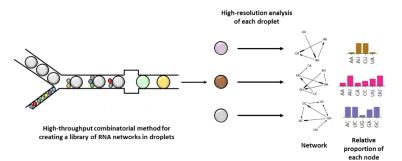
## Networks of RNA replicators in origin of life

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**Introduction:** The 'RNA world' hypothesis suggests that RNA initially acted both as an information carrier and a catalyst, functions that were subsequently carried out by DNA and proteins. In such a prebiotic world, catalytic RNA sets or networks could have acted as evolutionary units<sup>1-3</sup>. However it is not immediately clear how such collective systems could evolve as several ingredients are needed to start a Darwinian mode of evolution: reproduction with inheritance, variation and selection. Though many theoretical works explored evolutionary mechanisms with such networks<sup>2-6</sup>, there is a lack of empirical studies addressing these questions. In the current project, we are exploiting an experimental system derived from *Azoarcus* Group I intron where ribozymes are able to catalyze the formation of other ribozymes from smaller fragments<sup>7,8</sup>. As the catalytic relationship is directed and specific it allows us to create thousands of different catalytic RNA networks. To explore such a large network space, we have developed a high-throughput experimental set-up by combining droplet-microfluidics<sup>9</sup> with next-generation sequencing where a combinatorial library of RNA networks in droplets can be studied at an unprecedented resolution.



**Figure 1** – Schematic representation of a high-throughput method to create a diverse library of RNA networks from the fragments of *Azoarcus* group I intron ribozyme. Using droplet-based microfluidics each of the network from the library can be analyzed at high-resuloution.

Initial analysis suggest that both growth (amount of ribozymes formed) and composition (relative proportion of species or nodes) can be inferred solely from network topology. This will help us in addressing robustness and evolvability of such networks by mapping fitness (at a network or specific node level) on a large scale. Results will also reveal the experimental fitness landscape governing evolution processes with such systems.

## **References:**

[1] Higgs PG, Lehman N (2015) *Nature Reviens Genetics* 16:7-17. [2] Vasas V, Fernando C, Santos M, Kauffman S, Szathmáry E (2012) *Biology Direct* 7:1-14. [3] Hordijk W, Steel (2017) *BioSystems* 152:1-10. [4] Nghe P, Hordijk W, Kauffman SA, Walker SI, Schmidt FJ, Kemble H, Yeates JAM, Lehman N (2015) *Molecular BioSystems* 11: 3206-3217. [5] Segré D, Ben-Eli D, Lancet D (200) *Proceedings of the National Academy of Sciences USA* 97: 4112-4117. [6] Jain S, Krishna S (2001) *Proceedings of the National Academy of Sciences USA* 98: 543-47. [7] Hayden EJ, Lehman N (2006) *Chemistry and Biology* 13:909-918. [8] Vaidya N, Manapat ML, Chen IA, Xulvi-Brunet R, Hayden EJ, Lehman N (2012) *Nature* 491:72-77. [9] Eigen M, Schuster P (1977) *Die Naturwissenschaften* 64:541-565. [10] Matsumura S, Kun A, Ryckelynck M, Coldren F, Szilagyi A, Jossinet F, Rick C, Nghe P, Szathmáry E, Griffiths AD (2016) *Science* 354: 1293-1296.