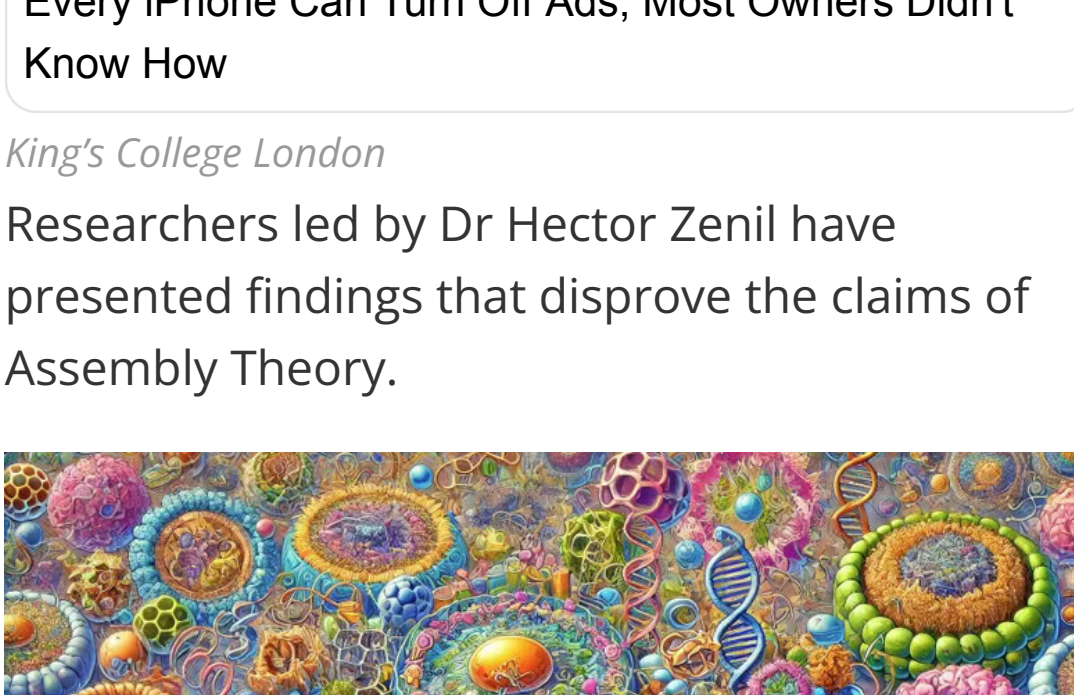


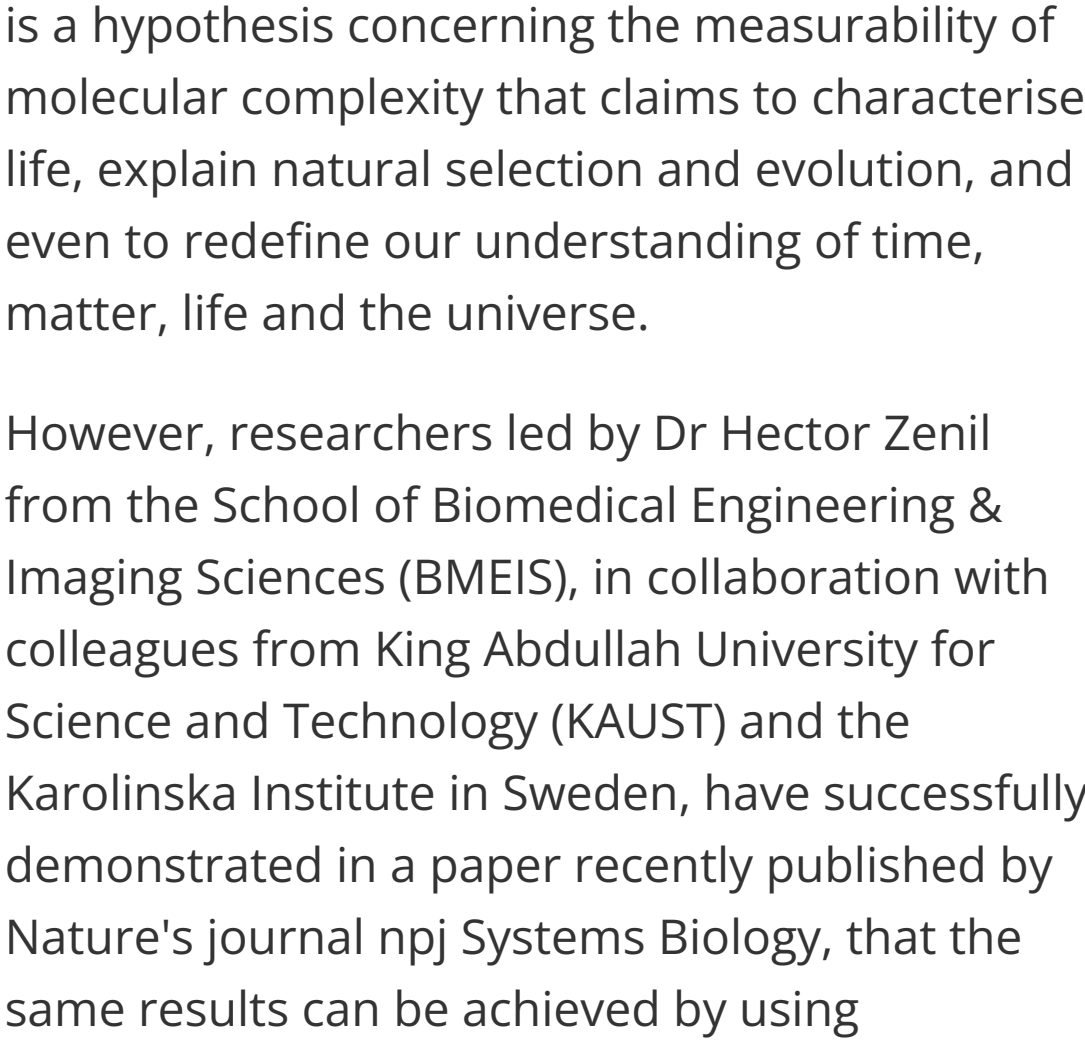
King's Researchers Debunk Assembly Theory Of Everything



Every iPhone Can Turn Off Ads, Most Owners Didn't Know How

King's College London

Researchers led by Dr Hector Zenil have presented findings that disprove the claims of Assembly Theory.



Three new papers refute claims for the Assembly Theory (AT) of molecular complexity being claimed as a new "theory of everything."

First publicly posited in 2017, Assembly Theory is a hypothesis concerning the measurability of molecular complexity that claims to characterise life, explain natural selection and evolution, and even to redefine our understanding of time, matter, life and the universe.

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

In a second paper just published by 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 used behind ZIP compression and image encoding formats such as PNG.

Our research demonstrated that the Assembly Index, the core component of Assembly Theory which determines the 'aliveness' of an object by the number of exact copies it possesses, as an original method, is not, and its conclusions are flawed.

Dr. Hector Zenil, Senior Lecturer/ Associate Professor, School of Biomedical Engineering and Imaging Sciences, and lead author.

Dr Zenil continued: "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 indistinguishable from other pre-existing measures of complexity. Yet, the original authors did not test for any other algorithms."

Despite some vegetables and plants such as Onions and Ferns having up to 50 times longer genomes with their many numerous gene copies, it is difficult to argue that onions or ferns are more complex or alive than humans like Assembly Theory would suggest based on such unidimensional index. 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 essential properties.

Prof Jesper Tegner, Professor of Bioscience and Computer Science at King Abdullah University of Sciences and Technology, Living Systems Lab, KAUST, and co-author.

Our analysis sheds light on the limitations of Assembly Theory's numerical indices, attempting to define 'aliveness' and life characteristics. What truly surprises me is the neglect of the crucial role of dynamic interactions in understanding life complexity. Even more alarming is the decision to propose a fixed life-detection threshold with no basis. The real breakthrough lies in building upon established knowledge, integrating seemingly diverse theories to unravel the complex multidimensional dynamics that shapes life rather than rehashing what we already knew with tools we had already developed.

Dr Narsis A. Kiani, Senior Researcher, Department of Oncology-Pathology, Center for Molecular Medicine, Karolinska Institute, co-author.

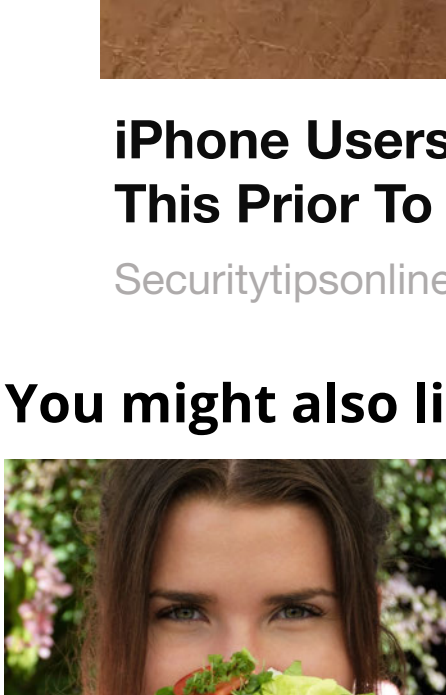
While characterising life is hard and still an open problem, it has been studied from many angles, from modular units by Gregor Mendel to thermodynamics by Erwin Schrödinger to Statistical Entropy by Claude Shannon to Algorithmic Information by Gregory Chaitin. Equipped with all this knowledge and much more from complexity sciences and systems' biology, we know today that one key aspect of life is that of open-endedness, the fact that life's agency seems not bounded to regular behaviour or repetition 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 in 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 before Assembly Theory as capable of separating organic compounds from non-organic as a function of molecular length.

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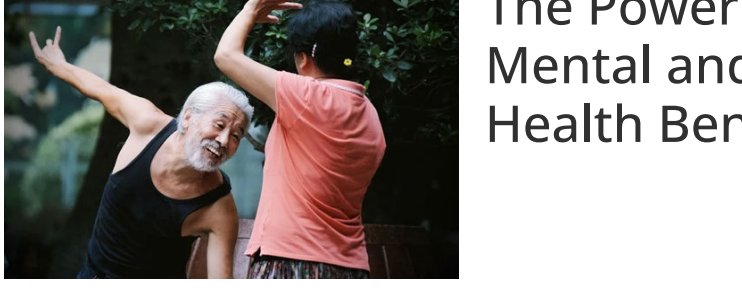
- [Nature.com: On the salient limitations of the methods of assembly theory and their classification of molecular biosignatures](#)
- [PLoS Complex Systems: Assembly Theory is an approximation to algorithmic complexity based on LZ compression that does not explain selection or evolution](#)
- [Assembly Theory Reduced to Shannon Entropy and Rendered Redundant by Naive Statistical Algorithms](#)

In this story



Dr Hector Zenil
Senior Lecturer / Associate Professor

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