Island-Genetic Algorithms Schema Theory
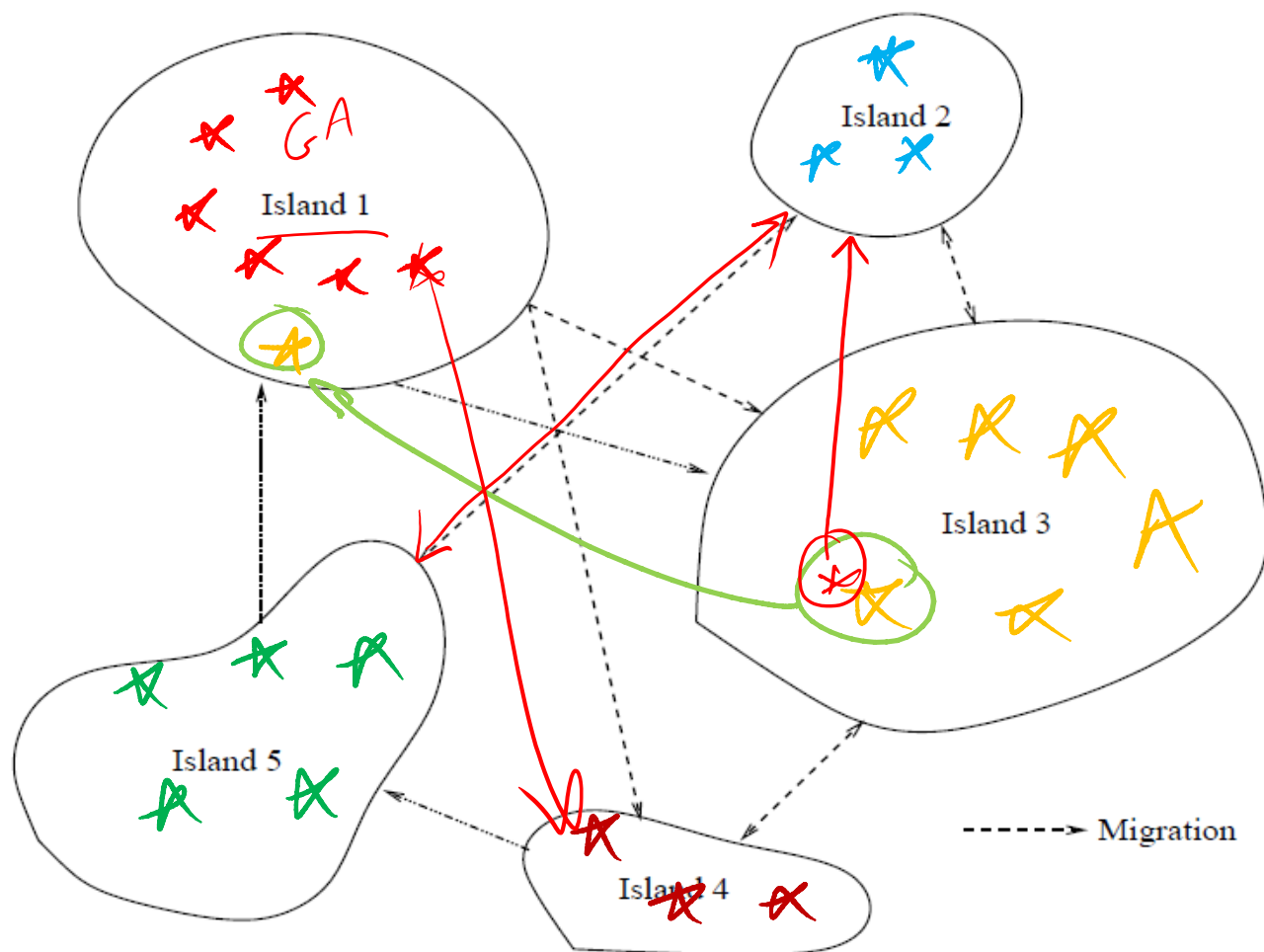
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Island Genetic Algorithm (I-GA)

- Each Island represents a separate GA with a separate sub-population

- One more operator is added: **Migration**

- Can be easily *parallelized* to run on multicore machines, clusters or GPU

Island Genetic Algorithm (I-GA)

Migration policies specify:

- A **communications topology**, which determines the migration paths between islands

- A **migration rate**, which determines the frequency of migration
  - If migration occurs too early, the number of good building blocks in the migrants may be too small to have any influence at their destinations
  - Usually, migration occurs when *each population has converged*
  - After exchange of individuals, all populations are restarted

- A **selection mechanism**, to decide which individuals will migrate *Source island*

- A **replacement strategy**, to decide which individual of the destination island will be replaced

Island Genetic Algorithm (I-GA)

Based on the selection and replacement strategies, Island GAs can be grouped into two classes of algorithms:

- Static island GAs
  - A **topology** is used to determine migration paths
- Dynamic island GAs
  - Migration decisions are made **probabilistically**

Island Genetic Algorithm (I-GA)

Static Island GAs:

- Deterministic selection and replacement strategies
    1. A *good migrant* [Source island] replaces a *bad individual* [dest. island]
    2. A *good migrant* replaces a *randomly selected individual*
    3. A *randomly selected migrant* replaces a *bad individual*
    4. A *randomly selected migrant* replaces a *randomly selected individual*

Island Genetic Algorithm (I-GA)

Dynamic Island GAs:

- **Migration** occurs at a probability

- **Destination** island is probabilistically selected

- Destination islands may use an **acceptance** strategy

    - *An immigrant is probabilistically accepted if its fitness is better than the average fitness of the island*

Schema Theory

Why do Genetic Algorithms work?

In this section we take an in-depth look at the working of the standard genetic algorithm, explaining why GA constitutes an effective search procedure

For simplicity we discuss binary string representation of individuals

Schema Theory

- Schema theory seeks to give a theoretical justification for the efficacy of the field of genetic algorithms.

- What is a Schema:
  - a template
    - the new gene alphabet $\Rightarrow$ {0,1,*} where * is a don't care

> *** * 1 1 0 * * 1 1 * * ***

  - Schema is favorable traits in a solution, where a favorable schema is called an above average schema
  - allows exploration of similarities among chromosomes
  - represents all matching strings

Schema Theory

Example:

the schema (* 1 1 1 1 0 0 1 0 0) matches two strings:

    (0 1 1 1 1 0 0 1 0 0) and

    (1 1 1 1 1 0 0 1 0 0)

Q. which strings does this schema match?

    (0 1 1 * 1 0 1 1 * *)

$2^3 = 8$

011 0 1011 00
011 0 1011 0 1
011 01011 1 0
⋮
011 1 1 011 11

- A schema matches 2^r strings

  r: # of (*) in the schema

Schema Properties

- **Order of schema S: o(S)**
  - number of **fixed** (non-*) positions
    S1 =   **11**101**
    12   345

    o(S1) = 5

  - The order of a schema is useful to calculate survival probability of the schema for mutations

- **Defining length of schema S: d(S)**
  - distance between first and last **fixed** string positions
    S1 = **11**101**   S2= **101***
    12 11 110 1 9   3 5
    3   5-3 = 2
    above d(S1) = 9-3= 6   d(S2)=?

  - The defining length of a schema is useful to calculate survival probability of the schema for crossovers

Effect of Operators on Schema
1-Selection

- Assume total number of chromosomes is PopSize.

- The number of above average individuals abiding by the above average schema S is P.

- f_i : fitness of chromosome i in the population of all chromosomes.

- Average fitness of population $= \frac{\sum_{i=1}^{PopSize} f_i}{PopSize} = \overline{F}$

Effect of Operators on Schema 1-Selection

- The average fitness of above average individuals abiding with favorable schema S=

$$\boldsymbol{F_{av}(S)} = \frac{\Sigma_{j=1}^{P} f_j}{\boldsymbol{P}}$$

  - **where P is the number of individuals abiding by S**

- Let :
  - **m(S, t)** denote the expected no. of individuals matched by schema S at time t.

  - **F** = total fitness of population, F=$\sum_{i=1}^{PopSize} f_i$

  - **m(S, t+1)** denote the expected no. of individuals matched by schema S at time t+1 (next iteration).

Effect of Operators on Schema 1-Selection

- $\text{m}(S, t+1) = m(S, t) * PopSize * \dfrac{f_{av}(S)}{F}$ (1)

- But F = total fitness
  where $\bar{\bar{F}} = \dfrac{F}{PopSize}$, so F= $\bar{F} * PopSize$

- Substitute in (1):
  $\text{m}(S, t+1) = m(S, t) * PopSize * \dfrac{f_{av}(S)}{\bar{F} * PopSize}$

  $\text{m}(S, t+1) = m(S, t) * \dfrac{f_{av}(S)}{\bar{F}}$ (2)

Effect of Operators on Schema 1-Selection

$$m(S, t+1) = m(S, t) * \frac{f_{av}(S)}{\overline{F}}$$

②

Note that $\boxed{\frac{f_{av}(S)}{\overline{F}}} > 1$

$f_{av}(s) > \overline{F}$

$f_{av}(s) = \overline{F} + \epsilon\overline{F}$ ➜ $f_{av}(s) = (1+\epsilon)\overline{F}$

$6 > 4 \Rightarrow 6 = 4 + \left(\frac{1}{2}\right)4$

Substitute in (2):

$m(S,t) = m(S,0) * (1+\epsilon)$

- $m(S, t+1) = m(S, t) * \frac{(1+\epsilon)\overline{F}}{\overline{F}}$

  $m(S, 2) = m(S, 1) * (1+\epsilon)$

  $= m(S, t) * (1+\epsilon) - - - - -(1+\epsilon) > 1$

  $m(S, 2) = m(S, 0) * (1+\epsilon) * (1+\epsilon)$

  $= m(S, 0) * (1+\epsilon)$ ②

- $m(S, t) = m(S, 0) * (1+\epsilon)^t$ — **Geometric Series!**
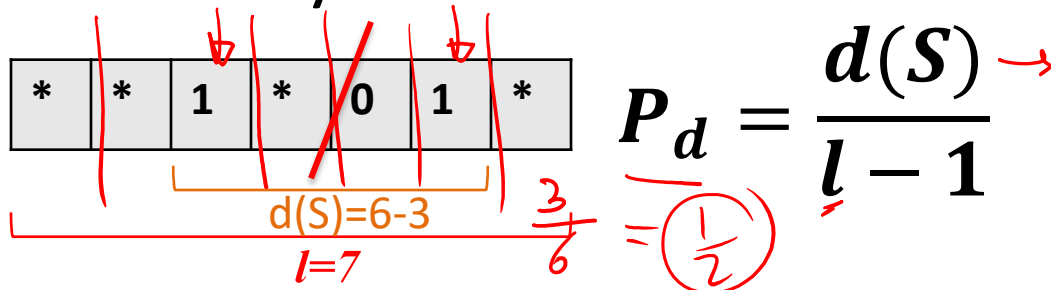
Effect of Operators on Schema 2-Crossover

Remember: Effect of selection on schema:

$$\text{m}(S, t+1) = m(S, t) * \frac{f_{av}(S)}{\overline{F}} \quad \textcircled{1}$$

Effect of Crossover:

What is the probability of **destruction** of a schema by crossover?

*	*	1	*	0	1	*

d(S)=6-3

l=7

$$P_d = \frac{d(S)}{l-1}$$

$$\frac{3}{6} = \frac{1}{2}$$

$1 \rightarrow l-1$

$1 \rightarrow 6$

where **d(S)** is the defining length of the schema, and **l** is length of chromosome.

Effect of Operators on Schema
2-Crossover

What is the probability of **<u>survival</u>** of a schema after crossover?

-->It should be (1-probability of destruction), but… destruction only happens if crossover will occur, and crossover occurs with a probability of **P_c**. So:

$$P_s = 1 - P_c \frac{d(S)}{l-1}$$

Substitute in equation (1):

$$m(S, t+1) = m(S, t) * \frac{f_{av}(S)}{\bar{F}} * \left(1 - P_c \frac{d(S)}{l-1}\right)$$

Equation (2) represents the combined effects of selection and crossover.

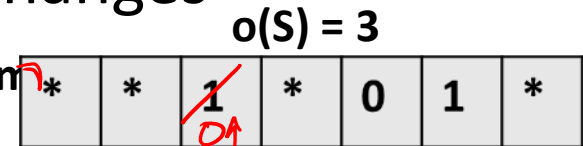# Effect of Operators on Schema 3-Mutation

What is the probability of **<u>survival</u>** of a schema after mutation?

i.e. all bits survive mutation without any changes

→probability of destruction of 1 bit: $\mathbf{P_d = P_m}$

→probability of survival of 1 bit:

$$\boldsymbol{P_s = 1 - P_d = 1 - P_m}$$

o(S) = 3

*	*	1	*	0	1	*

$(1 - P_m)^3$

→probability of survival of <u>schema</u>: [given order of schema o(S)]

$$\boldsymbol{P_s(S) = (1 - P_m) * (1 - P_m) * \cdots} \text{[for o(S) times]}$$

$$\boldsymbol{P_s(S) = (1 - P_m)^{o(S)}} \qquad \text{-- but Pm is a small number}$$

$$\boldsymbol{P_s(S) \simeq 1 - o(S)P_m}$$

Effect of Operators on Schema 3-Mutation

So probability of **survival** of a schema after crossover and mutation is:

$$P_s = 1 - P_c \frac{d(S)}{l-1} - o(S)P_m$$

→Substitute in (2):

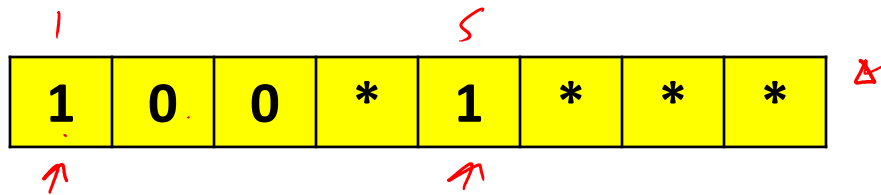$$m(S, t+1) = m(S, t) * \frac{f_{av}(S)}{\bar{F}} * \left(1 - P_c\frac{d(S)}{l-1} - o(S)P_m\right)$$

which is called the **Reproductive Schema Growth** Equation **RSG**

Conclusion:

'Short', 'low-order' & 'above-average' schema are liable to grow, increase and flourish in population

Exercise

Given the following schema 'S':

A- What is the probability of schema S survival after crossover knowing that Pc = 0.8?

$$P_S = 1 - P_c \cdot \frac{d(s)}{L-1}$$

$$\overset{0.8}{P_c} \cdot \frac{4}{7}$$

B- What is the probability of schema S survival after mutation knowing that Pm = 0.1?

$$P_S = 1 - P_m \cdot O(s)$$

$$\overset{0.1}{P_m} \cdot 4$$