Origins of Life

The Double Origin Hypothesis by Freeman Dyson

Seminar Life in Universe
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- Dyson's Toy Model for the Origin of Life
- Interpretation and Conclusions

Basic Background

- A living cell has two dominant components: proteins and nucleic acids
- Proteins are the hardware
  → catalysts for chemical reactions
- Nucleic acids are the software
  → tell the proteins what to do

Basic Background

- Living cells have two primary functions: metabolism and replication
- Metabolism: any chemical process occurring in cells (Stoffwechsel)
- Replication: exact copying of information by specific process

Theories of Origin

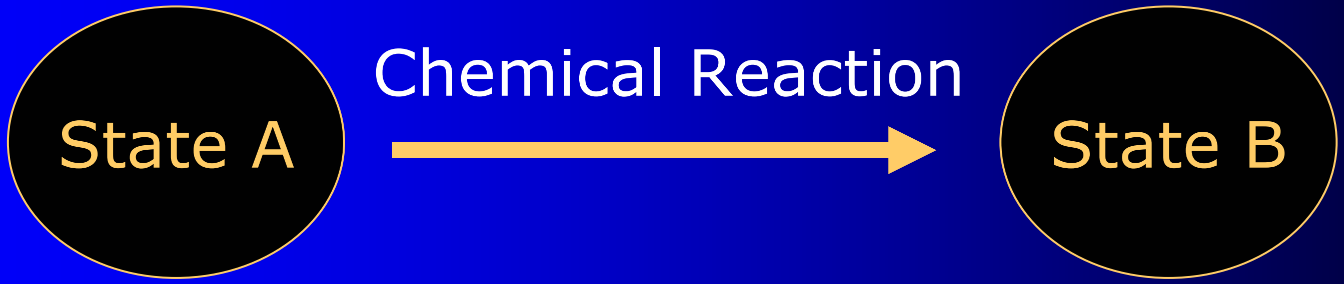
- Manfred Eigen:
  Genes → Enzymes → Cells
  Origin of replication (RNA-World)
- Alexander Oparin:
  Cells → Enzymes → Genes
  Origin of metabolism

Dyson`s Model

- Double origin of life! The first origin of life is the origin of metabolism! (Oparin)
  → First hardware then software!
- Genes enter later as parasites and form a symbiosis with the cells
  → symbiogenesis
- Lynn Margulis: parasitism and symbiosis were the driving force in the evolution of cellular complexity

The general Model

- Population of molecules (monomers) within a droplet
- Chemical reactions change population



State A

Chemical Reaction

State B

The general Model

- P is a probability distribution vector to be in any state
- M is the transition probability matrix where M_{ij} is the probability for a transition from state j to state i → stepwise evolution

$$P(k+1)=M\cdot P(k) \longrightarrow P(k)=M^{k}\cdot P(0)$$

The general Model

- Quasi-stationary probability distributions with different levels of chemical activity
- For simplicity only two quasi-stationary distributions

Low level of activity → disordered state

High level of activity → ordered state

The general Model

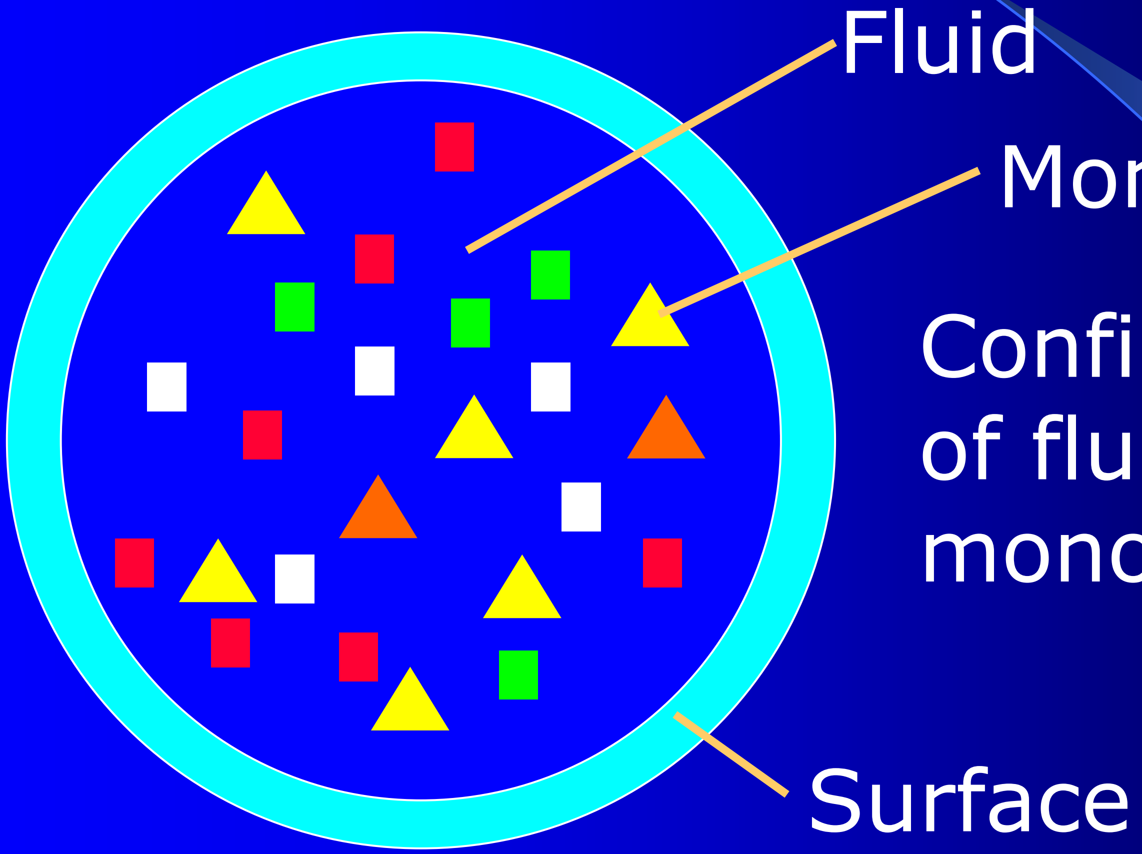
- Metabolism is the state of high chemical activity!
- How probably is the jump from the disordered state to the ordered?

disordered state → ordered state

The Toy Model

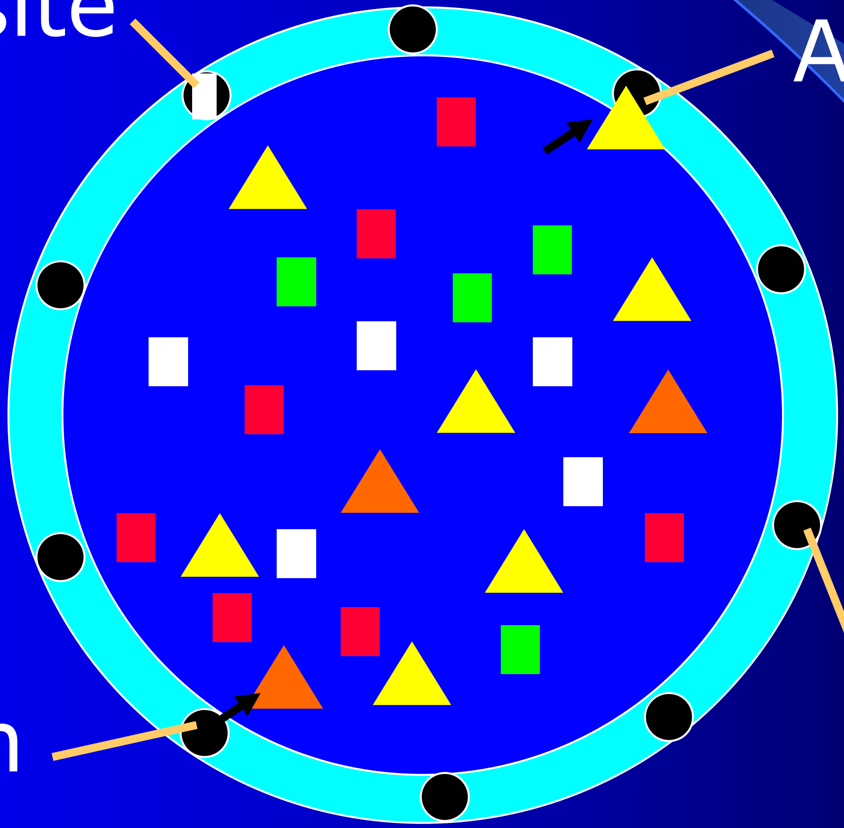
- Dyson presents a toy model with two quasi-stationary states, ordered and disordered, and determines the circumstances in which the jump will occur spontaneously

Cell



Confined volume of fluid with monomers inside

Active Surface with N sites



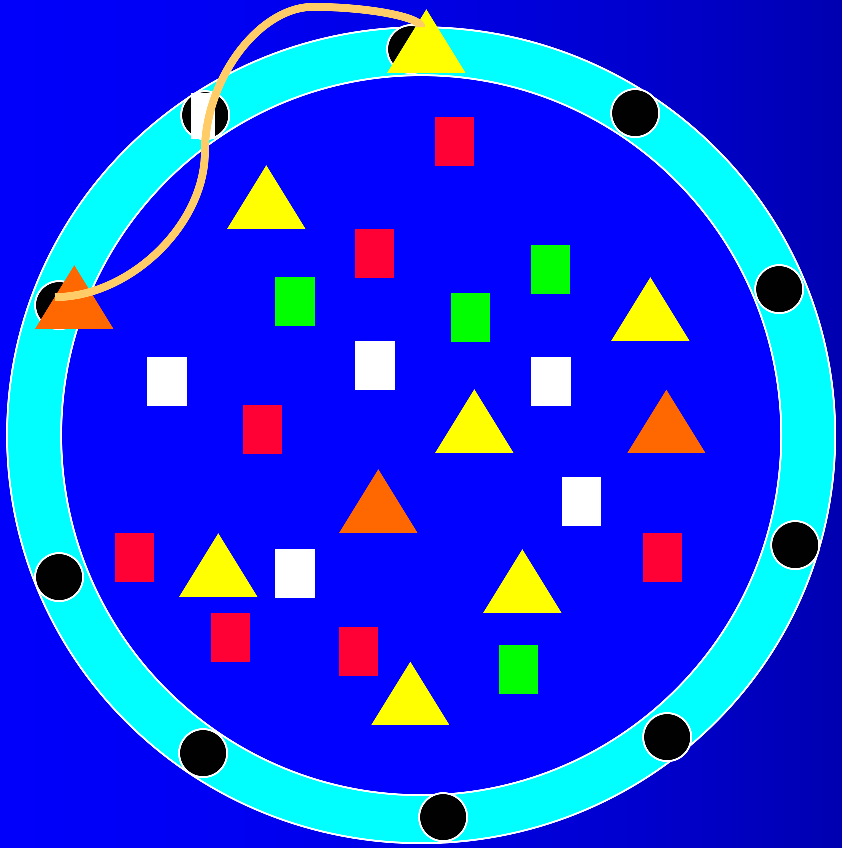
occupied site

Adsorption

empty site

Desorption

Polymers



Monomers adsorbed at neighbouring places link together to form polymers

Active/inactive monomers

- The active monomers are those that happen to be of the right species at the right sites, where they and their neighbours make a polymer that can act as an enzyme
- To act as an enzyme means to catalyse the adsorption of other monomers of the right species

Active/inactive monomers

- At each site, only 1 species is active
- The other n species are inactive
- Total n+1 species

An active monomer is one that helps other monomers to be active

Probabilities

- x ≡ # active sites / N
- w ≡ # inactive sites / N
- z ≡ # empty sites / N
- Site empty:
  adsorption of active monomer: $\Psi(x) \cdot p$
  adsorption of inactive monomer: p
- Site occupied:
  desorption of active and inactive monomers with $q \cdot p$

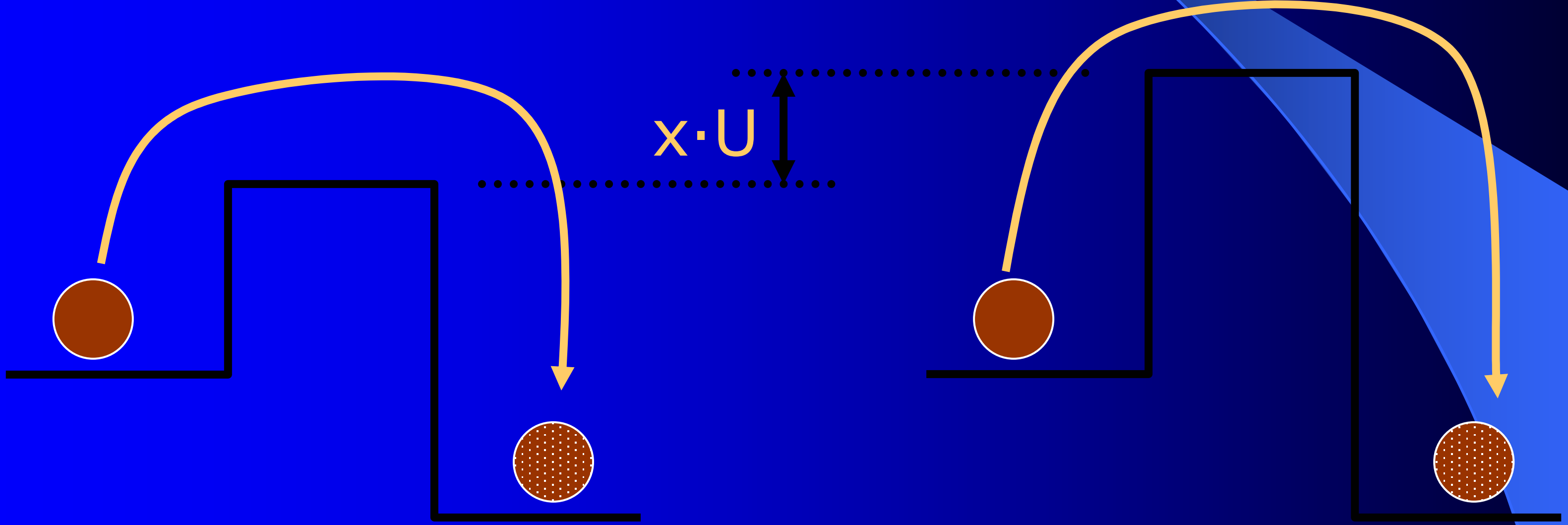
Steady State

- $x + w + z = 1$
- $(x, w, z) \sim (\Psi(x), n, q)$
- $a \equiv n + q$
- $\Phi(x) \equiv$ activity of daughter generation
- $x = \Phi(x) = \Psi(x) / (\Psi(x) + a)$

The Ψ(x) Function

Adsorption of an
active monomer

Adsorption of an
inactive monomer



Difference in activation energy of x·U

The $\Psi(x)$ Function

- The probability of an adsorption of an active monomer is increased over the adsorption of an inactive monomer

$$\Psi(x) = b^x$$

with $b \equiv \exp(U/k_B \cdot T)$

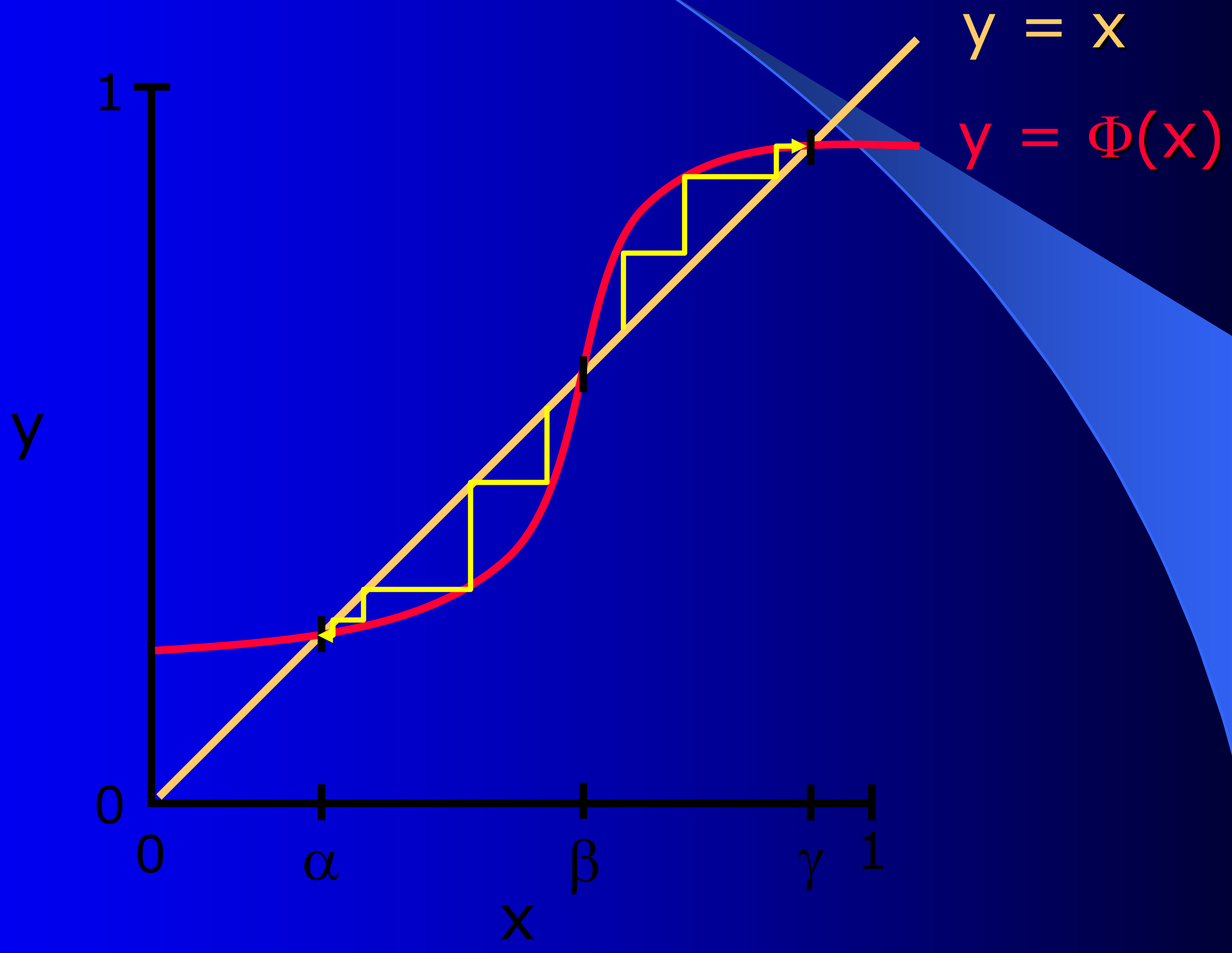
discrimination factor

The $\Phi(x)$ Function

- $a \equiv n + q$
- $b \equiv \exp(U/k_B \cdot T)$
- In steady state:
  $\Phi(x) = \Psi(x) / (\Psi(x) + a)$

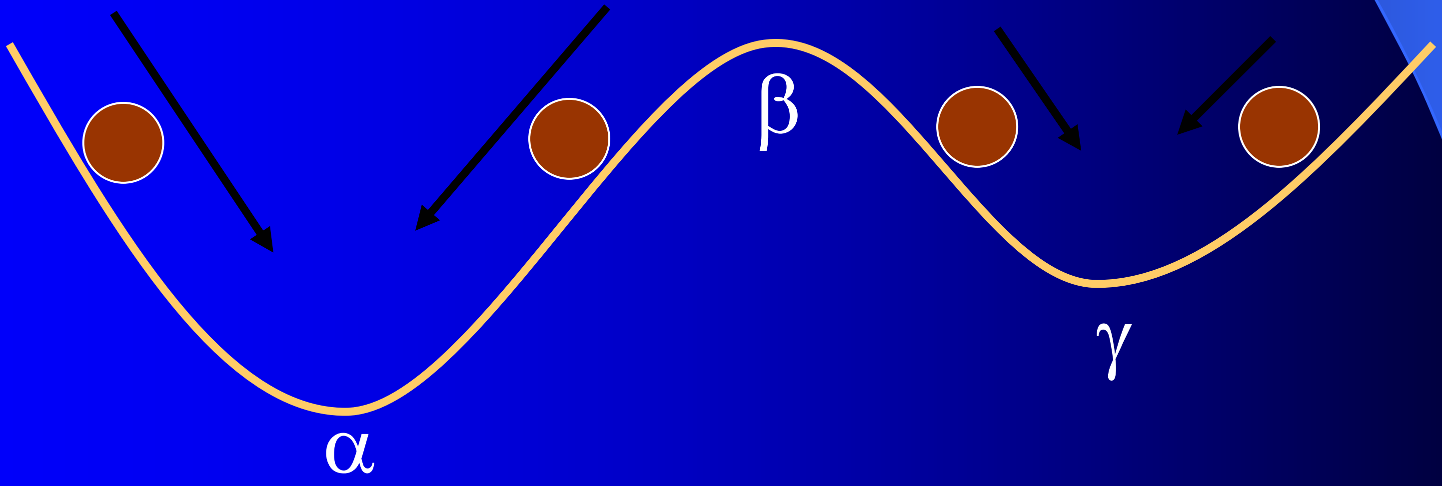
$$= (1 + a \cdot b^{-x})^{-1}$$

The Φ(x) Function



3 steady States

- α stable / disordered = low activity
- β unstable
- γ stable / ordered = high activity



Death and origin of life

- α disordered state → dead
- γ ordered state → alive

$\gamma \rightarrow \alpha$: Death

$\alpha \rightarrow \gamma$: Origin of life

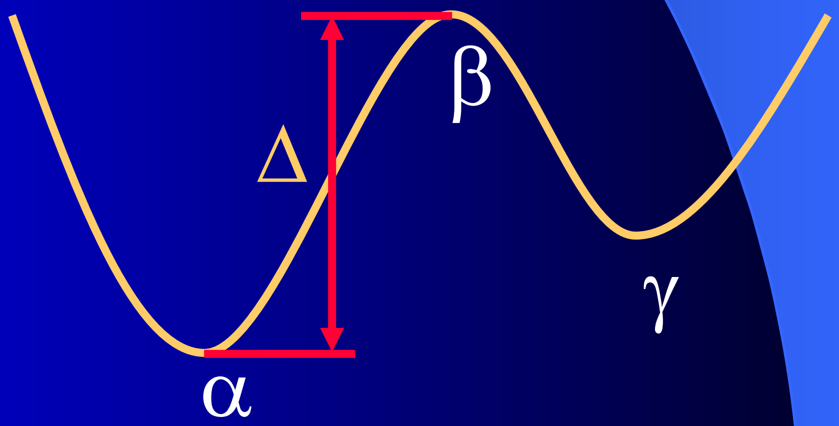
Transition Time

- After some math arising from the model we get an expression for the average time T required for a cell to make the transition from disorder to order (Transition time):

$$T = \tau \cdot \exp(\Delta \cdot N)$$

Transition Time

- $\tau \equiv$ average time interval between desorptions of a monomer at each site
- $N \equiv$ population size
- $\Delta \equiv V(\beta) - V(\alpha)$



Transition Time

- What is a reasonable transition time?
- $T \approx \tau \cdot 10^{13} \approx \tau \cdot \exp(30)$
  $\rightarrow$ population of 10^{10} droplets and a transition each $10^{3} \cdot \tau$
- $N_c \equiv 30 / \Delta$
  critical number of population

Preferred Ranges

- a = 8 – 10
- b = 60 – 100
- N = 2000 – 20000

a : Number of species

- $a \equiv n + q = 8 - 10$
→ 8 – 10 species of monomers
- Modern proteins: approximately 20 species of amino acids
- The model fails with only 3 – 4 species → polymerisation of RNA with 4 nucleotides not possible in this model!

b : discrimination factor

- $b \equiv \exp(U/k_B \cdot T) = 60 - 100$
  → discrimination factor b of 60 – 100
- Modern enzymes: b of 5000 – 10000
  → much more specialised by
  3 Gyr of fine-tuning!
- Simple inorganic catalysts: b of 50

N : population size

- N = 2000 – 20000
  → population of 2000 – 20000
- Large enough for chemical complexity of life
- Small enough to make transition to ordered state
  → Origin of life

Final Remarks

- Abstract mathematical model that is far too simple to be true!
- „If my remarks have any value, it is only insofar as they suggest new experiments. I leave it now to the experimenters to see whether they can condense some solid facts out of this philosophical hot air.“