

Ecce Homology

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1 Abstract

Ecce Homology, a physically interactive new-media work, visualizes genetic data as calligraphic forms. A novel computer-vision based user interface allows multiple participants, through their movement in the installation space, to select genes from the human genome for visualizing the Basic Local Alignment Search Tool (BLAST), a primary algorithm in comparative genomics. (<http://www.insilicov1.org>)



Figure 1: Visitors interacting with the installation at the UCLA Fowler Museum, November 6, 2003 - January 4, 2004.

2 Art and Science

For both ethical and technical reasons, the function of each gene in the human genome cannot currently be ascertained directly from the human genome itself. Usually, in order to determine the function of a gene, scientists must rely on comparisons between our genes/genome and those of other organisms. BLAST, the Basic Local Alignment Search Tool, (Altschul et al. 1990, 1997) allows researchers to compare DNA or protein sequences of unknown identity, function, and structure with "knowns" from validated databases, providing a measure of similarity or homology among sequences. BLAST analyses are conducted worldwide via web servers supported by major genome sequencing consortia in Europe, Japan, and North America, as well as in local laboratories on individual computers. Every day, an average of 100,000 unique BLAST runs from 70,000

unique IP addresses are conducted on the US National Center for Biotechnology Information's web servers. (Matten, 2003) BLAST is arguably the most widely used data-mining tool in history. Yet, despite its ubiquity, BLAST is a "black-box" process that is not well understood, even by researchers in the biological sciences.

For *Ecce Homology*, intermediate information about the progress of BLAST is revealed by an animation of the intermediate products of the algorithm as it operates on genomic data in real time overlaid on the calligraphic forms. This revelation of the operation of a normally invisible process is at the core of the installation's aesthetic experience. Transformed into an experience that proceeds at the scale of human-perceived time, BLAST is the engine and subject of this interactive installation.

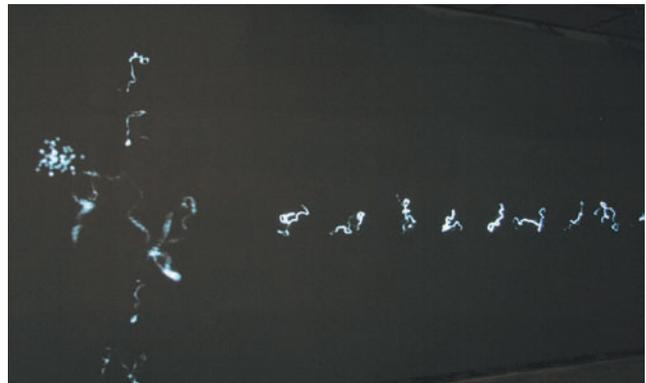


Figure 2: Human gene character undergoing BLAST

We believe that an artistic, holistic visualization of genomic data coupled with an esthetically engaging interactive experience of genomics-based biology can encourage the general public to engage the subject critically. Additionally, *Ecce Homology*'s novel calligraphic visualization of multi-dimensional genomic data is an example of art-science research that explores the possibility that artistic or aesthetic approaches can nurture discovery in the sciences. Unprecedented amounts of genomic data are generated daily. To capitalize on this wealth of data, new tools must be developed. The need to build knowledge from data, or to find patterns within vast datasets, is driving development and application of interdisciplinary and alternative approaches. *Ecce Homology* is one such approach. Its outcomes are both hybrid process and product.

3 Goals

To contribute simultaneously to the realms of science and art while retaining discipline-specific rigor. To investigate the nature of interdisciplinary collaboration. To foster awareness of tools that generate meaning and knowledge in science, particularly genomics. And to explore how artistic practice and aesthetic experience can nurture scientific discovery.

4 Innovation

Technical innovations include development of a novel calligraphic gene visualization incorporating multidimensional data and deployment of a new Java-based middle-ware framework: Kolo (and its associated scripting language Nebesko) developed at the UCLA Hypermedia Studio.



Figure 3: Brush strokes are shaped by atomic level properties of amino acids through entire gene sequences allowing for viewing of patterns or common properties among a group of sequences.

As users move in the installation space, hand-position information generated by the computer-vision module is forwarded to the pattern-matching module and the graphics modules that render user movement. When the pattern-matching module detects a match between a user-drawn form and a gene character, a BLAST run is triggered. As it runs, the BLAST module sends intermediate progress to the graphics modules for rendering. Finally, a separate state-management module manages the overall state of the installation.



Figure 4: *Ecce Homology* interactive experience is based on stillness, slow movement, and mindful or contemplative presence,

5 Vision

As the next era in the life sciences becomes increasingly dominated by interdisciplinary and discovery-based inquiry, *Ecce Homology* exemplifies an integrated art-science practice that goes beyond models of influence and convergence to explore the deep structures of science and technology in search of their expressive potentials and cultural relevance. Though it is driven by aesthetics, *Ecce Homology* suggests a new form of scientific visualization that may one day contribute to comparative genomics.

If the arts can nurture discovery in the sciences, it is possible that the process can bring about a new paradigm for our relationship to nature, one in which human creativity is the avenue for our rapprochement with nature.

6 References

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