Mutation-driven division of labour within population

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BACKGROUND

Classical studies of populations evolving at high mutation rates predict increases in mutational robustness.

- Quasispecies theory: neutrality increases even at the expenses of replication rate (Survival of the flattest effect).
- RNA evolution: neutral evolution of mutational robustness as the population moves to highly connected regions of the neutral network.

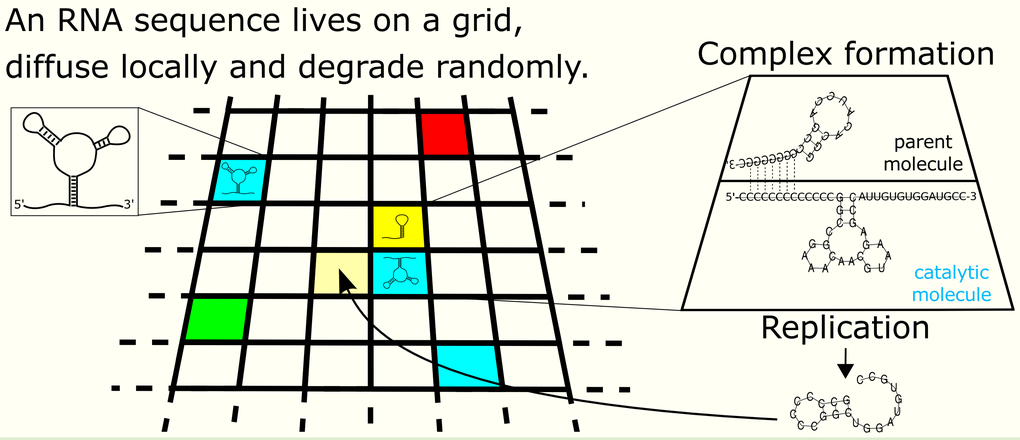
However, Error Threshold: upper mutation rate limit in order to maintain information in a single genome. Potenitally, more information can be stored within ecosystems, where multiple lineages coexist inter-dependently at high mutation rates.

- How can information increase within a single quasispecies?
- What would be its population structure?

MODEL / METHODS

Individual based, spatial system: RNA molecules form complexes to replicate each other.

An RNA sequence lives on a grid, diffuse locally and degrade randomly.



- A free 5' end is used to form complexes with close-by molecules.
- A free 3' end is used to let other molecules form complexes with it.
- If a complex forms, and if a sequence is catalytic (which depends on secondary structure), replication and mutations happens.

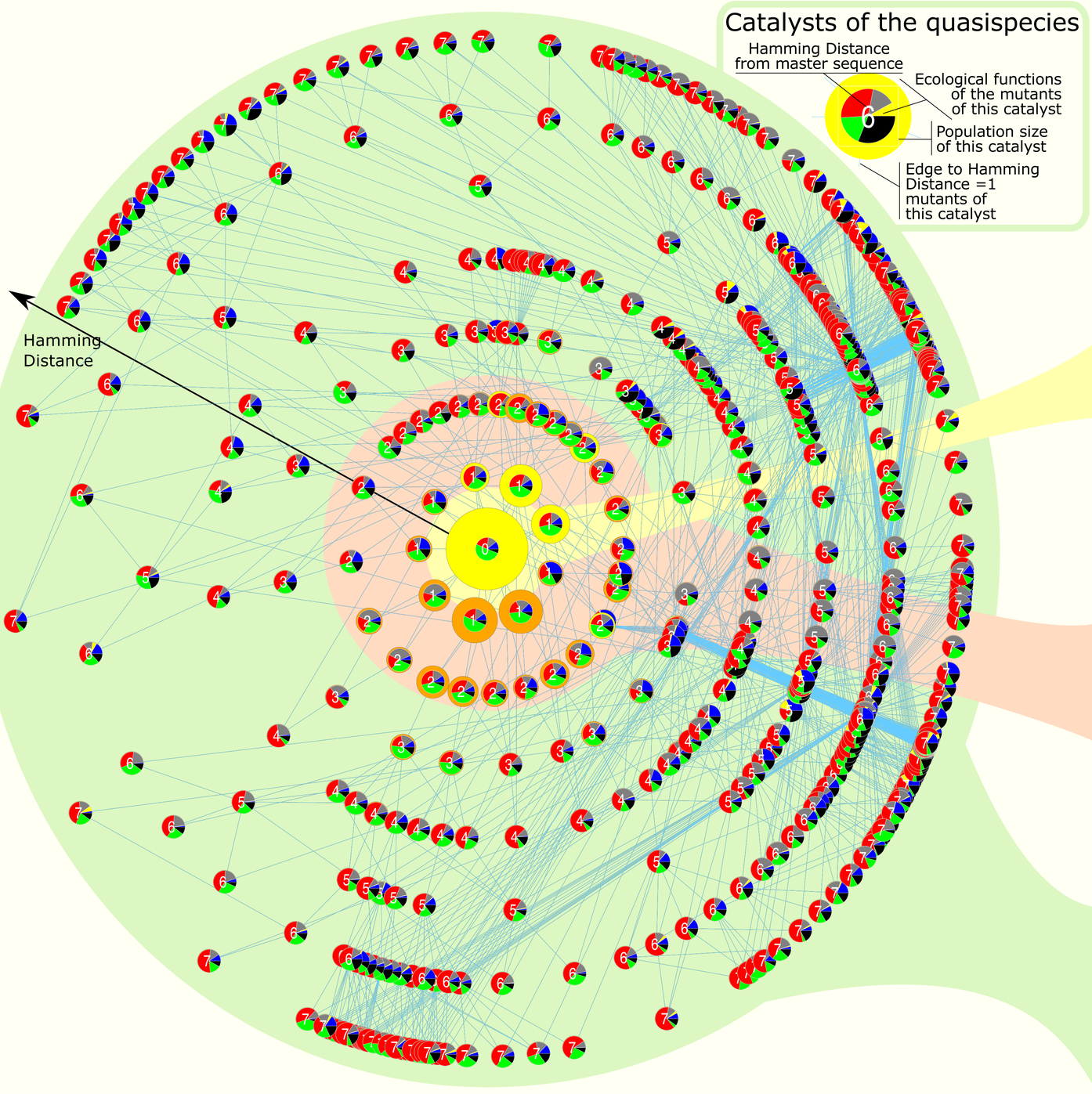
Phenotype recognition and classification

Catalysts	Parasites	Helpers	Stallers	Junk	Hybrid
Forms complex Gives replication Gets replication	Forms complex Gets replication	Forms complex Gives replication	 Forms complex	 (Inert)	Forms complex Gives replication or Gets replication
VIABLE	VIABLE	NOT VIABLE	NOT VIABLE	NOT VIABLE	NOT VIABLE

AT A GLANCE

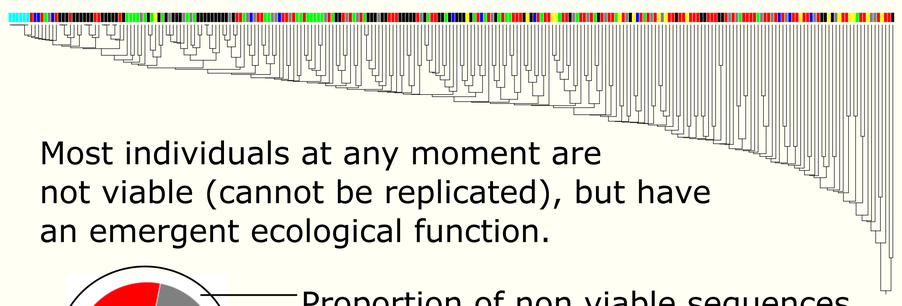
A quasispecies evolves at high mutation rates, it behaves like an ecosystem:

- High mutation rates are exploited so that small genotypic changes produce large phenotypic and functional differences,
- Emergent functions are carried out by non viable sequences,
- Individually coded, stochastically decoded ecosystem-based solution.

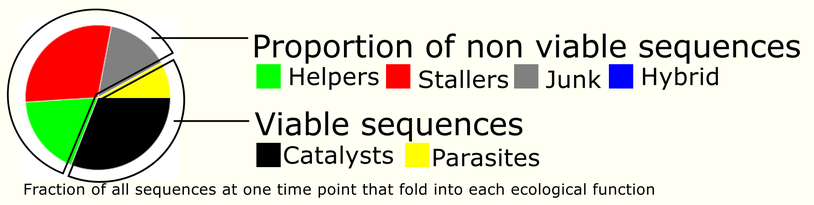


RESULTS: AT HIGH MUTATION RATES

A single, stable quasispecies evolves

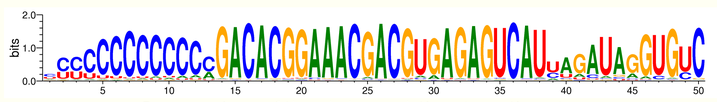


Most individuals at any moment are not viable (cannot be replicated), but have an emergent ecological function.



Fraction of all sequences at one time point that fold into each ecological function

One persisting master sequence at the centre of the quasispecies



Sequence Logo of the whole population at one time step

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CCCCCCCCCCCCCGACACGGAAACGACGUGAGAGUCAUUAGAUAGGUGUC
.............(((.((....)).(....).)))..............
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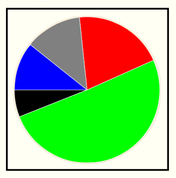
Consensus sequence and its secondary structure: the master sequence

Closer mutants of the master sequence are beneficial

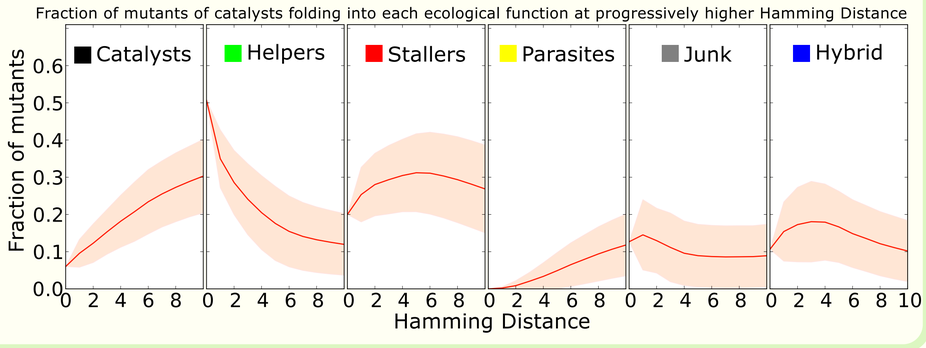
- minimised fraction of competitors (other ■Catalysts)
- no parasites (■)
- most of non viable mutants maximise the replication of the master sequence (■ Helpers)



Fraction of mutants of the master seq. that fold into each ecological function

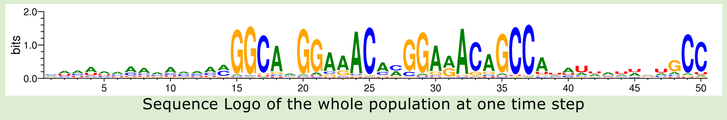
Mutants at higher Hamming Distances hinder competitors and rare parasites

- non viable mutants (■stallers), form complexes with close-by viable molecules impeding their replication
- fraction of helpers (■) drops drastically

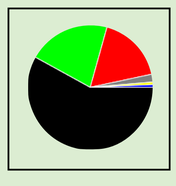


Steep vs. flat quasispecies

Steep - as opposed to flat - quasispecies evolve. However, flat quasispecies arise sometimes:



Sequence Logo of the whole population at one time step



Distribution of ecological functions among the mutants of the most frequent catalyst at one time point

- high variability, no master sequences
- different distribution of mutants
  - higher degree of neutrality (■)
  - fewer helpers (■)

Despite high replication rate of the flat quasispecies and high mutation rates, competitions steep vs. flat quasispecies result in the steep ones winning regularly. Hence, the survival of the flattest effect does not happen.

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