# What are the Chances? Probability Solves an Evolutionary Puzzle 

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The origin of species may be almost as random as a throw of the dice. Iosif Pinelis, a professor of mathematical sciences at Michigan Technological University, has worked out a mathematical solution to a biological puzzle: Why is the typical evolutionary tree so lopsided?

In other words, why do some descendants of a parent species evolve into hundreds of different species, while others produce so few they seem to be practicing family planning?

Natural selection may provide some answers, but simple probability yields a surprisingly elegant solution. Pinelis explains: Say you have a carp and a perch swimming in a pond and its equally likely that one of them will evolve a third species. Say the goldfish evolves from the common carp. Suddenly you have three fish species in your pond.

Assume again that it is equally likely for the carp, the goldfish, and the perch to split into two distinct species. The chances that the carp branch will develop a new species are now double that of the perch branch, because the carp family now has two members.

And so it goes, until the pond is overrun with carp and their relatives.
"If one branch has more species, the chances are greater that it will speciate," Pinelis says. "The rich get richer; money goes to money."

In real life, evolutionary trees are even more unbalanced than probability
would predict. So, Pinelis supposed that a significant number of species must change very slowly over time. His hunch is borne out in reality: Biologists have long puzzled over such species, which are sometimes called "living fossils."

One of these is the coelacanth, a species of fish first identified after being caught off the coast of Africa in 1938. Scientists believed it had gone extinct 80 million years earlier, but the discovery showed it had survived unchanged for over 340 million years.

In the fish evolutionary tree, the coelacanth branch is pretty straight. Other branches have thousands of limbs and twigs.

Pinelis believes his model may have practical applications, such as better understanding and control of the evolution of various microorganisms, including viruses and bacteria, which have especially high rates of change.

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Reference: Pinelis, et al. Evolutionary models of phylogenetic trees. Proceedings of the Royal Society B, Vol. 270, 1425-1431.

## Provided by Michigan Technological University

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