In Silico Evolution of Attenuated Parasites in Catalytic Regulatory Networks

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Outline



2 The Model

3 Methods





XP

RNA World - "Molecular Biologist's Dream" [Joyce and Orgel, 1999]

de novo origin ...

- prebiotic synthesis of nucleotides
- Prebiotic synthesis of polynucleotides
- emergence of RNAs catalyzing their own replication
- ④ evolution of primordial replicases to more efficient ones

Image and evolution of other catalytic RNAs

- regulatory network
- based on RNA
- life cycle simulation of a RNA virus

Question:

emergence & behavior of parasites within the model

- regulatory network
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Question:

emergence & behavior of parasites within the model

The Model



Basic assumptions

- 2D surface ~→
- 40mers of RNA ~→
- decreasing amount of "food"
- target structure
- parallel populations

e.g. Montmorillonite

"The generation of RNAs with chain lengths greater that 40 mers would have been long enough to initiate the first life on Earth." [Joyce and Orgel, 1999; Szostak and Ellington, 1993]



Simplification



2



The Reactions

$$M_{X} + M_{Y} \stackrel{h*k_{1}}{\underset{k_{-1}}{\rightleftharpoons}} D_{X \equiv Y}$$
(1)

$$M_{X} + food \stackrel{k_{2}}{\rightarrow} 2M_{X}$$
(2)

$$M_{X} + food \stackrel{k_{3}}{\rightarrow} M_{X} + P_{X}$$
(3)

$$D_{X \equiv Y} + P_{Z} \stackrel{k_{4}}{\rightarrow} V$$
(4)

$$Z \in \{X \equiv X; X \equiv Y; Y \equiv Y\}$$
(5)

Dimerization (reversible)

$$M_X + M_Y \stackrel{h*k_1}{\underset{k_{-1}}{\rightleftharpoons}} D_{X \equiv Y}$$
(1)

$$h = \sum_{(i,j)\in T_D} (1 - p_{ij}) + \sum_{(i,j)\notin T_D} (1 - p_{ij})$$
$$k_1 = 10^{-5}$$
$$k_{-1} = \frac{k_1}{K} \qquad \qquad \left[K = \frac{Z}{ZA * ZB} \right]$$

X

Translation & Replication

$$M_X + food \stackrel{k_2}{\rightarrow} 2M_X$$
 (2)

$$k_2 = \sum_{(i,j)\in \mathcal{T}_M} \left(1- p_{ij}
ight) + \sum_{(i,j)\notin \mathcal{T}_M} \left(1- p_{ij}
ight)$$

$$M_X + food \xrightarrow{k_3} M_X + P_X$$
 (3)

$$k_3 = 1 - k_2$$

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Encapsidation & Removal

$$D_{X \equiv Y} + P_Z \xrightarrow{k_4} V \tag{4}$$
$$Z \in \{X \equiv X; X \equiv Y; Y \equiv Y\}$$

$$k_4 = const * k_1$$

$$V \xrightarrow{k_5} V_{out}$$
 (5)

$$k_5 = const$$

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XII

• libSBML Systems Biology Markup Language

- Vienna RNA Package
- SOSlib SBML ODE Solver Library
- GA

Methods

The GA



X

Results



generations: 50 replacement: keep the best ρ : 6 μ : 10 λ : 12 $\tau: \mathbf{4}$ $p_{1-point-xover}$: 0.2 $p_{2-point-xover}$: 0.2 $p_{n-point-xover}$: 0.2 p_{bitmutation} : 0.01 p_{transloc-mutation} : 0.05 $p_{reverse-mutation}: 0.05$ $p_{xchange}: 0.05$

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Results



generations: 50 replacement: elitism ρ : 6 μ : 20 λ : 24 $\tau: \mathbf{4}$ $p_{1-point-xover}$: 0.2 $p_{2-point-xover}$: 0.2 $p_{n-point-xover}$: 0.2 p_{bitmutation} : 0.01 $p_{transloc-mutation}$: 0.05 $p_{reverse-mutation}$: 0.05 $p_{xchange}$: 0.05

- homodimeric RNAs
- heterodimeric RNAs with homodimeric protein coats
- no real parasitism
- combinatorial explosion
- rate parameters
- tracking history

Conclusion

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