Evolutive approaches to explorative design methods in architecture

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Current studies on the evolution of selected moss species reveal exciting new insights into the genetic mechanisms that lead to the creation of new species. One of these moss species, the spreading earthmoss, has been used in science as a model organism for many years, and its genetic information has been completely decrypted. This makes it and other members of its family ideal research objects for the transfer of these genetic mechanisms into algorithms—defined computational processes—and for their use in the developmental process of product design and architecture.

There is no doubt that no theory on the origin of species has molded our understanding of the worldwide diversity of species (biodiversity) in the same way as Charles Darwin's theory of evolution. Although Darwin was not the first to tackle this question in his studies, his work—for the first time—presented a comprehensive and well-founded approach that explains the underlying mechanisms of evolution. Based on the observations he made during his research trips, and his work on the biological materials collected and the fossils found on these trips, Darwin established the basic pillars of his theory, which he published in 1859. Fossils reflect the continuing changes occurring in nature. They make it possible for us to draw conclusions about shared ancestors within lineages. Evolution is a process in which species evolve from their ancestors in small steps. Darwin described the force driving evolution as natural selection. Changes can only take a foothold when they prove viable in the predominant environmental conditions. However, for new species to become established, they need to go through a process of reproductive, behavioral-biology, seasonal, geographic, or genetic isolation within a group of individuals of a species, what is termed a population. Over the course of the 20th century, Darwin's theory of evolution was expanded by the field of genetics. The theory was further underpinned by the advent of population genetics, by the discovery of DNA[1] as the carrier of genetic information, and, lastly, by the development of scientific methods in molecular biology and bioinformatics.

[1] *See glossary* **p. 141**

Evolution as the driving force of diversity and variation

A basic tenet of evolutionary theory holds that the increase in morphological diversity—the diversity of shape and form in the blueprints of living beings—is made possible through genetic changes and selection. Nowadays, biologists can trace these changes to the genetic code of the species, its genome, or even down to the single genes of an individual. In this case, the small changes described are random mutations of the DNA components. Such mutations can often be detected and characterized. In spite of this, it is mostly impossible to link these directly with a certain functional change or morphological characteristic. Instead, it has been shown again and again that biological processes are based on highly complex genetic networks of different genes and their gene products. They depend on constant feedback between genes and their products, and from the respective environment. Put simply, genes are translated from a DNA sequence into a sequence of transition molecules of RNA components and then finally into a protein ⌐**121**. Modern methods in molecular biology have made it possible to find out how highly regulated each of these steps is. This regulation applies to the accessibility of a gene on the DNA, to the activation of its decoding, to the structure of the RNA molecules and their subsequent modifications, through to the longevity of a protein after its formation. There is also the fact that not only proteins but also RNA molecules themselves can perform a wide range of biological functions. In eukaryotic organisms—creatures with a cell nucleus—the protein-coding genes are usually made up of exons and introns. Exons are areas that contain information for the structure of proteins. The introns lie in between these and do not have a coding function, that is, they do not contain information. The process of removing the introns is called "splicing." It is an indispensable step in the process of producing a functional protein. However, sometimes parts of exons are also removed in the process, which leads to a new gene product, and hence—possibly—to a new function of a protein. This process is referred to as

DNA

Replication

RNA

Transcription

Protein
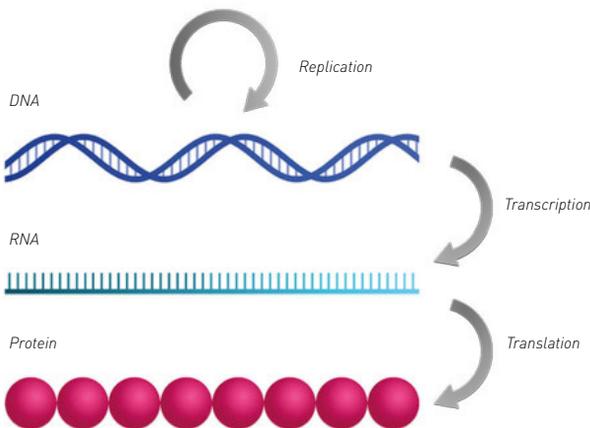
Translation

⌐**121** *The path from the DNA to the protein is a closely dovetailed and highly regulated biological process. Top: duplication of the DNA as part of cell division (replication). Middle: decoding functional sections on the DNA (gene) and translating into RNA molecules (transcription). Bottom: translating the RNA molecules into a protein (translation).*

"alternative splicing." In this way it is possible that additional gene products with a changed function are created without there being further genes in the genome. In addition to the protein-coding genes, a large part of the genetic information is composed of so-called noncoding DNA. We know today that a large part of this noncoding DNA contains transposons. These regions of DNA can spread themselves or copies of themselves in the genome through "jumps." When they carry out these jumps, they are able to also transfer adjoining DNA sections. This can lead to a dramatic change in the overall genome, and may explain how new genes are generated. Therefore, in addition to the exterior adaptation of shape and function, organisms are also subject to processes on the genetic level that favor the creation of diversity. Even though such genetic mechanisms are obviously critical in terms of evolutionary development, their role in the emergence of new species remains largely unclear.

Mosses and genetics

For the investigation of evolutionary processes at the genetic level, it is important to choose a suitable group of organisms that has already been well researched. An example is the Funariaceae, a family of mosses that does not contain too many species and includes the small spreading earthmoss ⌐123. Funariaceae occur worldwide on open or disturbed surfaces. In these places they grow either in single tufts or in the form of loose turf. The part of the moss plant that carries the leaves is called the gametophyte. Gametophytes have small, rosette-like stems surrounded by small leaves. On the side facing the substrate they form stringy, root-like structures (rhizoids) for the purpose of anchoring. Following fertilization, a sporophyte grows on the gametophyte. It consists of a spore capsule on a stem, which often extends above the moss cushion. Inside the spore capsule, spores are formed that are hardly visible to the naked eye. In Bryophytes, the opening mechanism of such a spore capsule is often extremely sophisticated. Within the Funariaceae, there are considerable differences between the species. The range of forms includes spore capsules with complex

┌122 *Intricately construct-ed spore capsule of the tropical Funariaceae species* Funaria calvescens *with a sophisticated toothed rim along the capsule open-ing, which allows the spores to discharge depending on the relative humidity.*

toothed rims at the opening of the cap-sule that can open or close depending on the relative humidity ┌**122** through to com-pletely closed, spherical spore capsules whence spores can emerge only when the wall of the capsule tears open ┌**124**.

The spreading earthmoss of the Funar-iaceae family is an annual plant, which is visually rather inconspicuous. It can often be found at the banks of drying-up lakes and in floodplains ┌**125**. The spores of this

pioneering species can survive long peri-ods in the ground and, given the right con-ditions, can grow up quickly when it col-onizes open areas in small tufts. The life cycle of the spreading earthmoss is very short, lasting approximately eight weeks, and is ideally completed before the water level rises again. The spore capsule looks like a simple sphere. It does not have any complex structures that would facilitate the release of the spores. In spite of its

┌123 *Typical Funariaceae representatives. From left to right: the bonfire moss (*Funaria hygrometrica*), the Norfolk bladder moss (*Phy-scomitrium eurystomum*), and the spreading earthmoss (*Physcomitrella patens*).*

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124 *Independent of wind and weather—the spore capsule of the spreading earthmoss simply bursts open as soon as the spores are mature.*

125 *Drained lakes or dried-out riverbanks are the typical habitat of the spreading earthmoss. At such locations the plants have little time to fulfill their life cycle and produce spores that can survive the next flooding.*

inconspicuous appearance, for years the spreading earthmoss has been used internationally as a model organism for biological studies. The fact that it can be easily cultivated in the laboratory, as well as its short life cycle, means that it is an ideal research object, making it possible to study how plants adapt to new habitats, for example. Thanks to specific methods and the successful mapping of the genome of the spreading earthmoss in 2008, molecular biologists are able to generate specific changes in the genetic code and thereby activate or repress specific genes.

What we can learn from the genetics of moss

Not knowing that DNA carries the genetic information, Darwin posited that geographic isolation and a resulting barrier to reproduction is a driving force in the evolution of species. However, as shown in molecular biology, spontaneous changes in the genome can also lead to repro-

ductive isolation. Using the Funariaceae as models, it is now possible to find out how changes in the genomes are related to morphological and functional innovation and diversity.

Such changes may involve the duplication or shifting of parts of the genome, or whole genome duplication. In the case of the Funariaceae investigated here, these occurred time and again in the course of evolution. For successful sexual reproduction of eukaryotes and the number of parental chromosomes—the DNA packaging units—must equal. Therefore, a duplication of the chromosomes owing to genome duplication represents a barrier to reproduction. It is assumed that the evolution of morphologically simpler species such as the spreading earthmoss and its close relatives is characterized by duplication events and the subsequent loss of individual chromosomes. But there are other factors, such as the transposons described above. Perhaps the conspicuously variable form of the spore capsule can also be traced back to such changes ⌐**126**.

┌126 *A direct comparison of the size of (A) bonfire moss, (B) Norfolk bladder moss, and (C) spreading earthmoss illustrates how different the spore capsules of the Funariaceae can look.*

A   B   C

Evolutionary design

In biology, every manifestation within a population is primarily based on a genome (i.e., the genetic information of an individual). These genomes have mutated in the course of evolution. In sexual reproduction they are combined with each other so that a new set of variants is created in the following generation.

Using so-called evolutionary algorithms, it is now also possible to apply these mechanisms in the field of evolutionary design of products, architecture, and art. Everything starts with a simple population, the digital genomes of which—in the form of numerical series—present random design variations. Gradually, new design variants are created through step-by-step mutation and the re-combination of the digital genomes. As in the natural selection process, every design variant is evaluated against defined design criteria and only the good ones are retained for the next evolutionary step. Over time, this leads to continually improving variants until finally a set of best suitable design variants is achieved. Normally, the sole purpose of these processes is the improvement of certain factors. However, an important characteristic of evolutionary processes is their strength of innovation, which again and again produces surprising new results. It follows that evolutionary approaches in design may lead not only to optimization but also to the exploration of new solutions.
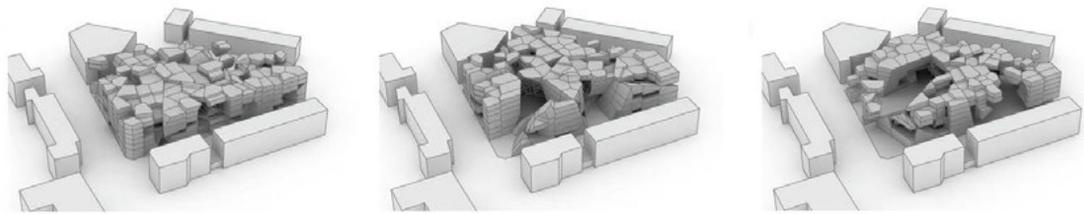
Transfer of evolutionary mechanisms to evolutionary design

The objective is to use selected genetic mechanisms of biological evolution to develop algorithms that allow the design to evolve analogously to the processes in nature. This makes it possible to utilize the innovative power of evolution and to proceed along new avenues in product design and architecture. However, two aspects must be taken into account in this endeavor: firstly, the variability of the size of genomes, and secondly, the importance of the noncoding DNA.

The digital genomes used in evolutionary design usually have a fixed size. This represents a simplified working model and reduces the computing time required. However, the variable size of genomes of the different species of Funariaceae illustrates that it is important to be able to modify the size of the digital genomes generated on the computer over the course of the evolution. Another factor is the simplified relationship between the genome and the resulting design compared to nature. In order to achieve free evolution of design these simplifications must be eliminated. Furthermore, the presence of noncoding DNA indicates that not every variable in the digital genome has to have a mandatory direct influence on the design. The seemingly superfluous variables are not necessarily decisive for the design of the following generation. However, if they are assessed as potentially useful as part of the selection mechanism, they are retained as part of the genome.

The part of the algorithm that converts the digital genome into a design is also referred to as digital embryogenesis. In biology, embryogenesis describes the development of the embryo following the fusion of the genomes of the egg and sperm cells. This analogy with biology indicates how the new type of design develops from the digital genetic makeup. The embryogenesis must be sufficiently complex that it does not limit the diversity of the possible design results and, at the same time, that it is able to benefit from the growing size of the genome. Tests carried out to date indicate that the complexity of this digital embryogenesis has heavily influenced the outcome of high-quality design variants. The structures that contribute to the evolution of the individual moss plant are similarly complex. Even though it is relatively easy to understand the individual steps involved, it is difficult to grasp how they all work together. Assuming that the developed evolutionary algorithm is helpful in solving the one specific design problem, it doesn't necessarily follow that this will apply to all design problems. The applicability of the evolutionary algorithm therefore depends heavily on the type of design problem and the algorithm has to be readjusted every time ⌐**127**.

The above prerequisites must be met before the genetic mechanisms of biological evolution, such as genome duplication, can be simulated digitally. Furthermore, processes such as alternative splicing or transposon jumps make it possible for new products to be created from one and the same gene. These different variants will then again be the starting point for
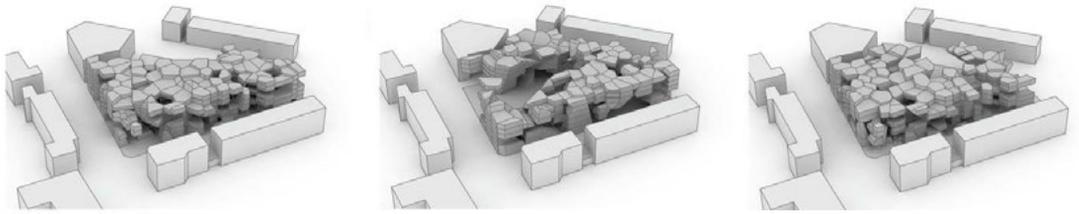
new design variants. We can conclude that understanding the processes underlying biological evolution and their implementation in evolutionary algorithms constitutes a key to fully utilizing design diversity and design innovation in product design and architecture.

⌐**127** *Development of urban apartment blocks (dark gray) using evolutionary algorithms. In this case, a specified genome size was used together with a complex embryogenesis.*

Glossary

Algorithm   *Stepwise process or set of rules to be followed in calculations*

Chromosome   *Packaging unit of the DNA*

DNA   *Deoxyribonucleic acid, molecule, carrier of genetic information*

Embryo-genesis   *Development of the embryo after the fusion of the genome of the egg cell with that of the sperm cell*

Encoding   *Containing information for making a gene product*

Eukaryotes   *Organisms in which the cells have a cell nucleus*

Exon   *Coding section of a gene that is decoded to produce a protein*

Gene product   *For example, a protein produced after a gene has been transcribed and translated*

Genome   *Total of the genetic makeup of a creature*

Intron   *Noncoding section of a gene that has to be removed before the transcript is translated*

Molecule   *Contains at least two equally linked atoms*

Morphological   *Relating to exterior shape or form*

Mutation   *Spontaneous modification of the genetic makeup*

Protein   *Protein molecule*

RNA   *Ribonucleic acid, a transition molecule that is created when decoding the DNA and is used (e.g., as a pattern for proteins)*

Splicing   *Removing the intron sections of a gene*

Splicing, alternative   *Removing the intron sections including certain parts of the adjoining exon areas or incomplete intron removal*

Transposon   *DNA area that can spread itself or copies of itself in the genome through jumps*