About 10 years ago, scientists finally worked out the basic outline of how modern life forms evolved. Now, parts of their tidy scheme are unraveling. Charles Darwin contended more than a century ago that all modern species diverged from a more limited set of ancestral groups, which themselves evolved from still fewer progenitors and so on back to the beginning of life. In principle, the relationships among all living and extinct organisms could be represented as a single genealogical tree. Discoveries made in the past few years have begun to cast serious doubt on some aspects of the tree, especially on the depiction of the relationships near the root.

Scientists could not even begin to contemplate constructing a universal tree until about 35 years ago. From the time of Aristotle to the 1960’s, research deduced the relatedness of organisms by comparing their anatomy or physiology or both. For complex organisms, scientists were frequently able to draw reasonable genealogical inferences in this manner. Microscopic single-celled organisms, however, often provided too little information for defining relationships. In the mid-1960’s, Emile Zuckerland and Linus Pauling of the California Institute of Technology came up with a different strategy other than just comparing anatomy and physiology. They proposed basing family trees on differences in the building block sequences for genes and proteins. Their approach is known as molecular phylogeny, and it states that individual genes are composed of unique sequences of nucleotides that typically serve as the blueprint for making specific proteins. These proteins are in turn composed of particular strings of amino acids. Consensus holds, that in the universal tree of life, the early descendant’s last common universal ancestor was a small cell without a nucleus. This ancestor was a prokaryote.

At this same time, Carl R. Woeses of the University of Illinois was turning his attention to a powerful new yardstick for evolutionary distances --- a small molecular subunit known as ribosomal RNA. Higher sections of the universal tree of life have based many of their branching patterns on sequence analysis of rRNA genes. By the 1960’s, microscopists had determined that the world of living
things could be divided into two separate groups ---eukaryotes and prokaryotes, depending on the structure of the cells that composed them. The endosymbiont hypothesis proposes that mitochondria formed after a prokaryote that had evolved into an early eukaryote engulfed and then kept one or more alpha-proteobacteria cell. Eventually the bacterium gave up its ability to live on its own and transferred some of its genes to the nucleus of the host becoming a mitochondrion. Later, some mitochondrion bearing eukaryote ingested a cyanobacterium that became a chloroplast. Eventually most scientists accepted this hypothesis because the overall structures of certain molecules in archaeal species of bacteria. Similarly, the archaeal proteins responsible for several crucial cellular processes have a distinct structure from the proteins that do the same tasks in more modern bacteria.

Once scientists accepted the idea of 3 domains of life instead of two, they naturally wanted to know which of the 2 structurally primitive groups --- true bacteria or archaic--- gave rise to the first eukaryotic cell. In 1989, research groups led by J. Peter Gogarten of the University of Connecticut and Takashi Miyata of the Kyushu University in Japan used sequence information from genes for other cellular components to establish the “root” for the universal tree of life. Comparisons of rRNA can indicate which organisms are closely related, but for technical reasons, cannot be themselves indicate which groups are the oldest and therefore closest to the root of the tree. DNA sequences encoding 2 essential cellular proteins agreed that the last common ancestor spawned both the true bacteria and archaic bacteria and then the eukaryotes (with a nucleus) branched from the archaic.

Still, as the DNA sequences of complete genomes have become increasingly available, research groups have noticed patterns that are disturbingly at odds with the prevailing beliefs. If the consensus tree were correct, transferred genes would be ones involved in cellular respiration or photosynthesis and not in other cellular processes. A good number of those bacterial genes though serve nonrespiratory and nonphotosynthetic processes critical to the cell’s survival. This classic tree also indicates that bacterial genes migrated only to a eukaryote, not to any archaic. However, archaic have been found to contain a substantial store of bacterial genes.
Quite possibly, the pattern of evolution is not as linear and treelike as Darwin imagined it. Although genes are passed vertically from generation to generation, this vertical inheritance is not the only process that has affected the evolution of the cells. Lateral or horizontal gene transfer of genes has also profoundly affected evolution. Such lateral transfer involves the delivery of genes, not from a parent cell to its offspring, but across species barriers. Lateral gene transfer would explain how eukaryotes that supposedly evolved from an archaeal cell obtained to many bacterial genes important to metabolism. The eukaryotes picked up genes from bacteria and kept those that proved most useful.

The “revised” tree of life retains a treelike structure at the top of the eukaryotic domain and acknowledges that eukaryotes obtained mitochondria and chloroplasts from bacteria. But it also includes an extensive network of untreelike links between branches. These links have been inserted somewhat randomly to symbolize the lateral gene transfers that occur between unicellular organisms. This “tree” also lacks a single cell at the root; the three major domains of life probably arose from a population of primitive cells that differed in their genes.