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Conditions to engineer evolvability

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- The Modern Synthesis has become the standard theory of biological evolution.
- Claim is that evolution is driven by existence of three major processes:
 - Heritability from genes
 - Introduction of variation (e.g. “random” mutation)
 - Selection
- According to this account, variation amongst individuals of a species is considered to be introduced randomly, with the directive force in the evolutionary process provided by natural selection, via the introduction of differential survival rates for fit and less fit organisms.
- Several mechanisms: mutation, cross-over, etc.
- Mutation considered to be the ultimate source of novelty (e.g. Clune et al. 2008).

- Major assumption: variation is ultimately random
- But “random” with respect to what?
 - Any mutation is equally likely?
 - Dawkins: evolution is random with respect to fitness
 - i.e. mutations (and other forms of introducing variation) are generated independently of their implications for the fitness of an organism
- So ... propensity to evolve set by physical constraints not linked to fitness implications (?)

Evolvability = propensity to evolve

- Kauffman (1996) postulated on theoretical grounds that evolution would favour organisms that were successful at evolution.
- More successful through ...
 - Better-than-random mechanisms for *generating* genetic variation
 - Mutation
 - Cross-over, etc.
 - Horizontal gene transfer
 - Better-than-random mechanisms for *using* (random) mutations
 - Through genotype-phenotype mapping
 - E.g. “gene regulatory networks” that (very roughly) control how genes are ultimately made into proteins
 - Or both!

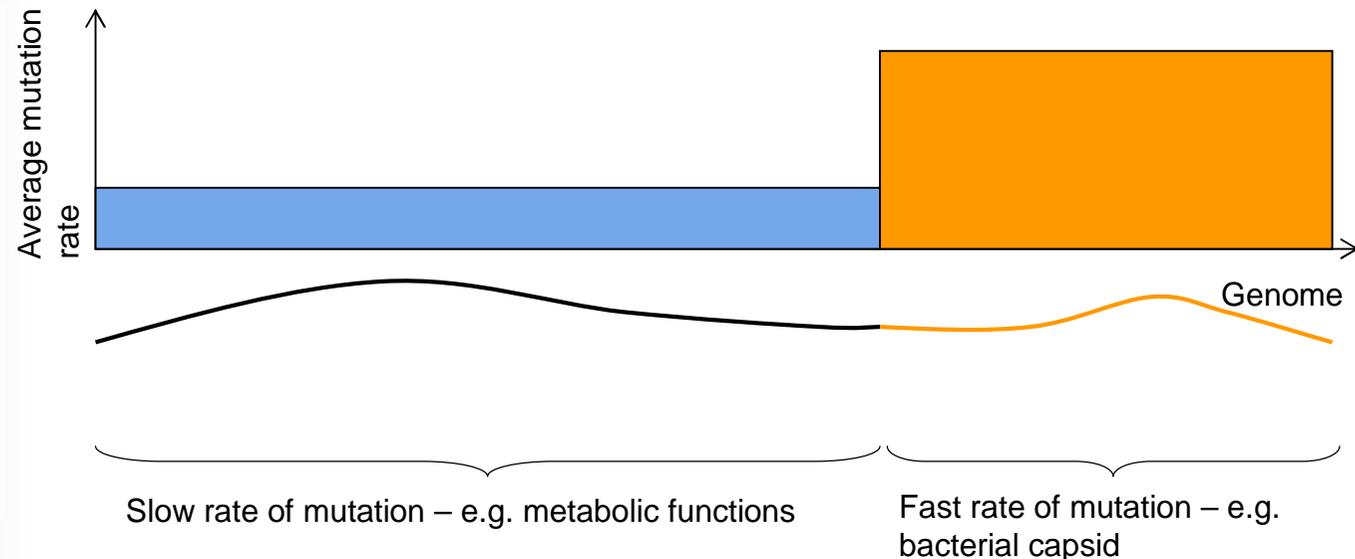
- **Genomic evolvability:** “mutation and recombination rates vary across species or clades and are influenced by the genetic makeup of an organism – they are not just passive results of external factors such as the level of background mutagenic radiation” (Pigliucci 2008 p78).
- **Phenotypic evolvability:** Large literature on potential mechanisms across genotype-phenotype mapping
- **Both(?):** Caporale (1998/2002) provides examples of organisms that demonstrate differential rates of genetic and phenotypic evolution across their genome in ways that appear adaptive
 - E.g. bacteria with higher mutation rates in capsid proteins than basic metabolic functions
 - More likely to evolve in ways that help them to avoid immune attack than in ways that alter basic functioning

- Clune et al. (2008) simulated evolution of mutation rate, asking a different question
 - Single mutation rate for the whole genome
 - Found that natural selection optimises this for long-term adaptation on smooth, but not on rugged landscapes
 - Unclear whether rates on rugged landscapes were nonetheless better-than-random
- E.g. Crombach & Hogeweg (2008) simulated mutation and selection of gene regulatory networks
 - demonstrated selection for network structures where [random] mutations tended to lead to favourable outcomes.
 - i.e. phenotype is evolvable whilst mutation remains random

- Caporale (2008) cites Conway Morris as asking the question of whether evolution would *always converge on evolvability*
- Test through computational model
 - For generality - abstract
 - For comparability - cellular automaton model
- Chosen genomic evolvability as the focus
 - Less studied
 - More fundamental as implies control of “ultimate source of variation” – i.e. of information available to the system, rather than how and whether information is processed

- To demonstrate evolvability, an organism or population does **not** need to:
 - produce **only** or even **primarily** adaptive changes
 - **optimise** its mutation rates
- Rather, it needs to demonstrate a **better-than-random distribution of mutations**

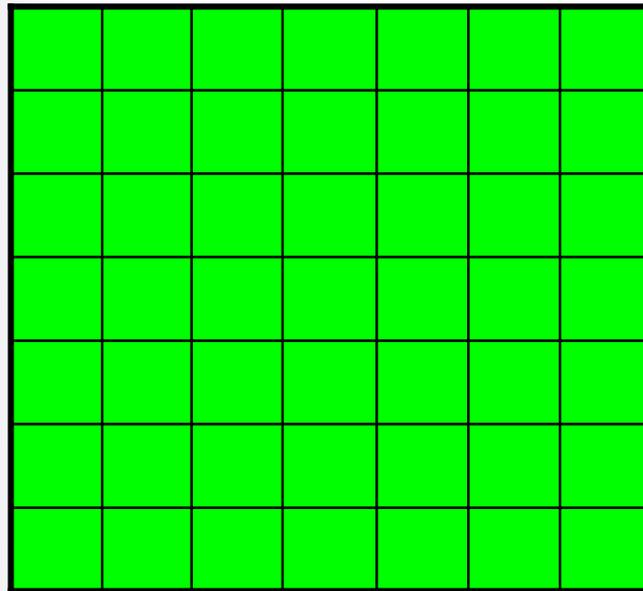
Demonstrate through differential rates of mutation across the genome, with higher rates for those parts that require to evolve quickly, and vice versa. These rates may not be “optimal”, but are nonetheless better than chance.



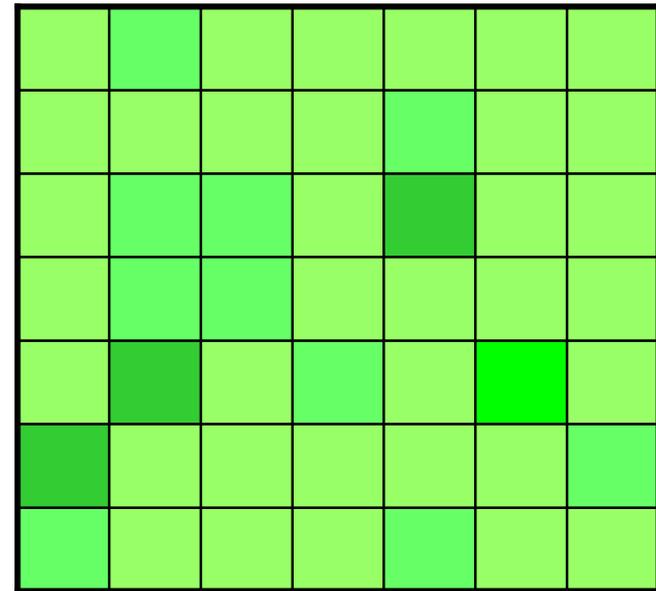
- But how can we be sure that simulated evolution is better-than-random?
 - In the real world, there probably *are* physical constraints that limit evolution, but it seems that within those limits there is variability
 - However, no easy way to know the optimal rate of evolution (and thus what constitutes a suboptimal rate) in the real world as physical constraints are poorly understood
 - Safer therefore to aim to demonstrate different rates in different parts of the genome that are adaptive
 - Avoids necessity to understand optimality

Cellular automaton model

- Camouflage metaphor – fitter organisms better camouflaged
- Each organism has:
 - (1) RGB colour values
 - (2) RGB mutation probabilities



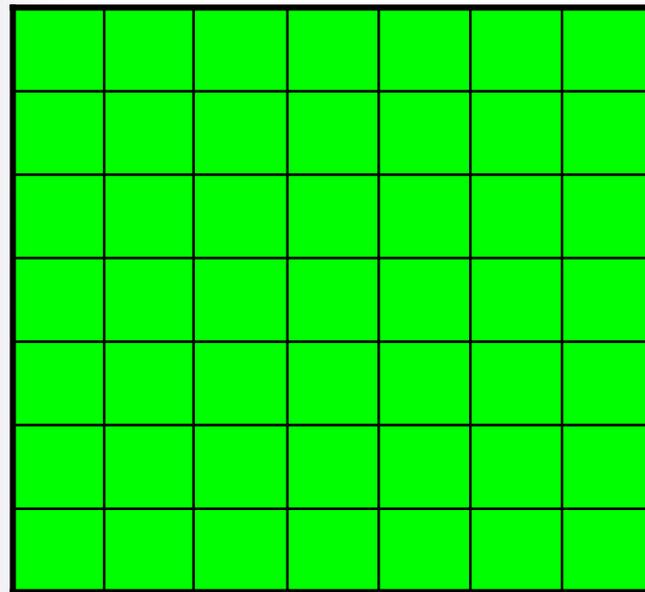
Background



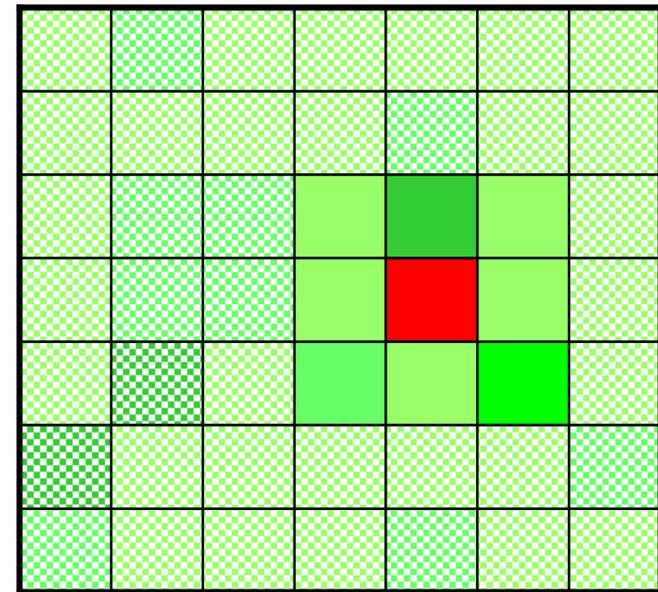
Organisms

Cellular automaton model

- Each time-step, organisms selected to be killed and replaced
- Fittest surrounding organism replicates
- Possible mutation in RGB values and RGB mutation probabilities



Background

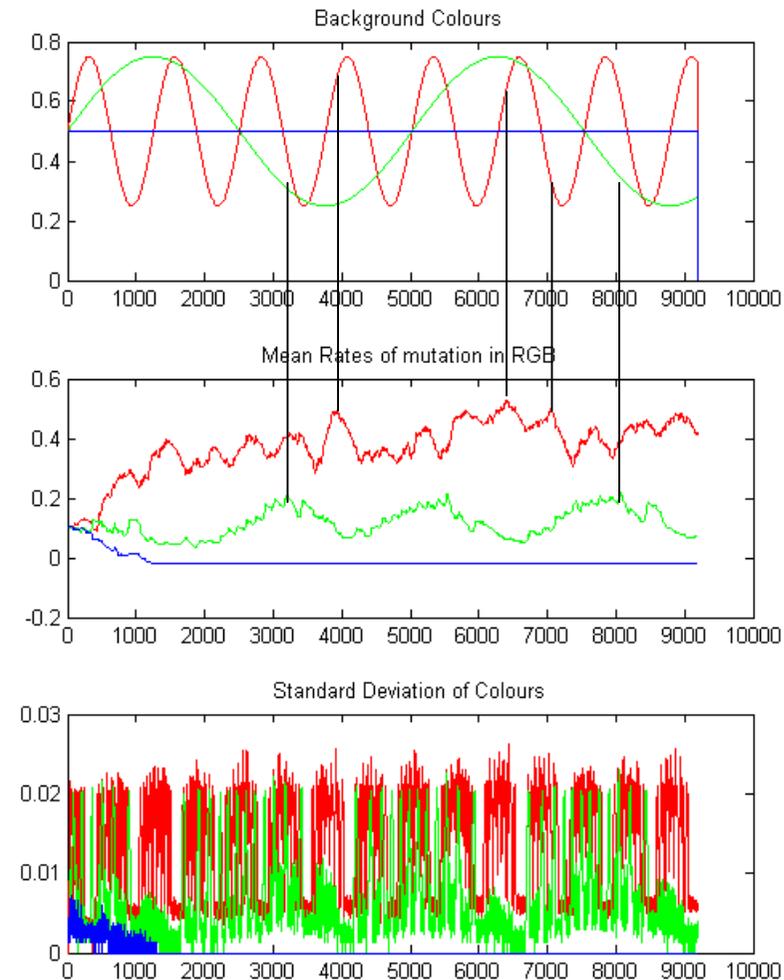


Organisms

- Fitness and thus selection is based solely on current camouflage
 - RGB values
- So, does evolvability emerge?
 - i.e. are RGB mutation probabilities adaptive
- Simulation demonstration – a work in progress
- “Proof by sample run”?

- 1) Average mutation rates correspond to rate of change of background – i.e. evolvability
- 2) Fastest mutation rates when background changing fastest (with lag)
- 3) Greatest diversity in fastest changing colour
- 4) Diversity tracks rate of change in background

Forgetting in the sense of returning to previous state



Next steps ...

- Robustness testing for different parameter values
 - Scale of grid, percentage to be killed, rate of change of background, functional form of background changes (i.e. not square, random, stochastic)
- Test different fitness functions
- Are the rates of mutation “optimal” over short/long timescales?
- Competition between evolvable and non-evolvable species
- Allow changes in step size as well as mutation probability
- Applications, perhaps in genetic algorithms ... ?

References

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