

Digital Code Mutation and Nucleotide Code Mutation is Not a Valid Comparison

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Abstract: DeJong & Degens (2011) conclude from the properties of digital codes that ‘nucleotide codes’ should have similar mutation protection. I argue that digital codes and ‘nucleotide codes’ are not sufficiently similar to draw conclusions about mutation protection and evolution. A ‘mutation protection paradox’ does therefore not exist in biology.

Keywords: Digital code, nucleotide code, mutation protection, evolution.

INTRODUCTION

DeJong & Degens (2011) [1] argue a distinction must be made between ‘random change within the boundaries of mutation protection’ and ‘unbounded random change’ outside the boundaries of mutation protection. DeJong & Degens present several lines of argument tending to the position that mutation outside the ‘boundary of mutation protection’ might neither be feasible nor robust. All lines of argument depend on the comparison of digital and nucleotide codes. Their first line of arguments is how digital codes are protected against mutation and programming error. A second line is asking whether digital constraints introduce restriction on individual based simulations and evolutionary programming as models for evolutionary change. A third line is the comparison of mutations in the genome to digital mutations.

RECONSIDERING THE ARGUMENTS

A comparison of the genome to a computer program is a well-known low level metaphor; however, DeJong & Degens (2011) seem to take the metaphor to be quite literal. This leads to an attempt to draw inferences about evolutionary change from the properties and possibilities of computer programming. The question is therefore whether their comparisons between ‘digital code’ and ‘nucleotide code’ are valid and biologically informative; especially, whether their major emphasis on the difference between ‘random change within the boundaries of mutation protection’ and ‘unbounded random change’ is equally warranted for genomic mutations and digital mutations.

DeJong & Degens point out that digital codes are strictly guarded against mutation at the bit level; no single mutation at the bit level is allowed, otherwise computers wouldn’t work. Digital code is therefore not comparable to DNA repair, as DNA repair is not 100% effective under any

circumstance [2], and, being costly in energy terms, depends upon the environment [3].

DeJong & Degens present an individual-based simulation intended to demonstrate the difference between random change with mutation protection versus unbounded random change. Individuals might belong to any of four genotypes; some random change of type is preprogrammed between parent and offspring. An individual gets two input values to make its output value. The core programming sentence might read somewhat like this:

“ consider individual i; if (type.i = x) then output.i := input1.i (X) input2.i”, where x equals 1,2,3,4 and (X) equals addition “+”, subtraction “-“, multiplication “*”, or division “/”. It will be clear that adding random bits of digital code to the individuals’ program module will lead to error messages and dead individuals in very many cases. Not in all potential cases: a typo “^”, exponentiation instead of addition “+”, is represented by a digital code that allows a valid mutation; a random digital code change might lead to “output.i := input1.i (X) input1.i”, again valid syntax. That is, random digital code change, or random syntax change, potentially lead to unbounded syntax changes in the module for individuals.

DeJong & Degens further argue that evolutionary programming only functions within a pre-determined program syntax. That might be true; however, nothing in their argument about digital codes or programming leads to their statement about genomic processes, that “mechanisms for random change of nucleotide codes operate within the boundaries of mutation protection present at the nucleotide-level and the higher levels of the code, and do neither produce new alleles nor expand the length of the nucleotide code”. Genomic processes are no digital codes. Mutation repair is not total, and mutations lead almost by definition to new alleles. As to expansion of the length of the nucleotide code, single base insertions lead to frame-shifts rather than expansion of the length of the nucleotide code. Larger scale mutations are ubiquitous. Genomic structural variation as DNA duplication, both of genes and of repeats, or insertion /

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deletions has been analyzed for its prevalence and function [4, 5].

CONCLUSION

A major stumbling block to DeJong & Degens seems to be that mutation causes dysfunction during an individual's life, as for instance cancer or aging, apart from adducing novel variation for selection to act on. The somatic mutation rate is higher than the germ line mutation rate, and seems subject to different selection strengths as it differently affects fitness [6]. The somatic mutation rate is not relevant for any change in gene content in genomes, or evolution of novel genes by gene duplication or *de novo* evolution from non-coding DNA [7, 8].

Mutational change as evidenced in populations and phylogenies seems unbounded. Any patterns in empirical mutation rates seem due a balance between genetic drift and natural selection [6].

CONFLICT OF INTEREST

The authors confirm that this article content has no conflicts of interest.

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REFERENCES

- [1] DeJong, W.; Degens, H. The evolutionary dynamics of digital and nucleotide codes: a mutation protection perspective. *Open. Evol. J.*, **2011**, *5*, 1-4.
- [2] Schofield, M.J.; Hsieh, P. DNA mismatch repair: Molecular mechanisms and biological function. *Ann. Rev. Microbiol.*, **2003**, *57*, 579-608.
- [3] Saint-Ruf, C. I. Matic. Environmental tuning of mutation rates. *Environ. Microbiol.*, **2006**, *8*, 193-199.
- [4] Emerson, J. J.; Cardoso-Moreira, M.; Borevitz, J.O.; *et al.* Natural selection shapes genome-wide patterns of copy-number polymorphism in *Drosophila melanogaster*. *Science*, **2008**, *320*, 1629-1631.
- [5] Zichner, T.; D.A.: Garfield, T. Rausch, *et al.* Impact of genomic structural variation in *Drosophila melanogaster* based on population-scale sequencing. *Gen. Res.*, **2013**, *23*, 568-579.
- [6] Lynch, M. Evolution of the mutation rate. *Trends Genet.*, **2010**, *26*, 345-352.
- [7] Chen, S; Krinsky, B.H.; long, M. New genes as drivers of phenotypic evolution. *Nat. Rev. Gen.*, **2013**, *14*, 646-660.
- [8] Neme, R and Tautz, D. Phylogenetic patterns of emergence of new genes support a model of frequent *de novo* evolution. *BMC Genomics*, **2013**, *14*, 117.

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