Genomic Complexity: Environmental Kolmogorov

- Kolmogorov complexity defined through an AE machine
- No need for a Turing machine, no need for infinite tape!
- Let $g$ be a genome of length $|g|$, $x$ a pattern, and $AE$ a developmental machine. Then, let

$$eK_{AE}(x) = \min_{|g|} \{ g \in G \mid g \vdash_{AE} x \}$$
May wish to define complexity functionally

Usually begin with an objective function and / or constraints

Can construct boolean objectives $O = \{ o_1, ..., o_k \}$

Then, all organisms which meet the above set:

$$S_O = \{ \alpha \mid \alpha \vdash_{AE} x \land o_1(x) \land ... \land o_k(x) \}$$

Then, the complexity of the niche:

$$\min \{|x| \mid \alpha \vdash_{AE} x \land \alpha \in S_O \}$$

So, we find out which niche a pattern belongs to, then determine the minimal organism (by genomic length) which also fits into that niche.
A simplification of Cellular Automata, defined on the space of stings of length $l$

$\alpha = (d, t, \phi)$, where $d$ a diameter, $t$ a running time, $\phi$ a transition function specifying output for each pattern of length $2^d$

A TCA $\alpha$ transforms a bit string from initial state “00...010...00” to some pattern.
Can compute the functional complexity with the following objectives:

- Objective set $O_1$: a symmetric, equally distributed pattern with few colour changes
- Objective set $O_2$: a pattern which is mostly 1s, with a right-most value of 0, also symmetric

Then, we can compute several measures of complexity for various lengths, and contrast the results.
Some correlations between complexity measures for TCAs: