FRACTAL DESCRIPTION OF BIOLOGICAL NANOSTRUCTURES

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Fractals were first introduced by B. Mandelbrot while trying to find a solution to the seemingly simple problem of determining the length of the British coastline. He found that Euclidean concepts fail in these and other situations, and that fractals were better suited for these purposes [1]. Unlike more familiar Euclidean constructs, every attempt to split a fractal into smaller pieces results in the resolution of more structure.

Fractals posses two basic distinguishing features:

1. Fractals typically (though not always) have a non-integer dimension.
2. Fractals typically exhibit statistical self-similarity over a range of length scales.

In fractal analysis, the Euclidean concept of "length" is characterized by a constant parameter D known as the fractal dimension:

$$D = \lim_{\varepsilon \to 0} \frac{\ln N(\varepsilon)}{\ln 1/\varepsilon}$$

where $N(\varepsilon)$ is the number of boxes in a square grid of side-size ε required to cover the object in question. The fractal dimension can be viewed as a relative measure of complexity, or as an index of the scale-dependency of a pattern.

Self-similarity, possible only for geometric fractals, is achieved only at infinity when every tiny part is identical to the whole. Fractal properties include scale independence infinite length or detail.

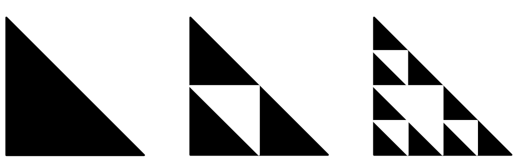

Fig. 1. Sierpinski gasket

The simplest fractals can be constructed by iterations. For example, for every filled-in triangle the midpoints of the sides should be connected and the middle triangle should be removed (Fig. 1). Iterating this process produces in the limit, we get the Sierpinski gasket. For 3D design Sierpinski tetrahedron can be constructed in a similar manner (Fig. 2).

The fractal concepts have been widely used in biological sciences because many natural objects show partial self-similarity in their structure.

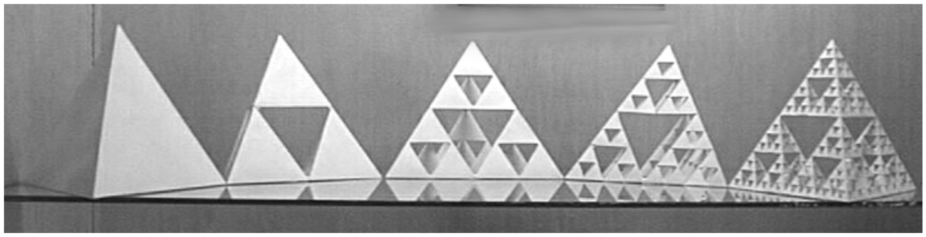

Fig. 2. Sierpinski tetrahedron [2]

This theory is fundamental to modeling of scale-related phenomena; from the molecular to ecosystem levels of organization [3]; from the relatively simple constructions of natural plants (Fig. 3 a) to the description of butterfly wings (fig 3 b), and human lungs (fig 3 c).

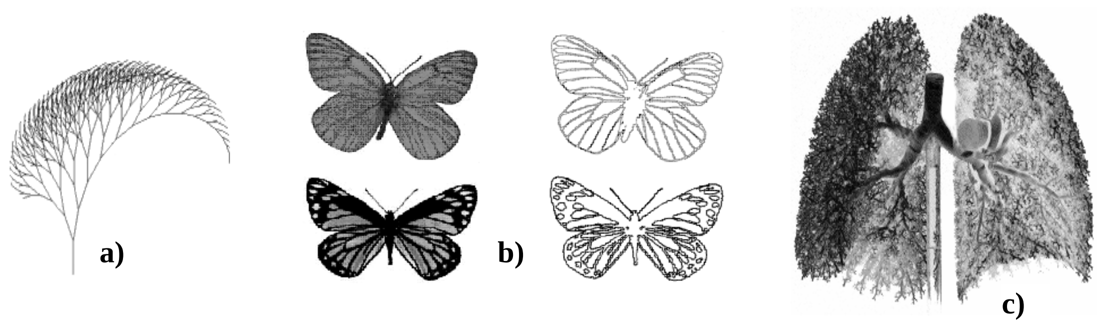

Fig. 3. Fractals in natures: plants modeled by L-fractals (a), fractal features in butterfly wings (b) [4], human lungs (c)

For example, Takahashi [5] hypothesized that the basic architecture of a chromosome is tree-like, consisting of a concatenation of mini-chromosomes. A fractal dimension of D=2.34 was determined from an analysis of first and second order branching patterns in a human metaphase chromosome.

Existing fractal techniques can be applied to classify and distinguish various types of cells. In particular, the use of fractal dimension to distinguish between cells is promising and could develop into a useful diagnostic tool of cancer [6].

A great number of examples can be presented, and each of them emphasizes new possibilities of fractal theory for the description of biological nanostructures.

References

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