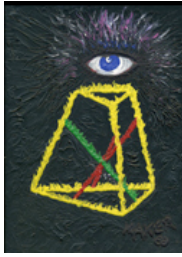


Brief Bio and (PR)²: Problems & Pitches – Rants & Raves by *Erik A Schultes*

Self Introduction



In lieu of a good digital image of myself, and when having relevance to visualization, I have on occasion used this rather providential acrylic painting (a gift from a colleague) as an iconic representation of my interests (see the RNA simplex below).

I have always been interested in visualization. As a child, I was obsessed with optics and drawing and colors. I loved lenses, prisms, microscopes, telescopes; made holograms, super-8 movies, and 3D computer graphics. Later in life, this interest in visualization shifted onto information design and information architectures, which I see as the presentation of large datasets where one can easily access any specific information while always remaining in the global context of the whole. Formally, my training is in organismal biology (BS, Oakland University, 1992), paleobiology (PhD, UCLA, 1997) and RNA biochemistry (postoc, MIT, 2005). My work most relevant to Knowledge Management and Visualization is the RNA simplex, a low-dimensional projection of the very-high dimensional sequence space of RNA. In a circuitous rout that makes little sense without a long explanation, the RNA simplex grew out of elements of evolutionary theory, optical mineralogy and physical chemistry. In recent years I have begun working with digital video and have growing interests in film documentary. I have worked as a private consultant since 2005.

Publications:

- (1) No Molecule is an Island: Molecular Evolution and the Science of Sequence Space, in *Algorithmic Bioprocesses*, ed. Condon A, Harel D, Kok JN, Salomaa A & Winfree E. (Springer, New York, forthcoming in 2008).
- (2) Compact and ordered collapse in randomly generated RNA sequences. *Nature Structural and Molecular Biology*, 12: 1130-1136 (2005).
- (3) One sequence, two ribozymes: implications for the emergence of new ribozyme folds. *Science* 289: 448-452 (2000).
- (4) A parameterization of RNA sequence space. *Complexity*, 4: 61-71 (1999).
- (5) Global similarities in nucleotide base composition among disparate functional classes of single-stranded RNA imply adaptive evolutionary convergence. *RNA*, 3: 792-806 (1997).

<http://hedgehogresearch.info/>

<http://www.santafe.edu/~pth/simplex.html>

General Questions

- 1) What is (are) your main interest(s) in attending the workshop?

With an interest in information design, my main interest in the workshop is to participate in and contribute to the design of large-scale information architectures in the biological sciences.

- 2) What information/knowledge management expertise do you have?

Most specifically, my skills focus on the structural biology of RNA and bioinformatics. More generally, I have developed tools for visualizing high-dimensional regular-graphs as low-dimensional projections. This work also focused on methodologies permitting meaningful (though incredibly sparse) sampling of large regular-graphs.

- 3) What is the most insightful visualization of static or dynamic phenomena you know?
I am obsessed with cellular automata because (1) they are visually intoxicating and (2) their formal structure is so simple, yet capable of capturing any possible dynamic without central control. Despite their many applications and all that has been discovered, I suspect the deepest secrets of cellular automata have yet to be revealed.
Also, see these hyperbolic viewers:
<http://www.caida.org/tools/visualization/walrus/gallery1/>
And anything to do with the light fields, e.g.:
<http://graphics.stanford.edu/projects/lightfield/>
- 4) What would you like to learn / achieve at the workshop?
I look forward to filling in the (gapping) holes in my knowledge about state-of-the-art visualization, and exploring opportunities with individuals and institutions for implementing large-scale projects in biology, history, and documentary studies.