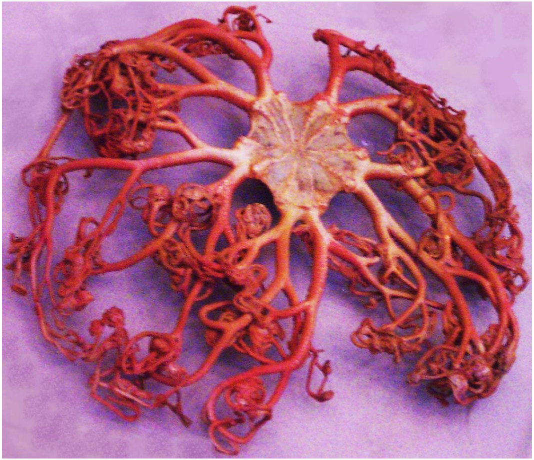
Complexity



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

$$eK_{AE}(x) = \min_{|g|}\{g \in G \mid g \vdash_{AE} x\}$$

Functional Complexity

- 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:

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

- Then, the complexity of the niche:

$$\min_{|x|}\{x \mid \alpha \vdash_{AE} x \ \wedge \ \alpha \in S_O\}$$

So, we find out which niche a pattern belongs to, then determine the minimal organism (by genomic length) which also fits into that niche.

Terminating Cellular Automata

- 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, ϕ a transition function specifying output for each pattern of length 2^d
- A TCA α transforms a bit string from initial state "00...010...00" to some pattern.

Computation of measures for TCAs

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.

Complexity

Some correlations between complexity measures for TCAs: