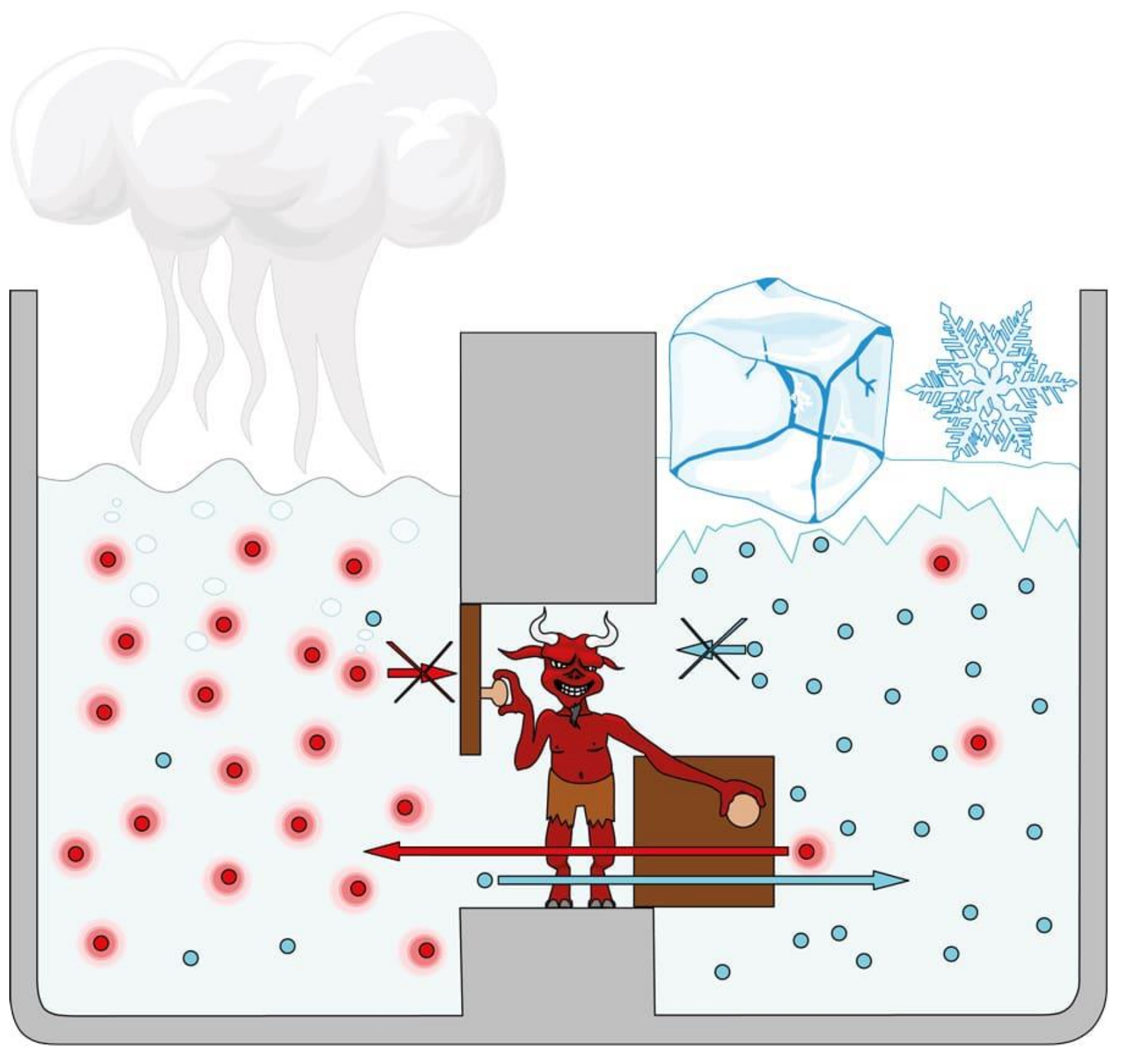




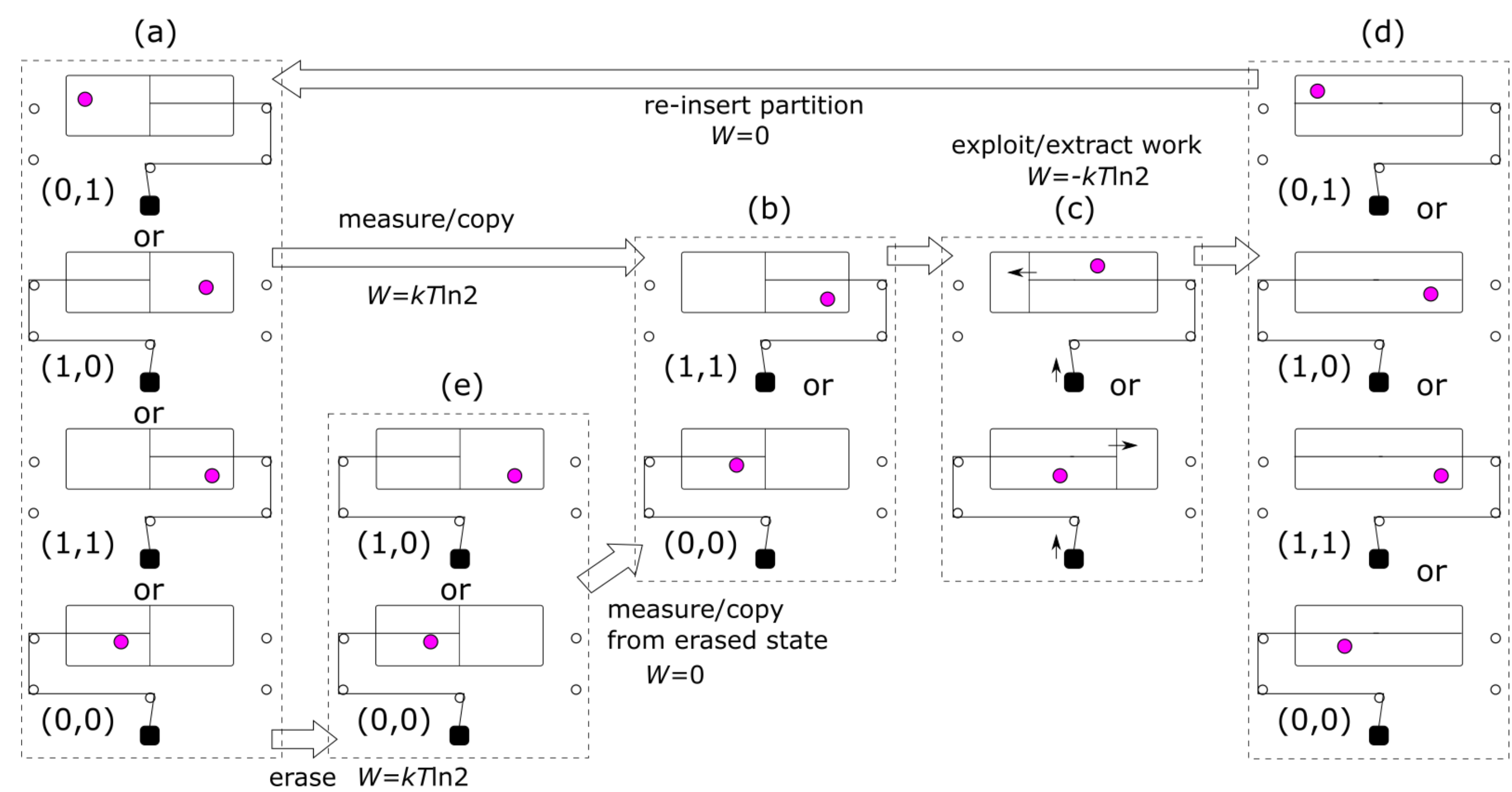
Thomas Ouldridge, Rory Brittain, Jenny Poulton, Javier Cabello Garcia, Nick Jones, Pieter Rein ten Wolde

Maxwell's demon and Szilard's engine – thought experiments from the 19th and early 20th centuries about the interplay of thermodynamics and information-processing – have long captured the imagination of theoretical physicists. Many still disagree about the interpretation of these ideas, the implications for the second law of thermodynamics, and the consequences for thermodynamics of computation. We have designed a theoretical Szilard engine from biomolecules; by explicitly rendering each step of the engine as a biochemical process, we are able to demystify the whole story. Doing so is helpful not only in resolving old thought experiments, but because the crucial idea - that the generation of correlation between non-interacting degrees of freedom is thermodynamically costly - is of fundamental significance to natural and synthetic molecular information-processing systems.

## Maxwell's Demon

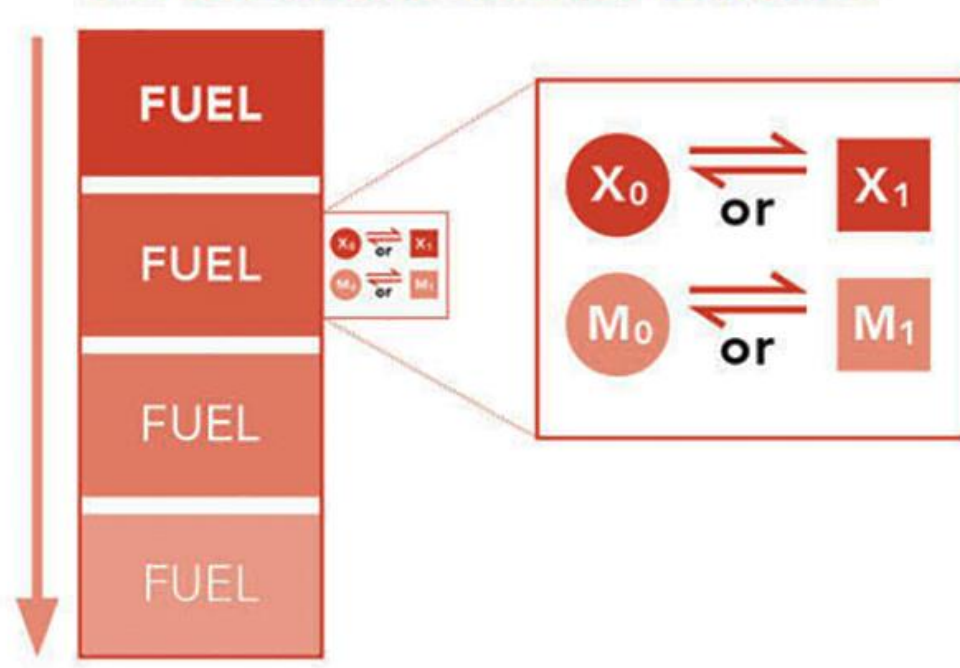


## Szilard's Engine



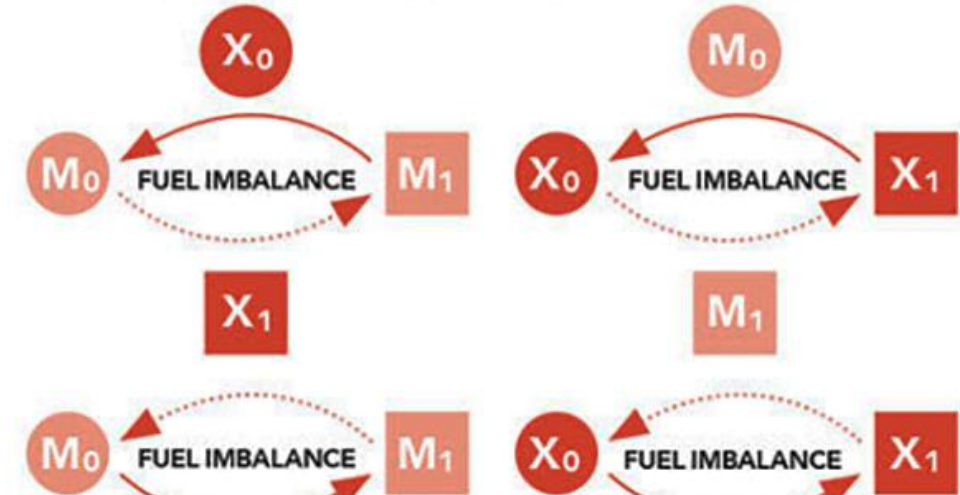
## A molecular Szilard engine

### APPARATUS FOR BUILDING A BIOCHEMICAL SZILARD ENGINE.



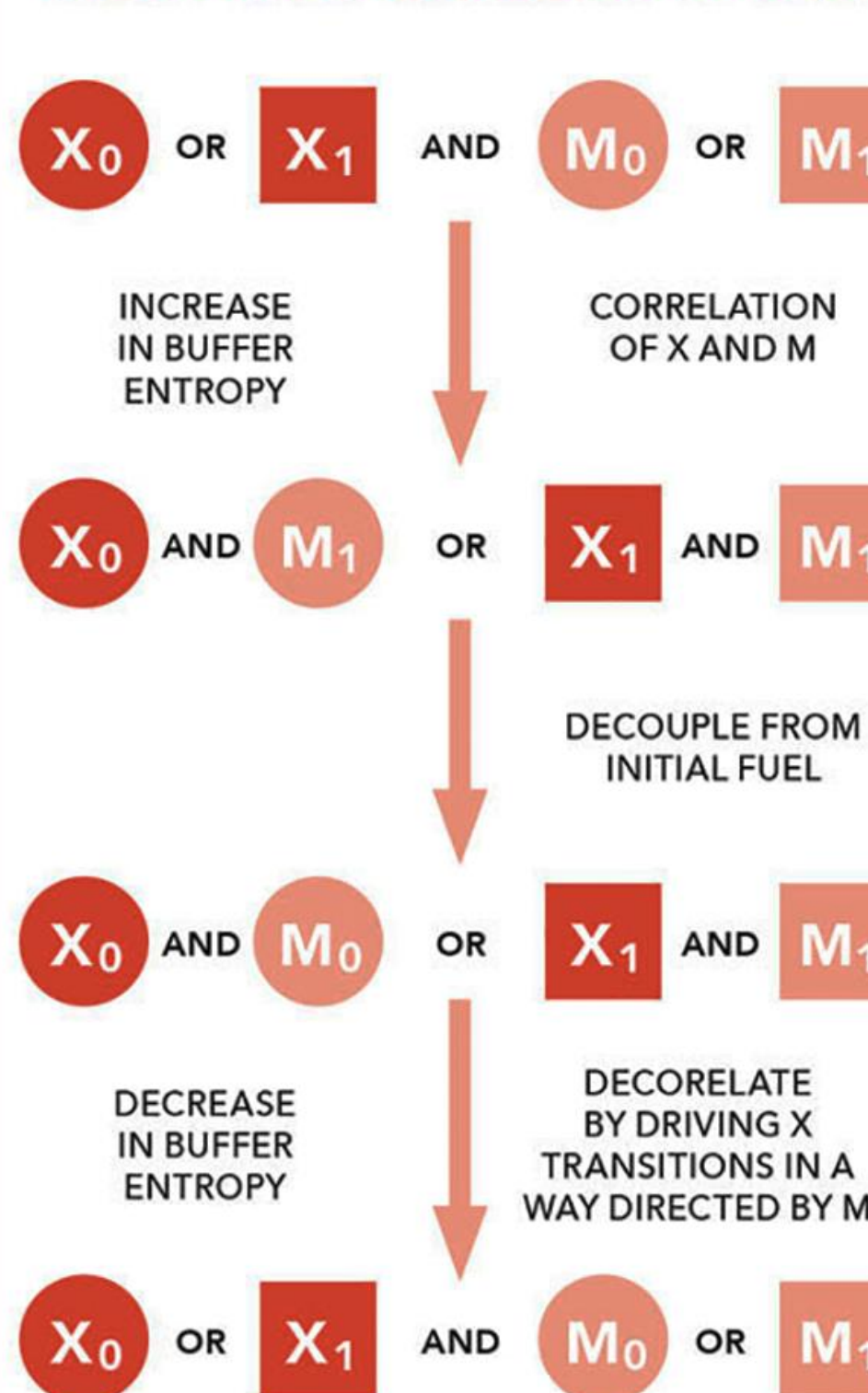
Two molecules of interest are trapped in a small volume. They are exposed to a series of chemical buffers with different concentrations of fuel molecules; these fuels drive reactions within the small volume, and function as a perfectly rechargeable battery.

### CATALYTIC REACTIONS WITHIN THE REACTION VOLUME.



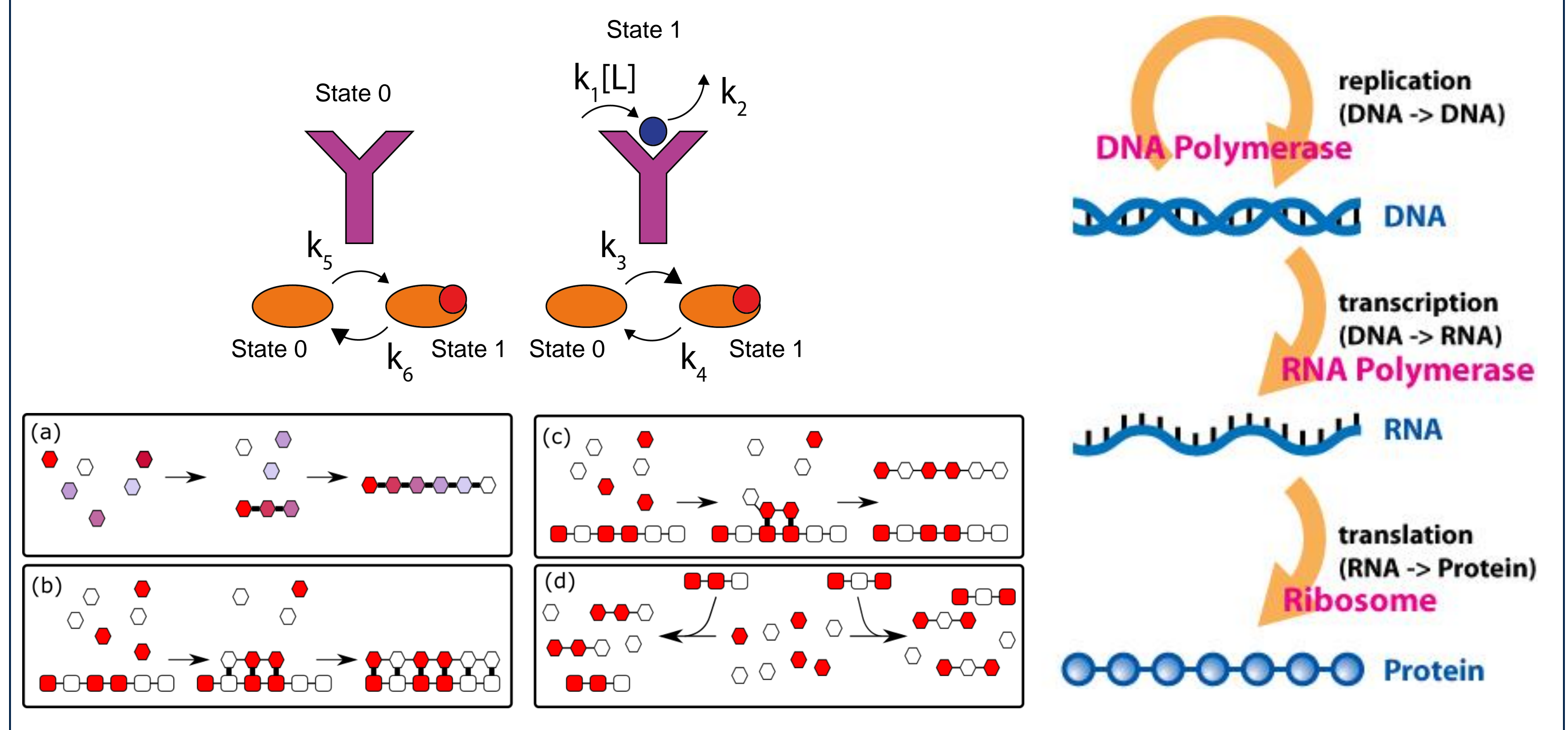
X and M have mutually catalytic reactions driven by imbalances in fuel concentrations. The state-dependence of these reactions allows information to be passed from one molecule to the other.

### SEQUENCE OF OPERATIONS IN THE BIOCHEMICAL SZILARD ENGINE.

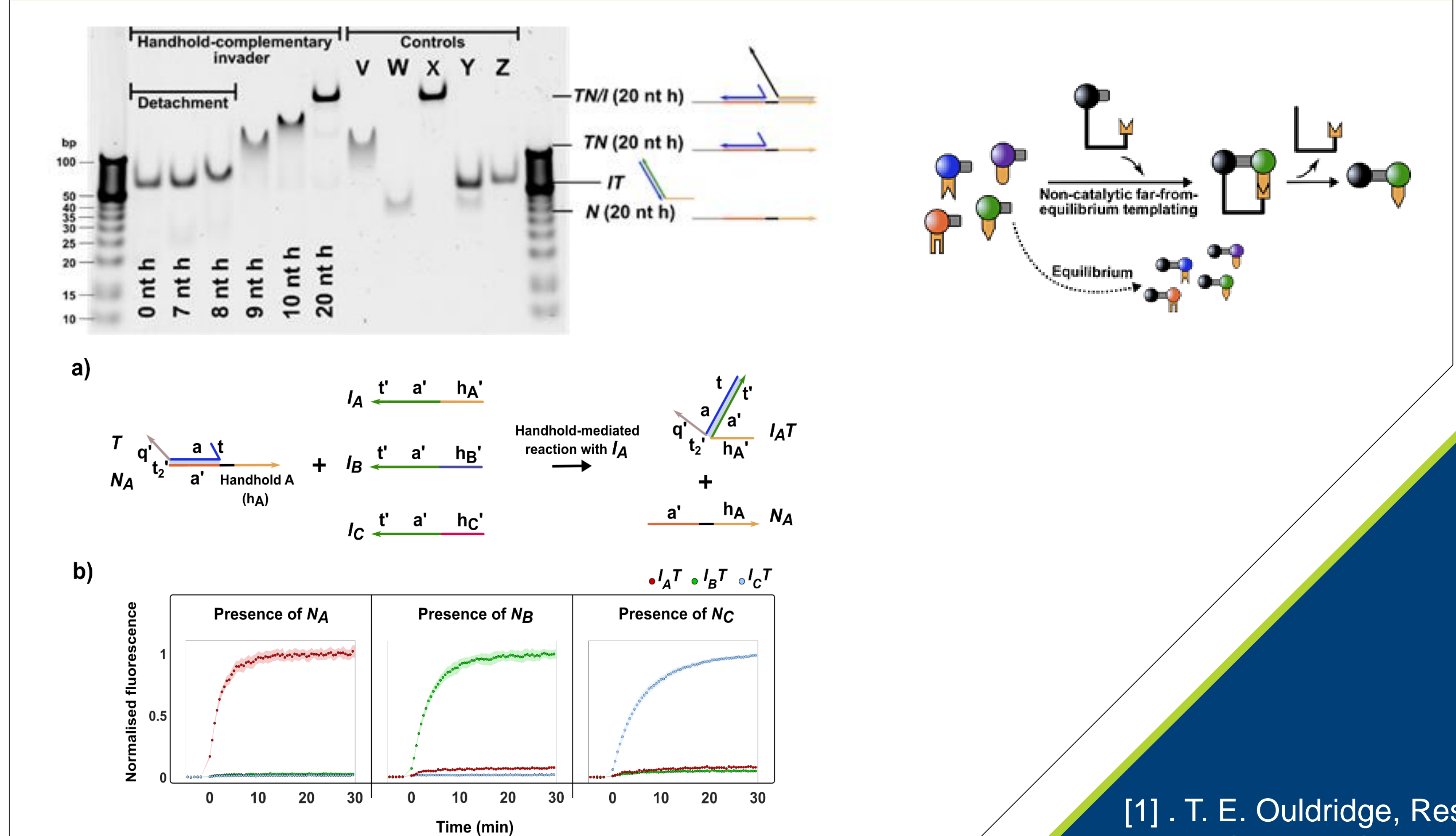


By carefully controlling the sequence of buffers, X and M can be first correlated, and then decorrelated from each other. The first stage decreases the entropy of X and M, but increases the entropy of the buffers to compensate. The final stage does the opposite.

## Non-equilibrium information in biology



## HMSD as a platform for non-equilibrium templating



## Can we build synthetic analogs?

