The program Funcopt will be used for finding the maximum of the function

$$f(x_1, x_2) = \frac{e^{-x_1^2 - x_2^2} + \sqrt{5}\sin^2(x_2 x_1^2) + 2\cos^2(2x_1 + 3x_2)}{1 + x_1^2 + x_2^2}.$$

in the interval x_1, x_2 in [-3,3].

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The program Funcopt consists of the following parts:

- funcopt.m (the main program)
- initpop.m (initializes the population)
- decode_chromosome.m (decodes the chromosomes)
- evaluate_individual.m (evaluates the individuals)
- tournament_select.m (carries out tournament selection)
- crossover.m (performs crossover)
- mutate.m (performs mutations)

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funcopt.m

```
npop = 50;
ngenes = 40;
pcross = 0.8;
pmut = 0.05;
ptour = 0.75;
range = 3.0;
maxgenerations = 200;

population = initpop(npop,ngenes);

for gen = 1:maxgenerations

 maxfitness = 0.0;
 for i = 1:npop
   x = decode_chromosome(population,i,range,ngenes);
   fitness(i) = evaluate_individual(x);
   if (fitness(i) > maxfitness)
    maxfitness = fitness(i);
    best_individual = i;
    xbest = x;
   end
 end

 temp_pop = population;

 temp_pop(1,:) = population(best_individual,:);
 temp_pop(2,:) = population(best_individual,:);


....
```

```
.... (cont'd)

 for i = 3:2:npop
  i1 = tournament_select(fitness,npop,ptour);
  i2 = tournament_select(fitness,npop,ptour);
  r = rand;
  if (r < pcross)
    new_individuals = crossover(population,i1,i2,ngenes);
    temp_pop(i,:) = new_individuals(1,:);
    temp_pop(i+1,:) = new_individuals(2,:);
  else
    temp_pop(i,:) = population(i1,:);
    temp_pop(i+1,:) = population(i2,:);
  end
 end

 for i = 3:npop
  temp_individual = mutate(temp_pop(i,:),pmut,ngenes);
  temp_pop(i,:) = temp_individual;
 end

 population = temp_pop;
 maxfitness, xbest

end
```

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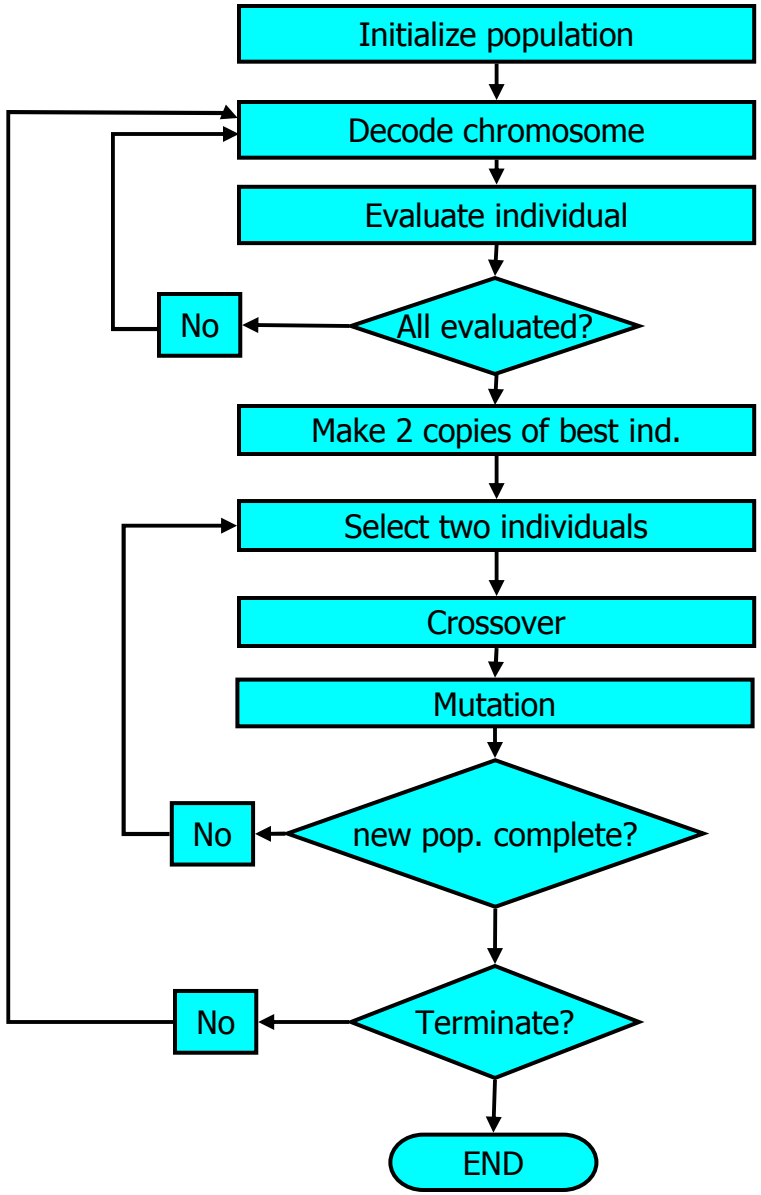


```
population = initpop(npop,ngenes);

x = decode_chromosome(population,i,range,ngenes);

fitness(i) = evaluate_individual(x);

temp_pop(1,:) = population(best_individual,:);
temp_pop(2,:) = population(best_individual,:);

i1 = tournament_select(fitness,npop,ptour);
i2 = tournament_select(fitness,npop,ptour);

new_individuals = crossover(population,i1,i2,ngenes);

temp_pop(i,:) = mutate(temp_pop(i,:),pmut,ngenes);
```

NOTE: unnecessary intermediate step in the lecture notes!

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Initialization of the population

```
function population = initpop(npop,ngenes);


for i = 1:npop
   for j = 1:ngenes
      s = rand;
      if (s < 0.5)
         population(i,j) = 0;
      else
         population(i,j) = 1;
      end
   end
end
```

Compact notation:

```
function population = initpop(npop,ngenes);

population = fix(2.0*rand(npop,ngenes));
```

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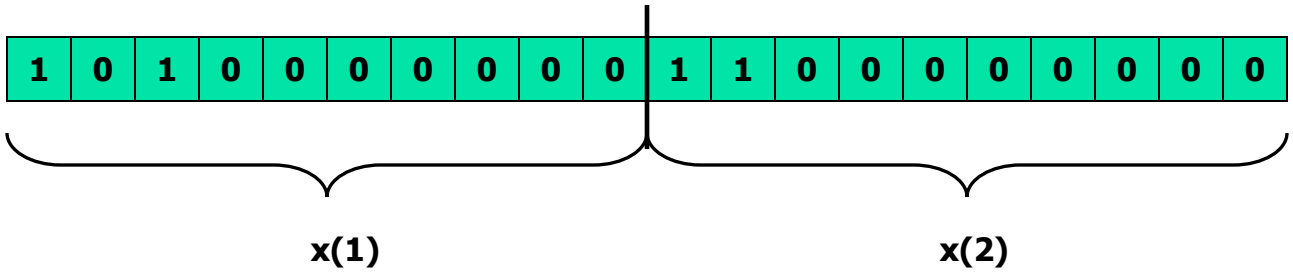
Decoding chromosomes:

```
function x = decode_chromosome(population,i,range,ngenes);

nhalf = fix(ngenes/2) ;
x(1) = 0.0;
for j = 1:nhalf
   x(1) = x(1) + population(i,j)*2^(-j);
end
x(1) = -range + 2*range*x(1);
x(2) = 0.0;
for j = 1:nhalf
   x(2) = x(2) + population(i,j+nhalf)*2^(-j);
end
x(2) = -range + 2*range*x(2);
```



(In this case: x(1) = -range + 2*0.625*range = 0.75, x(2) = -range + 2*0.75*range = 1.50)

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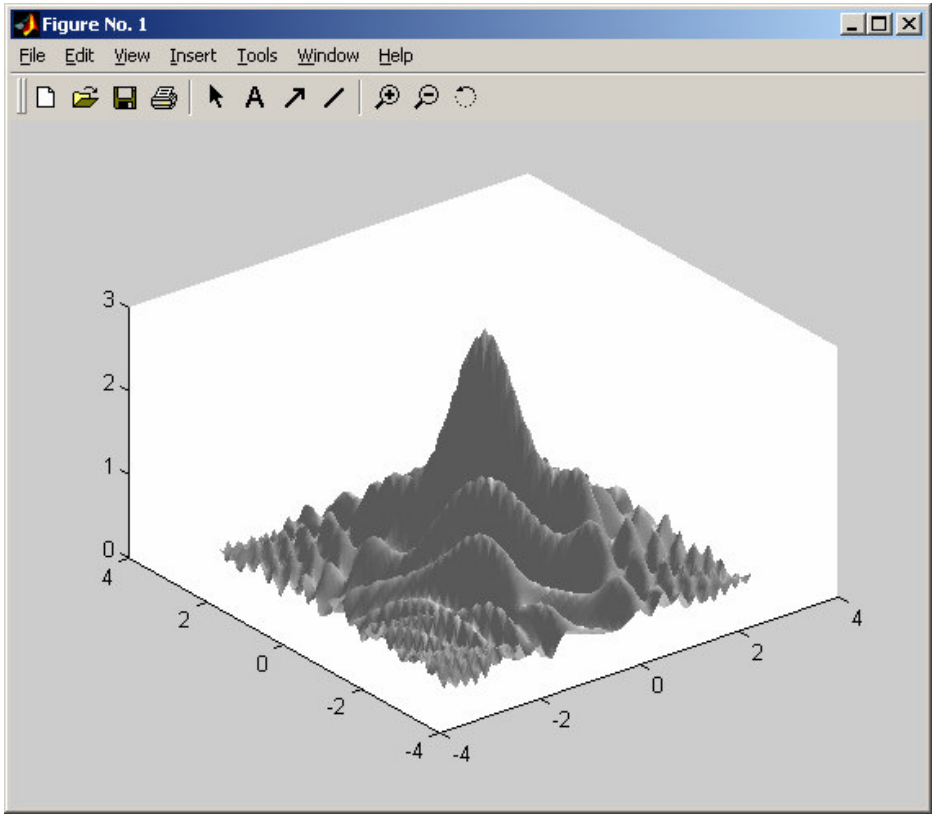
Evaluating individuals

```
function f = evaluate_individual(x);

f = (exp(-x(1)^2 - x(2)^2)+ ...
   sqrt(5)*(sin(x(2)*x(1)*x(1))^2) + ...
   2*(cos(2*x(1) + 3*x(2))^2))/(1 + x(1)^2 + x(2)^2);
```

Note: ... means that an expression continues on the next line.

f(1,1) = 0.62652...



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Tournament selection:

```
function i = tournament_select(fitness,npop,ptour);

itmp1 = 1+fix(rand*npop);
itmp2 = 1+fix(rand*npop);

r = rand;

if (r < ptour)
   if (fitness(itmp1)>fitness(itmp2))
      i = itmp1;
   else
      i = itmp2;
   end
else
   if (fitness(itmp1)>fitness(itmp2))
      i = itmp2;
   else
      i = itmp1;
   end
end
```

Note: in this simple example, the tournament size is set to 2.

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Crossover

```
function new_individuals = crossover(population,i1,i2,ngenes);

cp = 1 + fix(rand*(ngenes-1));

for j = 1:ngenes
   if (j < cp)
      new_individuals(1,j) = population(i1,j);
      new_individuals(2,j) = population(i2,j);
   else
      new_individuals(1,j) = population(i2,j);
      new_individuals(2,j) = population(i1,j);
   end
end
```

Note: selection from population (left unchanged during the whole selection cycle. New individuals inserted in temp_pop).

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Mutation

```
function mutated_individual = mutate(individual, pmut, ngenes);

mutated_individual = individual;
for i = 1:ngenes
   r = rand;
   if (r < pmut)
      mutated_individual(i) = fix(2.0*rand);
   end
end
```

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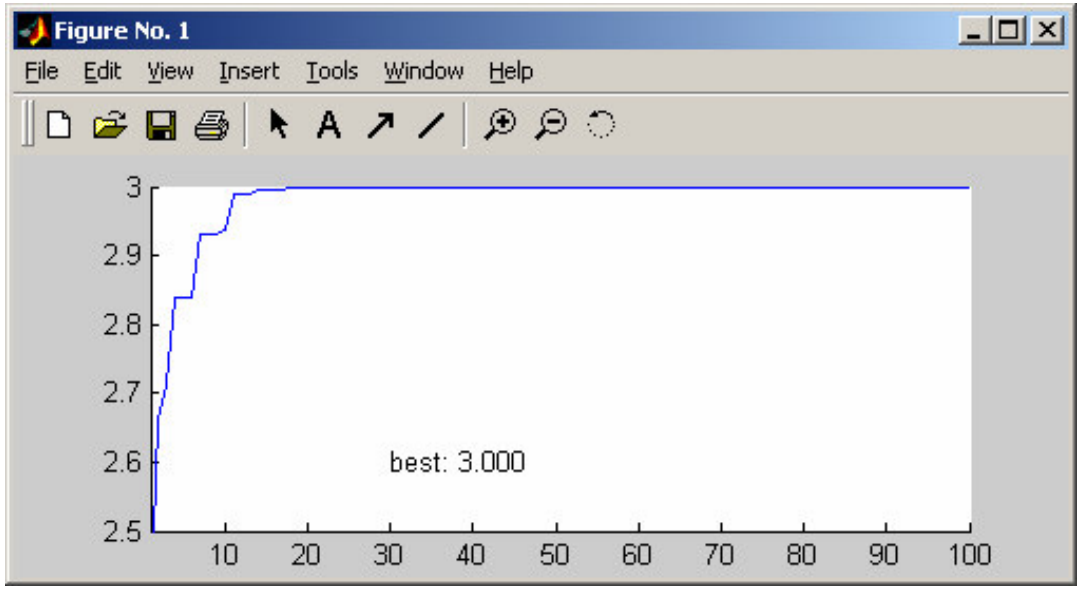
Running the program



Note: An introduction to Matlab programming (including *handle graphics*) can be found at

http://www.mathworks.com/access/helpdesk/help/pdf_doc/matlab/getstart.pdf

(In particular, see chapters 3 and 4).

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Handle graphics in Matlab (see also the online help files for Matlab)

```
npop = 100;
ngenes = 40;
pcross = 0.8;
pmut = 0.01;
ptour = 0.75;
range = 3.0;
maxgenerations = 100;
```

```
hfig = figure;
hold on
set(hfig, 'Position',[50,50,500,200]);
set(hfig, 'DoubleBuffer','on');
axis([1 maxgenerations 2.5 3]);
hbestplot = plot(1:maxgenerations,zeros(1,maxgenerations));
htext = text(30,2.6,sprintf('best: %4.3f',0.0));
hold off
drawnow;
```

```
population = initpop(npop,ngenes);
neval = 0
for gen = 1:maxgenerations
maxfitness = 0.0;
for i = 1:npop
   x = decode_chromosome(population,i,range,ngenes);
   fitness(i) = evaluate_individual(x);
   neval = neval +1;
   if (fitness(i) > maxfitness)
      maxfitness = fitness(i);
      best_individual = i;
      xbest = x;
      maxfitness, neval
   end
end
```

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```
plotvector = get(hbestplot,'YData');
plotvector(gen) = maxfitness;
set(hbestplot,'YData',plotvector);
set(htext,'String',sprintf('best: %4.3f',maxfitness));
drawnow;

temp_pop = population;

temp_pop(1,:) = population(best_individual,:);
temp_pop(2,:) = population(best_individual,:);

for i = 3:2:npop
  i1 = tournament_select(fitness,npop,ptour);
  i2 = tournament_select(fitness,npop,ptour);
  r = rand;
  if (r < pcross)
     new_individuals = crossover(population,i1,i2,ngenes);
     temp_pop(i,:) = new_individuals(1,:);
     temp_pop(i+1,:) = new_individuals(2,:);
  else
     temp_pop(i,:) = population(i1,:);
     temp_pop(i+1,:) = population(i2,:);
  end
end

for i = 3:npop
   temp_individual = mutate(temp_pop(i,:),pmut,ngenes);
   temp_pop(i,:) = temp_individual;
end

population = temp_pop;
end

x = decode_chromosome(population,1,range,ngenes)
```

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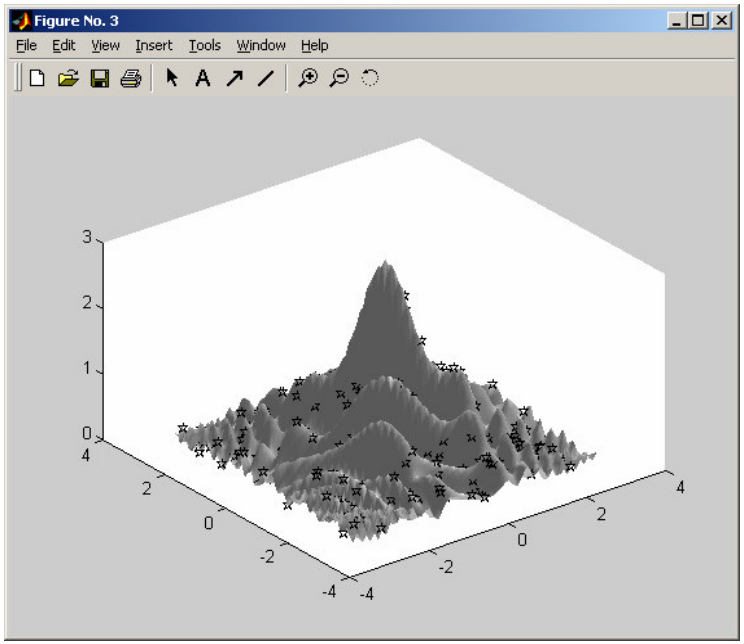
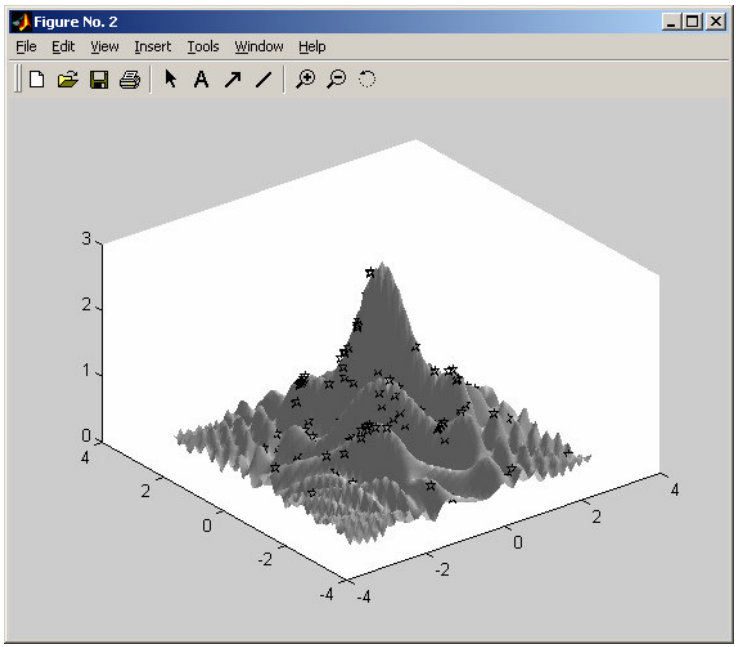
With 3D graphics





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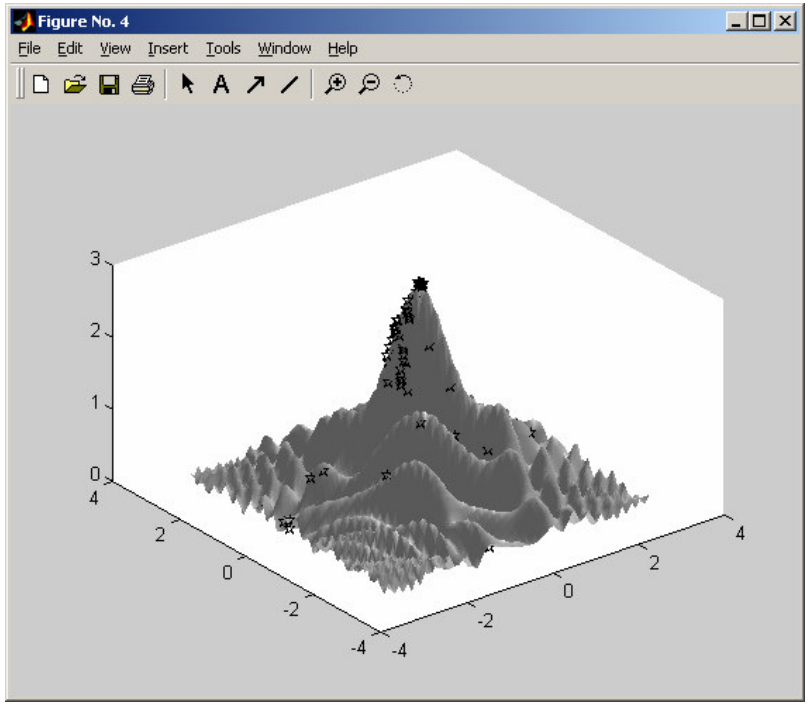

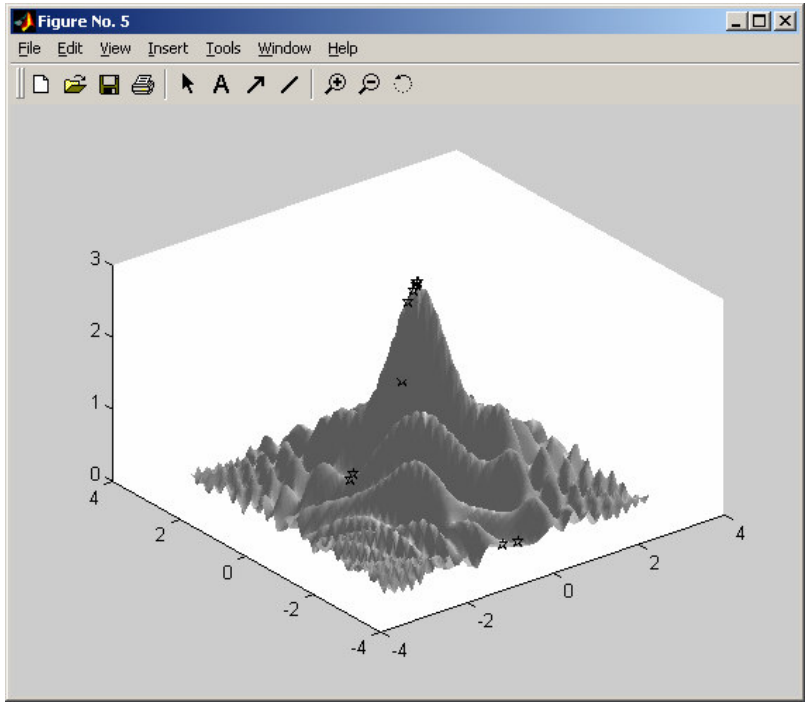

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3D graphics in Matlab (for more information, see e.g. the online Matlab help.)

```
npop = 200;
ngenes = 20;
pcross = 0.8;
pmut = 0.01;
ptour = 0.75;
range = 3.0;
maxgenerations = 100;
```

```
hfig = figure;
hold on;
set(hfig, 'DoubleBuffer','on');
delta = 0.1;
limit = fix(2*range/delta) + 1;
[xg,yg] = meshgrid(-range:delta:range,-range:delta:range);
zg = zeros(limit,limit);
for j = 1:limit
   for k = 1:limit
      zg(j,k) = evaluate_individual([xg(j,k) yg(j,k)]);
   end
end

surfl(xg,yg,zg)
colormap gray;
shading interp;
view([-7 -9 10]);

xind = zeros(npop,3);
h_indplot = plot3(xind(:,1),xind(:,2),xind(:,3),'kp');

hold off
drawnow
```

```
population = initpop(npop,ngenes);
```

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```
for gen = 1:maxgenerations
maxfitness = 0.0;

  for i = 1:npop
    x = decode_chromosome(population,i,range,ngenes);

    xind(i,1) = x(1);
    xind(i,2) = x(2);

    fitness(i) = evaluate_individual(x);

    xind(i,3)=fitness(i);

    if (fitness(i)>maxfitness)
      maxfitness = fitness(i);
      best_individual = i;
      xbest = x;
    end
  end

  set(h_indplot,'XData',xind(:,1),'YData',xind(:,2),'ZData',xind(:,3));
  drawnow;

  ETC...
```

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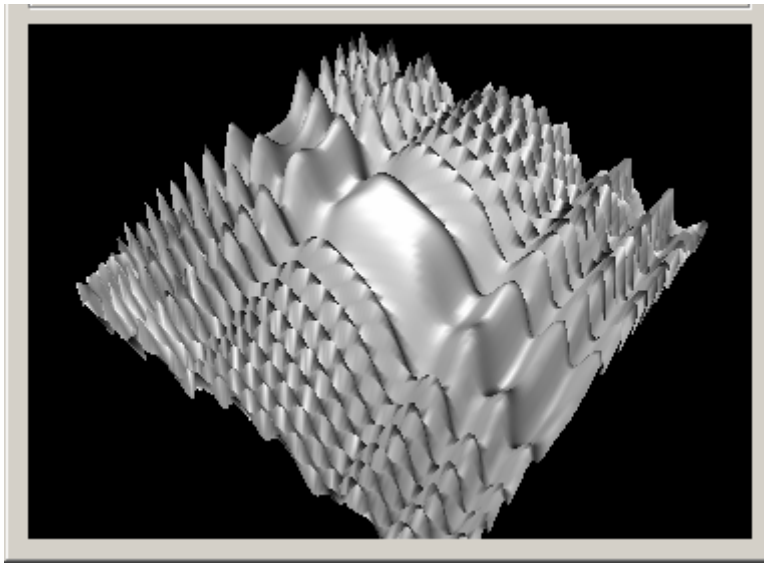
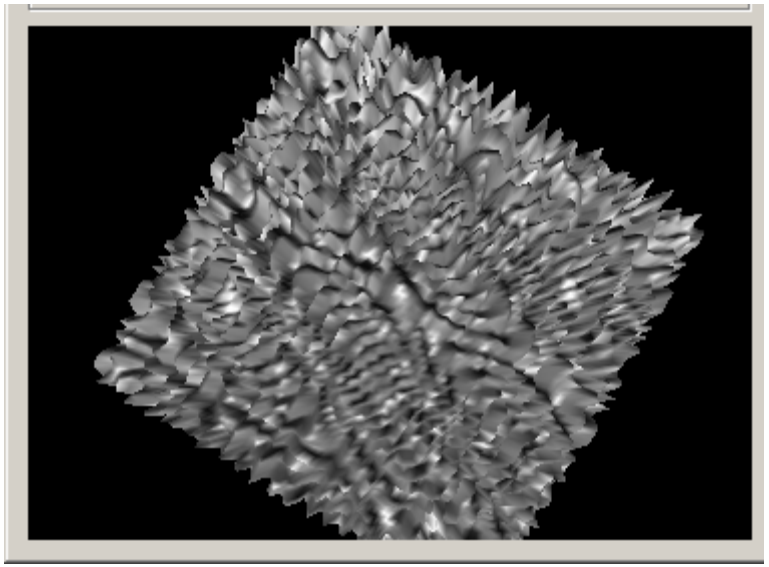
The function Psi(x1,...,x10):





$$\psi_n(x_1, x_2, ..., x_n) = \frac{1}{2} + \frac{1}{2n} \exp\left(-\alpha \sum_{i=1}^{n} x_i^2\right) \sum_{i=1}^{n} \cos\left(\beta \sqrt{i} x_i \sum_{j=1}^{i} j x_j\right),$$

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The schema theorem

Schemata: 100xx1, xx0xx0x1, 11x1 etc.

100001, 100011, 100101, 100111 are instances of the schema S = 100xx1.

GAs treat schemata so as to increase the number of schemata associated with high fitness

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Crossover (example)

S_1 = 000|11x

The schema survives if, for example, 000 is joined with 110 or 111

$$\begin{aligned}
\Gamma(S, g+1) &\geq \frac{\overline{f}(S)}{\overline{f}}\Gamma(S,g)\left(1 - p_c\frac{D(S)}{n-1}\right)(1-p_{\text{mut}})^{O(S)} \approx \\
&\approx \frac{\overline{f}(S)}{\overline{f}}\Gamma(S,g)\left(1 - p_c\frac{D(S)}{n-1}\right)(1-O(S)p_{\text{mut}}) \approx \\
&\approx \frac{\overline{f}(S)}{\overline{f}}\Gamma(S,g)\left(1 - p_c\frac{D(S)}{n-1} - O(S)p_{\text{mut}}\right),
\end{aligned}$$

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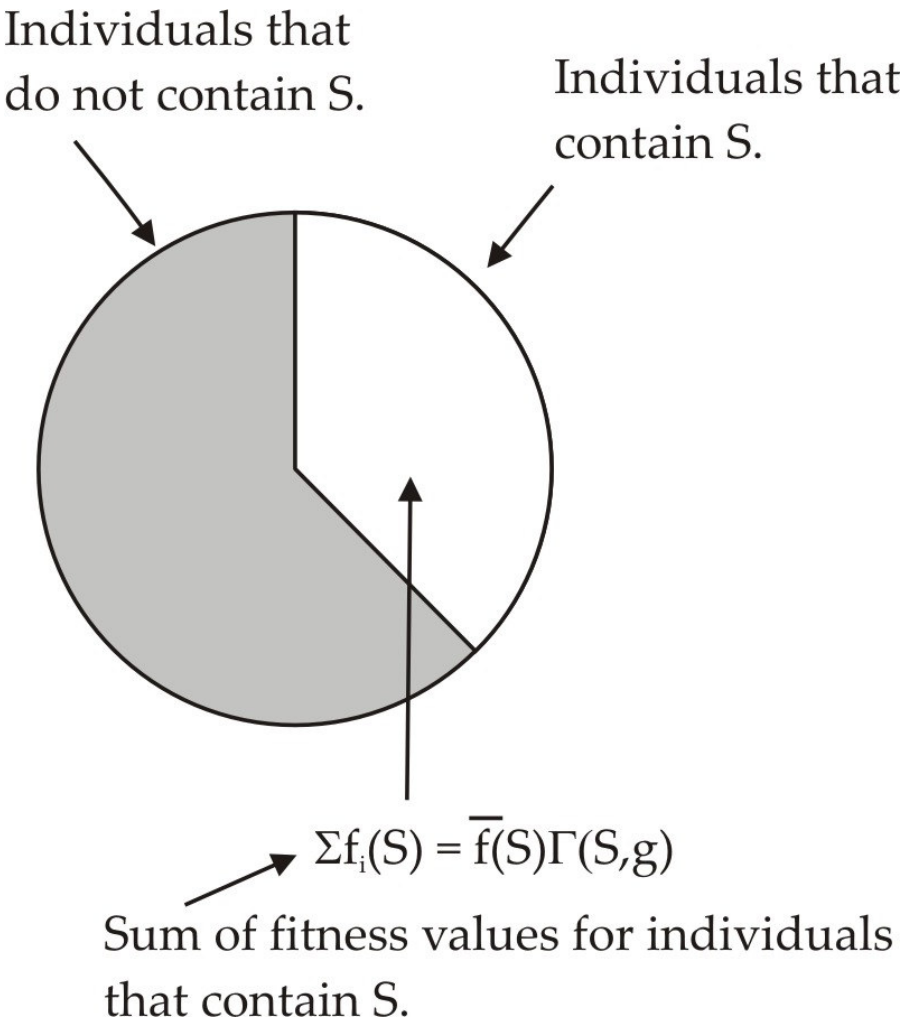
Schema theorem: selection of individuals containing a schema S



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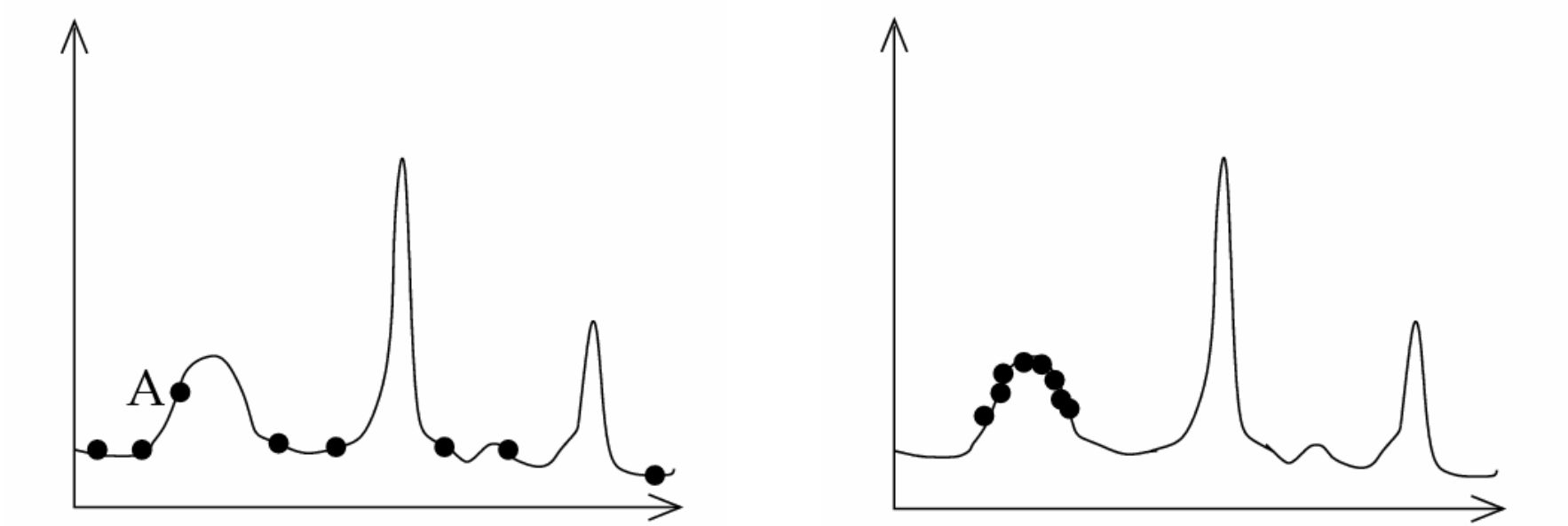
Premature convergence:



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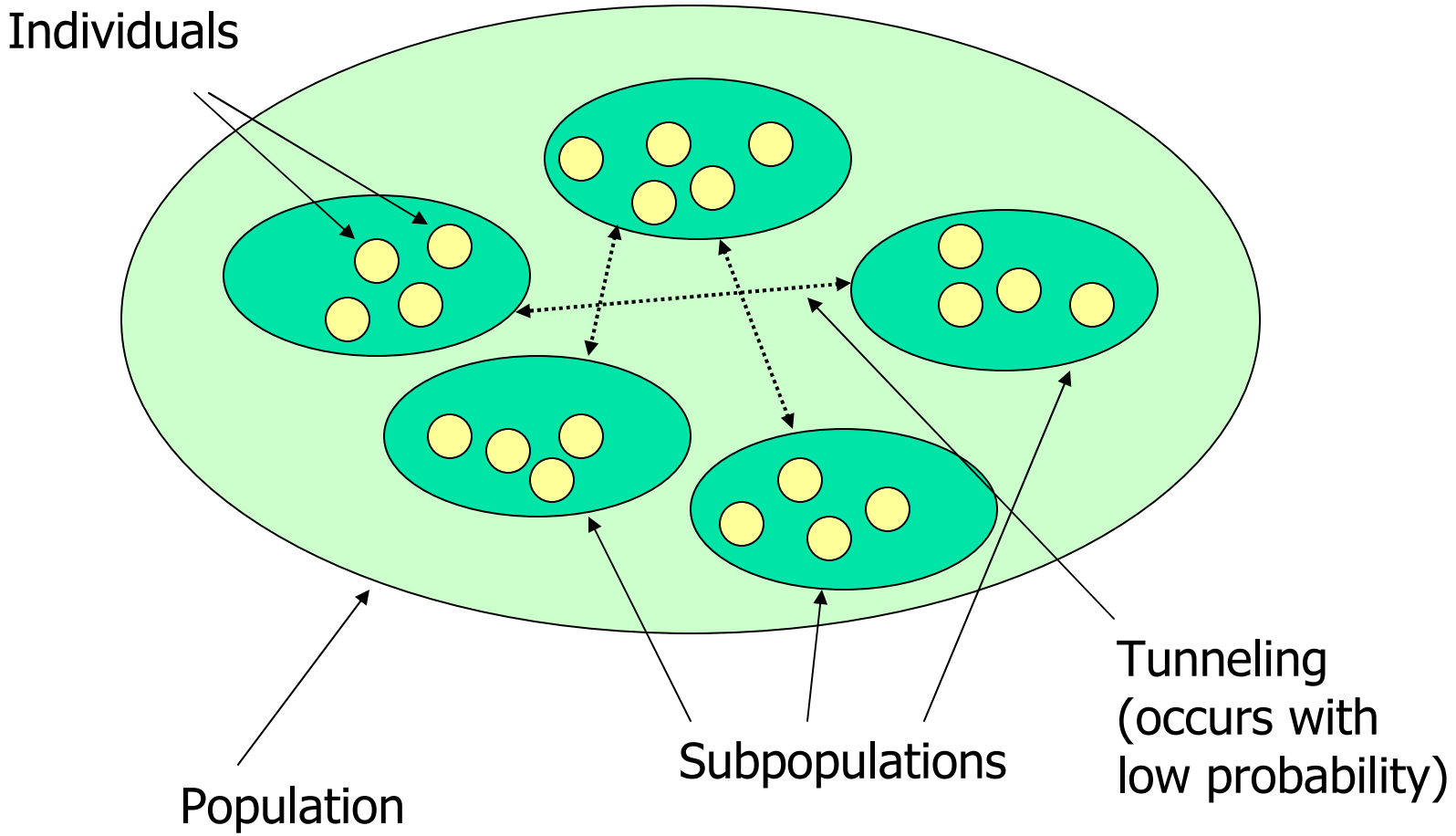

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The counting-ones problem:

Fitness = number of one-genes in the chromosome

EXAMPLE:

10101000101000 => Fitness = 5 etc.

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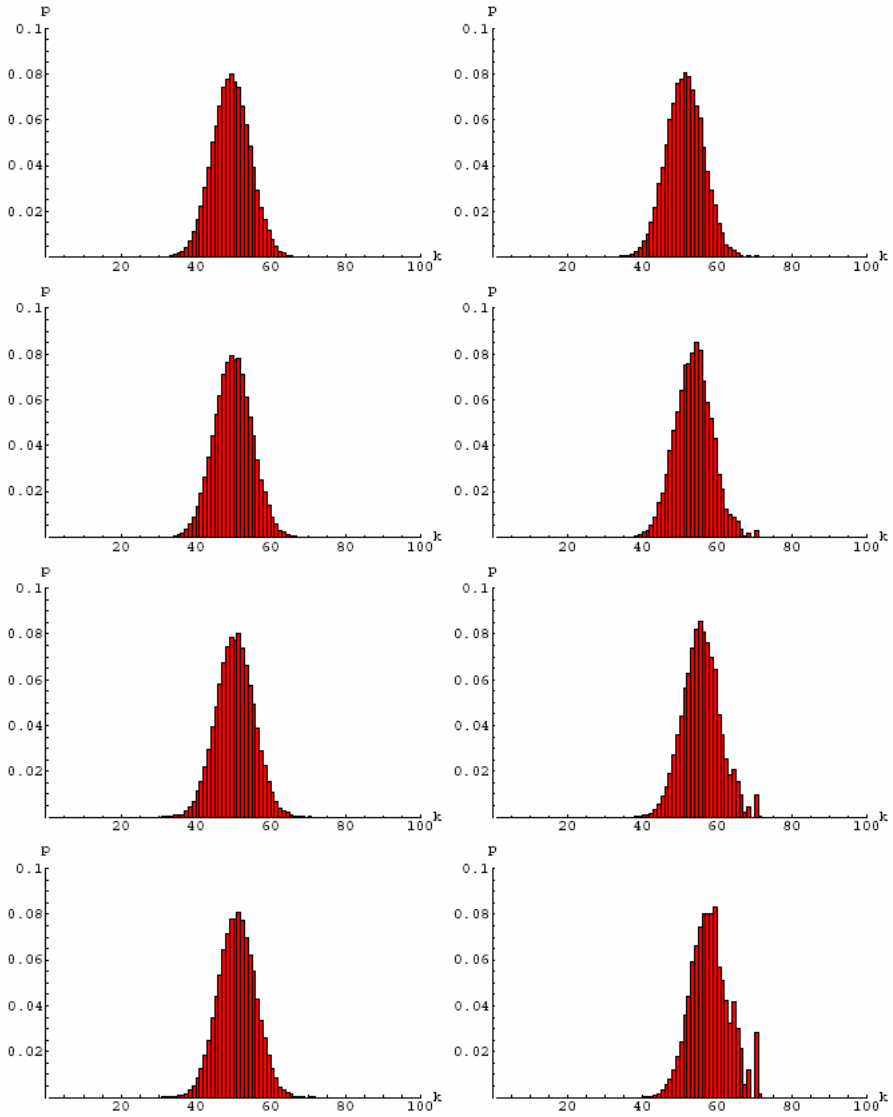

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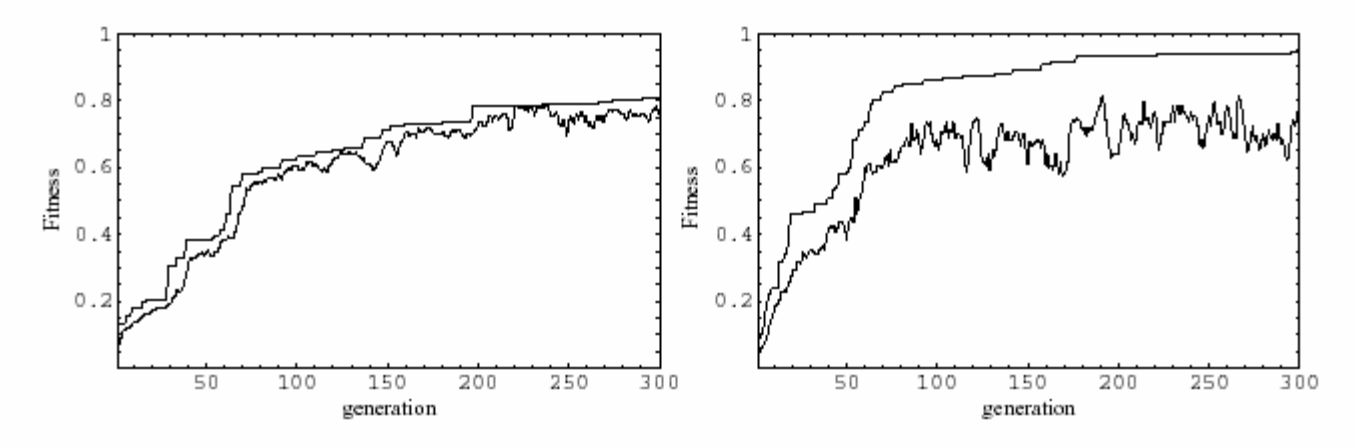
Generation (s)	Average fitness analytical	numerical	$p_s(n)$ $(n = 100)$
1	50.0000	49.9892	7.89×10^{-31}
2	50.5000	50.5011	1.58×10^{-30}
3	50.9901	51.0035	3.12×10^{-30}
4	51.4708	51.5013	6.13×10^{-30}



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