

Spontaneous emergence of autocatalytic information-coding polymers

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Recommended with a commentary by Alexander Grosberg, NYU

While it is a commonplace to compare a DNA or RNA with a string of a written text, the spontaneous emergence of its information content in pre-biological evolution is one of the biggest puzzles in modern science. Over the years, only a handful models were suggested, and none of them is even close to being completely satisfactory. In their recent article, cited above, Alexei Tkachenko and Sergei Maslov formulated a model which, although hardly pretends to be a complete solution, seems to me to offer certain significant advantages.

The model is a “soup” of monomers which is actively driven out of equilibrium by periodically changing temperature, with hotter conditions maintained for a while, followed for some comparable time by colder conditions; authors call these periods, respectively, day and night. The monomers are assumed capable of forming complementary pairs, just like modern nucleotides. In the night time, complementary pairs are stable and also monomers can polymerize. In the day time, pairs are unstable, and polymers can also break in any place. Finally, the last and decisive ingredient of the model, is this: if there are two oligomers (shorter chains) in the solution, and they are complementary to adjacent pieces of a longer chain, which is also present, then the two shorter pieces can hybridize with the longer chain, their ends coming within close proximity, and then these ends have a very high probability to connect (the process called ligation). This model is simple enough to allow for analytic investigation in a reasonable (mean field) approximation, and authors also simulate it numerically. Either way, the model does demonstrate intriguing ability to maintain (“memorize”) a spontaneously formed set of sequences which can be called “emergent information”.

In general, the main difficulty in these models is not so much initial emergence of information, but the fact that this information gets forgotten too fast. Indeed, energy selectivity δE between “correct” (complementary) and “wrong” pairing of monomers is far insufficient to fight against extensive entropy in the sequence space. Modern life machinery, of course, faces this problem, too, and employs kinetic proof-reading and other mechanisms to pay energy for improved accuracy of information copying. In the new model, the same end result is supposedly achieved by the cycling through active events (nights) and resets (days). Intriguingly, similar cycling is also an important ingredient of the recent experimental work [1]. It remains to be seen to which extent this new model is indeed immune to the error catastrophe and other problems arising from the extensive sequence entropy.

Another amusing aspect is the thermodynamic role of the emerging information, in the light of modern generalized formulations of the Second Law (see, e.g., [2]).

Whether this suggested model is right or wrong, it is in my opinion good enough to think about it.

References

- [1] P.M.Chaikin, “Some small steps toward Artificial Life”, talk in UCLA colloquium, 2015; <http://www.pa.ucla.edu/events/some-small-steps-toward-artificial-life-paul-chaikin-nyu>
- [2] D. Mandal, and C. Jarzynski “Work and information processing in a solvable model of Maxwells demon” Proc. Nat. Ac. Sci. v. **109** (29), p. 11641-11645, 2012.