How Neutrality allows for Self-Adaptating Search in Evolutionary Computation Toussaint's work, and Some of my Own.

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Evolution in Nature and in and Simple GAs

- In ordinary evolution, the search strategy is determined by independent mutations to the genotype.
- Unstructured variation at the genotypic level produces structured variation at the phenotypic level
- i.e. there is a high dependence between the different features of the phenotype.

Let's make this a little more (awkwardly) formal

Let $\mathcal{G} = G_1 \times \ldots \times G_n$ be a product space of Gene spaces and $\mathcal{P} = P_1 \times \ldots \times P_k$ be a product space of Phenotype traits.

Now, any exploration distribution over $\mathcal{G}$, induces an exploration distribution over $\mathcal{P}$.

Let us assume an independent exploration distribution over $\mathcal{G}$.

If there is any pleiotropy, i.e. if one gene g affects more than one phenotypic feature then the distribution over $\mathcal{P}$ will *not* be independent.

This is what it means for the phenotypic variation to be *structured*

Structured variation is not surprising. Adapted structured variation is.

So structured phenotypic variation in response to genotypic variation is not suprising. It occurs whenever there is pleiotropy in the genotype-phenotype map

What is suprising about natural evolution (and absent from simple GAs) is *adapted* structured variation.

It is then suprising that a search distribution that is independent over the genes produces a phenotypic search distribution with the *right* dependencies over the features.

- e.g. height and length of arms are dependent features, and vary correctly with each other.

No chance for adapted phenotypic search distributions in the Simple GA. What are the alternatives?

In a simple GA, the representation and the mutation operators are fixed, so there is no way that independent genotypic search distributions can produce adapted phenotypic search distributions.

One alternative to the un-adapted phenotypic search distributions of Simple GA's are so-called *Estimation of Distribution Algorithms*

The key point is that in these algorithms the search distribution over the genotypes is no longer indpendent.

How BOA works

1. set $t \leftarrow 0$ randomly generate initial population $P(0)$
2. select a set of promising strings $S(t)$ from $P(t)$
3. construct the network B using a chosen metric and constraints
4. generate a set of new strings $O(t)$ according to the joint distribution encoded by B
5. create a new population $P(t+1)$ by replacing some strings from $P(t)$ with $O(t)$ set $t \leftarrow t+1$
6. if the termination criteria are not met, go to 2.

Can independent elementary mutations at the genotypic level produce adapted, structured search strategies over the phenotypes?

"yes" if the representation is allowed to change.

> "Adapting the genetic representation of phenes while keeping mutation operators fixed is in some sense dual to adapting the mutation operators while keeping the representation of phenes fixed." (Toussaint, Thesis)

So How can the Representation Change?

One way is that the genotype-phenotype map changes. (Altenberg)

- this was the idea that I pursued during the my first year here.
- The idea that the interpretation of the genotype would change if the interpretter was some chemical bath that was modified in some small way.

Is there a way of adaptively changing the representation of the genotype while keeping the Genotype-Phenotype map fixed?

Doing so would allow open up the possibility for:

> "Simple adaptation mechanisms on suitable representations" instead of "Complex adaptation mechanisms on arbitrary representations".

Examples of Complex adaptation mechanisms on arbitrary representations are the Linkage Learning Genetic Algorithm, BOA, and many other algorithms that have come out of Goldberg's illEGAL lab.

Back to our question - Can we get "suitable representations" without changing the genotype-phenotype map?

Toussaint says "yes", and that the key is a non-trivial Genotype Phenotype mapping.

Non-trivial genotype-phenotype maps
In all cases (except *really* stupid ones) a non-trivial GP map is a non-injective i.e. many-to-one map between genotypes and phenotypes.

This map induces a partition over the space of genotypes and hence an equivalence relation over this space.

Non-trivial genotype-phenotype maps

A movement in the set of neutral genotypes doesn't change the phenotype, but it does change the way that the phenotype is represented.

Given neutral genotypes $g_1 \dots g_n \in [p]$, and a fixed pattern of mutation, what constitutes a *suitable* genotype?

One answer (not exactly the one that Toussaint gives) is as follows:

A Genotype g_i is suitable if the exploration distribution under fixed mutation $\mathcal{M}(\cdot|g_i)$ is "close" to the fitness distribution over all genotypes

If the exploration distribution is close to the fitness distribution, then phenotypic features that are independent w.r.t fitness (e.g. length of your right arm and eye color)vary independently and features that are dependent (e.g. length of your right leg and the length of your left leg) vary correctly.

How can we move around in the set of neutral genotypes?

1. Regular neutral mutations

2. Toussaint introduces Level 2 mutations, which "intelligently" change the genotype without changing the phenotype

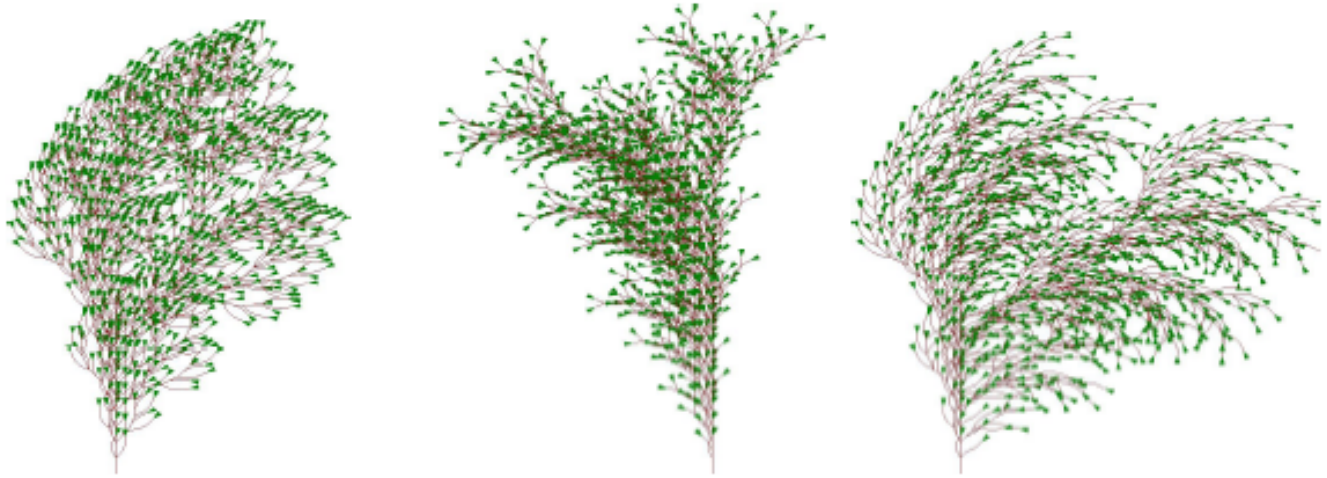
Level 2 mutations allow neutral cousins that are not accessible by regular mutation (Level 1) to be accessible

Examples of different search distributions corresponding to neutral L-Systemesq genotypes

genotype	phenotype	phenotypic neighbors
$\Psi^{(0)} = \langle \text{a} \rangle$, $\Pi = \langle\langle \text{a:bcbc} \rangle\rangle$	$\langle \text{bcbc} \rangle$	$\langle * \rangle$, $\langle *\text{cbc} \rangle$, $\langle \text{b}*\text{bc} \rangle$, $\langle \text{bc}*\text{c} \rangle$, $\langle \text{bcb}* \rangle$
$\Psi^{(0)} = \langle \text{a} \rangle$, $\Pi = \langle\langle \text{a:dd} \rangle, \langle \text{d:bc} \rangle\rangle$	$\langle \text{bcbc} \rangle$	$\langle * \rangle$, $\langle *\text{bc} \rangle$, $\langle \text{bc}* \rangle$, $\langle *\text{c}*\text{c} \rangle$, $\langle \text{b}*\text{b}* \rangle$
$\Psi^{(0)} = \langle \text{bcbc} \rangle$, $\Pi = \langle\ \rangle$	$\langle \text{bcbc} \rangle$	$\langle *\text{cbc} \rangle$, $\langle \text{b}*\text{bc} \rangle$, $\langle \text{bc}*\text{c} \rangle$, $\langle \text{bcb}* \rangle$

Note: In phenotype distributions with more than one * (e.g. $\langle$b*b*$\rangle$), both $*$'s will be replaced by the same letter (e.g. $\langle$baba$\rangle$).

Level 2 mutations can convert any one of these neutral genotypes into another.



Level 1 mutations to a genotype produces correlated changes to the phenotype. If the genotype is "suitable" then the changes to dependent phenotypic features will vary "correctly".

An experiment - Recall change of Bases

To represent a point p in some n-dimensional vector space $\mathbb{V}$

- pick a basis $\mathcal{B} = [B_1, \ldots, B_n]$,
- represent p as an n-tuple of co-ordinates $\mathbf{e}$ with respect to $\mathcal{B}$.

If you pick a new basis $\mathcal{B}'$, to represent p using $\mathcal{B}'$, apply the change of bases operation

$$\mathbf{e}' = \text{inverse}(\mathcal{B}') * \mathcal{B} * e$$

How it applies

Phenotype	Some point $\mathbf{p}$ e.g. $(3.7, 37.2)$ encoded in the cannonical basis
Genotype	$(\mathbf{e}, \mathcal{B})$
Genotype-Phenotype map	$\mathbf{p} = \mathcal{B} * \mathbf{e}$
Level 1 mutations	Gaussian changes to only to $\mathbf{e}$
Level 2 mutations	Gaussian changes to $\mathcal{B}$ followed by a change of co-ordinates $\mathbf{e}$ to preserve the phenotype