

Review of: "Modeling the structure and evolution of cultural information as Quasispecies"

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The discussion of the paper focuses on the ways in which cultural evolution can be studied within the framework of the evolution of information, including biological evolution. The paper presents models that illustrate the processes that lead to diversification of information in certain social contexts, and shows how variation in populations of cultural information can be modelled in the same way as biological information, in the form of genetic material. The paper also discusses the high rates of variation seen in cultural information, which can lead to an abundance of variants analogous to quasispecies in RNA viral populations. The article also touches on the effects of human behavior on error-prone replication of cultural information, and the formation of "textisms" or Emoji languages as analogous to defective interfering viral particles. The paper computes different measures of Shannon Diversity and Heterozygosity to judge diversification in model populations, and notes the importance of including survivability with reproduction rate to determine relative fitness of one variant to another. The paper proposes the use of this measure of fitness (w) in future analysis. The discussion also considers the principle of equivalence in genetic and cultural information, and how processes central to biological evolution are measurable in cultural evolution.

The model presented in the section for the selection and application of cultural information appears to be a well-researched and thought-through concept. The discussion of selection coefficients as describing the propensity of a sequence of cultural information to replicate is a useful way of framing the issue, and the inclusion of existing methodologies for determining the value of these coefficients adds rigor to the model.

The authors provide a clear explanation of the quasispecies model and its application to the study of cultural information. However, it should be noted that this model is not without limitations. For example, the assumption that the replication rate and mutation probability of information sequences are constant over time may not hold true in all cases. Also, the inclusion of external selection pressures in the model is a welcome addition, but more research may be needed to fully understand the complexity of these pressures and their effects on cultural evolution. Overall, this model presents a useful framework for studying the selection and application of cultural information, and its inclusion of the quasispecies model provides a mathematical approach to understanding the dynamics of cultural evolution.

Overall, the model presented in the topic of lexical variation and entropy appears to provide a useful framework for analyzing the diversity and entropy of language use within a cultural group. The use of Shannon entropy and heterozygosity indices allows for a quantitative assessment of the variation present within language, which can be used to track changes over time or compare between different cultural groups. The incorporation of mutation and population

growth dynamics is also a valuable addition, providing insight into how language diversity may alter over time due to these factors. However, there are some limitations to this model, particularly in its assumptions about the Infinite Allele Model and the speed of information transfer compared to the migration of people. These issues could potentially be addressed by incorporating additional complexity into the model, and future work may benefit from further exploring these dynamics.