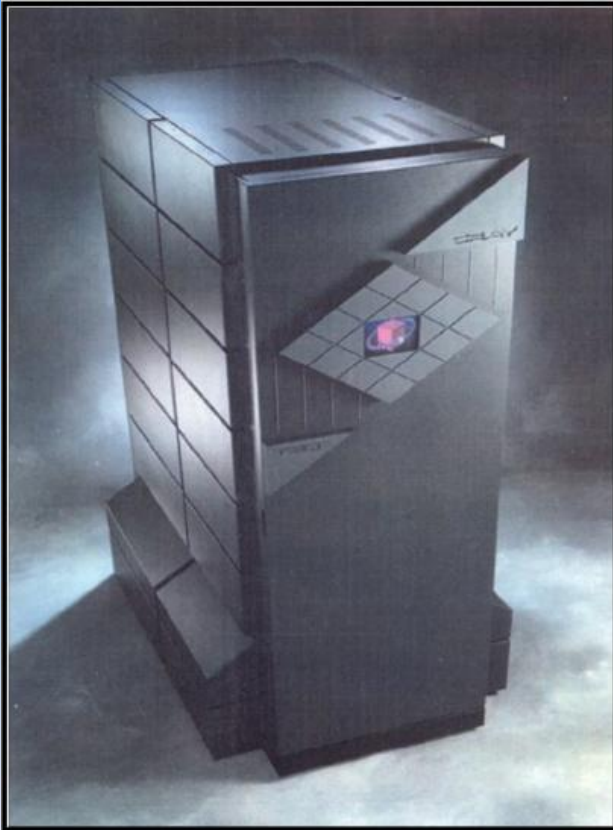


# Genetic Algorithms

# What Do the Following 3 Things Have in Common?



# Genetic Algorithms (GAs)

- GAs design jet engines.
- GAs draw criminals.
- GAs program computers.

# A Potpourri of Applications

1. General Electric's *EnGeneous* (generalized engineering optimization).
2. Face space (criminology).
3. Genetic programming (machine learning).

# Gas Turbine Design

## Jet engine design at General Electric (Powell, Tong, & Skolkick, 1989)

- Coarse optimization - 100 design variables.
- Hybrid GA + numerical optimization + expert system.
- Found **2%** increase in efficiency.
- Spending \$250K to test in laboratory.
- Boeing 777 design based on these results.

# Criminal-likeness Reconstruction

No closed form fitness function (Caldwell & Johnston, 1991).

- Human witness chooses faces that match best.
- GA creates new faces from which to choose.



# What are GAs?

- GAs are biologically inspired class of algorithms that can be applied to, among other things, the **optimization of nonlinear multimodal functions**.
- Solves problems in the same way that nature solves the problem of adapting living organisms to the harsh realities of life in a hostile world: **evolution**.

# What is a Genetic Algorithm (GA)?

A GA is an adaptation procedure based on the mechanics of natural selection and genetics.

GAs have 2 essential components:

1. Survival of the fittest (selection)
2. Variation

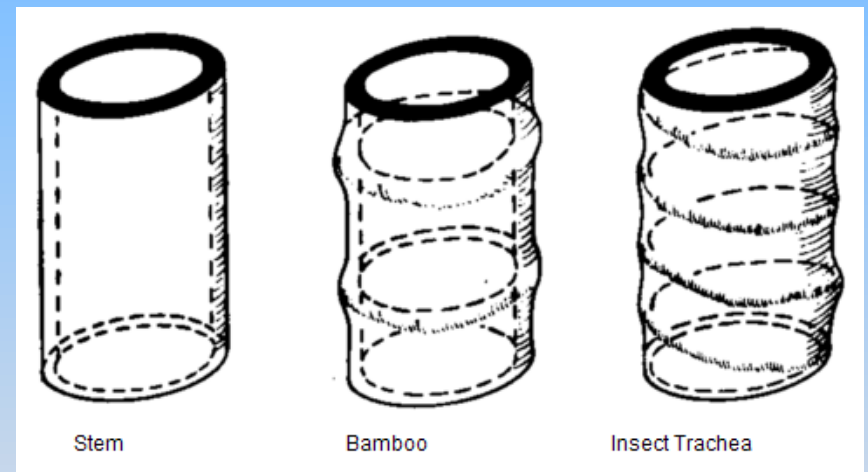


# Nature as Problem Solver

Beauty-of-nature  
argument

*How Life Learned to  
Live* (Tributsch, 1982,  
MIT Press)

**Example:** Nature as  
structural engineer



# Owl Butterfly



# Evolutionary is Revolutionary!

Street distinction evolutionary vs. revolutionary is false dichotomy.

3.5 Billion years of evolution can't be wrong.  
Complexity achieved in *short* time in nature.

Can we solve complex problems as quickly and reliably on a computer?

# Why Bother?

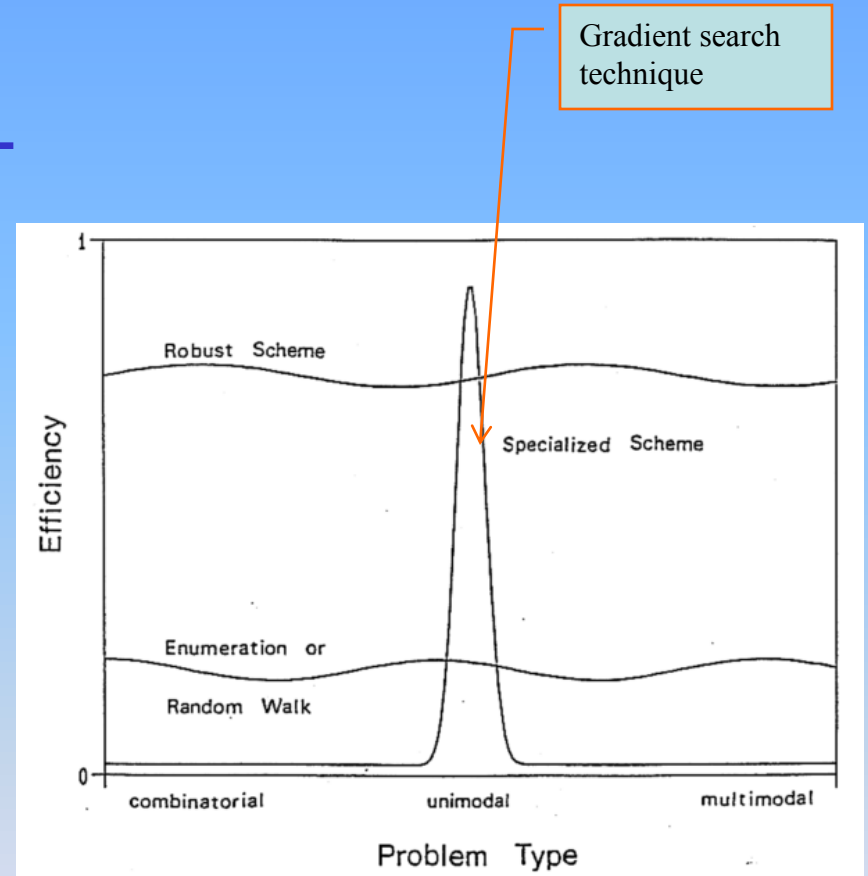
Lots of ways to solve problems:

- Calculus
- Hill-climbing
- Enumeration
- Operations research: linear, quadratic, nonlinear programming

Why bother with biology?

**Robustness** = Breadth + Efficiency.

A hypothetical  
problem  
spectrum:



# GAs Not New

**John Holland** at **University of Michigan**  
pioneered in the 50s.

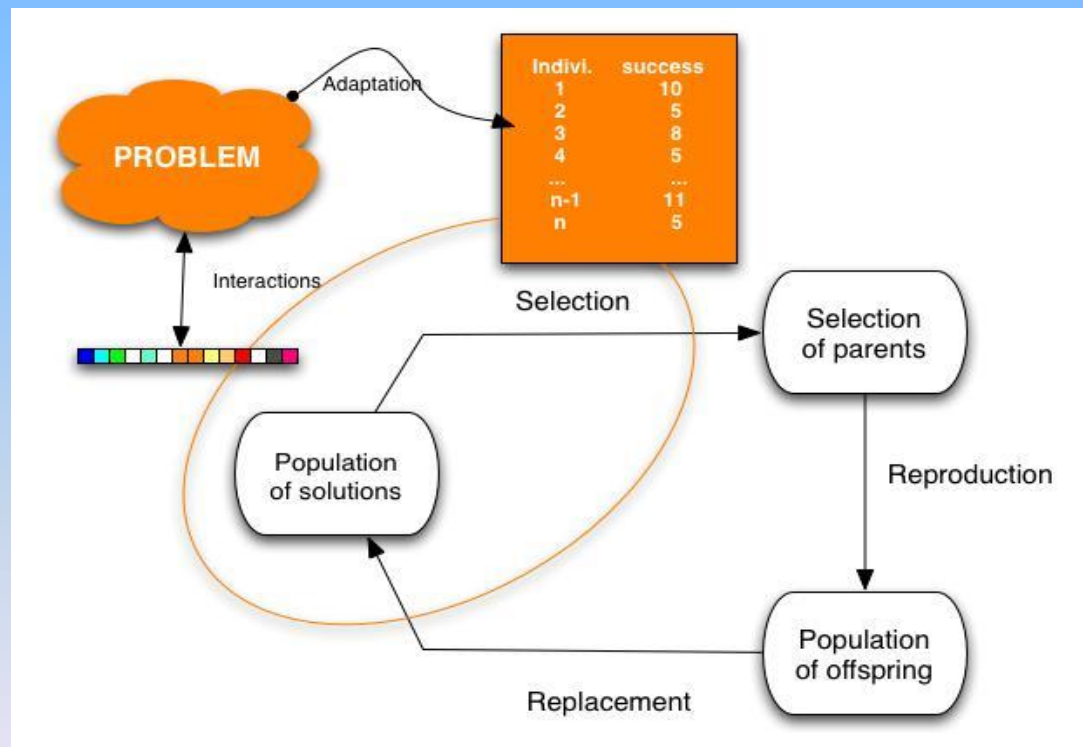
Other evolutionaries: Fogel, Rechenberg,  
Schwefel.

Back to the cybernetics movement and early  
computers.

Reborn in the 70s.

# Genetic algorithms

Variant of local beam search with *sexual recombination*.



# How GAs are different from traditional methods?

1. GAs work with a **coding of the parameter set**, not the parameter themselves.
2. GAs search from a **population of points**, not a single point.
3. GAs use payoff (**objective function**) information, not derivatives or other auxilliary knowledge.
4. GAs use **probabilistic transition rules**, not deterministic rules.



# Genetic Algorithm

## GAs APPROACH TO THE PROBLEM

Natural parameter set of the optimisation problem is represented as a finite-length string

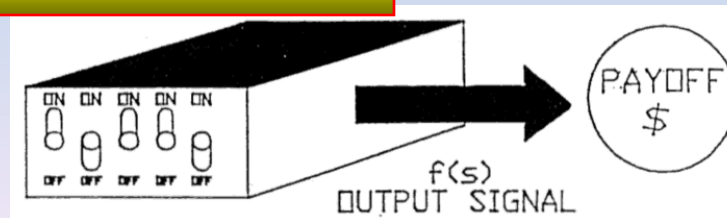
**Problem: Maximise the function  $f(x) = x^2$  on the integer interval  $[0, 31]$**

Traditional approach: twiddle with parameter  $x$

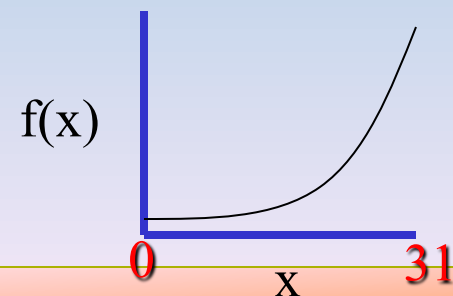
$$f = f(s)$$

Setting of five switches

output



GA doesn't need to know the workings of the black box.



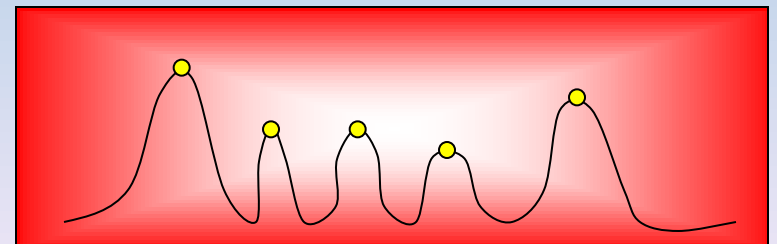
# Main Attractions of Genetic Algorithm

## GA

- Simplicity of operation and power of effect
- **unconstrained**
- work from a rich database of points **simultaneously**, climbing many peaks in parallel
- population of strings = points
- **Population of well-adapted diversity**

## Traditional Optimization Approaches

- Limitations: continuity, derivative existence, unimodality
- move gingerly from a single point in the decision space to the next using some transition rule



# Initial Population

# Genetic Algorithm

## GA

- **Initial Step:** random start using successive coin flips

GA uses coding

01101  
11000  
01000  
10011

population

- blind to auxiliary information

GAs are blind, **only payoff values** associated with individual strings are required

- Searches from a population

Uses probabilistic transition rules to guide their search towards regions of the search space with likely improvement

# Reproduction

# Genetic Algorithm

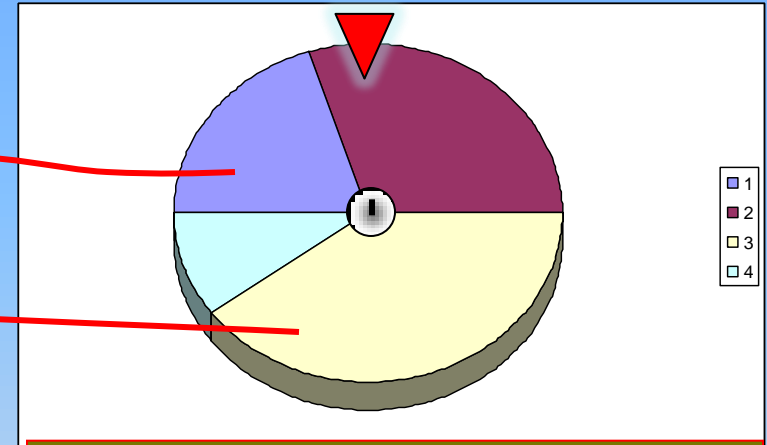
## REPRODUCTION

- **Selection** according to *fitness*

GA uses coding

01101  
11000  
01000  
10011

population



Weighted Roulette wheel

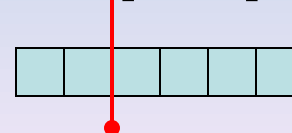
- **Replication**

Mating pool (tentative population)

## CROSSOVER

- **Crossover** – randomized information exchange

Crossover point  $k = [1, \ell-1]$



GA builds solutions from the past partial solutions of the previous trials

# Mutation

# Genetic Algorithm

## MUTATION

- **Reproduction and crossover** may become overzealous and lose some potentially useful genetic material
- **Mutation** protects against irrecoverable loss; it serves as an insurance policy against premature loss of important notions
- **Mutation rates:** in the order of **1 mutation per a thousand bit position transfers**



# Sample Problem

# Genetic Algorithm

## SAMPLE PROBLEM

- **Maximize  $f(x) = x^2$ ; where  $x$  is permitted to vary between 0 and 31**

### 1. Coding of decision variables as some finite length string

$X$  as binary unsigned integer of length 5

$[0, 31] = [00000, 11111]$

### 2. Constant settings

$P_{\text{mutation}} = 0.0333$

$P_{\text{cross}} = 0.6$

Population Size=30

DeJong(1975) suggests high crossover Probability, low mutation probability (inversely proportional to the pop.size), and A moderate population size

# Genetic Algorithm

## SAMPLE PROBLEM

- **Maximize  $f(x) = x^2$ ; where  $x$  is permitted to vary between 0 and 31**

**3. Select initial population at random** (use even numbered population size)

| String number | Initial Population | X value | $f(x)$ | pselect $\frac{f_i}{\sum f}$ | Expected count $\frac{f_i}{\bar{f}}$ | Actual count (Roulette Wheel) |
|---------------|--------------------|---------|--------|------------------------------|--------------------------------------|-------------------------------|
| 1             | 01101              | 13      | 169    | 0.14                         | 0.58                                 | 1                             |
| 2             | 11000              | 24      | 576    | 0.49                         | 1.97                                 | 2                             |
| 3             | 01000              | 8       | 64     | 0.06                         | 0.22                                 | 0                             |
| 4             | 10011              | 19      | 361    | 0.31                         | 1.23                                 | 1                             |

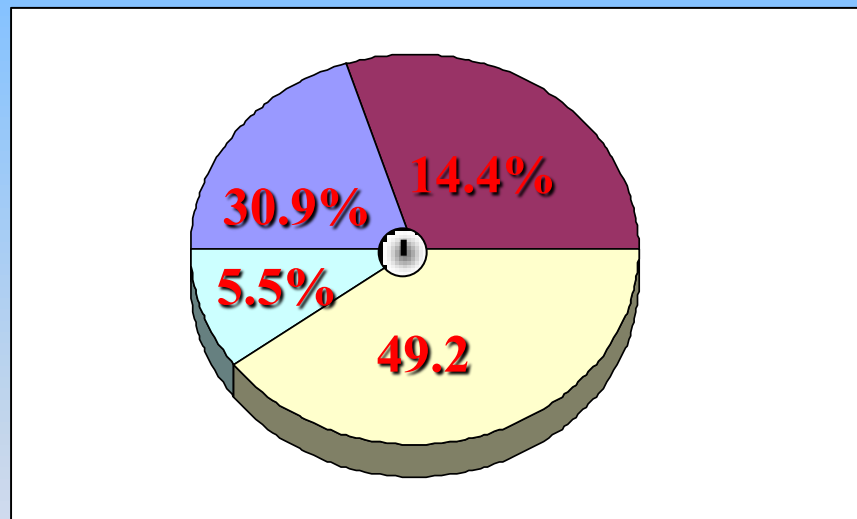
|      |      |
|------|------|
| Sum  | 1170 |
| Ave. | 293  |
| Max. | 576  |

# Genetic Algorithm

## SAMPLE PROBLEM

- **Maximize  $f(x) = x^2$ ; where  $x$  is permitted to vary between 0 and 31**

4. **Reproduction:** select mating pool by spinning roulette wheel 4 times.



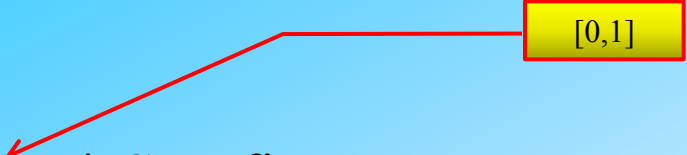
Weighted Roulette wheel

|       | <i>pselect</i> |
|-------|----------------|
| 01101 | 0.14           |
| 11000 | 0.49           |
| 01000 | 0.06           |
| 10011 | 0.31           |

The best get more copies.  
The average stay even.  
The worst die off.

# Choosing offspring for the next generation

```
int Select(int Popsiz, double Sumfitness, Population Pop){  
    partSum = 0  
  
    rand = Random * Sumfitness  
    j=0  
    Repeat  
        j++;  
        partSum = partSum + Pop[j].fitness  
    Until (partSum >= rand) or (j = Popsiz)  
  
    Return j  
}
```



A red arrow points from a yellow box containing the text "[0,1]" to the word "Random" in the code line "rand = **Random** \* Sumfitness".

# Genetic Algorithm

## SAMPLE PROBLEM

**5. Crossover** – strings are mated randomly using coin tosses to pair the couples

- mated string couples crossover using coin tosses to select the crossing site

| String number | Mating Pool after Reproduction | Mate (randomly selected) | Crossover site (random) | New population | X-value | $f(x)=x^2$ |
|---------------|--------------------------------|--------------------------|-------------------------|----------------|---------|------------|
| 1             | 0110 1                         | 2                        | 4                       | 01100          | 12      | 144        |
| 2             | 1100 0                         | 1                        | 4                       | 11001          | 25      | 625        |
| 3             | 11 000                         | 4                        | 2                       | 11011          | 27      | 729        |
| 4             | 10 011                         | 3                        | 2                       | 10000          | 16      | 256        |

# Algorithmic Steps

# The Genetic Algorithm

1. **Initialize** the algorithm.

**Randomly** initialize each **individual chromosome** in the population of size **N** (N must be **even**), and compute each individual's **fitness**.



# The Genetic Algorithm

1. Initialize the algorithm. Randomly initialize each individual chromosome in the population of size  $N$  ( $N$  must be even), and compute each individual's fitness.
2. **Select  $N/2$  pairs** of individuals for **crossover**. The probability that an individual will be selected for crossover is **proportional** to its **fitness**.

# The Genetic Algorithm

1. Initialize the algorithm. Randomly initialize each individual chromosome in the population of size  $N$  ( $N$  must be even), and compute each individual's fitness.
2. Select  $N/2$  pairs of individuals for crossover. The probability that an individual will be selected for crossover is proportional to its fitness.
3. **Perform crossover operation** on  **$N/2$  pairs** selected in Step1.  
**Randomly mutate bits** with a **small probability** during this operation.

# The Genetic Algorithm

1. Initialize the algorithm. Randomly initialize each individual chromosome in the population of size  $N$  ( $N$  must be even), and compute each individual's fitness.
2. Select  $N/2$  pairs of individuals for crossover. The probability that an individual will be selected for crossover is proportional to its fitness.
3. Perform crossover operation on  $N/2$  pairs selected in Step1. Randomly mutate bits with a small probability during this operation.
4. **Compute fitness** of **all** individuals in new population.

# The Genetic Algorithm

## 5. (Optional Optimization)

**Select  $N$  fittest individuals** from combined population of size  $2N$  consisting of **old** and **new populations** pooled together.

# The Genetic Algorithm

5. (Optional Optimization) Select  $N$  fittest individuals from combined population of size  $2N$  consisting of old and new populations pooled together.
6. (Optional Optimization)  
Rescale **fitness** of population.

# The Genetic Algorithm

5. (Optional Optimization) Select N fittest individuals from combined population of size  $2N$  consisting of old and new populations pooled together.
6. (Optional Optimization) Rescale fitness of population.
7. **Determine maximum fitness of individuals in the population.**

**If**  $|\text{max fitness} - \text{optimum fitness}| < \text{tolerance}$  **Then**  
**Stop**

**Else**

Go to Step1.

# A Simple GA Example

Let's see a demonstration for a **GA** that maximizes the function

$$f(x) = \left( \frac{x}{c} \right)^n$$


$$\mathbf{n} = 10$$

$$\mathbf{c} = 2^{30} - 1 = 1,073,741,823$$



# Simple GA Example

Function to evaluate:

$$f(x) = \left( \frac{x}{coeff} \right)^{10}$$


**Fitness Function  
or Objective  
Function**

*coeff* – chosen to normalize the *x* parameter when a bit string of length *lchrom* = 30 is chosen.

$$coeff = 2^{30} - 1$$

When the *x* value is normalized, the max. value of the function will be:

$$f(x) = 1.0$$

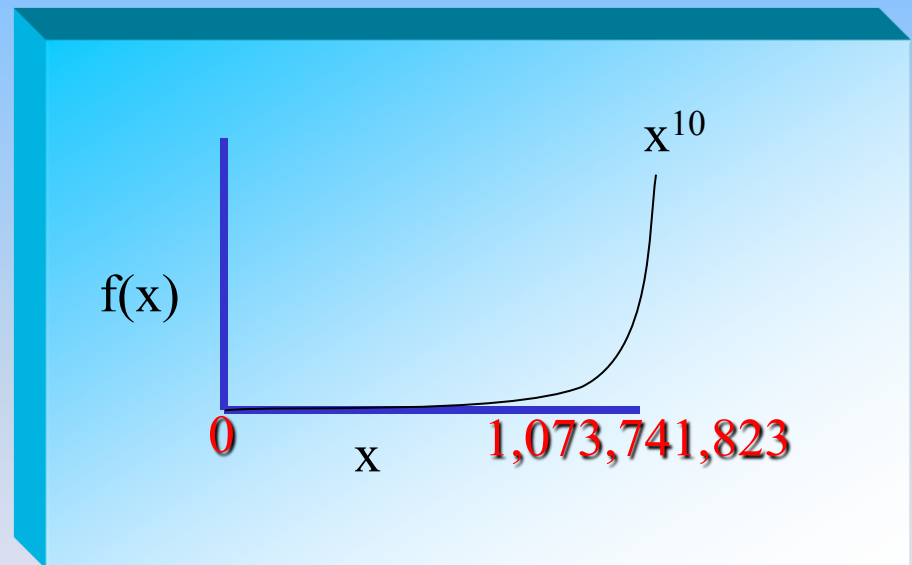
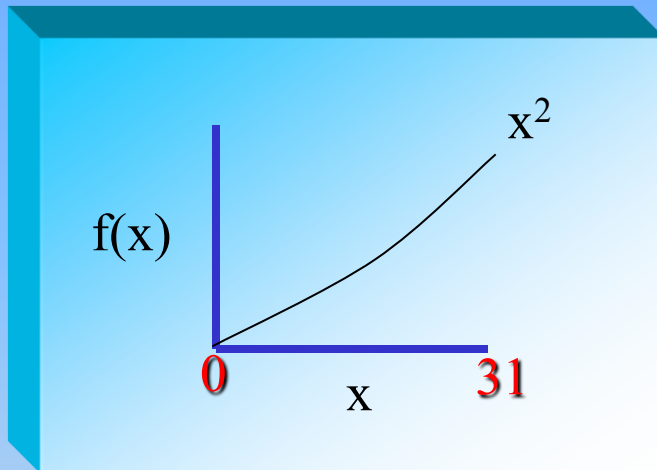
This happens when  $x = 2^{30} - 1$  for the case when *lchrom* = 30

# Test Problem Characteristics

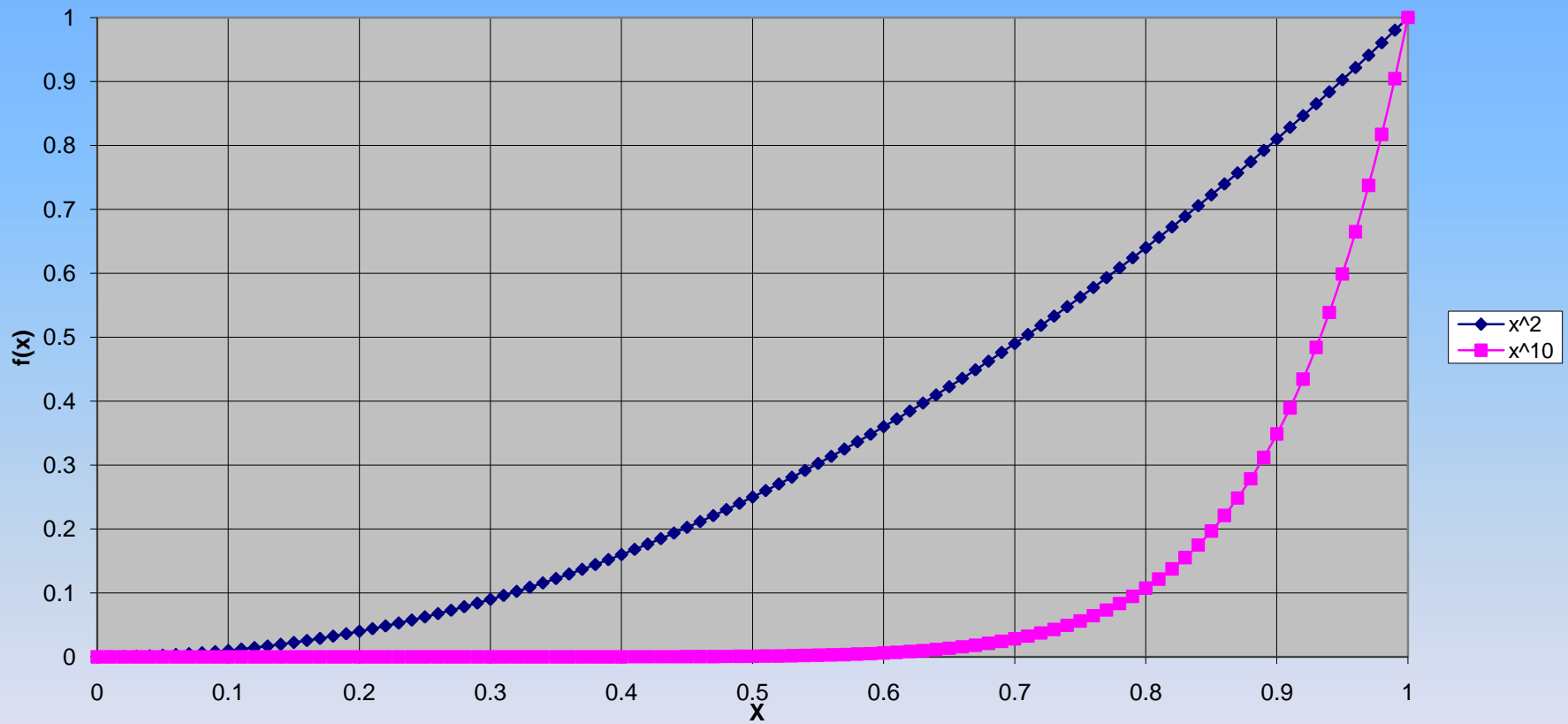
With a string length=**30**, the search space is much larger, and random walk or enumeration should not be so profitable.

There are  **$2^{30}=1.07(10^{10})$  points**. With over 1.07 billion points in the space, one-at-a-time methods are unlikely to do very much very quickly. Also, only **1.05** percent of the points have a value greater than **0.9**.

# Comparison of the functions on the unit interval

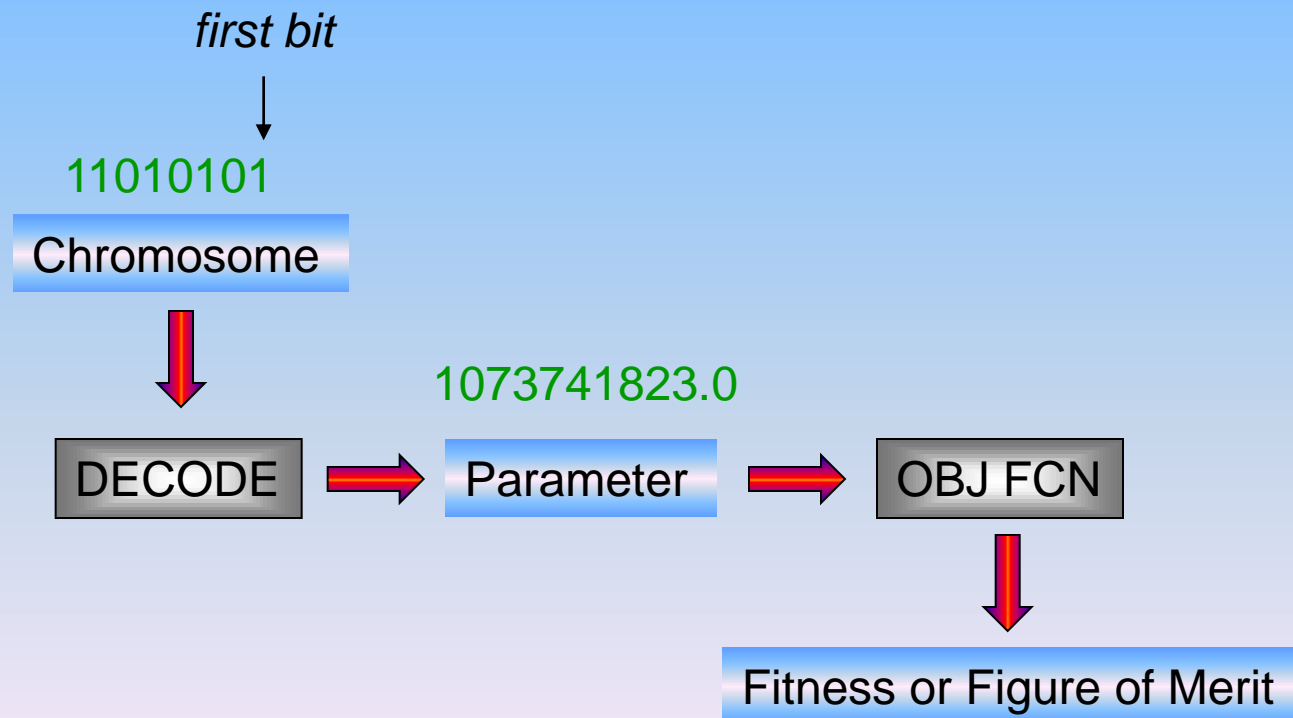


# Actual Plot



# Decoding a String

For every problem, we must create a procedure that decodes a string to create a parameter (or set of parameters) appropriate for that problem.



# GA Parameters

A series of parametric studies [De Jong, 1975] across a five function suite of optimization problems suggested that good GA performance requires the choice of:

- High crossover probability
- Low mutation probability (inversely proportional to the population size)
- Moderate Population Size

**(e.g.  $p_{\text{mutation}}=0.0333$ ,  $p_{\text{cross}}=0.6$ ,  $p_{\text{popsize}}=30$ )**

# Limits of GA

- GAs are characterized by a **voracious appetite** for **processing power** and **storage capacity**.
- GAs have **no convergence guarantees** in arbitrary problems.

# Limits of GAs

- **GAs** sort out interesting areas of a space **quickly**, but they are a **weak method**, without the guarantees of more convergent procedures.
- This does not reduce their utility however. More convergent methods sacrifice **globality** and **flexibility** for their convergence, and are limited to a narrow class of problem.
- GAs can be used where more convergent methods dare not tread.



# Advantages of GAs

- Well-suited to a **wide-class of problems**
- Do not rely on the **analytical properties** of the function to be optimized (such as the existence of a derivative)

# Advanced GA Architectures

## **GA + Any Local Convergent Method**

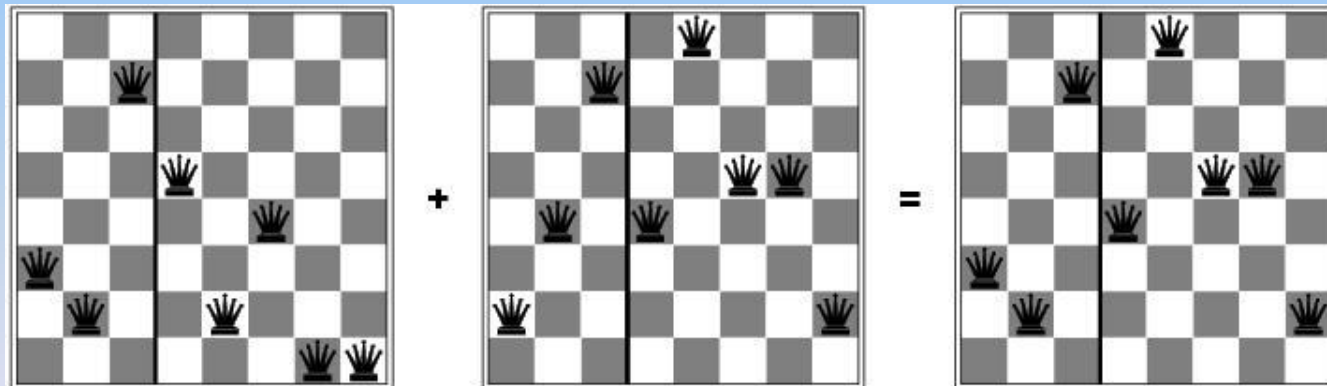
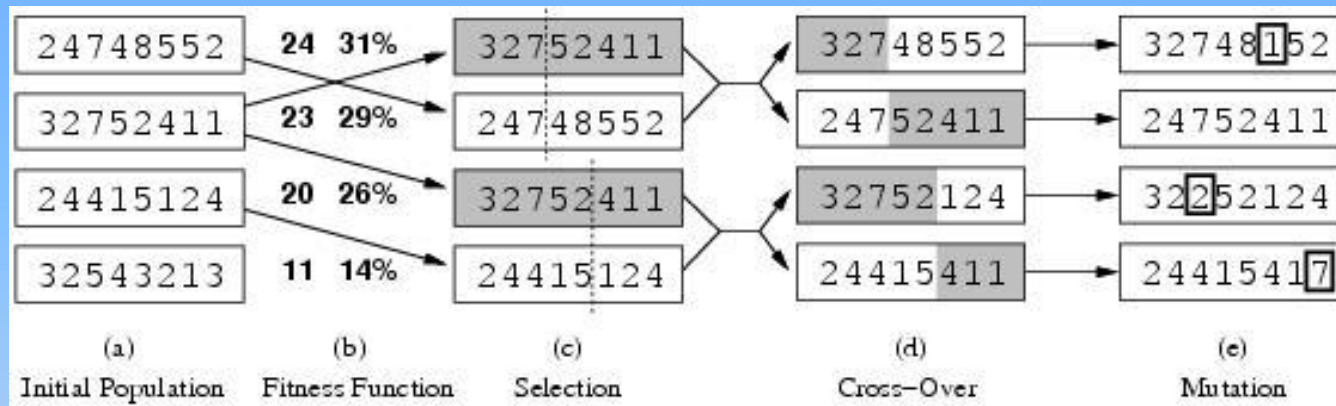
- **Start search using GA** to sort out the interesting hills in your problem. Once GA ferrets out the best regions, **apply locally convergent scheme** to climb the local peaks.

# Other Applications

Optimization of a choice of Fuzzy Logic parameters

# Genetic algorithms

Variant of local beam search with *sexual recombination*.

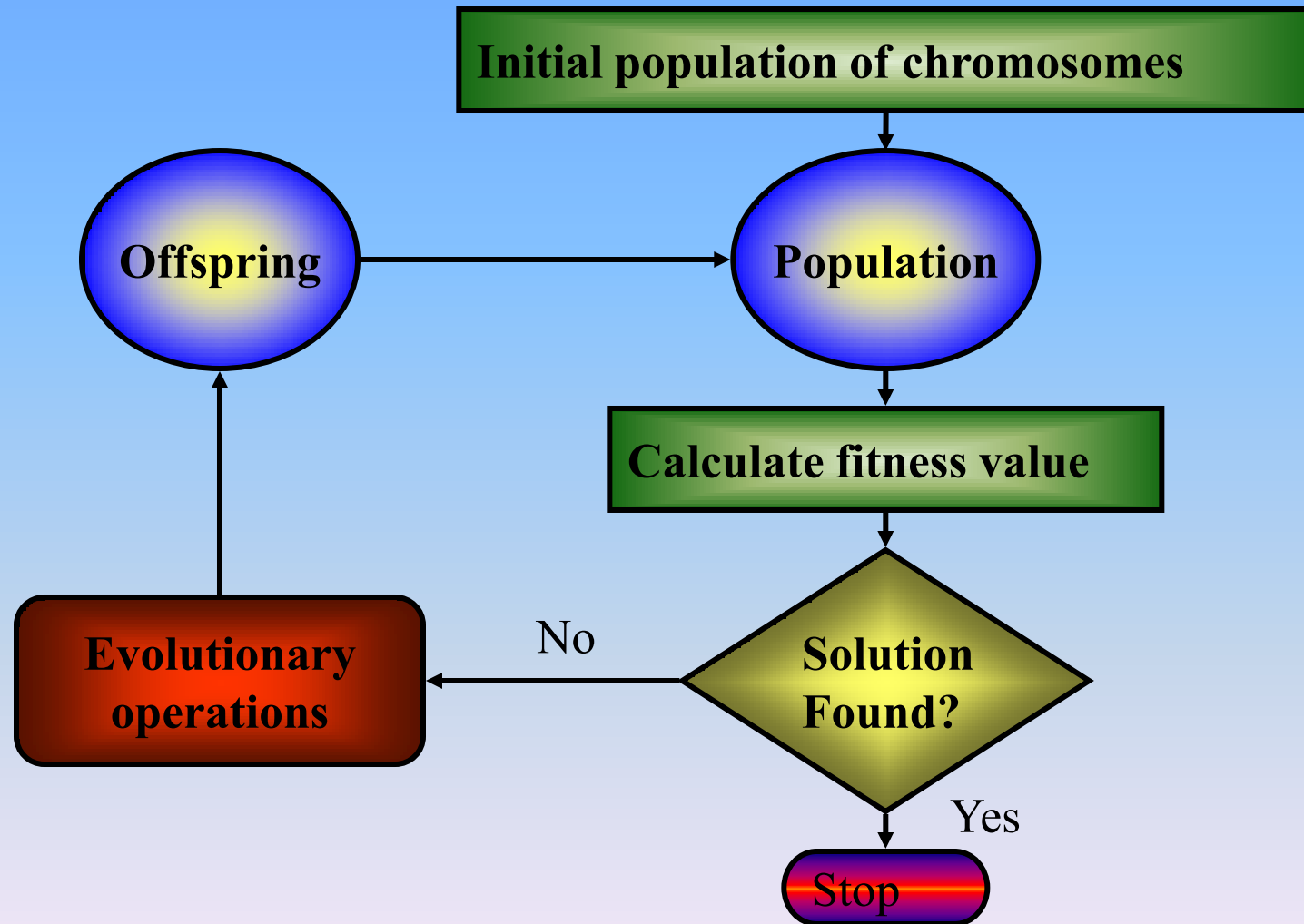


**Fitness function**: number of non-attacking pairs of queens (min = 0, max =  $8 \times 7/2 = 28$ );

$$24/(24+23+20+11) = 31\%$$

$$23/(24+23+20+11) = 29\% \text{ etc}$$

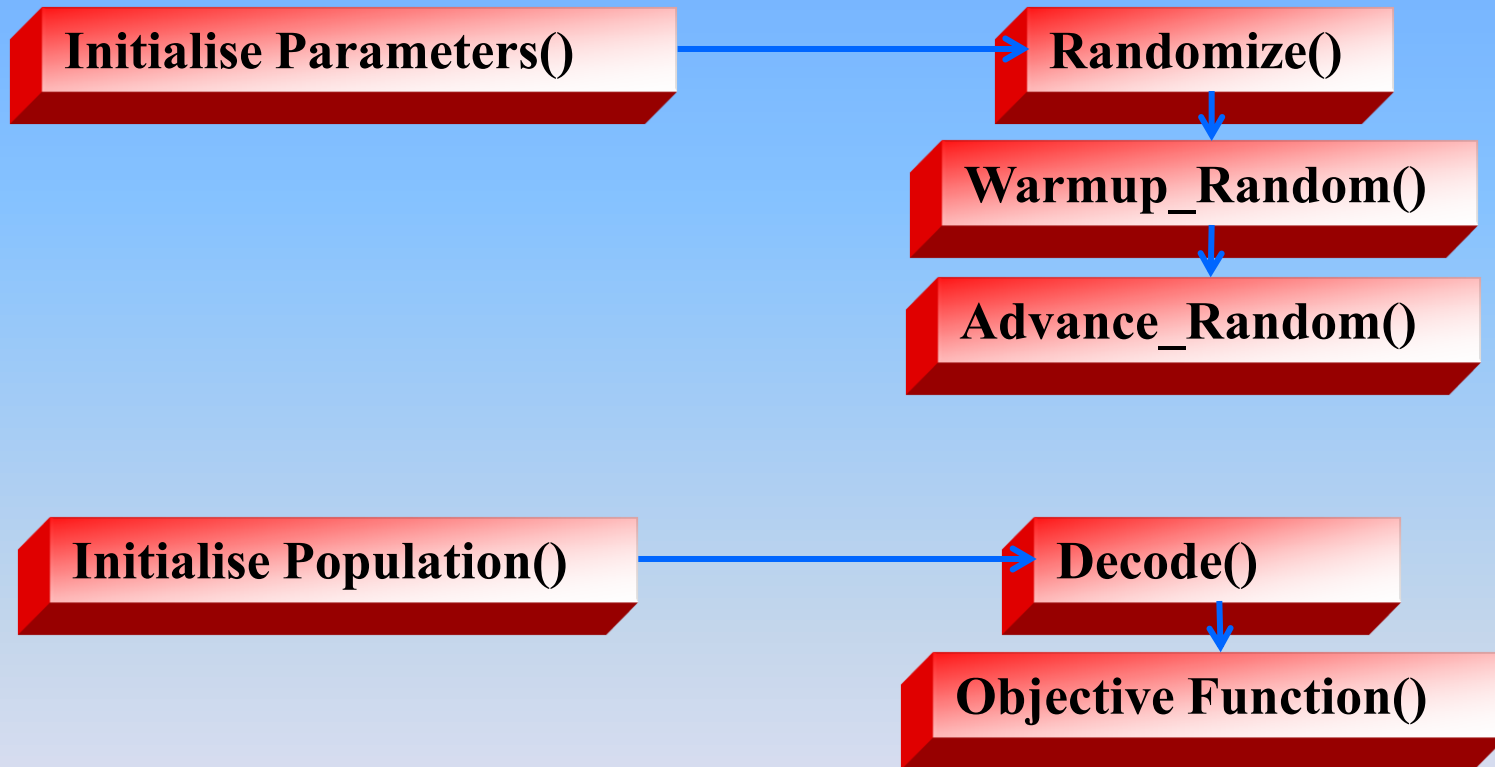
# Simple GA Implementation



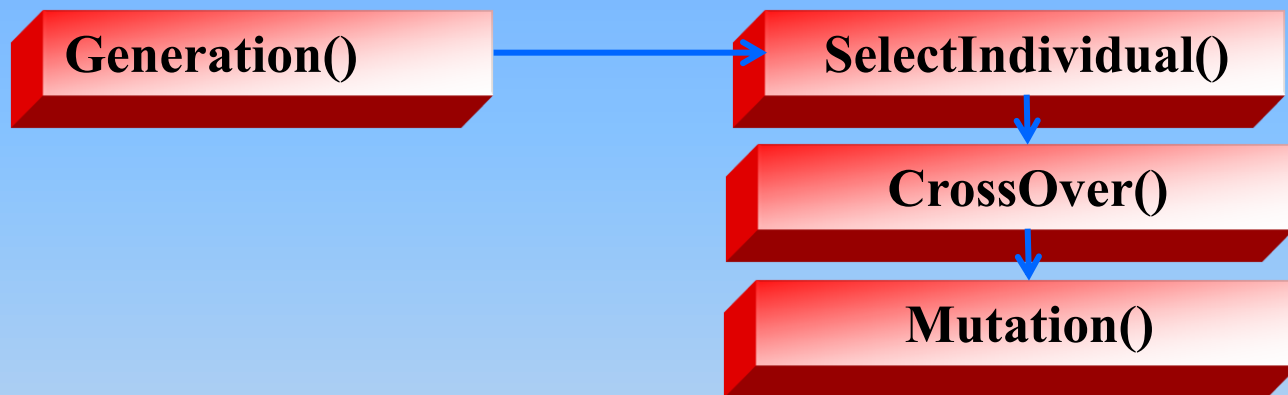
# Implementation

Based on **SGA-C**, A C-language Implementation of a Simple Genetic Algorithm

# Phase 1 – General Initialisation



# Phase 2 – Generation of Chromosomes





# Running the GA System

Gen = 0

Initialize( OldPop )

**Do**

Gen = Gen + 1

**Generation**( OldPop, NewPop )

For ii = 1 To PopSize

OldPop(ii) = NewPop(ii) 'advance the generation

Next ii

**Loop Until** ( (Gen > MaxGen) or (MaxFitness > DesiredFitness) )

# Initialisation

## Initialise Parameters

PopSize = 30      'population size  
lchrom = 30      'chromosome length  
MaxGen = 10  
PCross = 0.6  
PMutation = 0.0333

ReDim GenStat(1 To (MaxGen + 1))

'Initialize random number generator  
**Randomize**

'Initialize counters  
NMutation = 0  
NCross = 0

# Randomization

## Randomize

```
Sub Randomize()  
  Randomize Timer  
  Warmup_Random (Rnd * 1)  
End Sub
```

[0,1]



# Randomization

## Warmup\_Random()

Sub **Warmup\_Random**(RandomSeed As Single)

Dim j1 As Integer

Dim ii As Integer

Dim NewRandom As Single

Dim PrevRandom As Single

OldRand(55) = RandomSeed

NewRandom = 0.000000001

PrevRandom = RandomSeed

**For j1 = 1 To 54**

ii = (21 \* j1) Mod 55 'multiply first, before modulus

OldRand(ii) = NewRandom

NewRandom = PrevRandom - NewRandom

If (NewRandom < 0) Then NewRandom = NewRandom + 1

PrevRandom = OldRand(ii)

**Next j1**

Advance\_Random

Advance\_Random

Advance\_Random

jrand = 0

End Sub

[0, 1]

[0, 1]

# Randomization

## Advance\_Random()

Sub **Advance\_Random()**

Dim j1 As Integer

Dim New\_Random As Single

**For j1 = 1 To 24**

New\_Random = OldRand(j1) - OldRand(j1 + 31)

If (New\_Random < 0) Then New\_Random = New\_Random + 1

OldRand(j1) = New\_Random

**Next j1**

Max:  $24+31=55$

**For j1 = 25 To 55**

New\_Random = OldRand(j1) - OldRand(j1 - 24)

If (New\_Random < 0) Then New\_Random = New\_Random + 1

OldRand(j1) = New\_Random

**Next j1**

End Sub

Max:  $55-24=31$

# Random

'Fetch a single random number between 0.0 and 1.0 -  
Subtractive Method

'See Knuth, D. (1969), v. 2 for details

Function **Random()** As Single

    jrand = jrand + 1

    If jrand > 55 Then

        jrand = 1

        Advance\_Random

    End If

    Random = **OldRand**(jrand)

End Function

# Initialise Population

## InitPop()

Sub **InitPop()**

Dim j As Integer

Dim j1 As Integer

**For j = 1 To PopSize**

With OldPop(j)

For j1 = 1 To Ichrom

.Chromosome(j1) = Flip(0.5)

Next j1

.x = Decode(.Chromosome, Ichrom) **'decode the string**

.Fitness = ObjFunc(.x) **'evaluate initial fitness**

.Parent1 = 0

.Parent2 = 0

.XSite = 0

End With

**Next j**

End Sub

Max: 24+31=55

# Initialise Population

## Decode()

- 'decodes the string to create a parameter or set of parameters
- 'appropriate for that problem
- 'Decode string as unsigned binary integer: true=1, false=0

```
Function Decode(Chrom() As Boolean, lbits As Integer) As Single
    Dim j As Integer
    Dim Accum As Single
    Dim PowerOf2 As Single

    Accum = 0
    PowerOf2 = 1
    For j = 1 To lbits
        If Chrom(j) Then Accum = Accum + PowerOf2
        PowerOf2 = PowerOf2 * 2
    Next j
    Decode = Accum
End Function
```



# Initialise Population

## Objective Function()

'Fitness function =  $f(x) = (x/c)^n$

Function **ObjFunc**(x As Single) As Single 'coef =  $(2^{30})-1 = 1073741823$

'coef is chosen to normalize the x parameter when a bit string of length lchrom=30 is chosen

'since the x value has been normalized, the maximum value of the fcn will be  $f(x)=1$ ,  
'when  $x=(2^{30})-1$ , for the case when lchrom=30

Const coef As Single = 1073741823 'coefficient to normalize domain

Const n As Single = 10 'power of x

**ObjFunc** =  $(x / \text{coef})^n$

End Function

# Generation of Chromosomes

## SelectIndividual()

Function **SelectIndividual**(PopSize As Integer, SumFitness As Single, Pop() As IndividualType) As Integer

Dim RandPoint As Single

Dim PartSum As Single

Dim j As Integer

PartSum = 0

j = 0

RandPoint = Random \* SumFitness

Do **'find wheel slot**

j = j + 1

PartSum = PartSum + **Pop**(j).Fitness

**Loop Until** ((PartSum >= RandPoint) Or (j = PopSize))

SelectIndividual = j

End Function

Select a single individual or offspring for the next generation via roulette wheel selection

# Generation of Chromosomes

Function **CrossOver**(Parent1() As Boolean, Parent2() As Boolean, **Child1() As Boolean**, **Child2() As Boolean**,  
 lchrom As Integer, NCross As Integer, NMutation As Integer, jcross As Integer, PCross, PMutation As Single)

Dim j As Integer

If (Flip(PCross)) Then

    jcross = Rndx(1, lchrom - 1) 'cross-over site is selected between 1 and the last cross site

    NCross = NCross + 1

Else ' use full-length string l, and so a bit-by-bit mutation will take place despite the absence of a cross

    jcross = lchrom

End If

For j = 1 To jcross ' 1st exchange, 1 to 1 and 2 to 2

    Child1(j) = Mutation(Parent1(j), PMutation, NMutation)

    Child2(j) = Mutation(Parent2(j), PMutation, NMutation)

Next j

If jcross <> lchrom Then ' 2nd exchange, 1 to 2 and 2 to 1

    For j = jcross + 1 To lchrom

        Child1(j) = Mutation(Parent2(j), PMutation, NMutation)

        Child2(j) = Mutation(Parent1(j), PMutation, NMutation)

    Next j

End If

End Function

**CrossOver** OldPop(Mate1).Chromosome, OldPop(Mate2).Chromosome, \_  
                     **NewPop(j).Chromosome**, **NewPop(j + 1).Chromosome**, \_  
                     lchrom, NCross, NMutation, jcross, PCross, PMutation

# Generation of Chromosomes

## Mutation()

'Mutate an allele with PMutation, count number of mutations

Function **Mutation**(Alleleval As Boolean, PMutation As Single, NMutation As Integer)  
As Boolean

Dim Mutate As Boolean

Mutate = **Flip**(PMutation)

If Mutate Then

    NMutation = NMutation + 1

    Mutation = Not Alleleval

Else

    Mutation = Alleleval

End If

End Function

Function **Flip**(Probability As Single) As  
Boolean

    If Probability = 1 Then

        Flip = True

    Else

        Flip = (Rnd <= Probability)

    End If

End Function

# Generation of Chromosomes

## Generation()

Sub **Generation()**

Dim j As Integer  
Dim Mate1 As Integer  
Dim Mate2 As Integer  
Dim jcross As Integer

j = 1  
Do

**'Pick a pair of mates**

Mate1 = **SelectIndividual**(PopSize, SumFitness, OldPop)  
Mate2 = **SelectIndividual**(PopSize, SumFitness, OldPop)

**'Crossover and mutation - mutation embedded within crossover**

**CrossOver** OldPop(Mate1).Chromosome, OldPop(Mate2).Chromosome, \_  
NewPop(j).Chromosome, NewPop(j + 1).Chromosome, \_  
Ichrom, NCross, NMutation, jcross, PCross, PMutation

**'Decode string, evaluate fitness & record parentage data on both children**

With **NewPop(j)**

.x = Decode(.Chromosome, Ichrom)  
.Fitness = ObjFunc(.x)  
.Parent1 = Mate1  
.Parent2 = Mate2  
.XSite = jcross

End With

With **NewPop(j + 1)**

.x = Decode(.Chromosome, Ichrom)  
.Fitness = ObjFunc(.x)  
.Parent1 = Mate1  
.Parent2 = Mate2  
.XSite = jcross

End With

**j = j + 2** 'increment population index

Loop Until (j > PopSize)  
End Sub

# Why use Fitness Scaling?

**At the start of the GA run**, it is common to have a few extraordinary individuals in a population of mediocre colleagues.

If left to the selection rule

$$p_{\text{select}_i} = \frac{f_i}{\sum f}$$

the extraordinary individuals would take over a significant proportion of the finite population in a single generation.

This is undesirable, leading to a premature convergence!

# Why use Fitness Scaling?

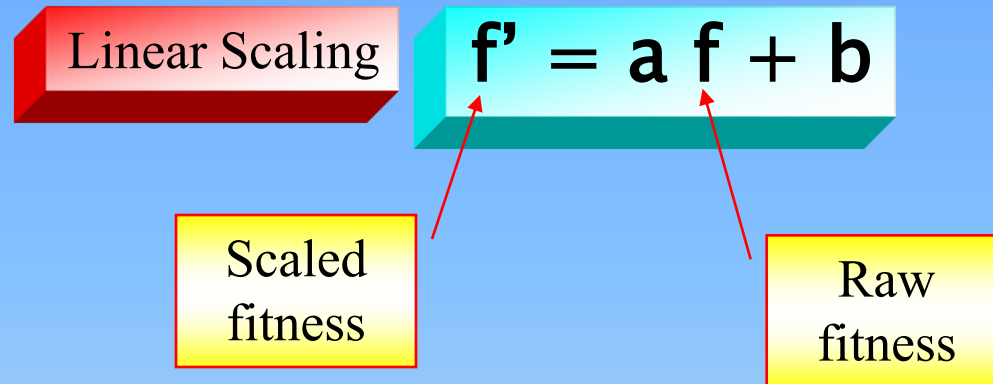
**Late in the run**, there may still be significant diversity within the population. However, the population's **average fitness** may be close to the population's **best fitness**.

If this is left alone,

- **average members** get nearly the same number of copies in future generations, and
- the survival of the fittest necessary for improvement becomes a **random walk** among the **mediocre**.

In both cases, at the beginning of the run, and as the run matures, **fitness scaling** can help.

# Why use Fitness Scaling?



In all cases, we want  $f'_{ave} = f_{ave}$  because subsequent use of the selection procedure will insure that each average population member contributes one expected offspring to the next generation.



# Why use Fitness Scaling?

To control the number of offspring given to the population **member with the maximum raw fitness**, we choose the other scaling relationship to obtain a **scaled maximum fitness**.

Scaled Maximum Fitness:

$$f'_{\max} = c_{\text{mult}} * f_{\text{ave}}$$

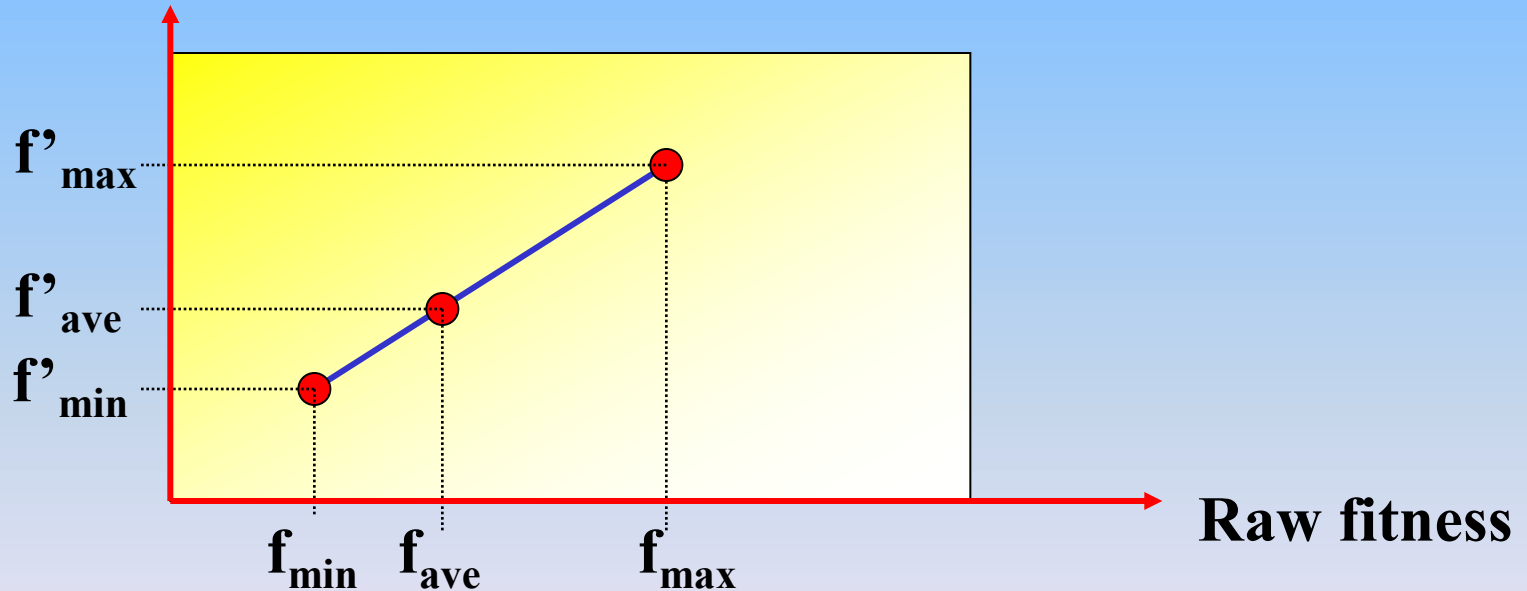
For a typical population size of  $n = 50$  to  $100$ ,  
 $c_{\text{mult}} = [1.2, 2]$  has been used successfully

Number of expected  
copies desired for the  
best population  
member

# Fitness Scaling

## Linear Scaling Under Normal Conditions

Scaled fitness



# Problem with Linear Scaling

Toward the end of a run, the choice of  $C_{\text{mult}}$  stretches the raw fitness values significantly.

This may in turn cause difficulty in applying the linear scaling rule.

The effects of the Linear Scaling rule works during the **initial run** of the GA:

- few extraordinary individuals get scaled down, and
- the lowly members of the population get scaled up

*The problem:* As the run matures, points with low fitness can be scaled to **negative values**!

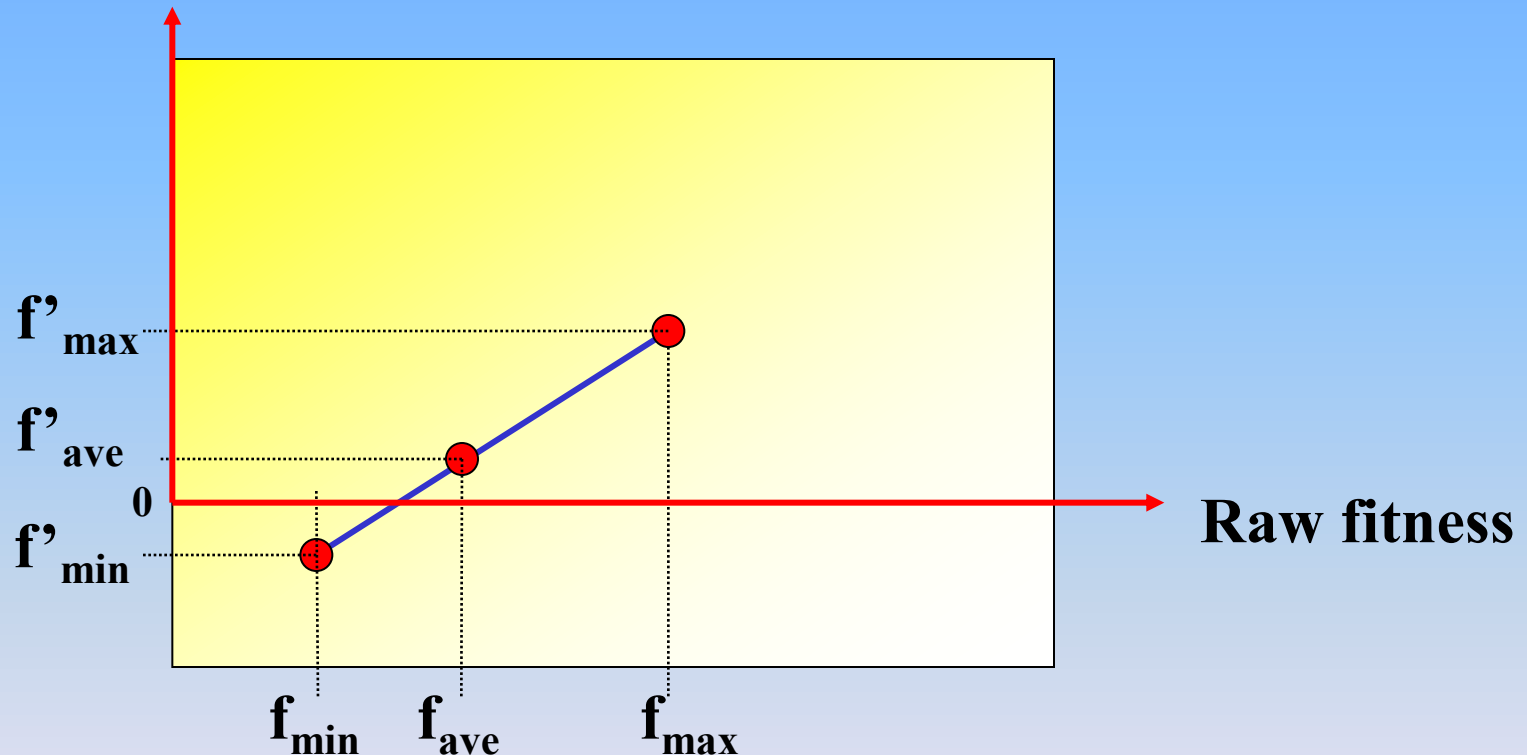
The stretching required on the relatively close average and maximum raw fitness values causes the low fitness values to go **negative** after scaling.

See for yourself, [TestGA2.xls](#)



# Why use Fitness Scaling?

Difficult situation for a linear scaling in mature run



Negative fitness violates  
non-negativity  
requirement!



# Fitness Scaling

**If** it's possible to scale to the desired multiple, **Cmult**

**Then**

Perform linear scaling

**Else**

Scaling is performed by pivoting about the average value and stretching the fitness until the minimum value maps to zero.

# Scaling

## Non-negative test:

```
If( min > (fmultiple*avg - max) / (fmultiple - 1.0) ) {  
    Perform Normal Scaling  
}
```

# Eliminating **negative fitness** values

## Solution:

When we cannot scale to the desired  $c_{mult}$ , we still maintain equality of the raw and scaled **fitness averages** and we map the minimum raw fitness  $f_{min}$  to a scaled fitness  $f'_{min} = 0$ .

## Description of Routines:

**Prescale** – takes the **average**, **maximum** and **minimum** raw fitness values and calculates linear scaling of the coefficients **a** and **b** based on the logic described previously. It takes into account whether the desired  $c_{mult}$  can be reached or not.

**Scalepop** – called after Prescaling is done. It scales all the individual raw fitness values using the function **Scale**.

# Fitness Scaling

```
procedure scalepop(popsiz:integer; var max, avg, min, sumfitness:real;  
    var pop:population);  
{ Scale entire population }  
var j:integer;  
    a, b:real; { slope & intercept for linear equation }  
begin  
    prescale(max, avg, min, a, b); { Get slope and intercept for function }  
    sumfitness := 0.0;  
    for j := 1 to popsiz do with pop[j] do begin  
        fitness := scale(objective, a, b);  
        sumfitness := sumfitness + fitness;  
    end;  
end;
```

```
function scale(u, a, b:real):real;  
{ Scale an objective function value }  
begin scale := a * u + b end;
```



# Fitness Scaling

```
{ scale.sga: contains prescale, scale, scalepop for scaling fitnesses }
```

```
procedure prescale (umax, uavg, umin:real; var a, b:real);
```

```
{ Calculate scaling coefficients for linear scaling }
```

```
const fmultiple = 2.0; { Fitness multiple is 2 }
```

```
var delta:real; { Divisor }
```

```
begin
```

```
if umin > (fmultiple*uavg - umax) / (fmultiple - 1.0) { Non-negative test }
```

```
then begin { Normal Scaling }
```

```
delta := umax - uavg;
```

```
a := (fmultiple - 1.0) * uavg / delta;
```

```
b := uavg * (umax - fmultiple*uavg) / delta;
```

```
end else begin { Scale as much as possible }
```

```
delta := uavg - umin;
```

```
a := uavg / delta;
```

```
b := -umin * uavg / delta;
```

```
end;
```

```
end;
```

**Linear Scaling**

**Stretch fitness until  
Minimum maps to zero.**

Let's try to solve an  
example using a  
stored GA run.



# Why Scaling?

Simple scaling helps prevent the early domination of extraordinary individuals, while it later on encourages a healthy competition among near equals.

# Multiparameter Code

Constructed from concatenated, mapped, fixed point codes

```
procedure extract_parm(var chromfrom, chromto:chromosome;  
                        var jposition, lchrom, lparm:integer);  
{ Extract a substring from a full string }  
var j, jtarget:integer;  
begin  
    j := 1;  
    jtarget := jposition + lparm - 1;  
    if jtarget > lchrom then jtarget := lchrom; { Clamp if excessive }  
    while (jposition <= jtarget) do begin  
        chromto[j] := chromfrom[jposition];  
        jposition := jposition + 1;  
        j := j + 1;  
    end;  
end;
```

# Multiparameter Code

Constructed from concatenated, mapped, fixed point codes

```
procedure decode_parms(var nparms, lchrom:integer;
    var chrom:chromosome;
    var parms:parmspecs);
var j, jposition:integer;
    chromtemp:chromosome; { Temporary string buffer }
begin
    j := 1; { Parameter counter }
    jposition := 1; { String position counter }
    repeat
        with parms[j] do if lparm>0 then begin
            extract_parm(chrom, chromtemp, jposition, lchrom, lparm);
            parameter := map_parm( decode(chromtemp, lparm),
                maxparm, minparm, power(2.0, lparm)-1.0 );
        end else parameter := 0.0;
        j := j + 1;
    until j > nparms;
end;
```

```
function map_parm(x, maxparm, minparm, fullscale:real):real;
{ Map an unsigned binary integer to range [minparm,maxparm] }
begin
    map_parm := minparm + (maxparm -minparm)/fullscale*x
end;
```

# Multiparameter Code

```
function decode(chrom:chromosome; lbits:integer):real;  
{ Decode string as unsigned binary integer - true=1, false=0 }  
var j:integer;  
    accum, powerof2:real;  
begin  
    accum := 0.0; powerof2 := 1;  
    for j := 1 to lbits do begin  
        if chrom[j] then accum := accum + powerof2;  
        powerof2 := powerof2 * 2;  
    end;  
    decode := accum;  
end;
```

# References

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University of Illinois at Urbana-Champaign  
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by Stephen Welstead

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# References

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Darrell Whitley

Computer Science Department