

# **Parallel Genetic Algorithm (PGA)**

# Introduction

In natural populations, thousands or even millions of individuals exist in parallel.

When GAs are executed in parallel, the time required to execute a single generation is independent of population size.

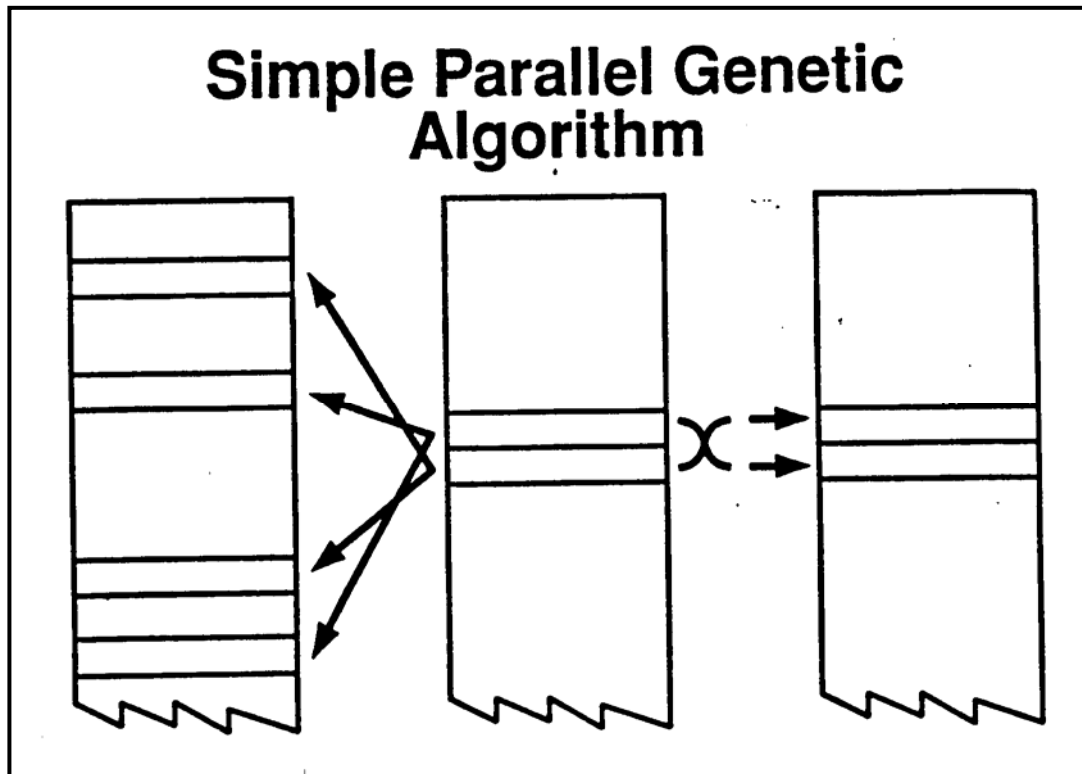
Large populations display slower convergence, i.e., the number of generations to convergence may increase.

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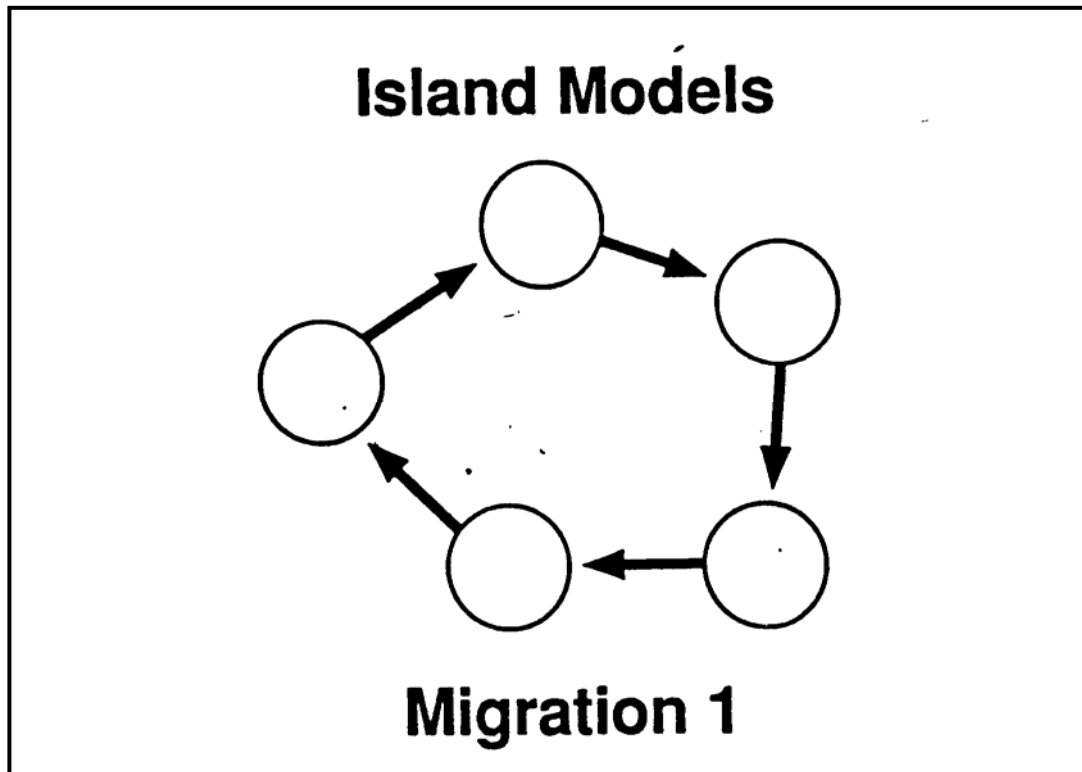
Three different ways of exploiting parallelism  
in GAs

1. Global populations with parallelism
2. Island model
3. Cellular GAs

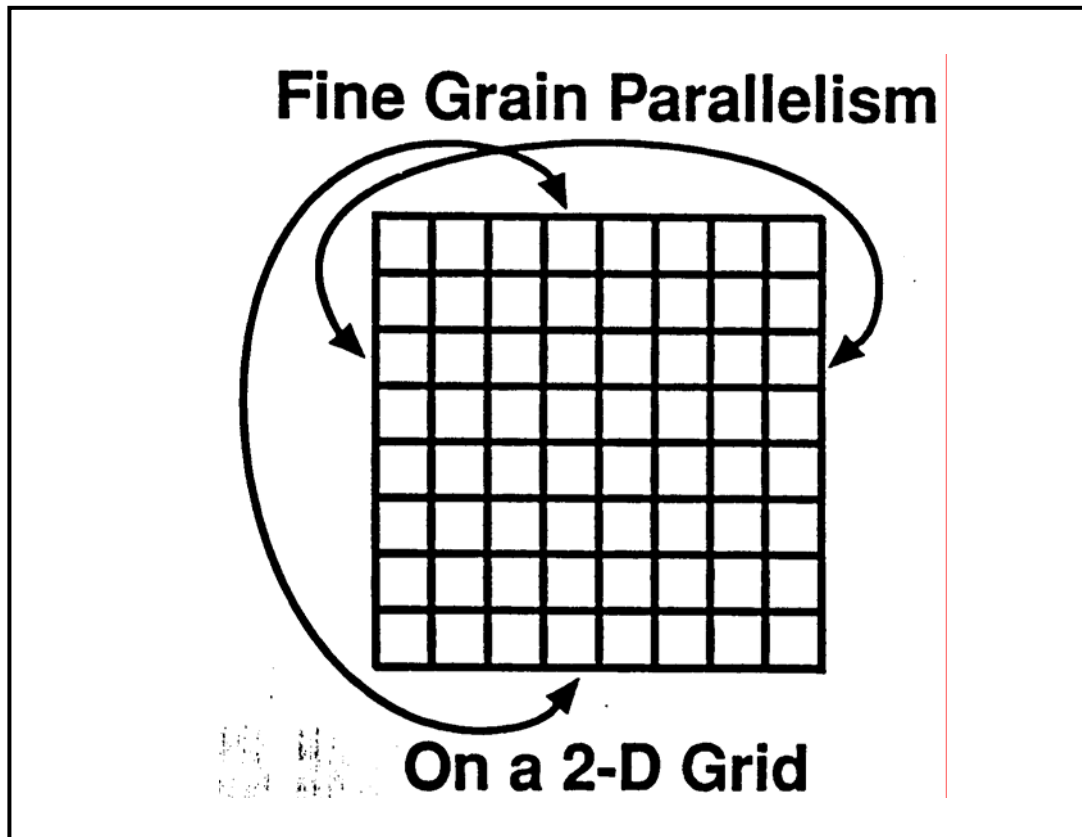
# Introduction



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Why parallelism?

Gain in speed

Much larger population size

Subpopulations interact and evolve in parallel

# Introduction

Strings are mapped to processors in a way that maximizes parallelism while avoiding unnecessary processors.

Different model has different role of local vs. global communication.



# Global Populations with Parallelism

Close to canonical GA. The only change is selection method which is done by tournament selection (Goldberg, 1990).

Instead of using fitness proportionate reproduction or directly using ranking, tournaments are held to fill the population before crossover and mutation.

Assuming two strings are selected, the better of the two strings is placed in the population. This process of randomly selecting two strings from the current population placing the best in the new population is repeated until the new population is full.

# Global Populations with Parallelism

This form of tournament selection is the same as expectation of ranking using a linear 2.0 bias.

With the addition of tournament selection, a parallel form of the canonical GA can be implemented in two (or 4, 6, ...) processors.

## Island Models

Breaks the total population down into subpopulations. Each subpopulation could then be executed as a normal GA.

Migration: occasionally, the subpopulation would swap a few strings.

# Island Models

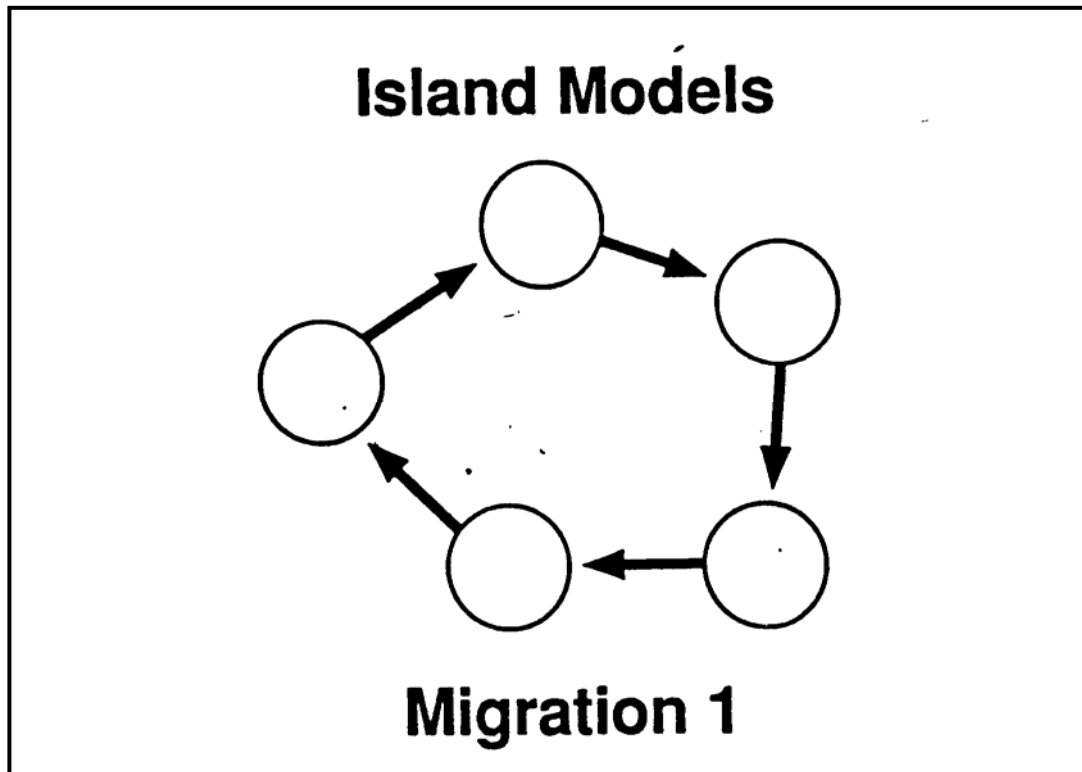
Migration allows subpopulation to share genetic material.

It may reduce the genetic drift (stochastic errors in sampling small population) in each subpopulation.

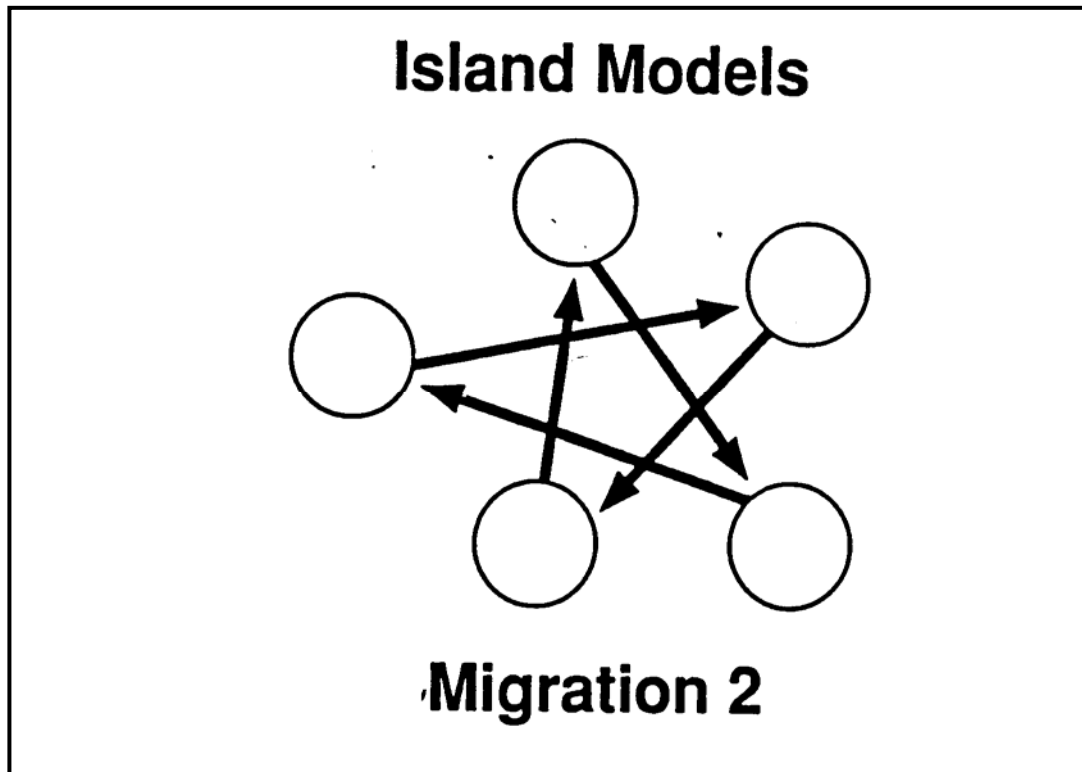
It may prevent premature convergence of subpopulations.

Several large populations with little interaction

# Island Models



# Island Models



# Cellular GAs (fgpGA)

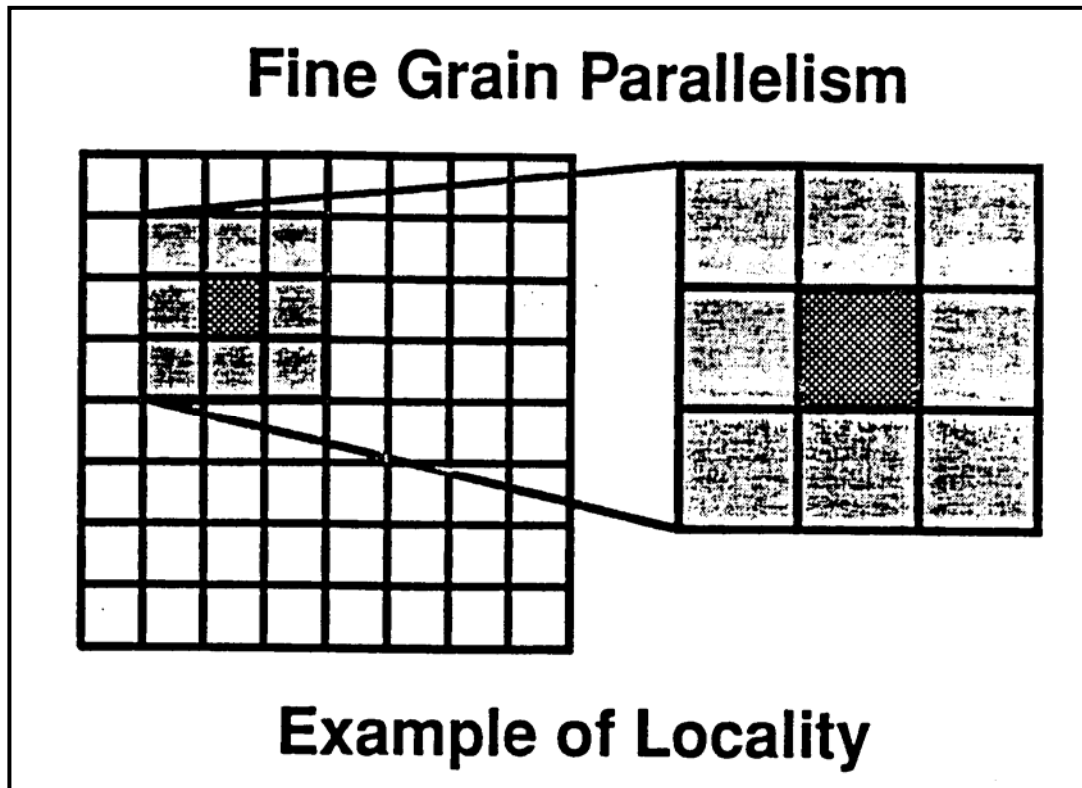
One or even number of strings per one processor (cell)

Processors only communicate with their intermediate localized neighbors (e.g., north, south, east and west: NSEW)

Each string seeks a mate close to home. Each processor checks the location to the NSEW, makes a copy of the best string, then recombine the resident string with the selected string.

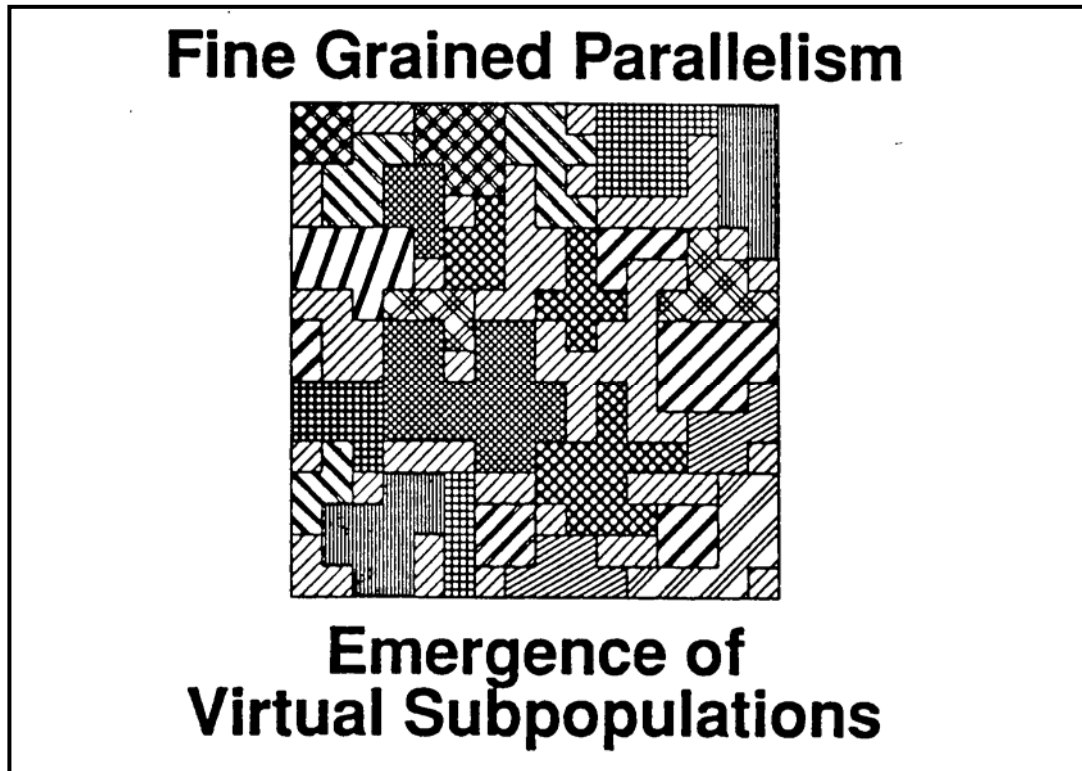
Interactions between subpopulations: Local optima can quickly spread.

# Cellular GAs (fgpGA)

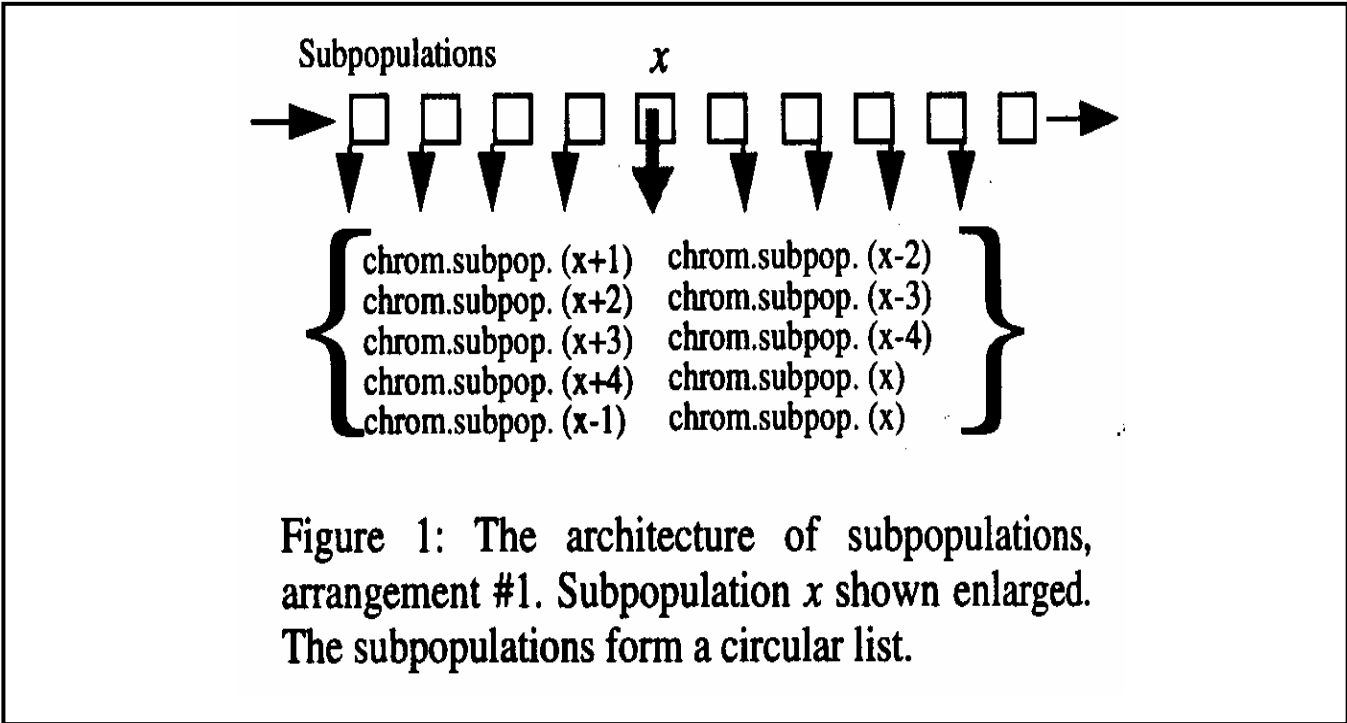




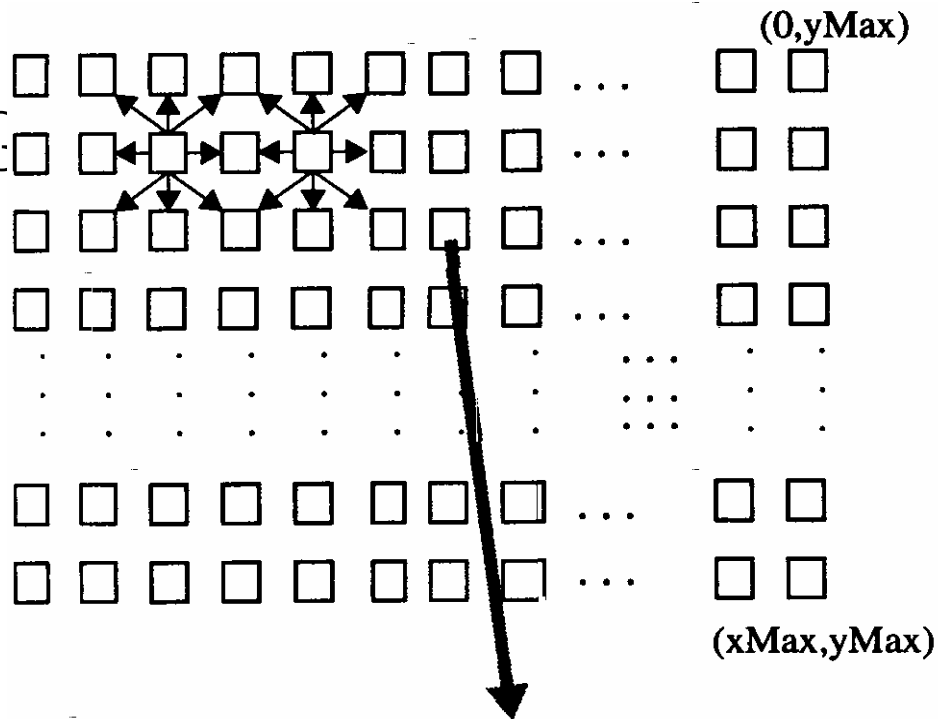
# Cellular GAs (fgpGA)



# Cellular GAs (fgpGA)



# Cellular C



**SUBPOPULATION (X,Y)**

chrom.subpop. $(x+1,y)$	chrom.subpop. $(x,y+1)$
chrom.subpop. $(x+1,y-1)$	chrom.subpop. $(x+1,y+1)$
chrom.subpop. $(x-1,y-1)$	chrom.subpop. $(x,y-1)$
chrom.subpop. $(x-1,y)$	chrom.subpop. $(x,y)$
chrom.subpop. $(x-1,y+1)$	chrom.subpop. $(x,y)$

Figure 2: Each subpopulation contributes one of its two chromosomes to each of its 8 nearest neighbors. The composition of subpopulation  $(x,y)$  is shown. Both of the chromosomes evolved at subpopulation  $(x,y)$  are included. The subpopulations form a toroid.