not at all based on the selection of the results of random mutations, but the interaction of dominant-recessive and blending inheritance in the process of re-combination with unknown, genetically unexpressed Biomorphs that the user isn't shown!

A genetic algorithm generates random solutions to a problem that has to be solved. In the case of Biomorphs, the problem at hand is defined by the selection criterion of the user. Let's first have a look at Richard Dawkins' program:



In this population of Biomorphs, all outer individuals are slightly changed replicas of the inner individuum.
These randomly altered individuals are being generated by executing a pre-programmed mathematical formula 8 times in a row while slightly changing and saving its variables. The formula itself can be considered to be the genotype of a Biomorph-phenotype. ***Only the variables can be changed by the genetic algorithm.*** Those are ***depicted*** in the GUI ***as*** simple ***integer sliders*** as you can see in the picture below:

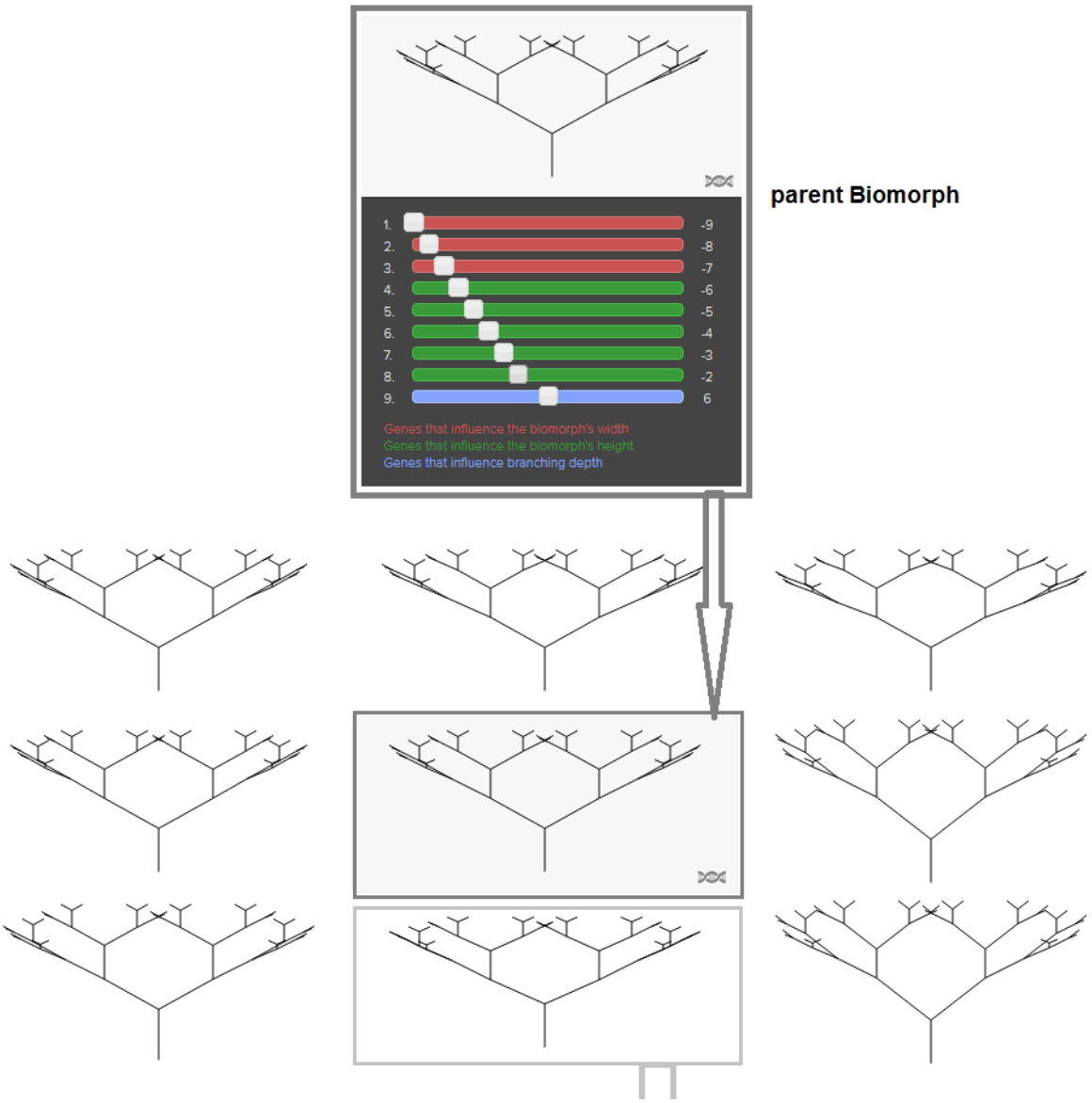


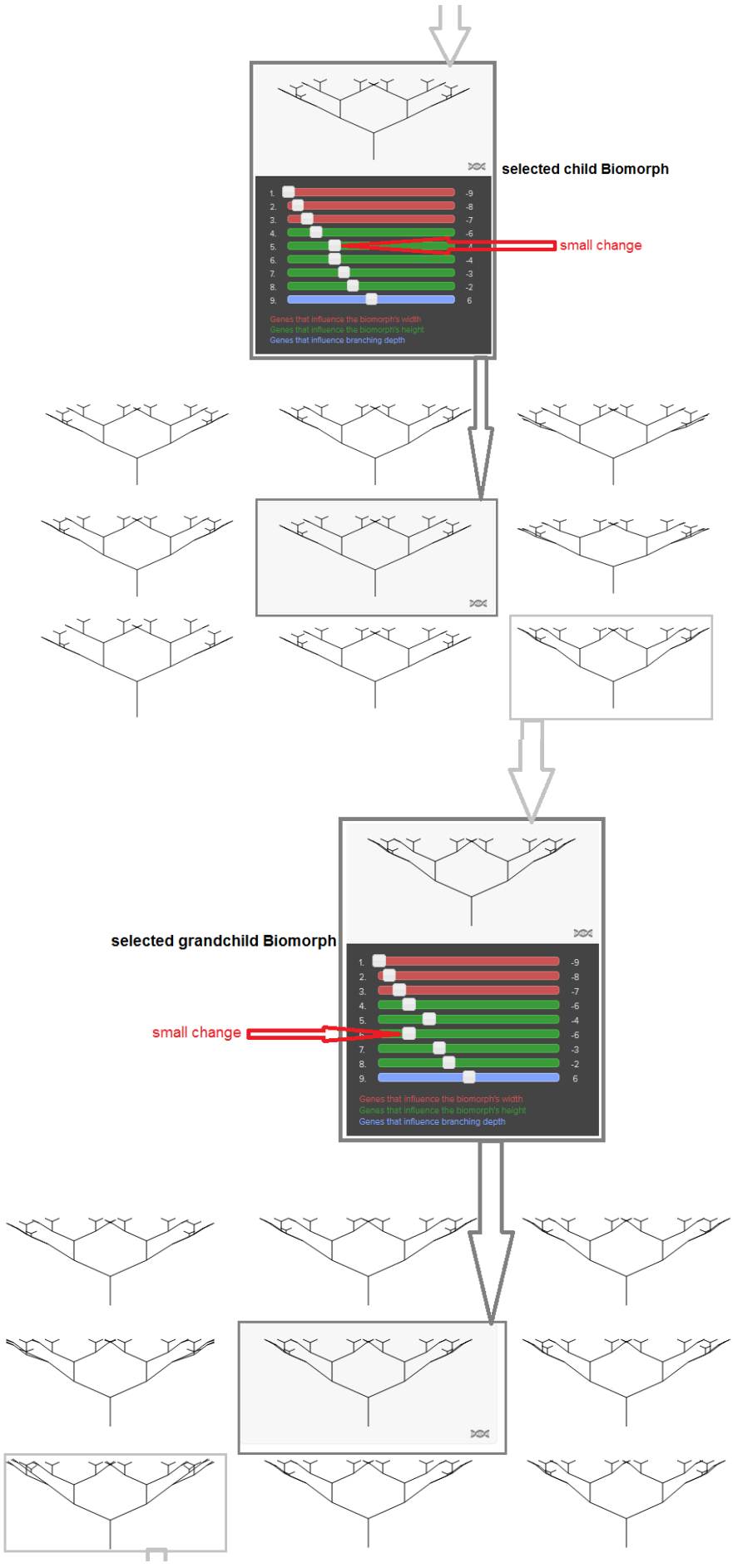
That technical limitation is claimed to be the allegedly *only* reason why the Biomorphs-program can only generate Biomorphs, hence couldn't evidence macroevolution.
It is believed, though, that this limitation doesn't exist in nature, so the narrative goes that the same mechanism driving the Biomorphs-program - namely ***selection acting on randomly generated changes*** - which Dawkins believes resemble genetic mutations - would ***a) be the main reason for adaptation*** and ***b) suffice for macroevolution*** in nature.
To find out, if that really is true, we have to explore the functioning of the genetic algorithm used in Richard Dawkins' book "the blind watchmaker".:

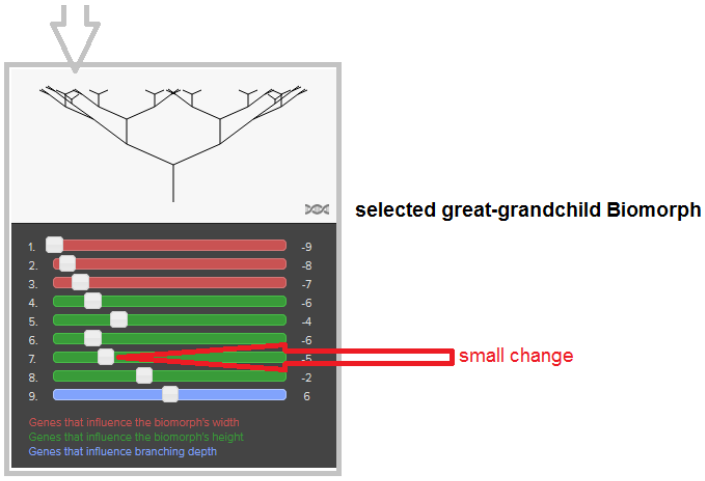
the possible implementations of genetic inheritance

1) Darwinian approach: randomizing a few parametric genes by small values

The following depiction shows progressive genetic changes over three generations.
You will notice the very small value alterations per generation in the parametric genes.:

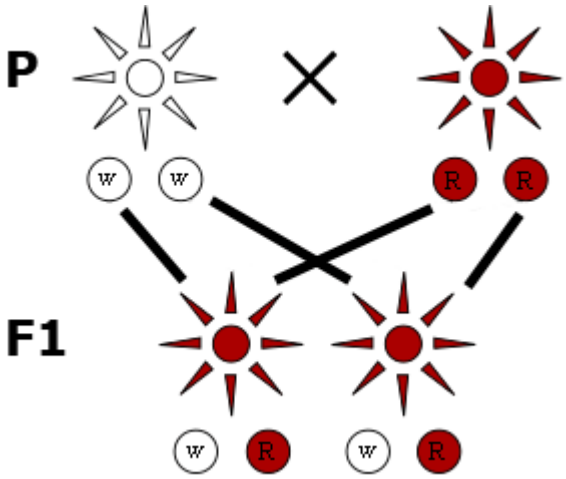



selected child Biomorph
small change
selected grandchild Biomorph
small change
Genes that influence the biomorph's width
Genes that influence the biomorph's height
Genes that influence branching depth

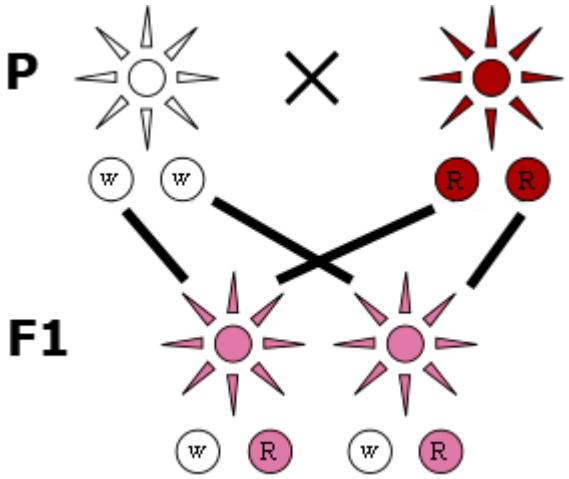


2) Mendelian approach: randomizing all parametric genes plus re-combination

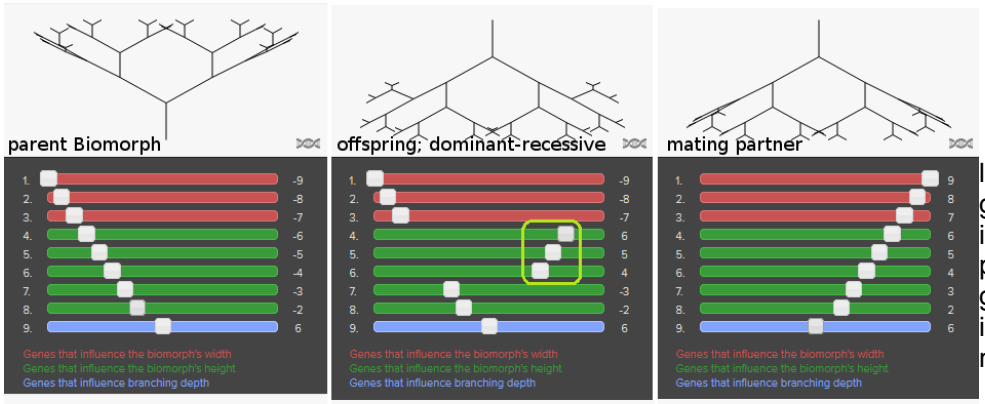
In order to be able to re-combine the parent Biomorphs with new ones, we first would need to randomize completely new Biomorphs from scratch, to generate some potential mating partners while keeping our parent Biomorph.
Secondly, we interpolate the parametric gene-values of the parent Biomorph into the values of the respective randomized mating partner Biomorphs. To do so in a genetically accurate way, we need to distinguish between dominant-recessive and blending inheritance.
If a trait is being inherited in a ***dominant-recessive*** way, it is expressed unchanged in the offspring - either coming from the parent or the mating partner Biomorph.
We can implement this by not interpolating the respective parameter value from the parent Biomorph into the new mating partner's parameter value, if the value of the parent Biomorph shall be dominating the respective counterpart value of the new mating partner.
If the new mating partner's value shall dominate the value of the parent Biomorph, the new mating partner Biomorph's parametric gene value is being inherited to the offspring, hence the interpolation between the parent's and the mating partner's value is maximum.



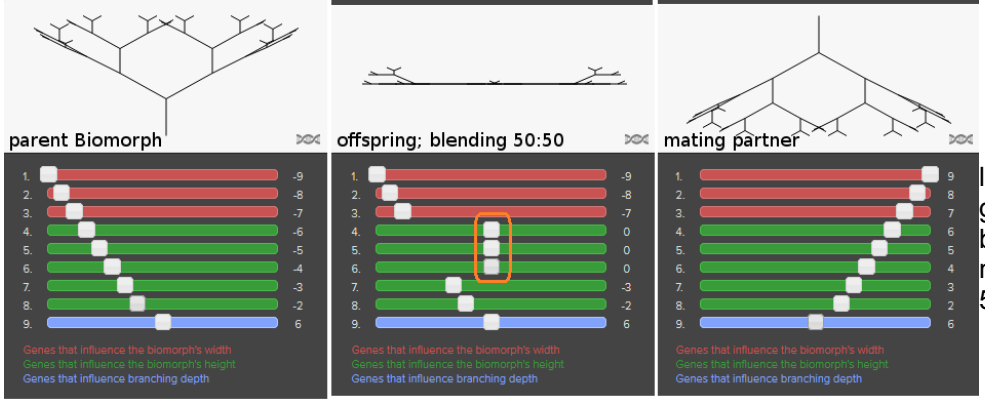
In the case of ***blending inheritance***, the respective parametric gene values are being interpolated in certain ratios.



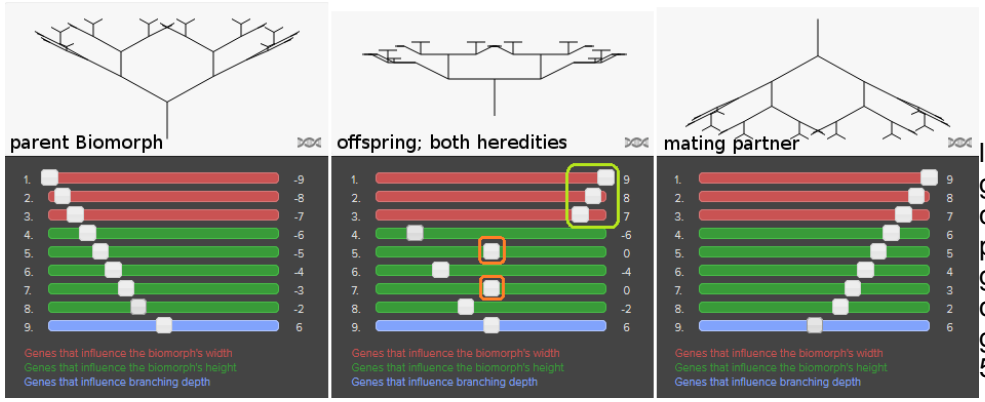
The following depiction schematically shows the **effects of** the different heredities of **re-combination on** the genotype and phenotype of the **Biomorphs**.
For the sake of clarity, the genotypes of parent and selected mating partner have been designed to form an optical pattern that's better recognizable.



left:
genes 1,2,3,7,8,9 inherited dominantly from parent Biomorph;
genes 4,5,6 inherited dominantly from mating partner Biomorph



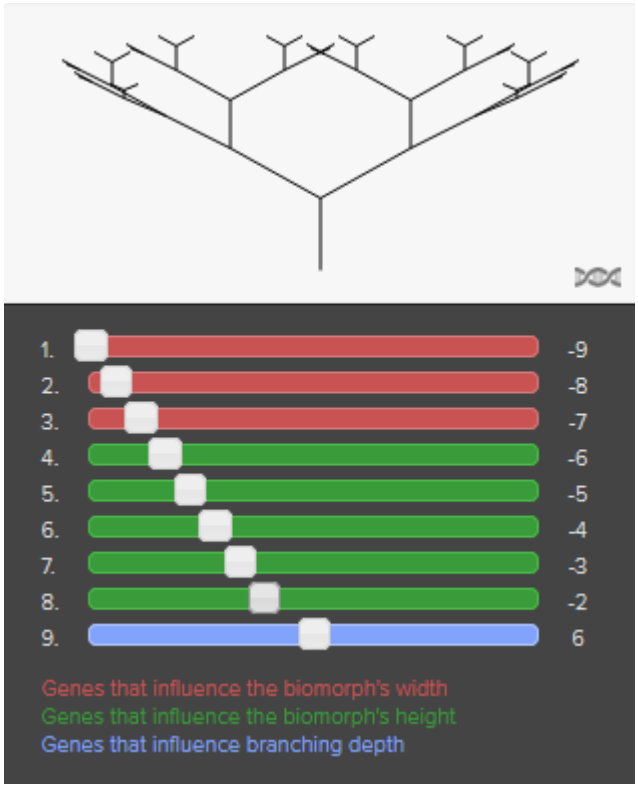
left:
genes 4,5,6 blend between parent and mating partner in a 50:50 ratio



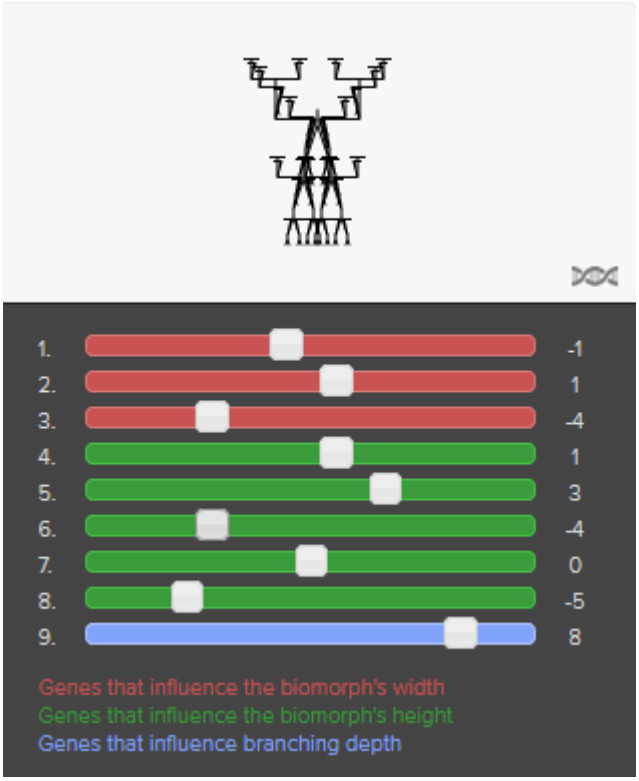
left:
genes 1,2,3 inherited dominantly from mating partner;
genes 4,6,8,9 inherited dominantly from parent;
genes 5,7 blending in 50:50 ratio

Now we keep the parent Biomorph and randomize all of the mating partner's parametric genes by big values.:

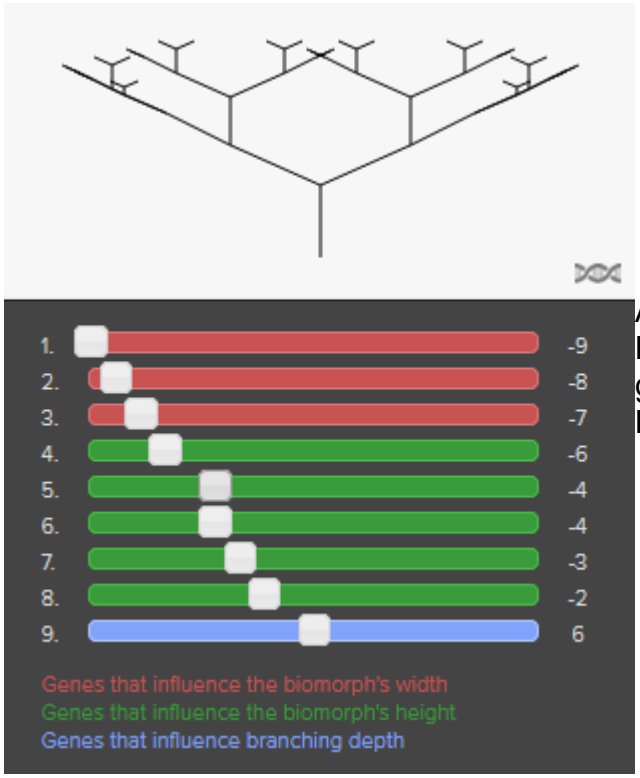
parent Biomorph



randomized mating partner



Now let's blend the 5th gene between parent and mating partner by the ratio of 12.5:87.5 and inherit all other genes dominantly from the parent Biomorph.
The resulting offspring Biomorph will be this one:



As you can see, this is the exact same Biomorph that we got in the first offspring generation (entitled "selected child Biomorph") using the Darwinian approach.

significance

The reason why the Mendelian approach can lead to the exact same results like the Darwinian approach is that the Darwinian approach is just a dumbed down version of the Mendelian approach! It ignores the randomization of a whole populations of mating partners for each generation with each having an own pattern of heredities and blending ratios in order to speed up the selection processed and save computation power!
The user is shown 8 actual children resulting from a quasi-re-combination of the parent Biomorph and 8 random mating partners that are not shown in the User Interface for the reason mentioned above.
The alleged Darwinian approach Richard Dawkins uses to argue for "descent with modification" is therefore actually not Darwinian at all and could
only evidence Mendelian inheritance and therefore variation within a created kind - like the Biomorph-kind.
As obvious, if we look at the parametric genome of a Biomorph, no genes are being added or deleted. All information to build every Biomorph possible is already encoded in the combinations of the variable parametric gene sliders. The volume of information therein is called the "genetic variation range" and in the case of the Biomorphs program it contains 5 x 8^19 = 144.115.188.075.855.873 different Biomorphs.
The genetic algorithm only helps to find them.

The Weasel Program

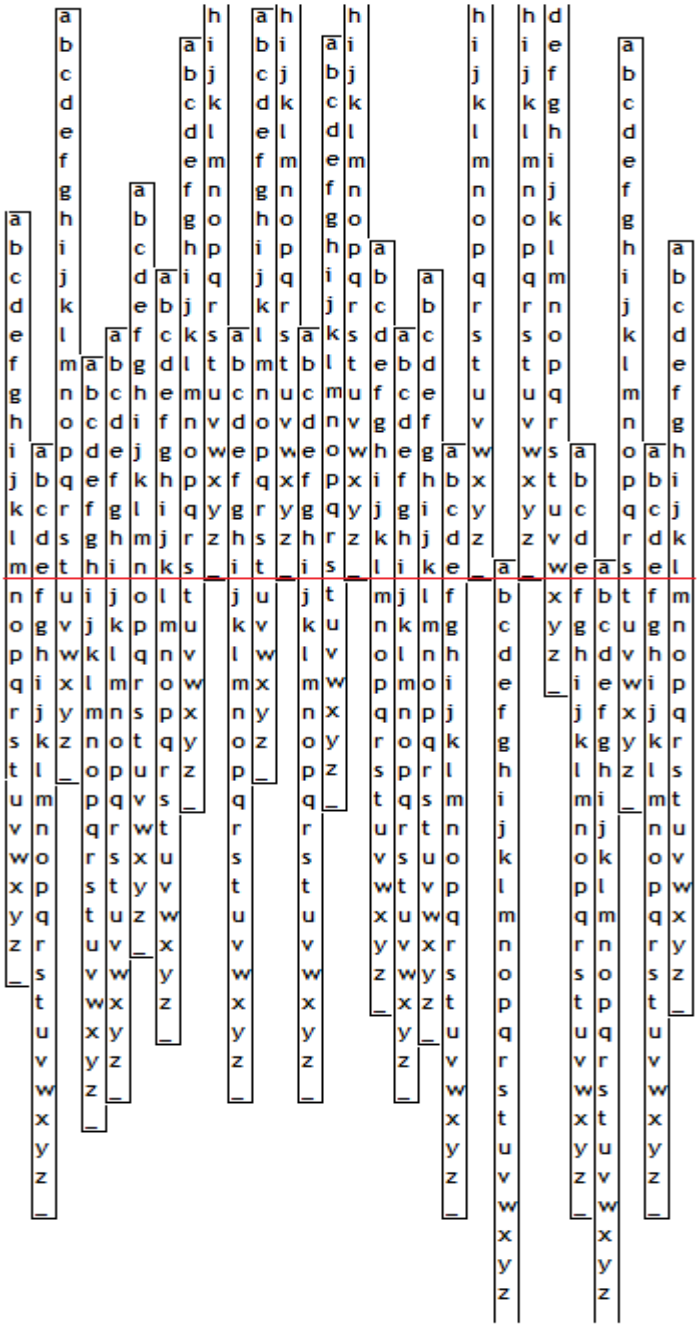
Now let's look at another example by Richard Dawkins: the famous ***"Weasel-program"***.
As you will notice, you can't see any population per generation and neither can you actively select any individual sentence yourself.

```
Generation 01:   WDLTMNLT DTJBKWIRZREZLMQCO P
Generation 02:   WDLTMNLT DTJBSWIRZREZLMQCO P
Generation 10:   MDLDMNLS ITJISWHRZREZ MECS P
Generation 20:   MELDINLS IT ISWPRKE Z WECSEL
Generation 30:   METHINGS IT ISWLIKE B WECSEL
Generation 40:   METHINKS IT IS LIKE I WEASEL
Generation 43:   METHINKS IT IS LIKE A WEASEL
```

The sentence "Methinks it is like a weasel" by Shakespeare is being found by the same genetic algorithm in use for the Biomorphs example combined with an additional target-driven selection mechanism that checks every generation's population of random sentences for the individual sentence that's nearest to the target sentence.
This special case of an automatic genetic algorithm is called "hill climbing algorithm”.

Although every randomization and selection happens "under the hood" and therefore doesn't need a graphical representation, the genetic representation of the sentences is quite similar like that of the Biomorphs. Both use integer variables that can be represented as parametric gene sliders that can be treated the same way - with the exact same implications I already pointed out above.

The following depiction shows the parametric genes of the target sentence and their respective positions. You can imagine the positions for the selected random sentences for each generation.



As in the Biomorphs example above, no new gene sliders are being added and the information for each sentence -no matter how meaningless- is already encoded in the combinations of the slider positions.
The algorithm only finds the right combination resulting in the target sentence.

Conclusion

Richard Dawkins' big claim that evolution is a “blind watchmaker"
could not be evidenced at all, therefore **the *teleological argument* has not been refuted by atheists to this day!**