Thermodynamics of sequence and exploration in prebiotic scenarios

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Using classical and stochastic thermodynamics[1], we study polymers with a sequence (e.g. RNA, peptides) in solution. In the first part, we study (I) closed systems with sequence exchange reactions[2], and (II) open systems with exchange reactions that exchange polymers with reservoirs. We show that these open systems can exhibit exotic behavior. For example, we can obtain increasingly large polymers, by exploiting entropic thermodynamic forces. In the second part, we revisit ligation-fragmentation models of prebiotic RNA and explicitly consider chemical activation. This leads to modified polymer length distributions and general statements about energy and material requirements of such models. More importantly, it introduces a general energy cost for maintenance and sequence exploration. This cost severely limits the emergence of prebiotic functionality (e.g. ribozymes). By accounting for such costs, we can refine prebiotic scenarios.

[1] M. Esposito and C. V. den Broeck (2015) *Physica A* 418:6. [2] N. Lehman (2008) *Biodiversity* 5:1707.

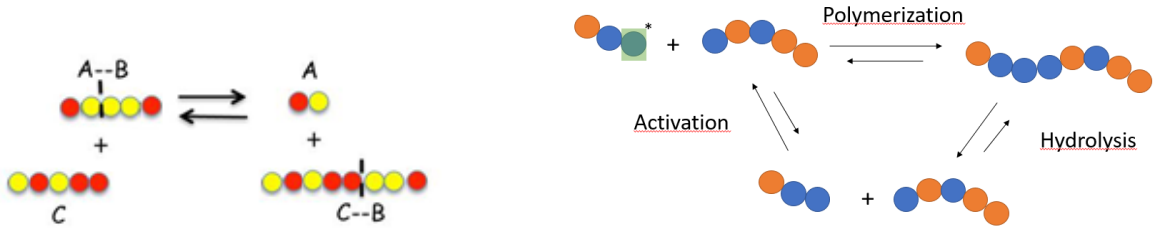

Figure – (left) an example of a (simplified) exchange reaction. (right) a ligation-hydrolysis-activation cycle.