

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. *Ecce Homology* was successfully installed in the UCLA Fowler Museum, November 6, 2003 – January 4, 2004. (<http://www.insilicov1.org>)

2 Motivation

Advances in molecular biology make genomics an increasingly important topic for public discourse. BLAST [Altschul et al. 1990] is foundational to genomic biology. Yet, despite its ubiquity, BLAST is a “black box” process whose workings are little understood, even by researchers in the biological sciences. We believe that an artistically founded 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.

3 Visualization

Ecce Homology's gene visualization is based on an ideographic and pictographic language reminiscent of Chinese calligraphy or Sanskrit writing. Motivated by the desire to move beyond the traditional representation of genes as long strings of ‘ACTG’ nucleotide lists, *Ecce Homology* visualizes characteristics of genes as the strokes and radicals of a non-phonetic alphabet.

Stroke curvature, width, pressure, and the brush profile are varied according to the physical and chemical qualities of each individual gene. A naturalistic rendering of gene characters is achieved by modeling a brush depositing ink as it is drawn across a textured sheet of paper. By using this holistic representation of genes we hope to gain insight into the structure and configuration of the genome.

4 Interaction

Five projectors present *Ecce Homology's* calligraphic forms across a thirty-five feet wide wall. Multiple users can simultaneously interact with the installation through its computer-vision system in which hand movement (or hand-like movement) is detected and rendered in front of the user for feedback. By moving in the installation space users are able to draw their own calligraphic characters. A pattern-matching algorithm compares

the user-drawn forms with the existing visualizations of genes in a genome database to select a character from that database. The system then visualizes a BLAST experiment with the selected character as its target. BLAST is a statistical pattern-matching algorithm that involves multiple passes over genomic data, each pass employing powerful but computationally inexpensive scoring mechanisms. This process involves cutting genes into millions of ‘words’, looking for ‘hits’ and ‘high scoring pairs’ and then ‘growing matches’. As opposed to the standard “black box” implantation of BLAST, which returns a result with no information on intermediary process, all of these aspects of BLAST are visualized for users.

5 Implementation

Because of the complexity and computational requirements of this installation, *Ecce Homology* is implemented as a collection of independent software modules running on multiple machines and networked together over TCP/IP using a Java-based middleware framework called Kolo developed at the UCLA Hypermedia Studio. [Burke et al. 2002]

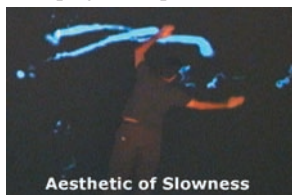
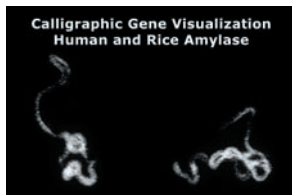
As users move in the installation space, hand position information generated by the computer vision module is forwarded to the pattern matching module and the graphics modules that render user movement. (Three graphics modules are used collectively to project over five projectors.) When the pattern-matching module detects a match between a user drawn form and a gene character a BLAST run is triggered. When run, 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.

6 Conclusion

Ecce Homology is based upon a ‘transdisciplinary’ framework that attempts to retain the depth and rigor of discipline-specific practices of both the arts and sciences. *Ecce Homology* implements a unique holistic calligraphic gene visualization that incorporates multidimensional biological (genomic and protein) data. Through movement within the installation space, multiple users are able to interact simultaneously with BLAST, the Basic Local Alignment Search Tool, shedding light on what is normally a “black box.”

7 References

- Altschul, S. F., et al. 1990. Basic Local Alignment Search Tool, *Journal of Molecular Biology* 215, 403-410.
- Burke, Jeff, Eitan Mendelowitz, Joseph Kim, and Rex Lorenzo. 2002. Networking with Knobs and Knats: Towards Ubiquitous Computing for Artists. In *Ubiquitous Computing 2002, Concepts and Models Workshop, Gothenburg, Sweden, September 29 - October 2, 2002*.



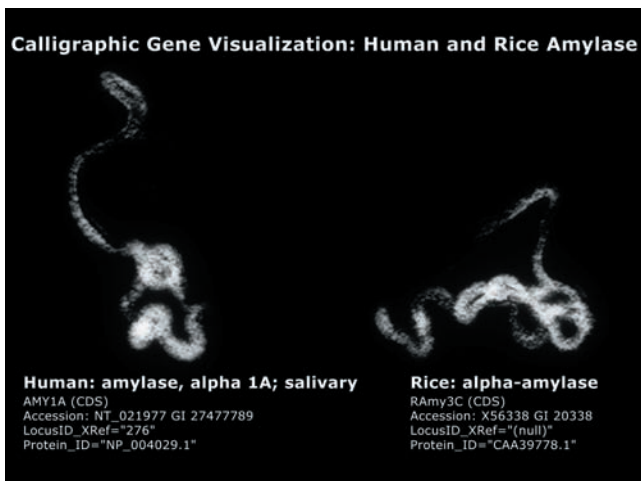


Figure 1: Brush strokes are shaped by atomic level properties of amino acids through entire gene sequences allowing for viewing of patterns or common properties among a group of sequences.



Figure 2: *Ecce Homology*'s interactive experience is based on stillness, slow movement, and mindful or contemplative presence,

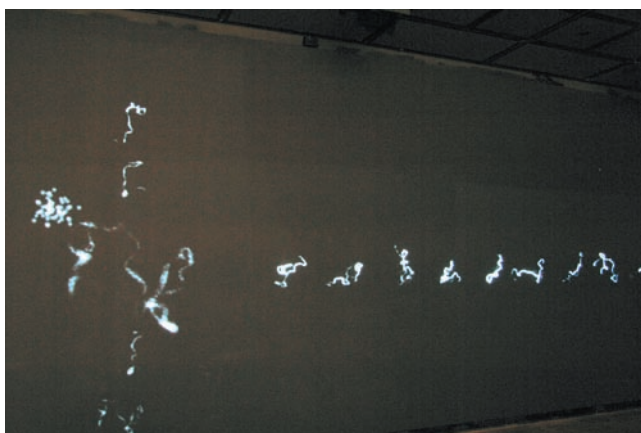


Figure 3: Human gene character undergoing BLAST

Visualization

The stroke curvature, brush width, pressure and the brush profile vary according to secondary structure information as well as chemical and physical information about each position in the sequence. Genomic data selected from human and rice genomes maintained by the National Center for Biotechnology Information (NCBI), The Institute for Genomic Research (TIGR), and the Rice database at Gramene: A Comparative Mapping Resource for Grains (Cornell University) were used for the installation of *Ecce Homology* in the UCLA Fowler Museum of Cultural History.

Aesthetic of Slowness

The expansion of the projection from a small shimmering form at the scale of the human body to a scale that engages our peripheral vision indicates the vast and abstract nature of the genomic datasets and our relation to them at this point in time. At the conclusion of the expansion, multiple users can simultaneously interact with the piece through a computer-vision and feature-extraction system in which hand movement (or hand-like movement) is detected and rendered in real-time near the calligraphic forms. By moving in the space, users draw their own light-filled calligraphic characters. The more deliberate and contemplative one's motion, the more continuous the light-filled gesture traces and the longer they persist. This results in an aesthetic of slowness, which creates a sustained sense of presence and contemplation for visitors.

BLAST Visualization

Simple pattern matching is performed to compare the user-created forms with those of human genes. When a sufficiently close match is found, a human gene character from the vertical axis is selected. This use of pattern matching as a selection process is a metaphor for BLAST. Upon selection, a human gene character is enlarged and displayed in the central space where the user's gesture traces had been, and the BLAST engine compares it to the genes from other organisms residing in the 'target' database. For *Ecce Homology*, the 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, is overlaid on the calligraphic forms. It includes segmentation, neighbor location, dynamic programming, and ranking based on likelihood of homology, or evolutionary similarity. This produces an inversion of scale at the level of time, making the normally imperceptible algorithmic process visible and visceral.



Figure 4: Images from the installation at the UCLA Fowler Museum, November 6, 2003 - January 4, 2004.

Acknowledgements

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Ecce Homology is available online at: <http://www.insilicov1.org>

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