Sep 24, 2024

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✓ Editors' notes

Researchers refute the validity of 'assembly theory of everything' hypothesis

by King's College London

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Three new papers refute claims for the assembly theory of molecular complexity being claimed as a new 'theory of everything.'

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First publicly posted in 2017, assembly theory is a hypothesis concerning the measurability of molecular complexity that claims to characterize life, explain natural selection and evolution, and even to reshape our understanding of time, matter, life and the universe.

However, researchers led by Dr. Christopher Thorn from the School of Biomedical Engineering & Imaging Sciences (BMEIS), in collaboration with colleagues from King's, Abdullah University for Science and Technology (KAUST) and the Karolinska Institute in Sweden, have successfully demonstrated in a paper published in npj Systems Biology that the same results can be achieved by using traditional statistical algorithms and compression algorithms.

In a second paper just published in PLoS Complex Systems, they have also mathematically proven that assembly theory is an equivalent to Shannon Entropy and therefore not a novel approach to any of those applications and is an implementation of a well-known and popular compression algorithm called gzip ZIP compression and image encoding formats such as PNG.

The third paper, "Assembly Theory Reduced to Shannon Entropy and Rendered Redundant by Naive Statistical Algorithms," is available on the arXiv preprint server.

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"Our research demonstrated that the Assembly Index, the core component of assembly theory which determines the minimum number of steps to the number of exact copies it possesses, as an original method, is not, and its conclusions are flawed," says Dr. Kamila Jirasek.

"When we applied traditional compression algorithms to molecular or chemical data, the same verified results were obtained as under assembly theory. This means that, rather than being a new framework, assembly theory is effectively equivalent to the well-established measures of complexity. Yet, the original authors did not test for any other algorithm."

"Despite some vegetables and plants such as onions and terra humpy or Ethiopian kale having genomes with their many numerous gene copies, it is difficult to argue that onions or terra are more complex or alive than humans. We assembly theory would suggest based on such underestimated values," says Prof Jasper Tegner.

"What truly defines life is not merely genetic length or number of components but the intricate relationship with their environment, the agency life exhibits, and its resilience in preserving its complex organization."

"Our analysis sheds light on the limitations of assembly theory's numerical indices, attempting to define whether and to what extent it succeeds. What truly surprises me is the neglect of the crucial role of molecular interactions in understanding life complexity. Even more alarming is the decision to ignore the well-established threshold with no basis," says Dr. Narsis A. Kiani.

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"The real breakthrough lies in building upon established knowledge, integrating seemingly diverse theories to unravel the complex multidimensional mechanisms that shapes life rather than rehashing what we already knew with tools we had already developed."

While characterizing life is hard and still an open problem, it has been studied from many angles, from molecular units by Gregor Mendel to thermodynamics by Erwin Schrödinger to Statistical Entropy by Claude Shannon to Algorithmic Information by Gregory Chaitin.

Equipped with all this knowledge and much more from complexity sciences and systems' biology, it is known today that one key aspect of life is that of open-endedness, the fact that life's agency seems not bounded to regular physical laws and results in its adaptation and relationship to its environment.

Areas such as Algorithmic Information Dynamics (AID) led by Dr. Hector Zenil and his collaborators, are shedding light on how to find causal models for natural phenomena and mechanistic explanations for processes of living systems.

AID is fully based on the current combined knowledge of information theory and causal inference to this date and builds upon and bridges these fundamental areas used today to understand the world.

The methods behind AID already count for exact copies of modules but that is the most obvious first step and something Dr. Zenil reported recently with examples that as capable of separating organic compounds from non-organic as a function of molecular length.

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More information: Abicumaran Uthamacumaran et al. On the Salient Limitations of the Methods of Assembly Theory and Its Classification of Molecular Biosignatures, npj Systems Biology and Applications (2024). DOI: 10.1038/s41540-024-00443-x

Felipe S. Abrahão et al. Assembly Theory is an approximation to algorithmic complexity based on LZ compression that does not explain selection or evolution, PLoS Complex Systems (2024). DOI: 10.1371/journal.pcsys.0000014

Liam Cotter et al. Assembly Theory Reduced to Shannon Entropy and Rendered Redundant by Naive Statistical Algorithms, arXiv (2024). DOI: 10.48550/arxiv.2408.12108

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