Sequence Evolution

Carsten Kemena & Inken Wohlers

FU Berlin

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Introduction

Molecular Evolution

Information Content

Hypercycles

Summary

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Big Steps in Evolution

- 1. Molecular replication
- 2. Translation and genetic code
- 3. Procariotic cells
- 4. Eucariotic cells
- 5. Multicellular live

Question

- How do macromolecules evolve?
- How can information content of genes be maintained/increased?

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Quasispecies und Hypercycles

- ▶ Model from M. Eigen and P. Schuster [1]
- Explains evolution from simple self-replicating units to complex forms of self-organization
- Based on a mathematical model

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Necessary Properties for Darwinian Behaviour

- 1. Metabolism
- 2. Self-reproduction
- 3. Mutability

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Metabolism

- ► Formation and degradation of molecular species ⇒ independent and spontanious
- System away from equilibration
- Selection effective only for intermediate states

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Self-reproduction

- Necessary for any selection process involving destabilization
- Constant degeneration
 - \Rightarrow Conservation of information

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Mutability

- Physical associated with self-reproduction
- Main source of new information
- Has to be limited danger of information loss

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Modelling of Self-reproduction

$$A + X \xrightarrow{k} 2X, \quad X \xrightarrow{k'} F$$

- X = molecular species
- A = raw material
- F = final product
- k = rate of self-replication
- ▶ k'= rate of degeneration

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Modelling with a Differential Equation

$$\frac{dn}{dt} = kn - k'n = (k - k')n$$

solution:

$$n(t) = n_0 e^{(k-k')t}$$

n = start concentration

t = time

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Development of Concentrations



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Modelling of Molecular Evolution

Usually there exist several different species X_i

$$A + X_1 \xrightarrow{k_1} 2X_1, \quad X_1 \xrightarrow{k'_1} F$$
$$A + X_2 \xrightarrow{k_2} 2X_2, \quad X_2 \xrightarrow{k'_2} F$$
$$\vdots$$
$$A + X_n \xrightarrow{k_n} 2X_n, \quad X_n \xrightarrow{k'_n} F$$

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Generalized Differential Equation

$$\frac{dn_i}{dt} = k_i n_i - k'_i n_i = (k_i - k'_i) n_i$$

solution:

$$n_i(t) = n_{i,0}e^{(k_i-k_i')t}$$

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Including the Selection Process

- A selection process needs selection pressure
 - 1. limited raw material
 - 2. limited total number of macromolecules
 - $\Rightarrow \mathsf{permanent}\ \mathsf{dilution}$

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Differential Equation

$$\frac{dn_i}{dt} = (k_i - k_i')n_i - \varphi n_i$$

Determining φ

$$0 = \sum_{i} \frac{dn_{i}}{dt} = \sum_{i} (k_{i} - k_{i}')n_{i} - \varphi \sum_{i} n_{i}$$
$$\Rightarrow \varphi = \frac{\sum_{i} (k_{i} - k_{i}')n_{i}}{\sum_{i} n_{i}} = \frac{\sum_{i} E_{i}n_{i}}{\sum_{i} n_{i}} = \bar{E}$$

• $\varphi = rate of dilution$

•
$$E_i = k_i - k'_i$$
 (selection value)

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Selection Equation

$$\frac{dn_i}{dt} = (E_i - \bar{E})n_i$$

• \bar{E} = mean excess productivity (selection threshold)

Observation Species with

> • $E_i > \overline{E} \Rightarrow \frac{dn_i}{dt} > 0$: concentration increases • $E_i < \overline{E} \Rightarrow \frac{dn_i}{dt} < 0$: concentration decreases

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Development of Concentration





 \Rightarrow Only one species survives

Ebeling et. al.

Carsten Kemena & Inken Wohlers Sequence

Sequence Evolution

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Development of the Selection Threshold





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Mutation

$$\frac{dn_i}{dt} = F_i n_i - k'_i n_i + \sum_j m_{ij} n_j - \varphi n_i$$

 Q_i = fraction of error-free replication $F_i = k_i Q_i$ (error free replication rate) m_{ii} = mutation rate from species j to species i

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Selection Value W_i

$$\blacktriangleright W_i = k_i Q_i - k'_i$$

•
$$W_i > \bar{E} \Rightarrow$$
 concentration increases

Quasi Species Distribution

• Mutations \Rightarrow not a selection of a single species

• Case
$$W_m \gg W_j$$
, $j \neq m$

- \Rightarrow high concentration of master species X_m
- \Rightarrow positive concentration of closely related species
- \Rightarrow selection of one quasi species

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The Quasi Species

- Average sequence is called wild-type
- Only a small fraction equals the wild-type

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Distribution of the Quasi Sequence



Conservation of Information Minimal Probability of Error-free Replication Sequence Length

Stable Conservation of Information

The quasi species is a steady distribution around the master sequence. If Mutation rate gets too high

- Too many mutations are produced and the master sequence can not survive
- The quasi species distribution gets unsteady
- Process of inheritence of information collapses



Conservation of Information Minimal Probability of Error-free Replication Sequence Length

Three Questions

- 1. What is the lower bound for the probability of an error-free replication?
- 2. Given an error rate how much information (number of nucleotides) can be conserved?
- 3. How can the information content (number of nucleotides) be increased?



Conservation of Information Minimal Probability of Error-free Replication Sequence Length

Minimal Probability for Error-free Replication

$$Q_m = q_m^{N_m}$$

 Q_m : Probability for error-free replication of the master sequence, Quality factor

 q_m : Probability for error-free replication of one monomer in master sequence

 N_m : Length of master sequence

Correct master sequence copies must be able to compete with their error copies:

$$1 > Q_m > Q_{min}$$
.

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Minimal Probability for Error-free Replication

- Depends on superiority of the master sequence
- Minimal probability of error free replication of one monomer depends on sequence length

$$Q_m > Q_{min} = q_{min}^{N_m} = rac{1}{\sigma_m}$$

 \Leftrightarrow
 $q_{min} = \sqrt[N_m]{rac{1}{\sigma_m}}$

 σ_m : Superiority of master sequence

Conservation of Information Minimal Probability of Error-free Replication Sequence Length

Superiority of the Master Sequence

 Weighted Quotient of the master sequence's fitness divided by the rest of the population's fitness

$$\sigma_m = \frac{A_m}{D_m + \overline{E}_{k \neq m}}$$

 σ_m : Superiority of the master sequence A_m : Reproduction rate of master sequence D_m : Degradation rate of master sequence $\overline{E}_{k\neq m}$: average productivity of all competitors

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Maximum Sequence Length

• Limit inversely proportional to the average error rate per symbol $1 - q_m$

$$N_{max} = \frac{\ln \sigma_m}{1 - q_m}$$

Expectation Value of an Error

 Expectation value of an error in the master sequence must always remain below a sharply defined threshold

$$\mathbb{E}(\varepsilon_m) = N_m(1-q_m) \Leftrightarrow \exp(\mathbb{E}(\varepsilon_m)) < \sigma_m$$

Conservation of Information Minimal Probability of Error-free Replication Sequence Length

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Error rate per monomer	Superiority σ_m	Sequence length N _{max}	Molecular mechanism	Biological Example
$1 - q_m$ 5×10^{-2}	2 20 200	14 60 106	enzyme-free RNA replication	t-RNA precursor, N = 80
5×10 ⁻⁴	2 20 200	1386 5991 10597	single-stranded RNA replication via specific replicases	phage Q_eta , $N=4500$
1×10 ⁻⁶	2 20 200	0.7×10 ⁶ 3.0×10 ⁶ 5.3×10 ⁶	DNA replication via polymerases including proofreading by exonuclease	E.coli, $N = 4 \times 10^6$
1×10 ⁻⁹	2 20 200	0.7×10 ⁹ 3.0×10 ⁹ 5.3×10 ⁹	DNA replication and recombination in eucaryotic cells	vertebrates (man), $N = 3 \times 10^9$

Conservation of Information Minimal Probability of Error-free Replication Sequence Length

Cooperation in Sequence Evolution

Lower error rates and thus larger sequence lengths can be achieved if enzymes catalyse replication.



Cooperation = Selective Advantage

Catalyst Catalytic Cycle Catalytic Hypercycles Competition of Hypercycles

Catalyst

- Sequence of reactions where any product is identical with a rectant of a preceeding step
- Example: Catalytic mechanism of an enzyme



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Catalytic Cycle

- One up to all intermediates are catalysts
- Example: Replication of single stranded RNA (linear growth)



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Autocatalyst

- Self-replicative Unit
- Example: DNA-Replication (exponential growth)





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Catalytic Hypercycles



- Cycle of self-replicating or autocatalytic units
- RNA/DNA molecules catalyse synthesis of enzymes which in return catalyse Synthesis of RNA/DNA molecules

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RNA-Phage Infection of a Bacterial Cell

- Translation of infectious strand instructs synthesis of a protein subunit (E) which, associated to host proteins, forms a phage-specific RNA-replicase
- This replicase complex exclusively recognizes phenotypic features of the phage-RNA
- Results in burst of phage-specific RNA-replicase



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Simple Hypercycle



$$\frac{dn_E}{dt} = A_T n_I - D_E n_E$$
$$\frac{dn_I}{dt} = A_R n_I n_E - D_I n_I$$





Figure: $A_R = A_T = D_I = D_E = 1$

Decay for $n_I(0) > 1$ Growth for $n_I(0) < 1$

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Competition of Hypercycles



Why has only one basic molecular maschinery of the cell evolved, common for all species?

 Hypercycles compete with each other if they need the same chemical building blocks and if they do not cooperate in higher order linkage

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Competition of Hypercycles

$$\frac{dn_{E,i}}{dt} = A_{T,i}n_{I,i} - \varphi_E(t)n_{E,i}$$
$$\frac{dn_{I,i}}{dt} = A_{R,i}n_{I,i}n_{E,i} - \varphi_I(t)n_{I,i}$$

From

$$\sum_{i} \frac{dn_{E,i}}{dt} = 0 , \ \sum_{i} \frac{dn_{I,i}}{dt} = 0$$

follows

$$\varphi_E = \frac{\sum_i A_{T,i} n_{I,i}}{\sum_k n_{E,k}} , \varphi_I = \frac{\sum_i A_{R,i} n_{I,i} n_{E,i}}{\sum_k n_{I,k}}$$

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Steady States for Competition of Two Hypercycles

There are two possible stable steady states:

$$(n_{E,1}, n_{I,1}, n_{E,2}, n_{I,2}) = (0, 0, C_E, C_I)$$

 $(n_{E,1}, n_{I,1}, n_{E,2}, n_{I,2}) = (C_E, C_I, 0, 0)$

Depending on the initial value the number of molecules tends to one of the steady states.

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Figure: $A_{T,1} = A_{R,1} = 1, A_{T,2} = A_{R,2} = 0.5$

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Once-forever-selection

- If two hypercycles compete with each other only one of them can survive.
- The lower the number of molecules belonging to a competing hypercycle the smaller the chance it survives.
- With (coincidentally) good initial values also non-optimal systems could have prevailed

Only one hypercycle survived and developed to become the molecular machinery of the cell.

Summary

Quasi species

Explain the inner diversity of species

Hypercycles

- Explain how to increase the information content of self-replicating units
- Are a possible explanation why there is no diversity of the molecular maschinery of the cell.

Open Questions

- How were more and more specific enzymes added during evolution?
- How did a genetic code emerge?

Thanks for your attention!

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Literature

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