MOLECULAR ALGORITHMS

- The most sophisticated organization of matter is biology, spanning 24 orders of magnitude ($10^{-18}$ TO $10^6$ Grams)

Biological organization is information based. DNA sequences, refined by evolution, encode both the COMPONENTS and the PROCESS that guide the development into an organism. It is a world of molecular algorithms.

Molecular algorithms, energy, entropy are essential concepts to understand how physical processes create order.

A single group of atoms existing in one copy produces orderly events, marvelously tuned with each other and with the environment. The “statistical mechanism” produces order from disorder and the “biological mechanism” order from order.

E. Schrodinger, What is life (1944)

A. TURING UNIVERSAL COMPUTATION

If you construct an automaton right, then any additional requirements about the automaton can be handled by sufficiently elaborated instructions. This is only true if A is sufficiently complicated, if it has reached a minimal level of complexity. A simpler thing will never perform certain operations, no matter what instructions you give it; but there is a definite finite point where an automaton of this complexity can, when given suitable instructions, do anything that can be done by automata at all.

The laws of physics “happen to” permit the existence of physical models for the operations of arithmetic. Thus, at least at the level of investigation of “reasonable” instances of computation, the theory of computation is part of physics.

D. Deutsch, on computation.
Towards a minimal cell
A vesicle bioreactor
V. NOIREAUX

In his Theory of Automata, J. Von Neumann compared computing machines and living organisms. The self reproduction of automata was discussed and linked to a Turing like principle. In parallel the biological sciences have raised the question of how to engineer a minimal self-reproducing living cell. Any attempt would give clues to how self-replication emerges and also lead to insights on replicators based on inorganic materials.
Fig. 5.1. Schematic of the structure of a lipid bilayer membrane. On a scale hundreds or thousands of times larger than its thickness (40 Å), the bilayer curves to enclose a finite volume. Within the bilayer itself, the lipid molecules are aligned perpendicular to the plane of the membrane and are disordered (liquid-like) in the plane.

Encapsulation of the Extract in Vesicles

- Feeding Solution
- Emulsion
- Cell-free Feeding Solution
- Vortex
- Centrifugation
- M. Oil + PC
- Reaction (CFE-DNA-RNA)
Gene Expression Inside Vesicle

Tauxin C. et al, Osmotic pressure induced pores in phospholipid vesicles, Biochem., 1975

STA PHYLO COCCUS AUREUS

1. HEMOLYSIN

Diagram showing the time course of eGFP production in vesicles and bulk.
Some Physical Aspects of the Origin of Life and of Artificial Cells

Dr. Albert Libchaber, Rockefeller (KITP 1-19-05)
Figure 1. (A) Protolytic cycle: EM images of CipX degrading lambda 0 protein. Left-most panel: CipX, CipX, CipX, CipX, CipX, CipX. Center panel: CipX, CipX, CipX, CipX, CipX, CipX. Right-most panel: CipX, CipX, CipX, CipX, CipX, CipX. (B) Schematic of CipX protease function: The substrates are bound, then cleaved, and finally released. (C) Time course of CipX activity: Fluorescence intensity versus time (hours).
Fig. 5. Specific protein degradation with the ClpXP complex of E. coli. (A) SDS PAGE
15% showing the protein purified. Lane 1 and 4, marker (75, 50, 37, 25, 15 kDa); lane 2,
His-ClpX; lane 3, ClpP-His; lane 5, eGFP-srrA. (B) kinetics of degradation in a buffer of
His-eGFP-srrA (closed circles) and His-eGFP-srrA/DD (closed squares), with 1.5µM
ClpP and 2µM ClpP. (C) Fluorescence images of two droplets on a cover glass after a
few hour incubation, left with His-eGFP-srrA and right with His-eGFP-srrA/DD.