

Attribute-Efficient Evolvability of Linear Functions

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Joint work with Elaine Angelino (Harvard University)

Outline

- 1 Summary : Previous Talks
- 2 Representation of Functions
- 3 Evolving Sparse Linear Functions
- 4 Conclusions and Future Work

Evolution as computational learning

Leslie Valiant (2006)

- **Genotype**: string representation (e.g., as encoded in DNA)
- **Phenotype**: function $X \rightarrow Y$
 - (x_1, \dots, x_n) — represents the environment
 - y — desired output, e.g., expression level of protein

Evolution as computational learning

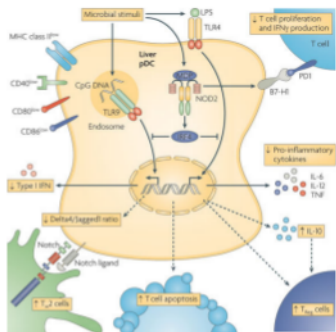
Leslie Valiant (2006)

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Ideal function: best behaviour in each possible setting

For what classes of ideal functions is evolution feasible?

Inside a Cell



From: Angus W. Thomson and Percy A. Kole, Nature Review Immunology 10, 753-766, 2010

- Snapshot of environment through sensors (e.g., transcription factors)
- These factors affect gene production through interactions with DNA

Last talk : From learning to evolution

- At a very high level (reductions of Feldman, P. Valiant)
 - representation encodes **state** of SQ learning algorithm, **queries** and their possible **responses**
 - selection “chooses” representation corresponding to correct query response

Last talk : From learning to evolution

- At a very high level (reductions of Feldman, P. Valiant)
 - representation encodes **state** of SQ learning algorithm, **queries** and their possible **responses**
 - selection “chooses” representation corresponding to correct query response
- These mechanisms indeed fit in Valiant’s model
 - but the **representations** may be quite complex

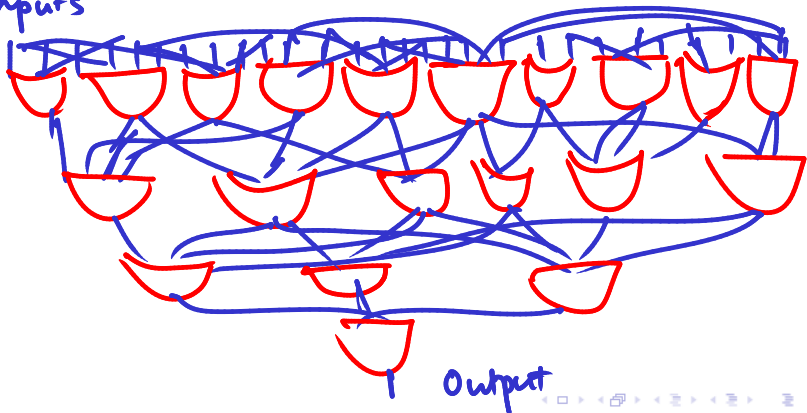
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Representation

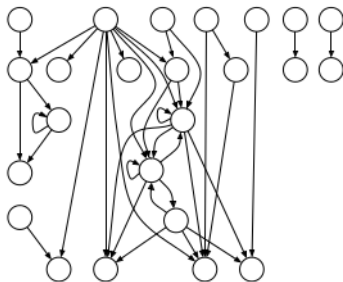
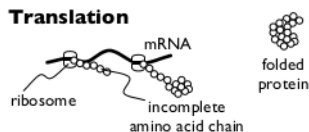
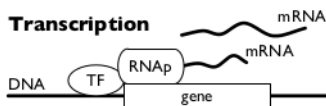
- Representation is a string describing a function (description of circuit)
00011101011000110001100110000100011100001100000011110
- Valiant's model : Arbitrary circuit of **polynomial** size

Inputs



Gene Expression

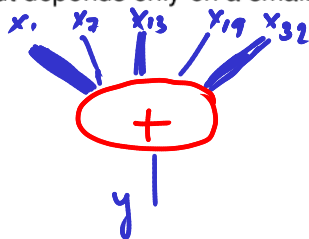
- DNA is transcribed into mRNA, which is subsequently translated into protein
- Gene expression level is controlled by binding of RNA polymerase (RNAP)



- Transcription factors (TFs) bind to the promoter region to activate/repress expression (by affecting binding of RNAP)

Gene Expression Networks

- Transcription Networks in Prokaryotes:
 - The **degree** of networks is quite small, roughly 1 – 12 (short promoter region)
 - The **depth** of the network (cascade length) is also small (typically 1 – 4)
- Eukaryotic Regulation is more involved
- When viewed as circuits, small depth and fan-in
- Output depends only on a small number of input variables (juntas)



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Sparse Linear Functions

- Sparse linear functions
 - (Ideal) $f(x_1, \dots, x_n) = 5x_1 + 7x_{17} - 3x_{45} + 100x_{100}$
 - Notion of performance (squared loss)

$$\text{Perf}(r) = -\mathbb{E}_{\mathbf{x} \sim D}[(f(\mathbf{x}) - r(\mathbf{x}))^2]$$

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- Evolutionary mechanism where each intermediate **representation** is a sparse linear function
 - sparse linear functions expressed as depth 1 weighted arithmetic circuit
 - representations may be less sparse than the ideal function

Aside: Learning sparse linear functions

- Sparse linear regression (Machine Learning)
- Sparse signal recovery (Compressed Sensing)
- Sparsest solution to an underdetermined linear system of equations
- In general the problem is NP-hard
- However, if the distributions are somewhat “nice” the hardness results are broken

Setting

Sparse Linear Functions:

$$\text{Lin}_{l,u}^k = \{ \mathbf{x} \mapsto \mathbf{w} \cdot \mathbf{x} \mid \text{sparsity}(\mathbf{w}) \leq k, \forall i, w_i = 0 \text{ or } l \leq |w_i| \leq u \}$$

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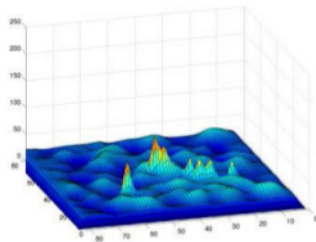
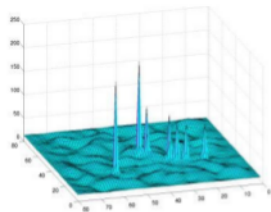
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Smooth Distributions:

- Let \tilde{D} be an arbitrary distribution over \mathbb{R}^n (bounded support)
- Draw $\tilde{\mathbf{x}} \sim \tilde{D}$
- For each i , $x_i = \tilde{x}_i + \eta_i$, where $\eta_i \in [-\Delta, \Delta]$ uniformly at random
- D is the smooth (noisy) distribution over \mathbf{x}
- Further, let $\mathbb{E}[x_i^2] \leq 1$ and support of D is bounded

Smooth Distributions

Inspired by work of Spielman and Teng



Representations

- Representations also sparse linear functions

$$\text{Rep} = \{\mathbf{x} \mapsto \mathbf{w} \cdot \mathbf{x} \mid \text{sparsity}(\mathbf{w}) \leq K, |w_i| \leq B\}$$

- Here K, B depend on k, u, l, Δ , (but not on n)

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Notation:

- Represent $r(\mathbf{x}) = \mathbf{w} \cdot \mathbf{x}$ by vector \mathbf{w}
- $\text{NZ}(\mathbf{w}) = \{i \mid w_i \neq 0\}$
- Denote $\langle \mathbf{w}, \mathbf{w}' \rangle = \mathbb{E}_{\mathbf{x} \sim D}[(\mathbf{w} \cdot \mathbf{x})(\mathbf{w}' \cdot \mathbf{x})]$
- Denote $\|\mathbf{w} - \mathbf{w}'\| = \mathbb{E}_{\mathbf{x} \sim D}[(\mathbf{w} \cdot \mathbf{x} - \mathbf{w}' \cdot \mathbf{x})^2]$

Properties of Smooth Distributions

- Let D be a “smooth” (bounded) distribution over \mathbb{R}^n
- Let \mathbf{w} be a vector representing function $\mathbf{x} \mapsto \mathbf{w} \cdot \mathbf{x}$
- **Useful Properties:**
 - 1 For each i , $w_i^2 \leq \frac{\langle \mathbf{w}, \mathbf{w} \rangle}{\Delta^2}$
 - 2 There exists an i , such that $w_i^2 \leq \frac{\langle \mathbf{w}, \mathbf{w} \rangle}{|\text{NZ}(\mathbf{w})| \Delta^2}$
 - 3 \mathbf{e}^i represents the function x_i , $\|\mathbf{e}^i\| = \Theta(\Delta)$

Mutation Algorithm

- Sparse representation: $r(x_1, \dots, x_n) = \sum_i w_i x_i$

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- Adjustments: (improve within current set of variables)

- 1 Random rescaling:

$$\mathbf{w} \leftarrow \alpha \mathbf{w} \text{ for some } \alpha \in [-1, 1]$$

- 2 Reset a random coordinate

$$\mathbf{w} \leftarrow \mathbf{w} - w_i \mathbf{e}^i + \beta_i \mathbf{e}^i \text{ for random } i \in \text{NZ}(\mathbf{w}), \beta_i \in [-B, B]$$

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- Jump improvements: (add new variables into consideration)

- 1 Add a random coordinate

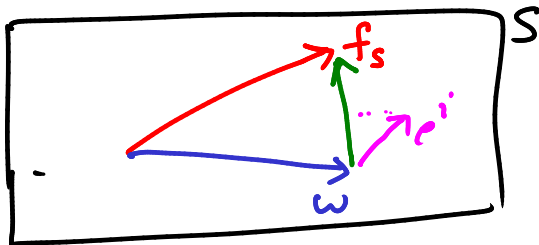
$$\mathbf{w} \leftarrow \mathbf{w} + \beta_i \mathbf{e}^i \text{ for random } i \in [n] \setminus \text{NZ}(\mathbf{w})$$

- 2 Swap a random coordinate

$$\mathbf{w} \leftarrow \mathbf{w} - w_i \mathbf{e}^i + \beta_j \mathbf{e}^j \text{ for random } i \in \text{NZ}(\mathbf{w}), j \in [n] \setminus \text{NZ}(\mathbf{w})$$

Adjustment Mutations

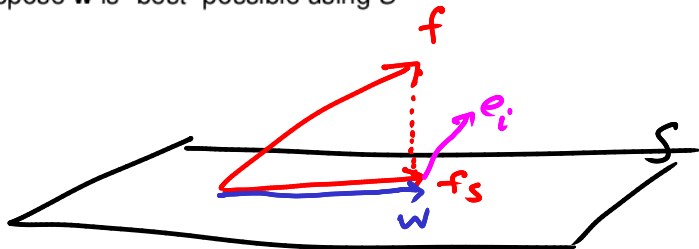
- Let $S = \text{NZ}(\mathbf{w})$ be the current set of non-zero variables in \mathbf{w} , $|S| \leq K$
- Either \mathbf{w} is “best” possible using S
- Or adjustment to some co-ordinate is an improvement



- \mathbf{f}_S best using variables in S , $\mathbf{r} = \mathbf{f}_S - \mathbf{w}$
- $\langle \mathbf{r}, \mathbf{r} \rangle = \sum_{i \in S} r_i \langle \mathbf{e}^i, \mathbf{r} \rangle$
- Beneficial Mutations Exist!

Adding/Swapping a New Variable

- Let $S = \text{NZ}(\mathbf{w})$ be the current set of non-zero variables in \mathbf{w} , $|S| \leq K$
- Suppose \mathbf{w} is “best” possible using S



- $\mathbf{f}_S \approx \mathbf{w}$ best using variables in S , $\mathbf{r} = \mathbf{f} - \mathbf{w}$
- $\langle \mathbf{r}, \mathbf{r} \rangle = \sum_{i \in \text{NZ}(\mathbf{f}) \setminus S} r_i \langle \mathbf{e}^i, \mathbf{r} \rangle$
- Some variable from S can be discarded (has low influence)
- Beneficial Mutations Exist!

Main result

Theorem (Informal)

The class of sparse functions is evolvable under smooth distributions. Furthermore, it has the following strong attribute-efficient properties:

- *the representations are all sparse linear functions*
- *the number of generations depends only on the sparsity of the ideal function and the accuracy ϵ (independent of n)*

The population (number of mutations) at each generation is polynomial in n and $1/\epsilon$.

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Conclusions and future work

Valiant's Framework and Computational Learning Theory provide a language to study several complexity measures for evolution

- This talk: sparsity inspired by transcription networks
- Other systems in biology: different constraints, similar analysis?
- Can richer classes of sparse functions be evolved?
 - sparse low-degree polynomials?
 - sparse linear functions with nonlinear filters?
 $f(x) = \text{NL}(w \cdot x)$, where NL is a one-variable function
e.g., sigmoid, Hill, etc.
- Next Talk: What functions do gene expression levels represent?