

# Examining Forms of Inductive Bias Towards 'Simplicity' in Genetic Algorithms to Enhance Evolvability of Boolean Functions

Hetvi Jethwani, Sumeet Agarwal

Indian Institute of Technology, Delhi

16th June 2021

# Outline

Components

    Evolvability

    Metabiology

COLT and AIT

Framework

Conclusion

Future work



Figure: Scan to visit paper pdf

# Motivation

- Keratin, a protein found in human hair, nails, and skin, is about 550 amino acids long- out of  $\approx (20)^{550}$  possible combinations, nature somehow stumbled upon this particular arrangement.
- Definitely not tractable to explore the whole space
- How exactly does nature 'reduce' this exponential possibility to weed out potentially good combinations?



# Motivation

- In a sense, we're "learning" what's fit and what's not enabled by some constraints
- These 'constraints' are known as priors or the inductive bias
- Typically represent selectivity for low-complexity structures

# Goal

- o Existing approaches which seek to incorporate such priors-
  1. As a restricted case of PAC learnability Valiant (2009)
  2. Meta-biology - evolving software Chaitin (2011),Hernández-Orozco et al. (2018)
- o We propose common framework to examine how these different priors affect the notion of evolvability of boolean function classes

# 1: A Computational Learning Theory (COLT) description

Evolution is modelled as a learning problem guided by aggregate fitness

Facilitated by restricting the search space to a chosen class of functions (such as conjunctions)

Simpler classes like conjunctions are shown to be more evolvable

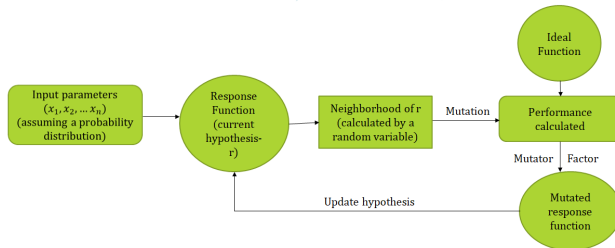


Figure: Visualization of this framework [Kaushal (2018)]

## 2: The algorithmic information theory (AIT) approach

Impose the universal distribution over the mutation neighbourhood- probability of picking an algorithmically simpler structure is exponentially more

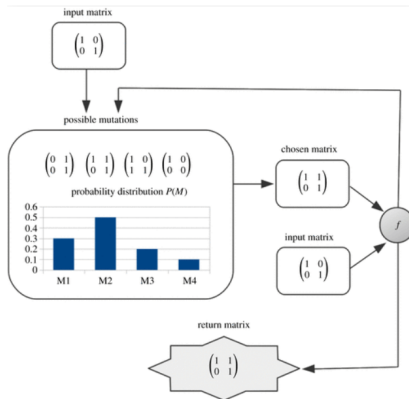
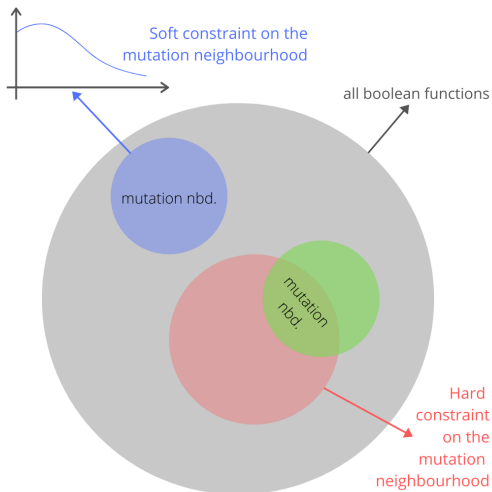


Figure: Framework proposed by Hernández-Orozco et al. (2018)

# Finding common ground





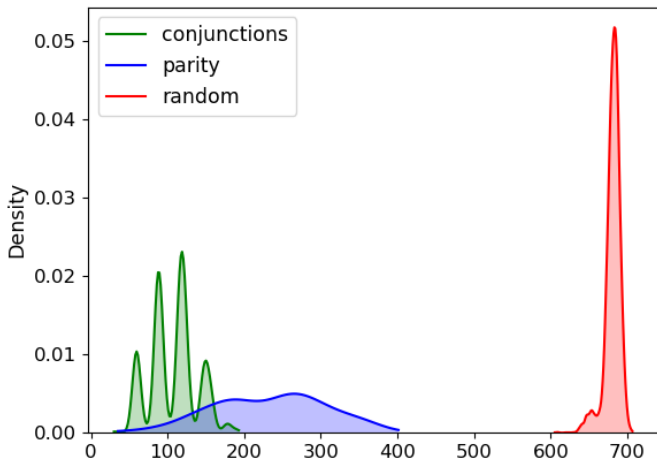
# Framework: Soft $\rightarrow$ Hard

*How does the Valiant (2009) notion of inductive bias translate to the setting proposed in Hernández-Orozco et al. (2018)?*

- Represent individuals as  $2^n \times 1$  matrices, each representing minterms of a boolean function of  $n$  variables.
- Soft constraint: G.A. similar to Hernández-Orozco et al., 2018
- Hard constraint: restriction on the algorithmic information of individuals- our 'prior' here becomes a threshold on the Kolomogorov complexity or BDM value.

## But before we go on..

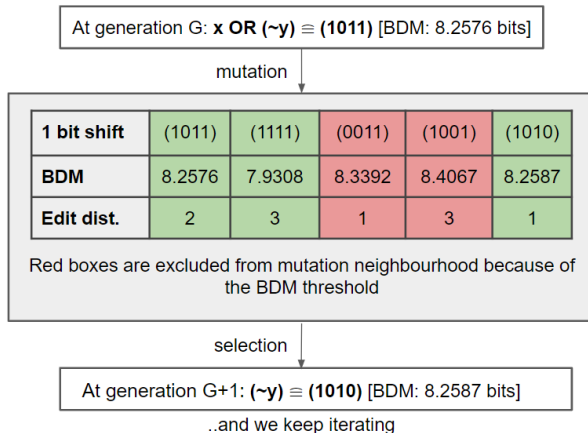
Can the "hard constraint" in the sense of belonging to a certain function class be emulated using a threshold on the information content?



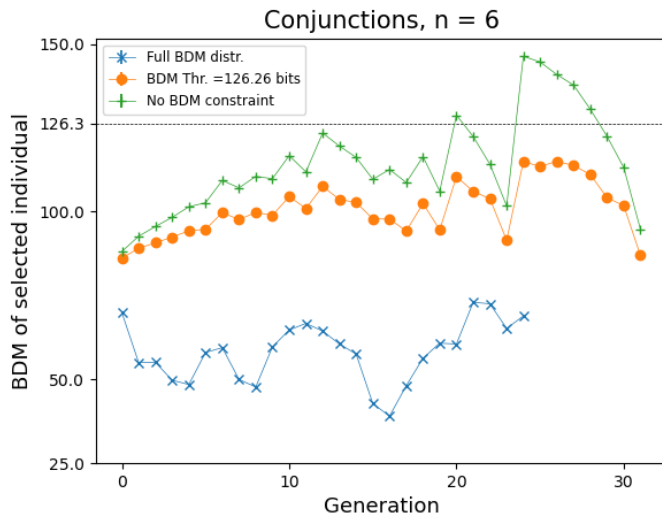
# Toy-example

Each boolean function is mapped to a binary string using its minterm representation

**Evolving to:  $X \text{ AND } (\sim y) \equiv (0010)$  [BDM 8.2576 bits]; Threshold: 8.3 bits**



# Observations



# Observations

- Classes are actually 'separable' by BDM
- Thresholded setting converges faster than no threshold, and as it becomes tighter, faster convergence
- Extinctions/Time-outs also increase
- Conjunctions converge considerably faster than parity functions
- Threshold weaker form of bias than the full universal distribution, but leads to a notable speed-up






# Conclusion

- Is it plausible to assume knowledge of a distribution over an exponentially large space?
- Restriction on realisable functional mechanisms (such as conjunctions) may be a more plausible constraint

# Further directions

- What's a feasible way to tune the BDM threshold?
- Exploring modifications of the representation space because the current one would require space exponential in  $n$

# References

-  Cepelewicz, J. (n.d.). Computer science and biology explore algorithmic evolution.  
<https://www.quantamagazine.org/computer-science-and-biology-explore-algorithmic-evolution-20181129/>
-  Chaitin, G. (2011). *Goedel's Way: Exploits into an undecidable world*. CRC Press. <https://cds.cern.ch/record/1486394>
-  Delahaye, J.-P. & Zenil, H. (2012). Numerical evaluation of algorithmic complexity for short strings: A glance into the innermost structure of randomness. *Applied Mathematics and Computation*, 219(1), 63–77.
-  Hernández-Orozco, S., Kiani, N. A. & Zenil, H. (2018). Algorithmically probable mutations reproduce aspects of evolution, such as convergence rate, genetic memory and modularity. *Royal Society Open Science*, 5(8), 180399.  
<https://doi.org/10.1098/rsos.180399>
-  Kaushal, S. (n.d.). Mathematical models of evolvability.