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Answering questions we did not know how to ask

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I want to be stunned by a visualization discovery, a WOW moment! And I do not mean that some variable values turned out to be much different than expected or the location of an event was different than expected, etc. But rather that something far-reaching we had no idea existed was found, something like penicillin. This should be the measure of visualization's success. And just how do we do that? For one thing luck helps but, as I tell my students, "When you work harder your luck improves"! For a data-set with M items there are 2M possible subsets anyone of which may turn out to be the one satisfying our objectives. With our fantastic pattern-recognition ability, we can cut great swaths through this combinatorial explosion discovering patterns corresponding to relational information from a good data display. This is something that simply cannot be automated … thank goodness! Patterns are geometrical creatures and so we need to learn geometry. Actually from our point-of-view, we are not interested in rigid patterns but malleable ones e.g. "gaps" which can be different in shape but are gaps, nonetheless. That is we are really in the topology of the patterns. It has been shown that multidimensional patterns cannot be discovered directly from their points. Rather they can be synthesized from lower dimensional information. Even in 3-D, we learn to look at planes not by their points but by their planar surface/shape consisting of their lines and ditto for surfaces. We need to discuss and adopt a rigorous syllabus for the discipline of visualization involving geometry, topology and cognition among others. This is our best investment for the future. Research on the geometry and topology induced by coords has made great strides. Many patterns corresponding to multivariate relations have been discovered. We have embarked on a project to transform these results into powerful tools for our exploration and data mining arsenal. They revolutionize the power of modern-coords.

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Information hiding in DNA sequences

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People are always looking for secure methods to protect valuable information against unauthorized access or use. That's why disciplines like cryptography and steganography are gaining a great interest among researchers. Although the origin of steganography goes back to the ancient Greeks, recent Information Hiding techniques embed data into various digital media such as sound, images, and videos. However, in this research we took a step further to utilize DNA sequences as a carrier of secret information. Two techniques will be presented. The first method hides the secret message into some reference DNA sequence using a generic substitution technique that is followed by a self-embedding phase such that the extraction process can be done blindly using only the secret key. The second technique is called the Least Significant Base Substitution or LSBase for short. This method exploits a remarkable property of codon redundancy to introduce silent mutations into DNA sequences in such a way that the carrier DNA sequence can be altered without affecting neither the type nor the structure of protein it produces.

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Page 98