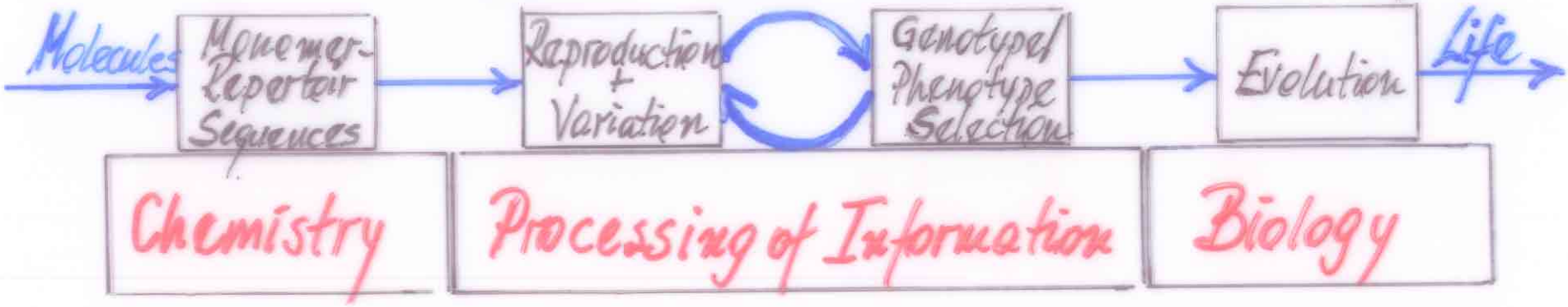
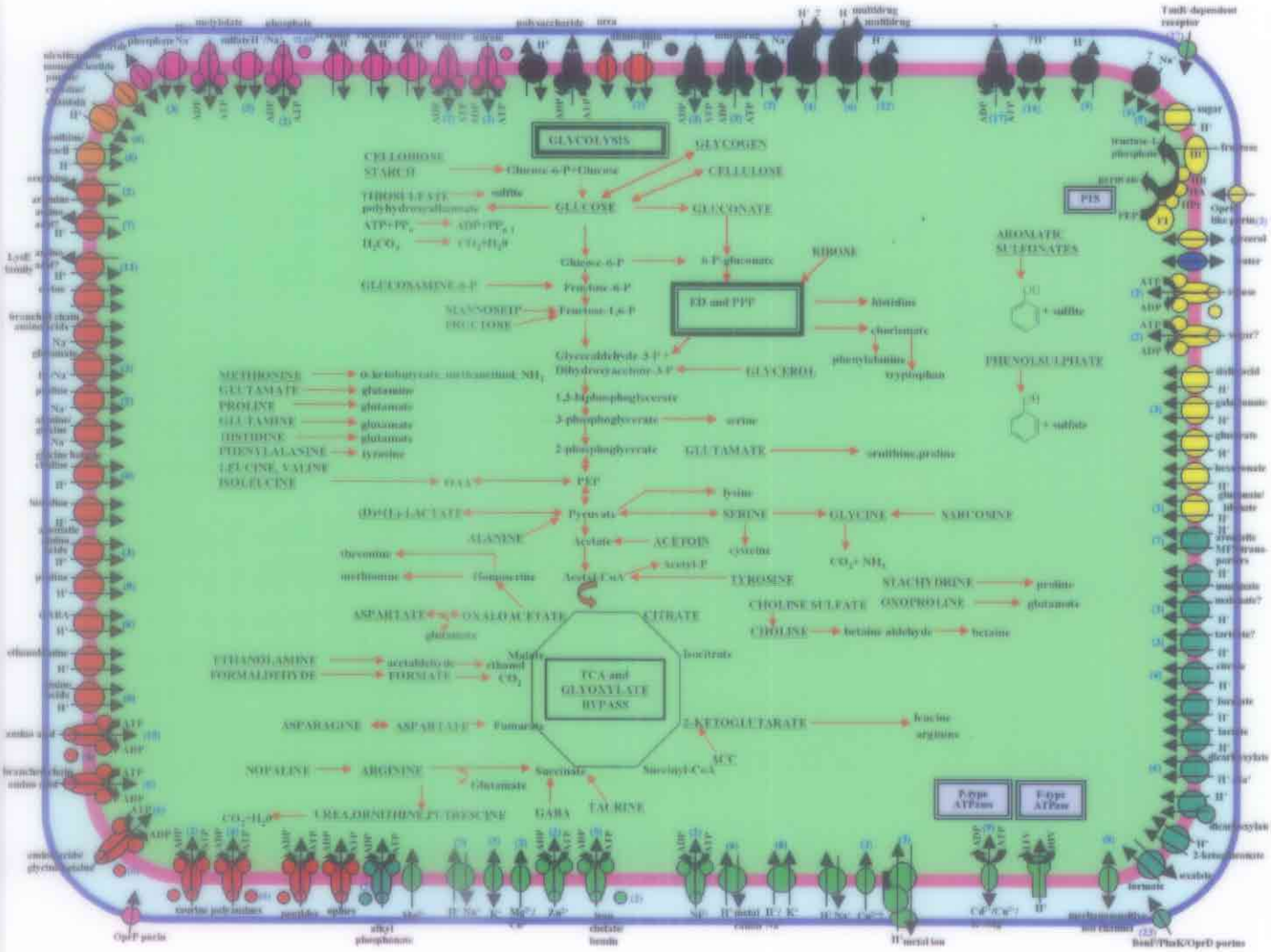
Manfred Eigen, Max Planck, Gottingen

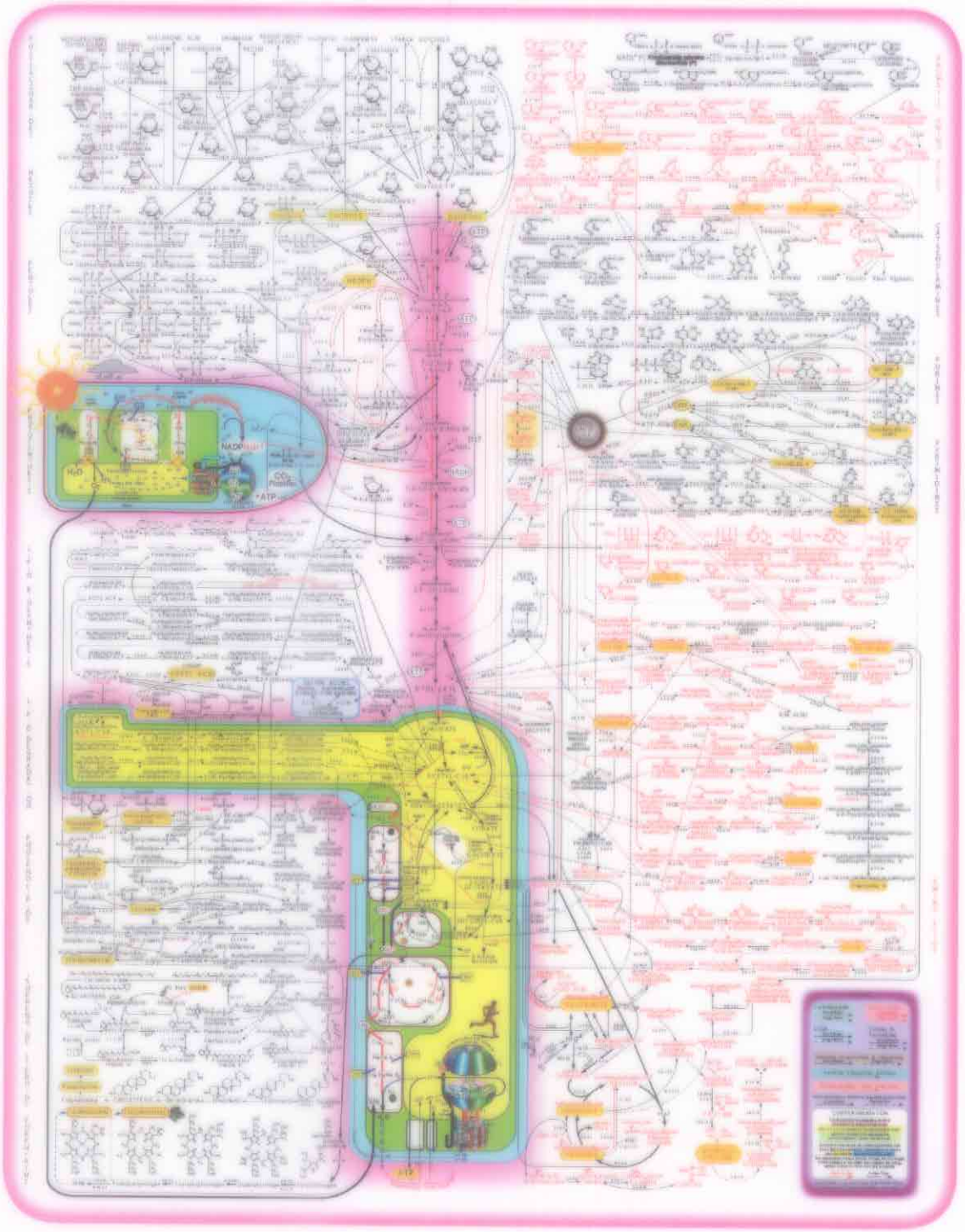
From Chemistry to Biology

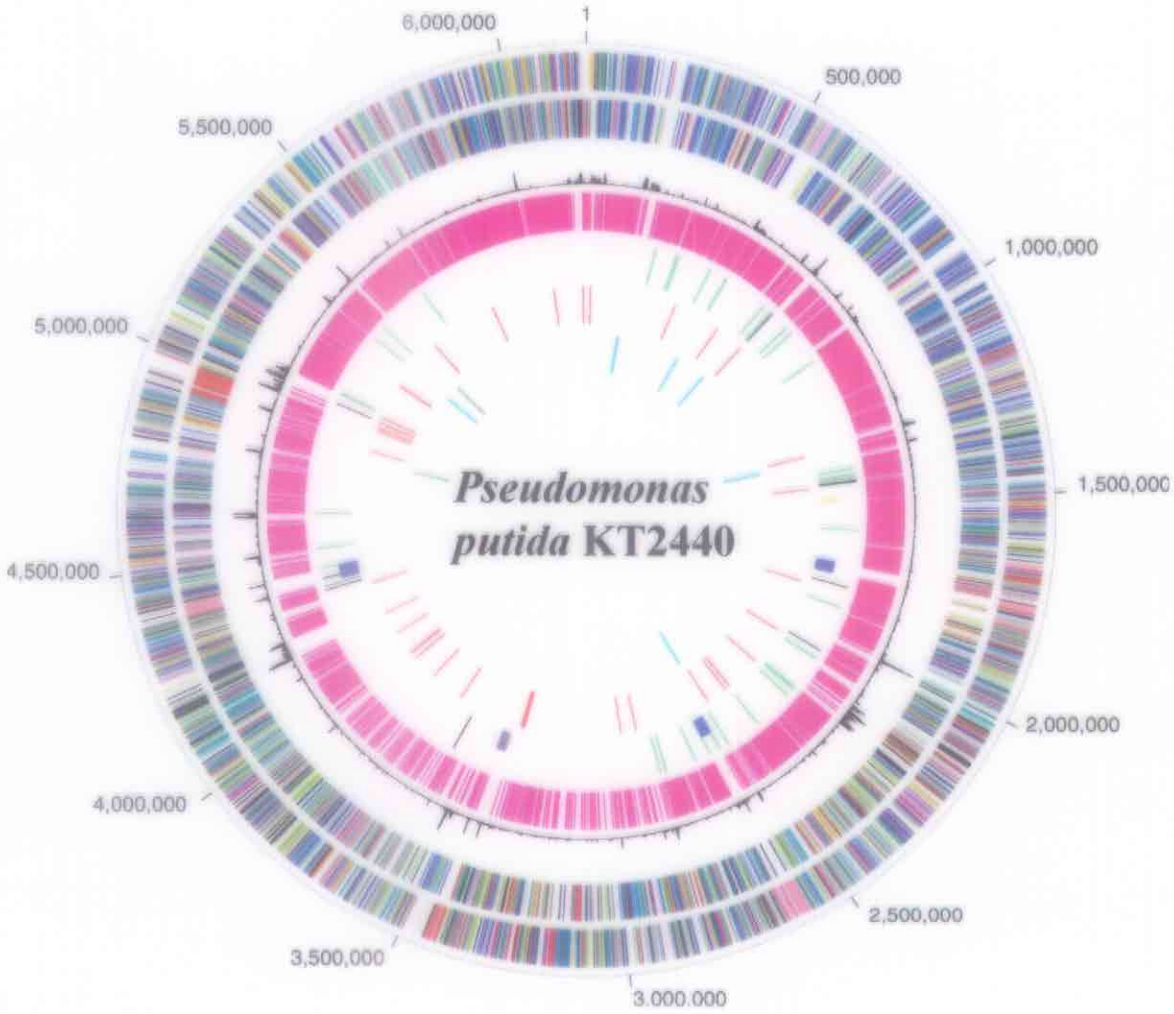
Schematic Representation :

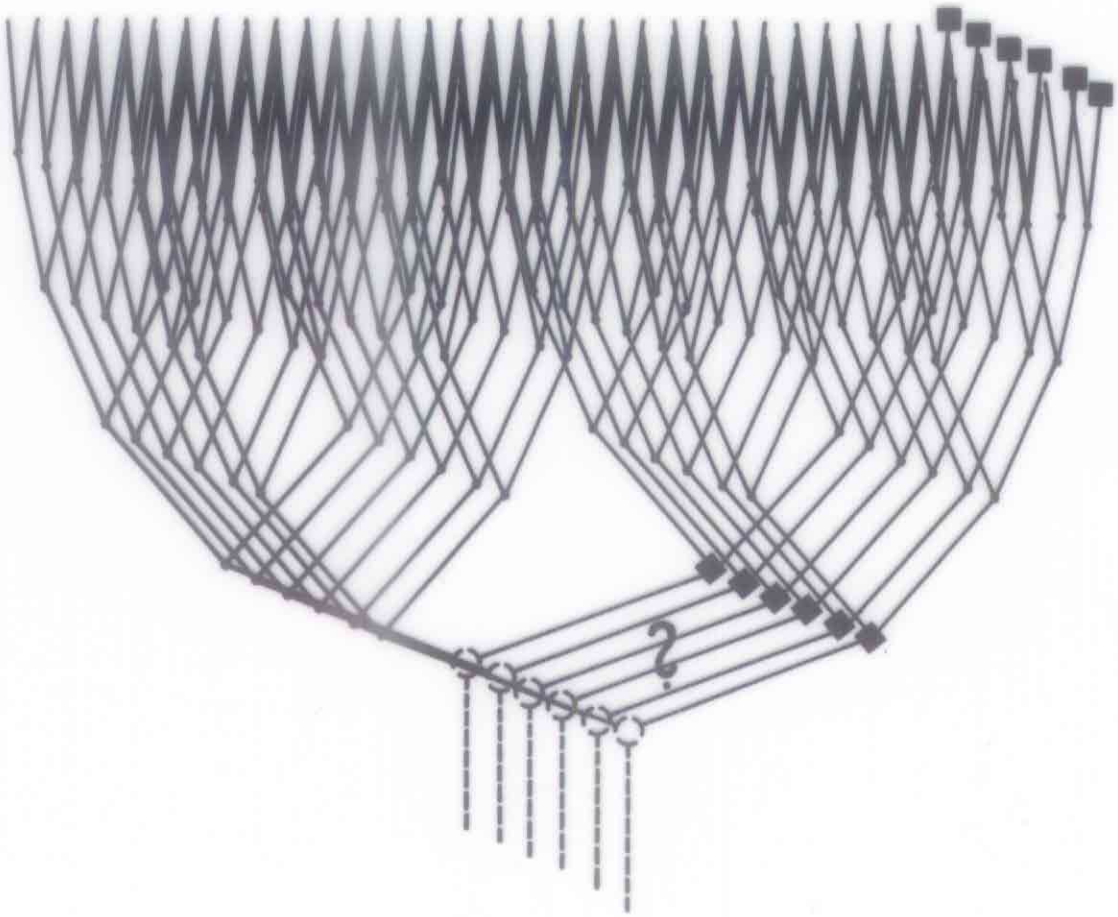
Origin and Evolutionary Optimisation of Life

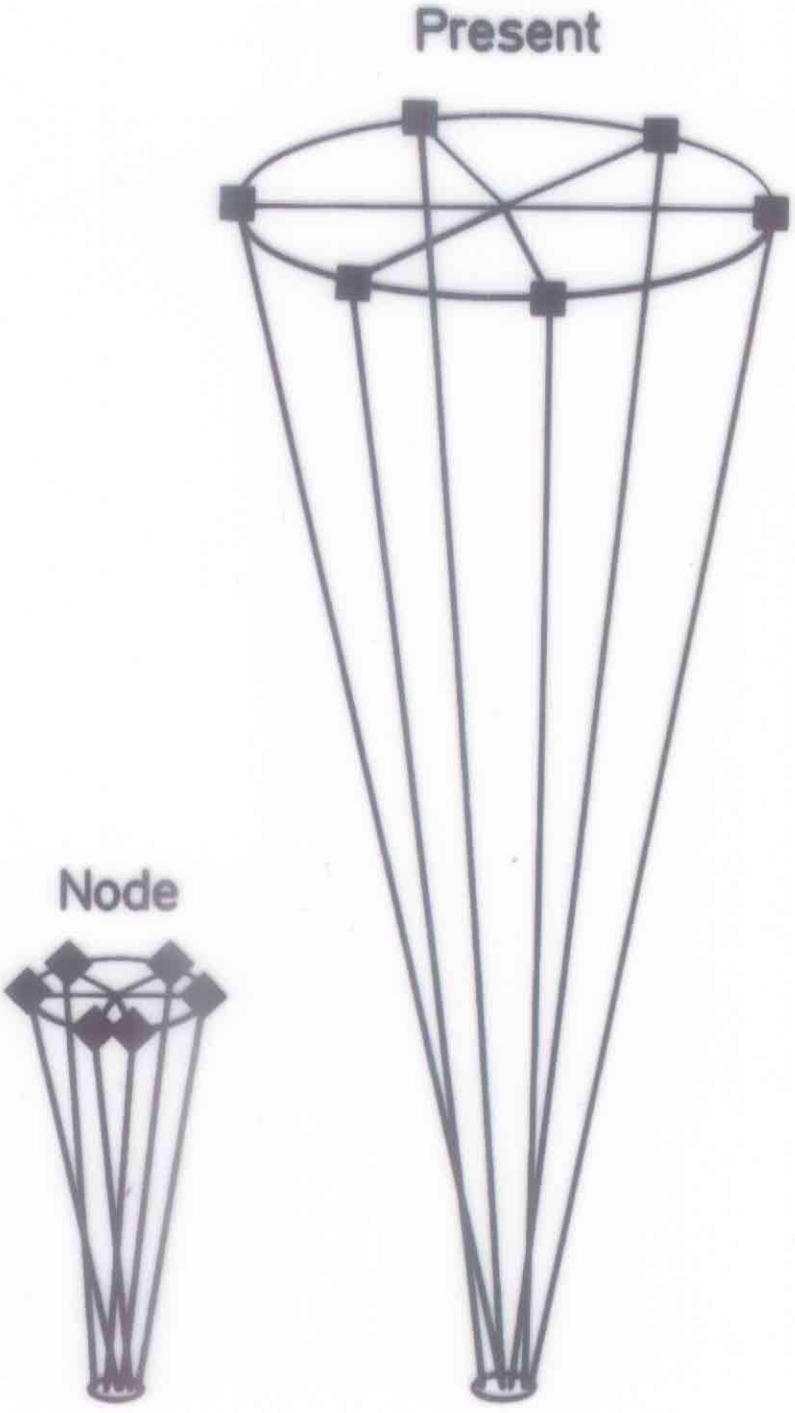


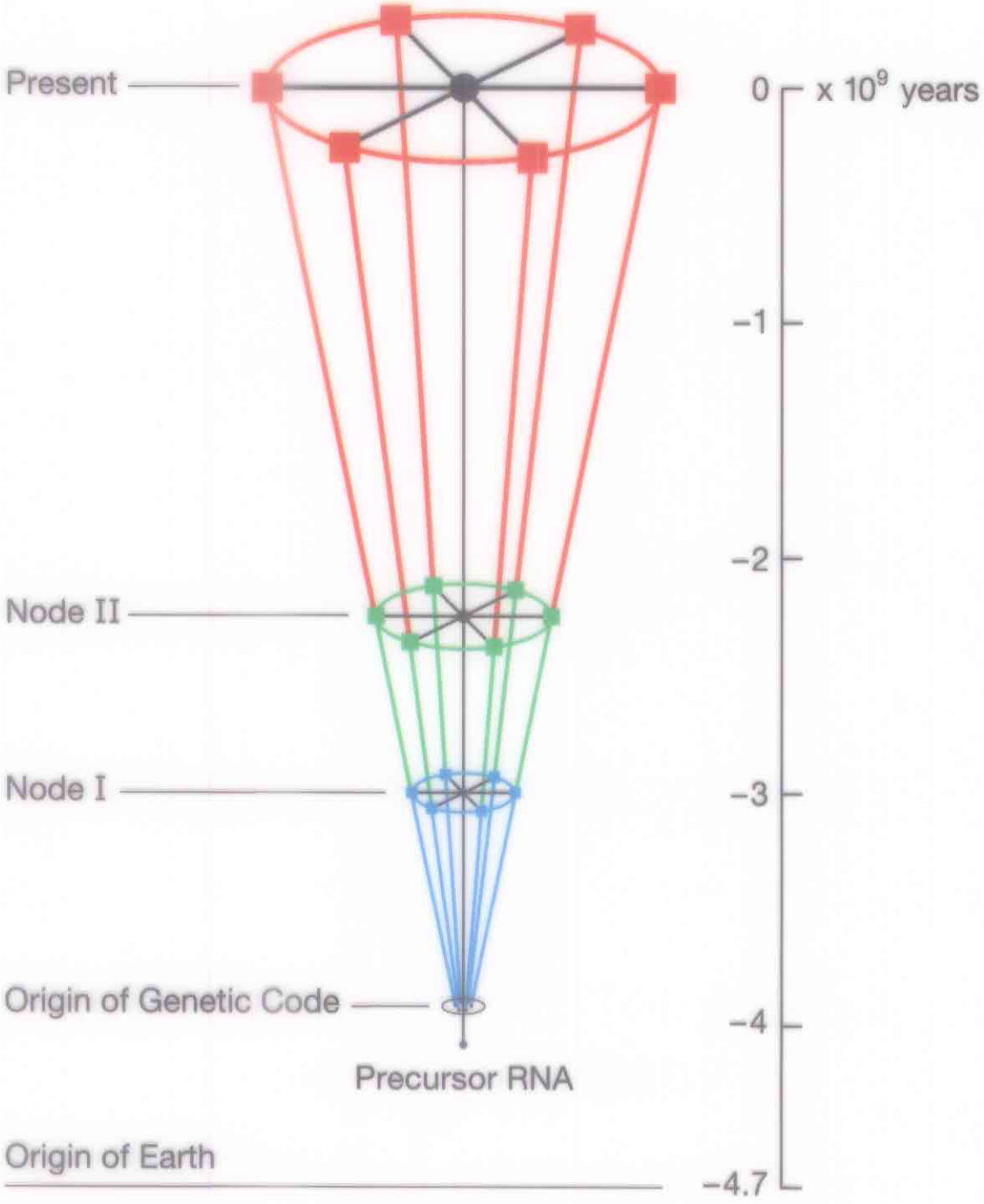

GLYCOLYSIS
GLYCOGEN
CELLULOSE
GLUCOSE
GLUCONATE
Glucose-6-P
6-P-gluconate
RIBOSE
ED and PPF
Fructose-6-P
Fructose-1,6-P
Glyceraldehyde-3-P
Dihydroxyacetone-3-P
GLYCEROL
1,3-bisphosphoglycerate
3-phosphoglycerate
2-phosphoglycerate
PEP
Pyruvate
Acetate
Acetyl-CoA
ACETOIN
CITRATE
Isocitrate
TCA and GLYOXYLATE BYPASS
2-KETOGLUTARATE
Succinate
Succinyl-CoA
Fumarate
OXALOACETATE
Malate
ASPARTATE
ASPARAGINE
ARGININE
GABA
TAURINE
SERINE
GLYCINE
ALANINE
CYSTEINE
TYROSINE
CHOLINE
PROLINE
GLUTAMATE
ornithine,proline
histidine
glutamine
phenylalanine
tryptophan
AROMATIC SULFONATES
PHENOLSULPHATE
PTS
F-type ATPase
V-type ATPase

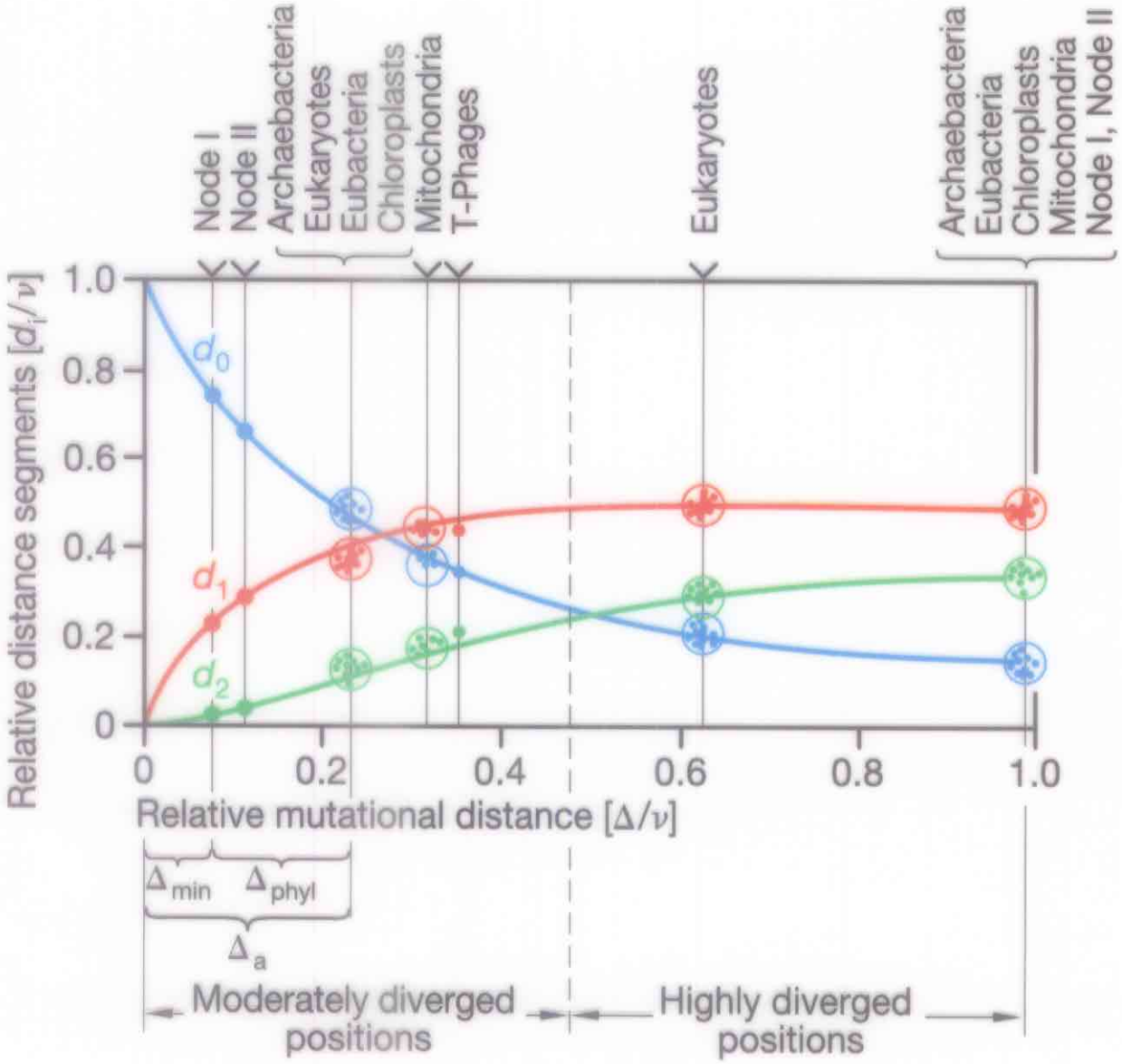


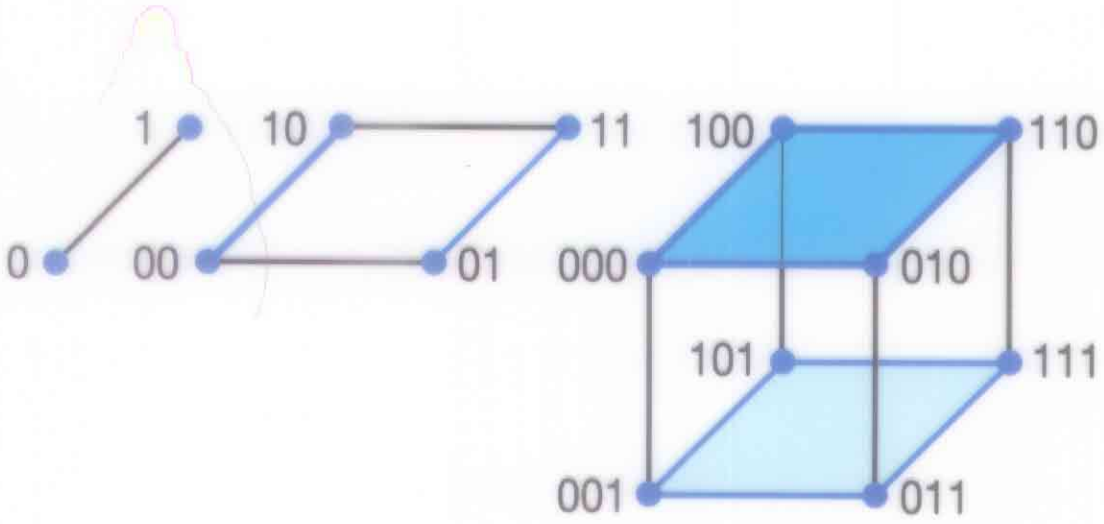

1
500,000
1,000,000
1,500,000
2,000,000
2,500,000
3,000,000
3,500,000
4,000,000
4,500,000
5,000,000
5,500,000
6,000,000
Pseudomonas
putida KT2440

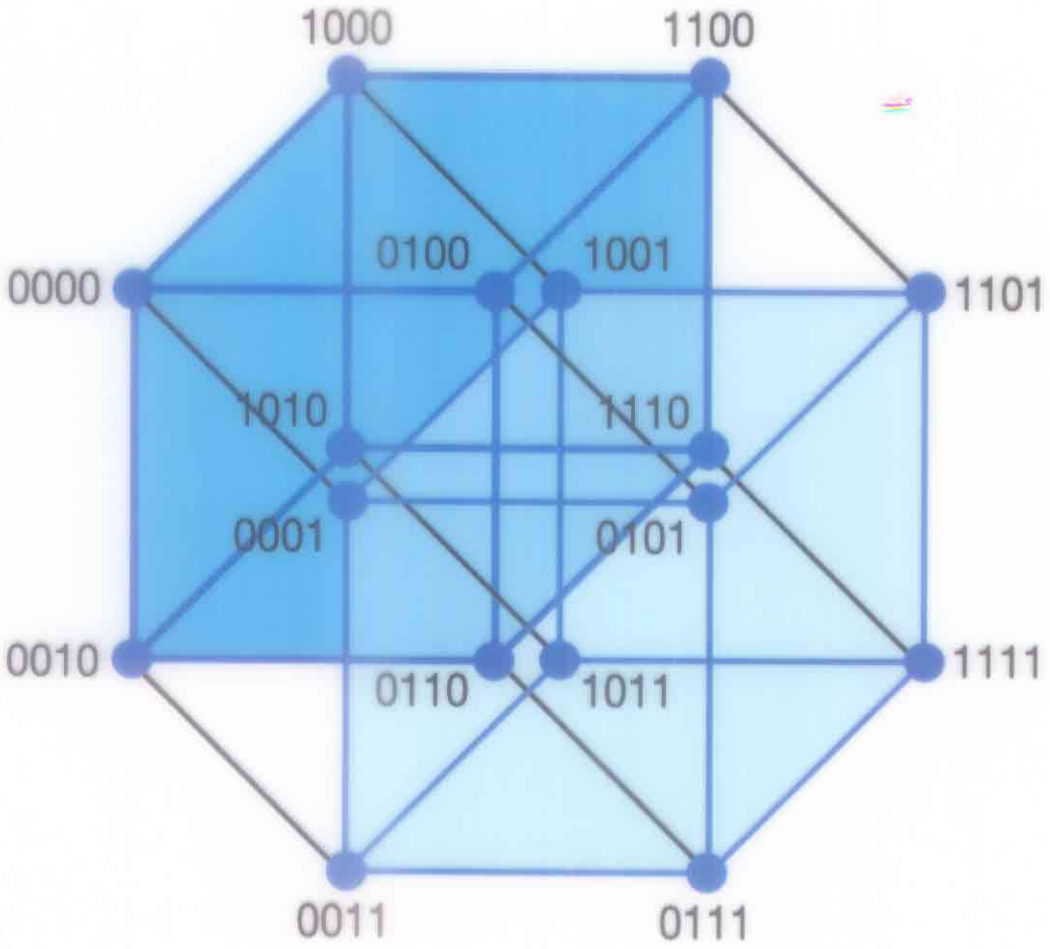


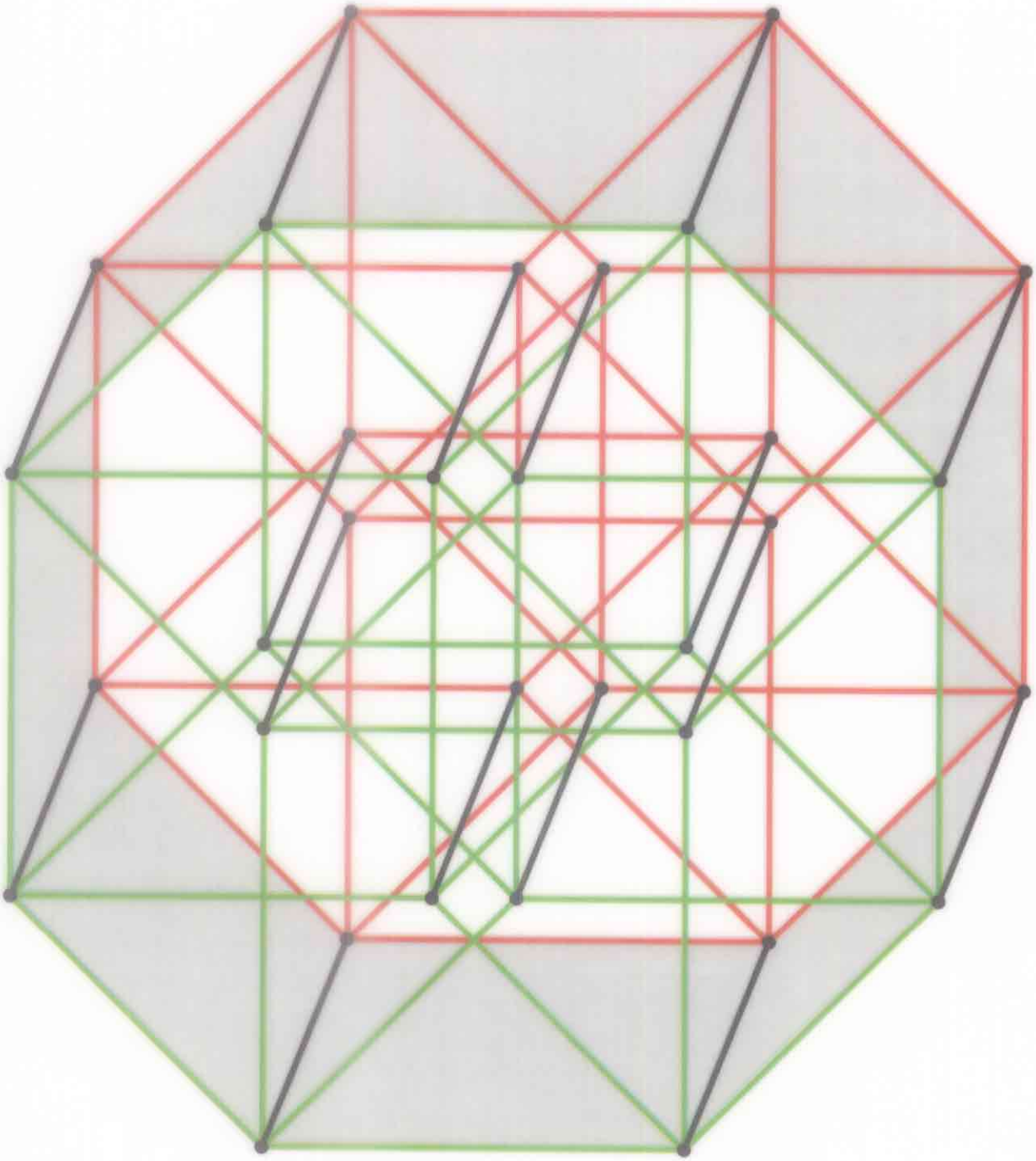

Present
Node

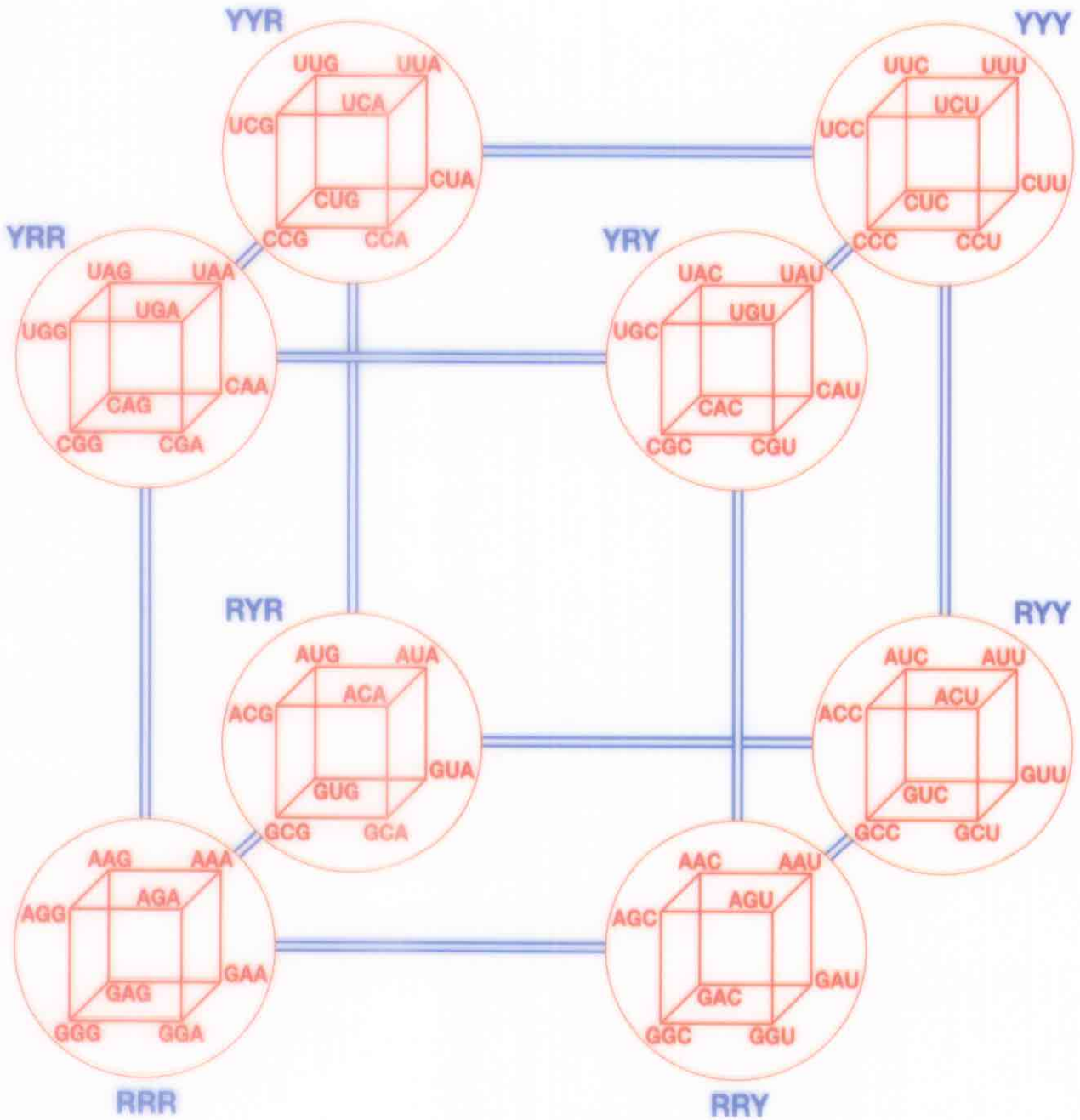

Present
Node II
Node I
Origin of Genetic Code
Precursor RNA
Origin of Earth
0
x 10^9 years
-1
-2
-3
-4
-4.7

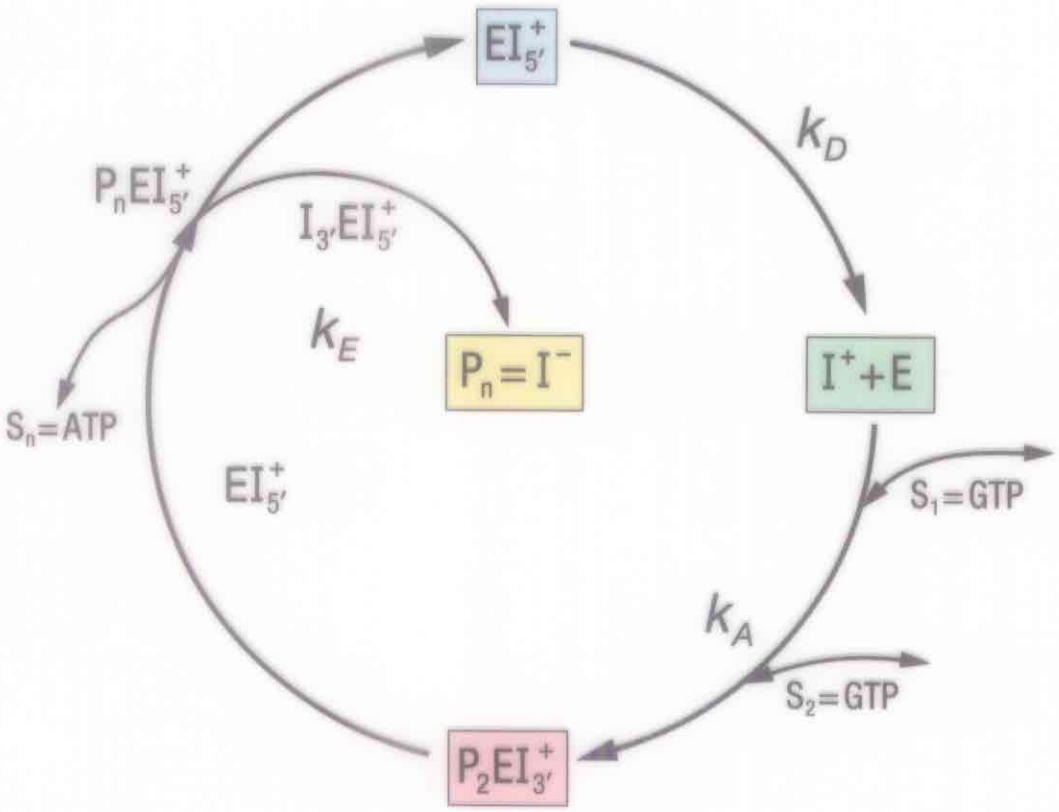

Node I
Node II
Archaebacteria
Eukaryotes
Eubacteria
Chloroplasts
Mitochondria
T-Phages
Eukaryotes
Archaebacteria
Eubacteria
Chloroplasts
Mitochondria
Node I, Node II
Relative distance segments [d_i/ν]
1.0
0.8
0.6
0.4
0.2
0
d_0
d_1
d_2
0
0.2
0.4
0.6
0.8
1.0
Relative mutational distance [Δ/ν]
Δ_{min}
Δ_{phyl}
Δ_a
Moderately diverged positions
Highly diverged positions

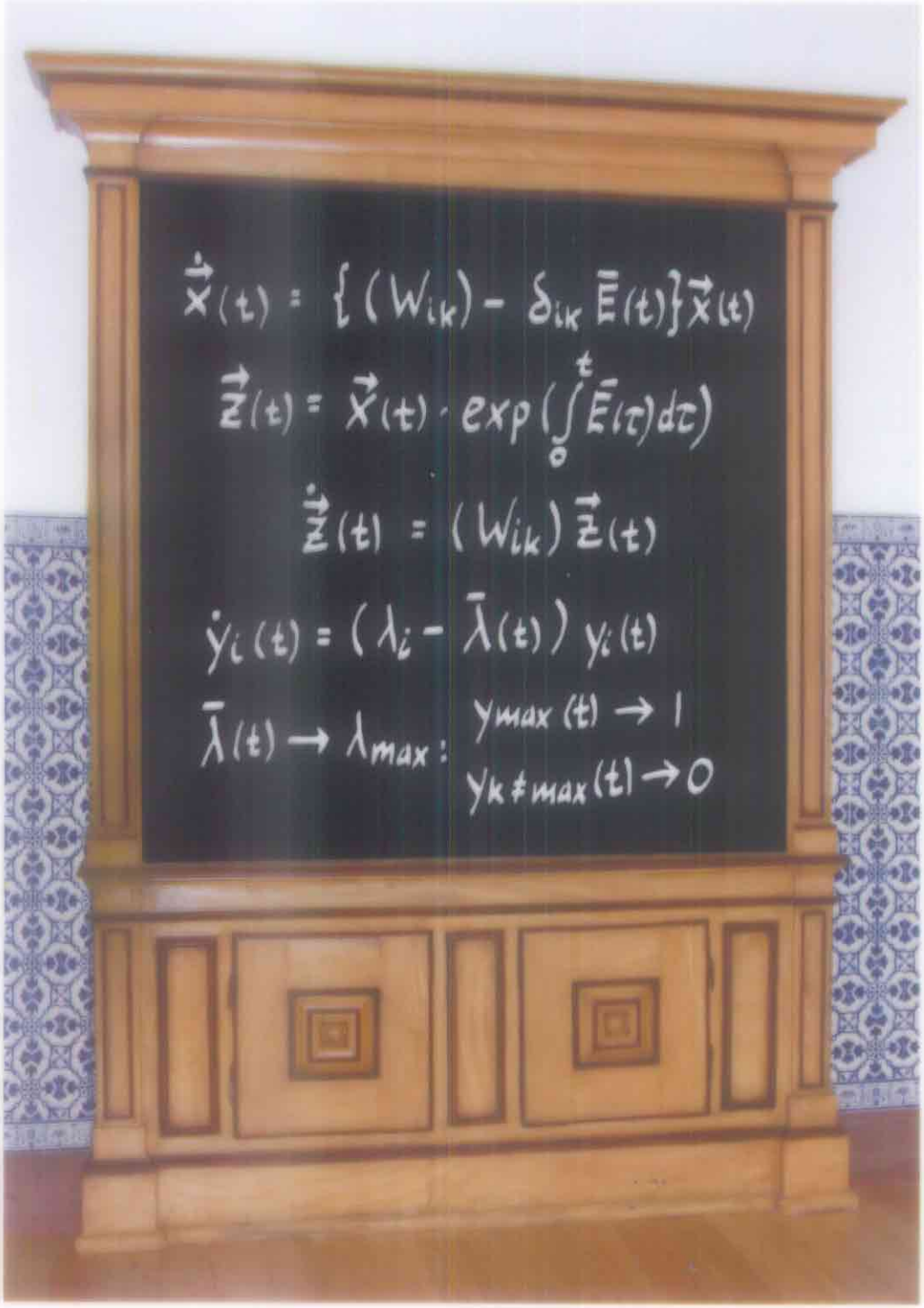

1
10
11
0
00
01
100
110
000
010
101
111
001
011

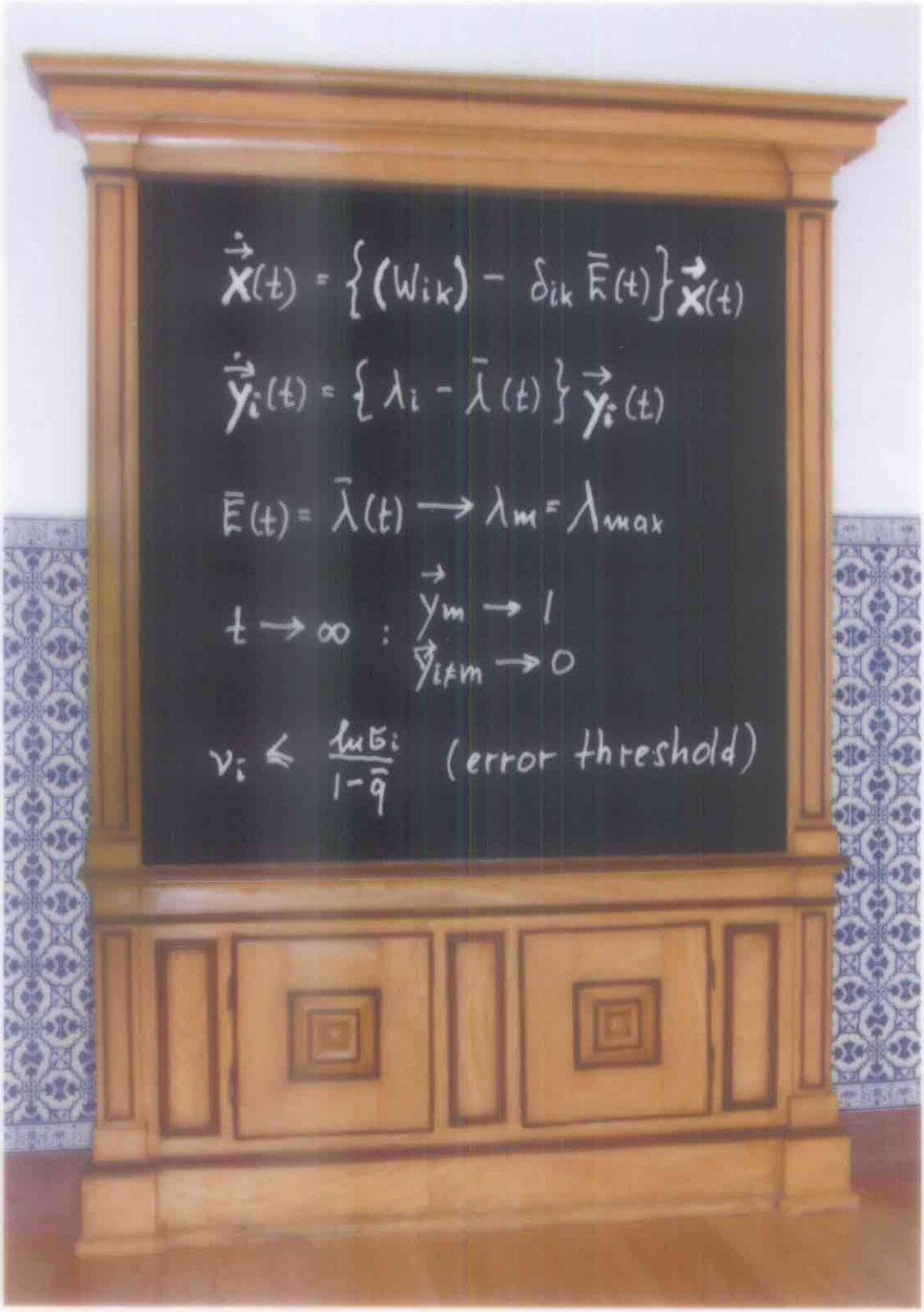

1000
1100
0100
1001
0000
1101
1010
1110
0001
0101
0010
1111
0110
1011
0011
0111

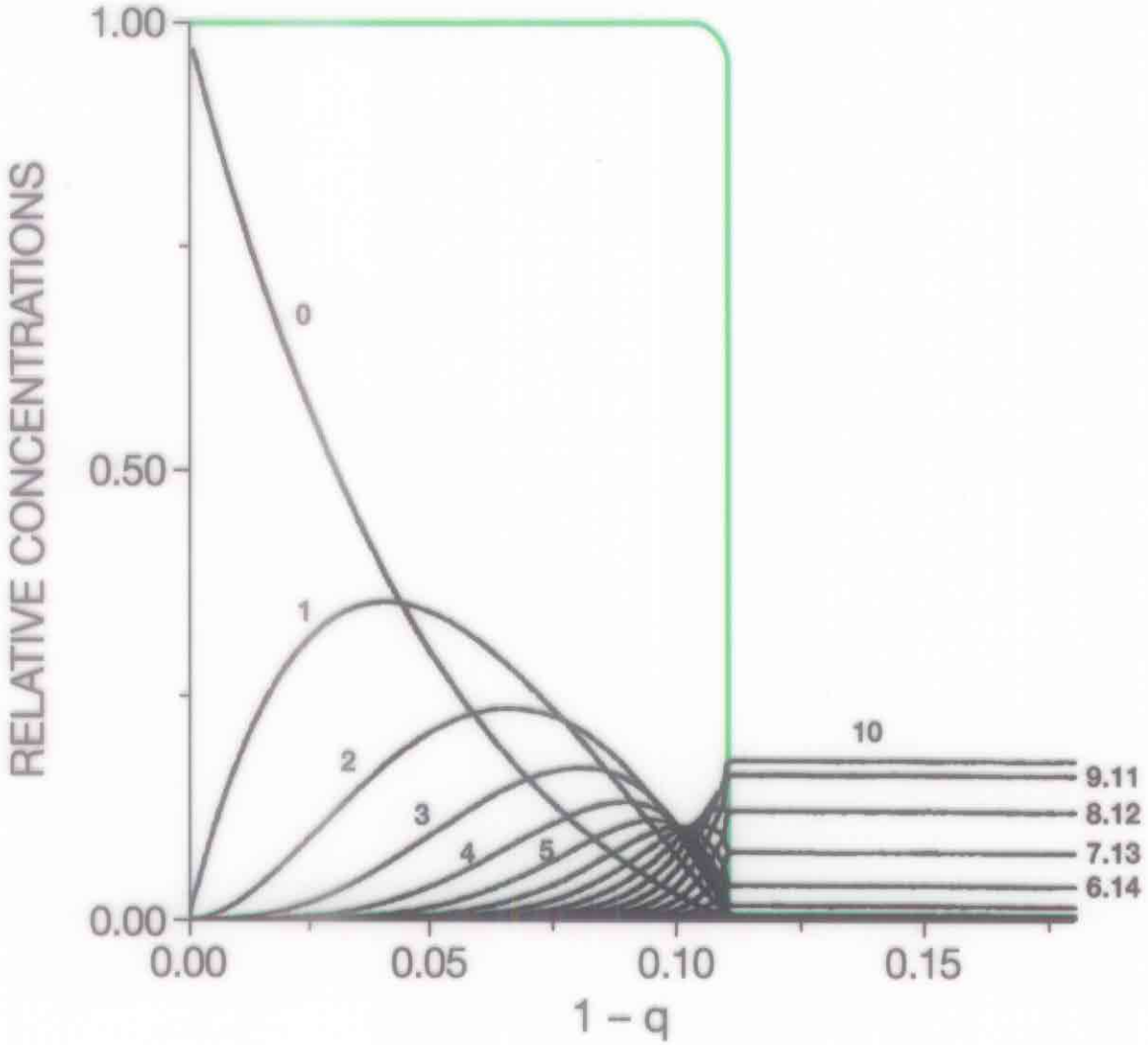


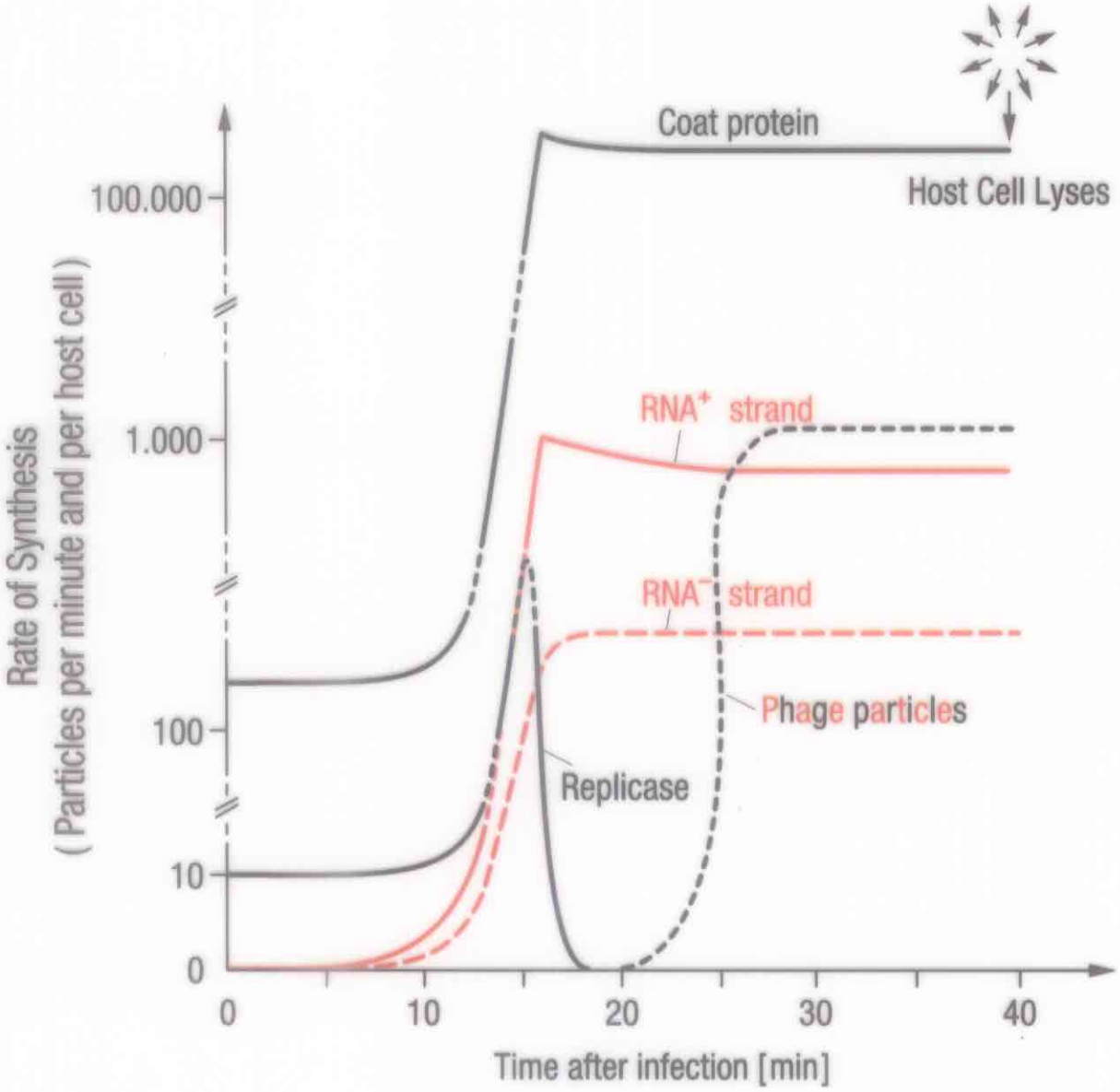

YYR
UUG
UUA
UCA
UCG
CUA
CUG
CCG
CCA
YYY
UUC
UUU
UCU
UCC
CUU
CUC
CCC
CCU
YRR
UAG
UAA
UGA
UGG
CAA
CAG
CGG
CGA
YRY
UAC
UAU
UGU
UGC
CAU
CAC
CGC
CGU
RYR
AUG
AUA
ACA
ACG
GUA
GUG
GCG
GCA
RYY
AUC
AUU
ACU
ACC
GUU
GUC
GCC
GCU
RRR
AAG
AAA
AGA
AGG
GAA
GAG
GGG
GGA
RRY
AAC
AAU
AGU
AGC
GAU
GAC
GGC
GGU


$EI^+_{5'}$
k_D
$I^+ + E$
$S_1 = GTP$
k_A
$S_2 = GTP$
$P_2EI^+_{3'}$
$P_n EI^+_{5'}$
$I_{3'}EI^+_{5'}$
k_E
$P_n = I^-$
$S_n = ATP$
$EI^+_{5'}$


$\dot{\vec{x}}(t) = \{(W_{ik}) - \delta_{ik}\bar{E}(t)\}\vec{x}(t)$
$\vec{z}(t) = \vec{x}(t) \cdot \exp\left(\int_0^t \bar{E}(\tau)d\tau\right)$
$\dot{\vec{z}}(t) = (W_{ik})\vec{z}(t)$
$\dot{y}_i(t) = (\lambda_i - \bar{\lambda}(t))\, y_i(t)$
$\bar{\lambda}(t) \to \lambda_{max}$: $y_{max}(t) \to 1$
$y_{k \neq max}(t) \to 0$


$\dot{\vec{x}}(t) = \{(W_{ik}) - \delta_{ik}\bar{E}(t)\}\vec{x}(t)$
$\dot{\vec{y}}_i(t) = \{\lambda_i - \bar{\lambda}(t)\}\vec{y}_i(t)$
$\bar{E}(t) = \bar{\lambda}(t) \longrightarrow \lambda_m = \lambda_{max}$
$t \to \infty : \vec{y}_m \to 1$
$\vec{y}_{i \neq m} \to 0$
$\nu_i \leq \frac{\lambda_m \Sigma_i}{1-\bar{q}}$ (error threshold)


1.00
0.50
0.00
RELATIVE CONCENTRATIONS
0
1
2
3
4
5
10
9.11
8.12
7.13
6.14
0.00
0.05
0.10
0.15
1 – q


Coat protein
Host Cell Lyses
100.000
1.000
100
10
0
Rate of Synthesis
(Particles per minute and per host cell)
RNA+ strand
RNA− strand
Phage particles
Replicase
0
10
20
30
40
Time after infection [min]