Eric Holloway Publishes Paper on Specified Complexity

David Nemati and Blyth Institute fellow Eric Holloway recently published a new paper in the journal *BIO-Complexity* (Nemati and Holloway, 2019). The paper, titled "Expected Algorithmic Specified Complexity," explores the expected Algorithmic Specified Complexity (ASC) of a random variable, concluding that the expected ASC is always less than zero. This is true both of random variables and of "processed" random variables—variables which have undergone some sort of transformation. This indicates that the existence of positive ASC always counts as "surprise," and therefore always requires explanation.

New Thinking on Human Origins

This past year witnessed a plethora of new thinking on human origins. First up, new research by Ola Hössjer and Ann Gauger recently showed a unique model for looking at biodiversity (Hössjer and Gauger, 2019). Essentially, they looked at the ways in which minor allele frequency distributions can arise, and how long different distributions take to arise. New alleles essentially start out as one-off events, arising as a mutation in a single individual and later spreading through the population or dying out (or somewhere in-between). The frequency of these minor alleles can provide some amount of information about the history of the species in question. It takes time for an allele to spread through a population. Therefore, initially, from an initially homozygous pair, the low-frequency side of the minor allele frequency spectrum will contain all of the new mutations. The mutations will take time to spread throughout the population. What Hössjer and Gauger discovered, though, is that a *heterozygous* initial pair creates an allele frequency spectrum that looks much older than it is. This is because an allele can actually start as either 25%, 50%, 75%, or 100% of the population before any mutations even occur. Thus, the frequency spectrum will fill very quickly from the initial pair, and the initial heterozygosity will look equivalent to ancient mutations.

Using standard assumptions, Hössjer and Gauger calculated that the current allele frequency spectrum could be attained from an initial starting pair in 100,000–500,000 years. Using other alternative assumptions about the nature of the starting pair could result in attaining the current allele frequency spectrum in an even shorter period of time.

Another interesting paper was done by Nathaniel Jeanson and Ashley Holland, which analyzed the human Y chromosome (Jeanson and Holland, 2019). Analyzing the human genome as a whole leads to a number of model-specific issues. If we imagine a starting pair for humanity, were the original chromosomes identical or did they house diversity? Additionally, might the first human female have eggs that had additional diversity in their chromosomes?

However, nearly all considerations of single-couple human origins have exactly one starting Y chromosome, leading to fewer model-specific considerations. Jeanson and Holland aimed to improve the data available about Y chromosome mutation rates by examining pedigree-based studies which used high-coverage sequencing. According to Jeanson and Holland, (a) a Y chromosome molecular clock exists, and (b) it suggests a paternal history of the human race of about 4,500 years.

Finally, the year ended with the publication of Joshua Swamidass's new book titled *The Genealogical Adam and Eve* (Swamidass, 2019). This book aims to show that the practical difference between popular and scientific conceptions of "Adam and Eve" are not too far off. His viewpoint is that, although, according to the consensus view, there could be no single-couple *origin* of humans, there could be a single couple to whom all modern humans could trace their genealogies.

Communicating Science Through New Venues

New media becomes old media very quickly in the modern age. Email was once the best technological way to communicate interpersonally. This is now often replaced with various social media platforms such as Facebook, Twitter, and others. Likewise, YouTube was once at the center of

video-based media. While YouTube is still the de facto destination for video content, it is useful to look at some of the newer players.

First of all, some video is being distributed through apps on standard platforms. Developing an app for Roku, Amazon Fire, or Apple TV is a new way to get content to users. Additionally, streaming services such as Twitch, and now Mixer, are becoming the dominant social video platforms for the youth. Science communicators should explore ways of reaching the public through these outlets. One possibility would be to play video games with scientists, discussing what they do while shooting zombies, or discussing the latest theories of the universe while racing Nascar.

Growth opportunities are always with the latest technology. Asserting a strong position while they are still unproven is the best way to establish leadership for the future.

Austrian Society *Zentrum für BioKomplexität & NaturTeleologie* Opens with Special Symposium

A new Austria-focused scientific society, *Zentrum für BioKomplexität & NaturTeleologie*, recently formed and held their first symposium. The symposium featured many European scientists and mathematicians, as well as a few from the United States as well. The organizers of the conference were Günter Bechly, a prominent German paleontologist who presently works as a senior scientist for the Biologic Institute, and Siegfried Scherer, a professor of microbiology and chair of microbial ecology at the Technical University of Munich.

While the society is based in Austria, the symposium itself was largely in English. Many of the talks from the three day symposium are available on YouTube, at `https://www.youtube.com/playlist?list=PLkaKqUjdyg2JHNqeWQHnVTXZ-37h0tJMb`.

Breaking the Weismann Barrier and Closing the Loop for Lamarckian Evolution in Multicellular Organisms

A recent review paper in the Royal Society shows that the Weismann barrier is crumbling. In "The active role of spermatozoa in transgenerational inheritance," Sciamanna et al review the mounting evidence that there is a Lamarckian feedback loop in DNA inheritance (Sciamanna et al., 2019). The paper reviews evidence that mammalian somatic tissues release RNA-containing vesicles, and that these vesicles are then passed to epididymal spermatozoa. Additionally, epididymal spermatozoa are known to be able to internalize foreign nucleic acids into their nuclei. This completes the communication channel between somatic cells and germ cells required for Lamarckian inheritance.

This communication channel was original proposed in the 1990's. Steele et al's *Lamarck's Signature* suggested that somatic mutations might be passed to germ line cells through an RNA channel (Steele, Lindley, and Blanden, 1999). After decades of work across multiple groups, evidence is mounting that Steele's hypothesis was largely correct.

Overcoming Entrenched Dogma About Pseudogenes

Biologists have long known that not all non-coding DNA is junk DNA. However, pseudogenes have long been considered the standard bearer for the junk DNA concept. Since pseudogenes look like defective, non-coding copies of ordinary genes, it has been often assumed that these are evolutionary leftovers—genes which once coded for something, or a copy of a gene that once coded for something, but which some accident of mutation incapacitated its activity.

While the evidence for the activity of pseudogenes has long been known, the idea that pseudogenes indicate junk DNA has been ingrained in biologists. A group of researchers recently published a paper pointing out that the prejudices that biologists have about the status of pseudogenes as junk DNA is impeding the progress of understanding the way that the genome functions (Cheetham, Faulkner, and Dinger, 2019).

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