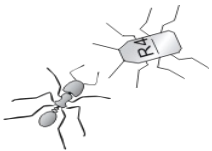


# Evolutionary Computation



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Companion slides for the book *Bio-Inspired Artificial Intelligence: Theories, Methods, and Technologies* by Dario Floreano and Claudio Mattiussi, MIT Press



# What you will learn today

4 pillars of evolution

Genetic basis of natural evolution

The algorithmic loop of artificial evolution

Choosing a genetic representations

Building an initial population

Devising a fitness function

Selection and reproduction methods

Mutations and crossover

Measuring evolution

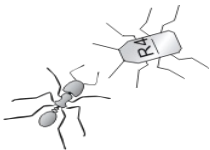
Function optimization by evolution

Types of evolutionary algorithms

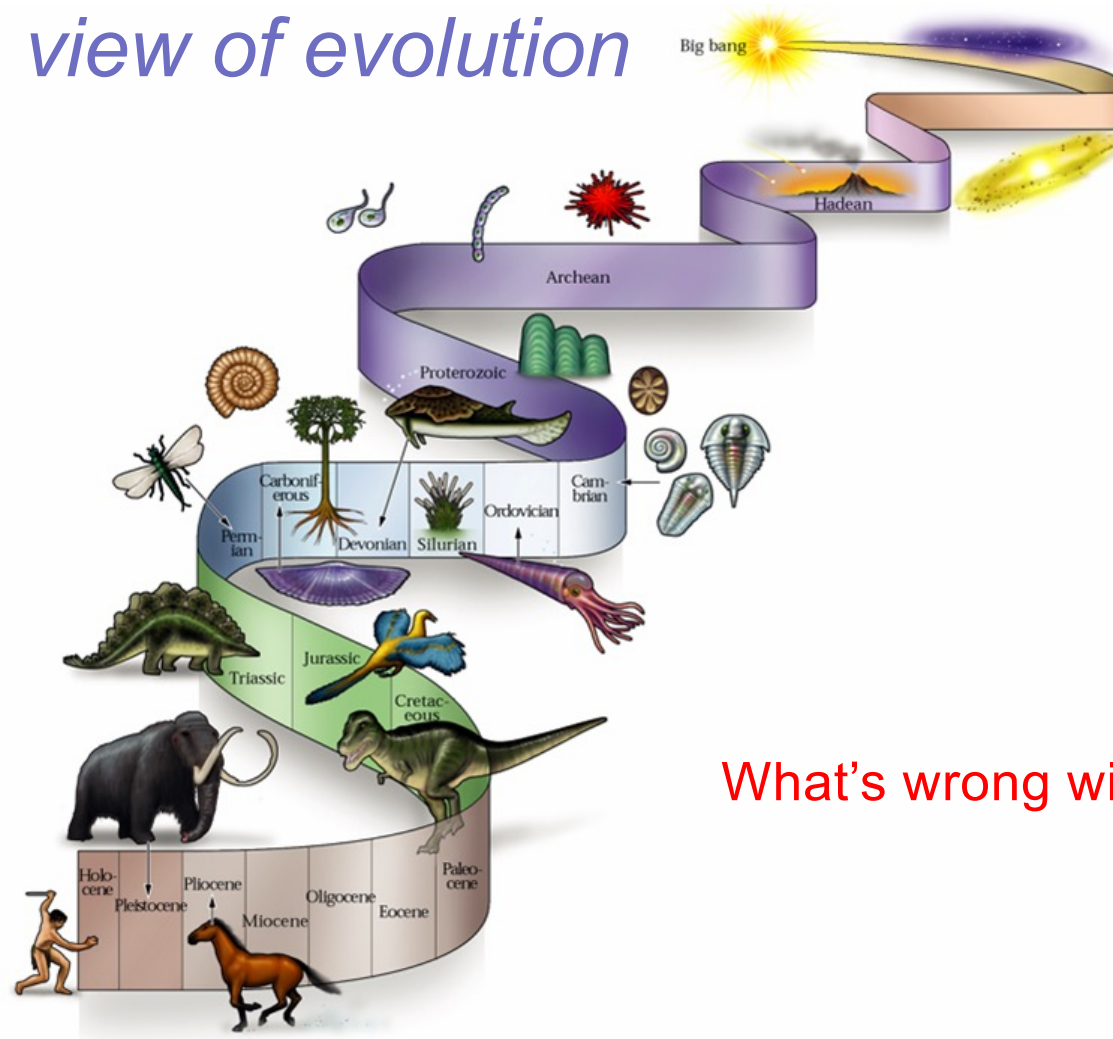
A simple example: evolving an antenna design

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Companion slides for the book *Bio-Inspired Artificial Intelligence: Theories, Methods, and Technologies* by Dario Floreano and Claudio Mattiussi, MIT Press

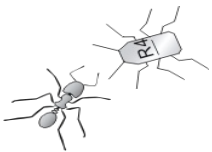


# A deceptive view of evolution

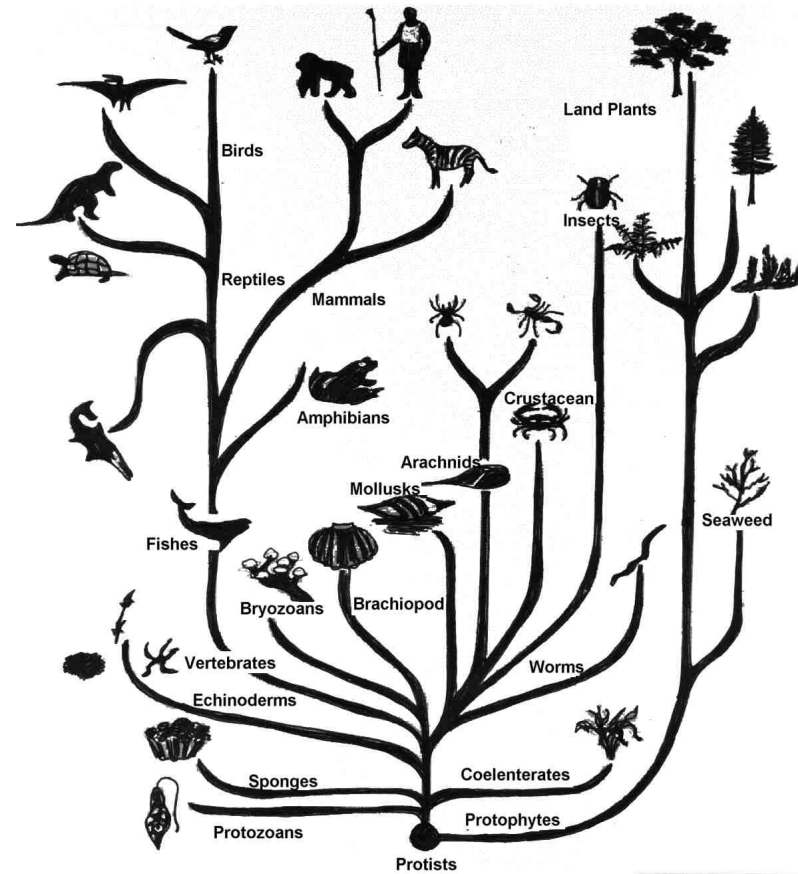


What's wrong with this image?

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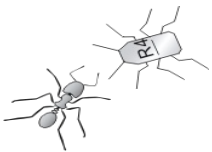


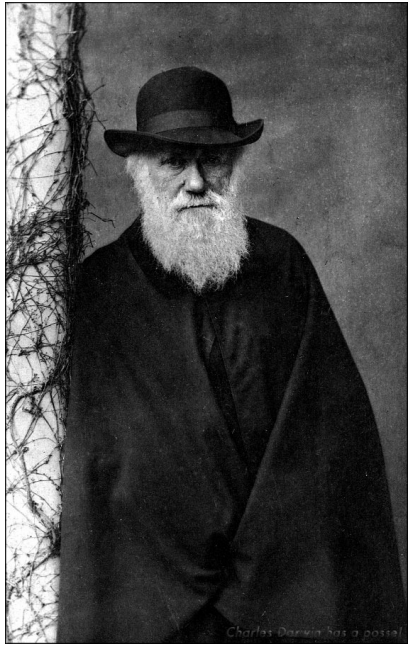
# Diversity generation



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Charles Darwin, 1859  
*On the Origins of Species*

## *Four Pillars of Evolution*

### **Population**

Group of several individuals

### **Diversity**

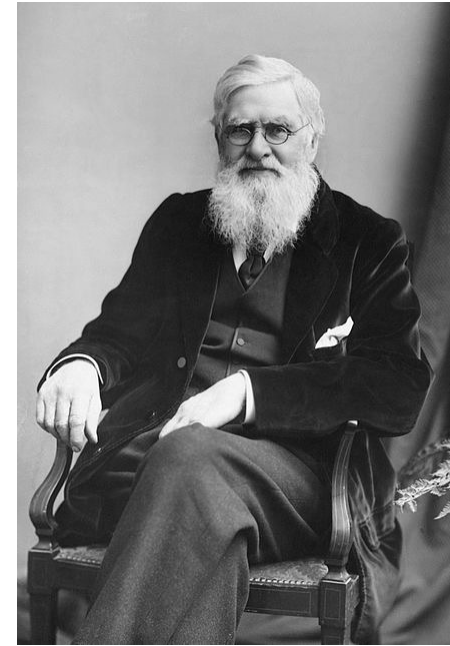
Individuals have different characteristics

### **Heredity**

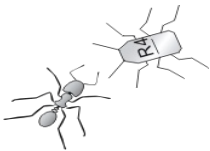
Characteristics are transmitted over generations

### **Selection**

- Individuals make more offspring than the environment can support
- Comparatively better ones have higher probability of reproducing



Alfred Russel Wallace, 1858



# Phenotype & Genotype

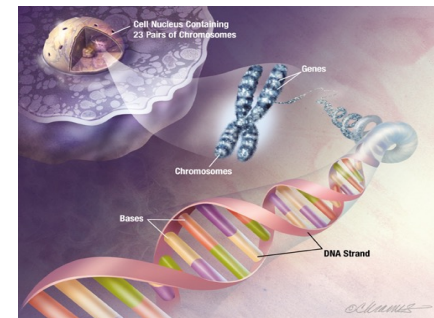
## Phenotype

The organism (physical instantiation, behavior, etc.)  
Selection operates on phenotype  
It is affected by environment, development, and learning



## Genotype

The genetic material of an organism.  
Selection does not operate directly on genotype  
It is affected only by mutations



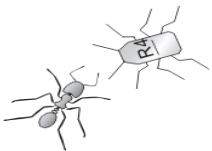
Gregor Mendel, 1858  
Genetic basis of inheritance



Huxley, 1940  
Modern synthesis of evolution

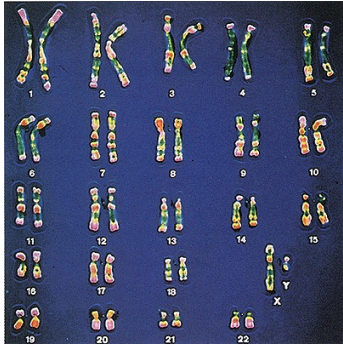
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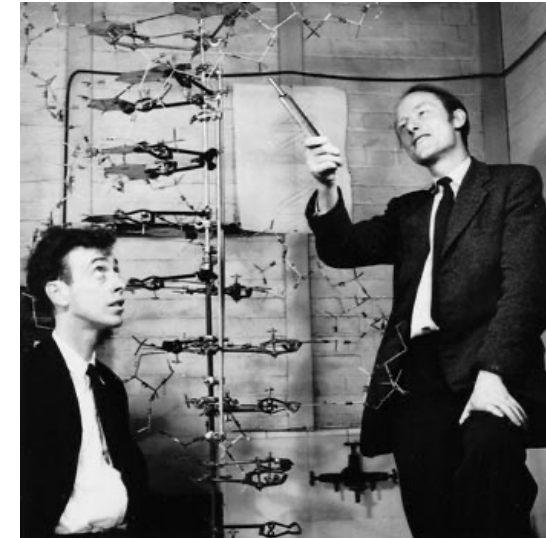
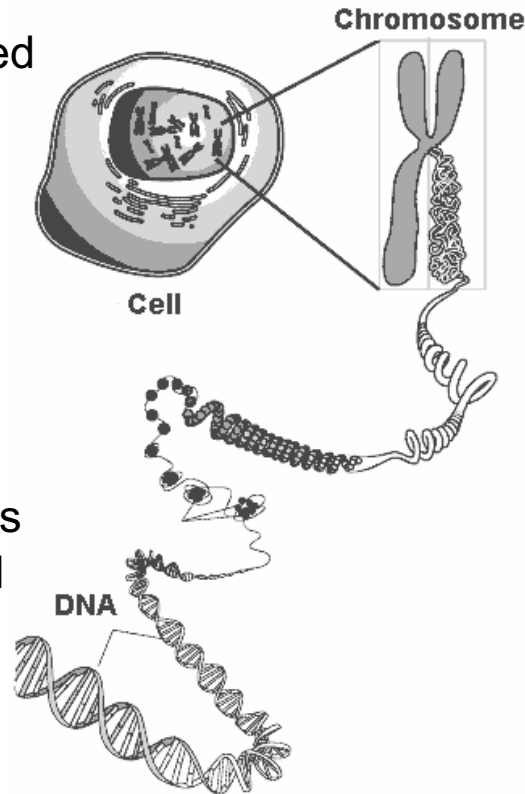
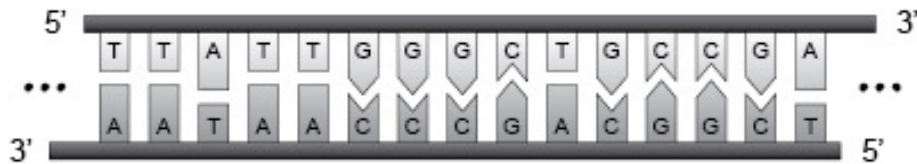
# Genotype: DNA (DeoxyriboNucleic Acid)

Long molecule, twisted in spiral, and compressed



Humans have 23 pairs of DNA molecules (chromosomes)

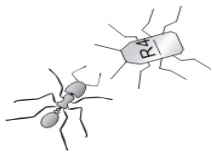
DNA is composed of 2 complementary sequences (strands) of 4 nucleotides (A, T, C, G), which bind together in pairs (A-T and C-G)



Crick 1953 Watson  
Discovery of DNA structure

**A gene** is a sequence of several nucleotides that produce a protein

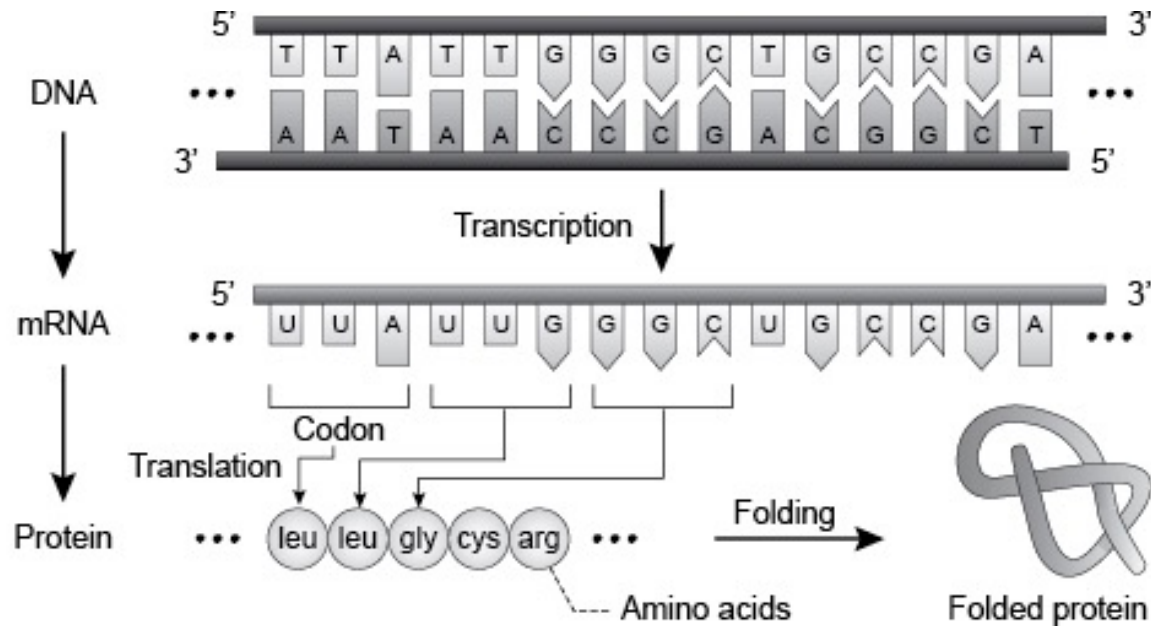
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# From Genotype to Phenotype: Gene Expression

Proteins are folded molecule chains whose shape define the type and function of cells (some proteins affect gene expression)

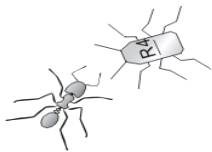
The sequence of nucleotides in one strand defines the type of protein. The expression of the gene into a protein is mediated by another molecule, known as messenger RNA.



AlphaFold, 2021

Computer prediction of 3D protein folding

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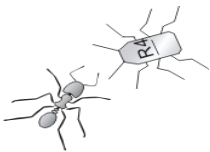
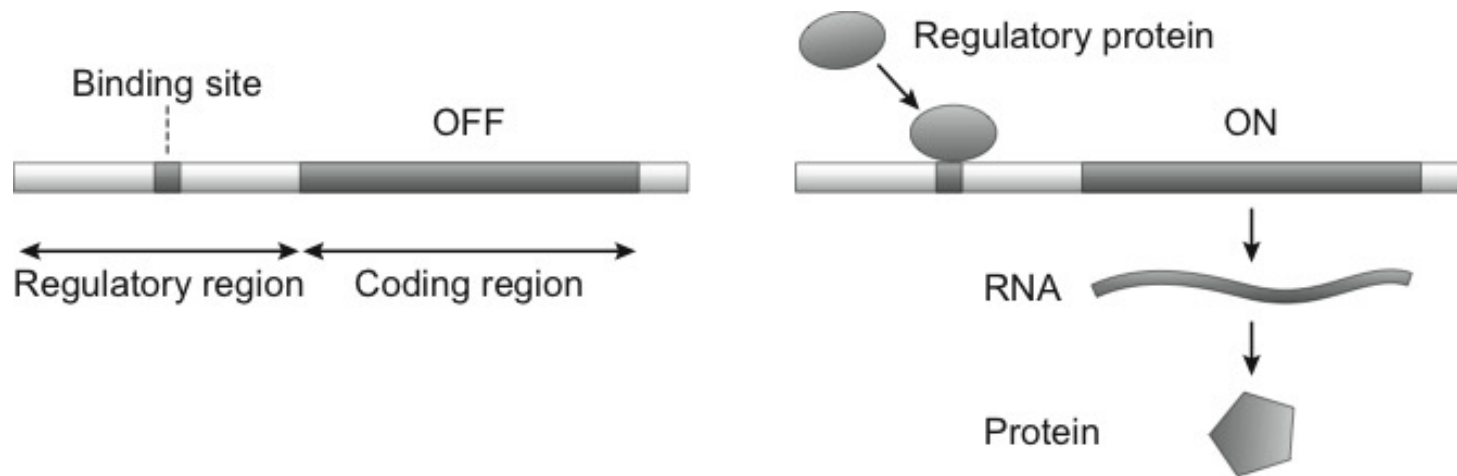


# Regulation of Gene Expression

Genes are composed of a regulatory region and of a coding region.

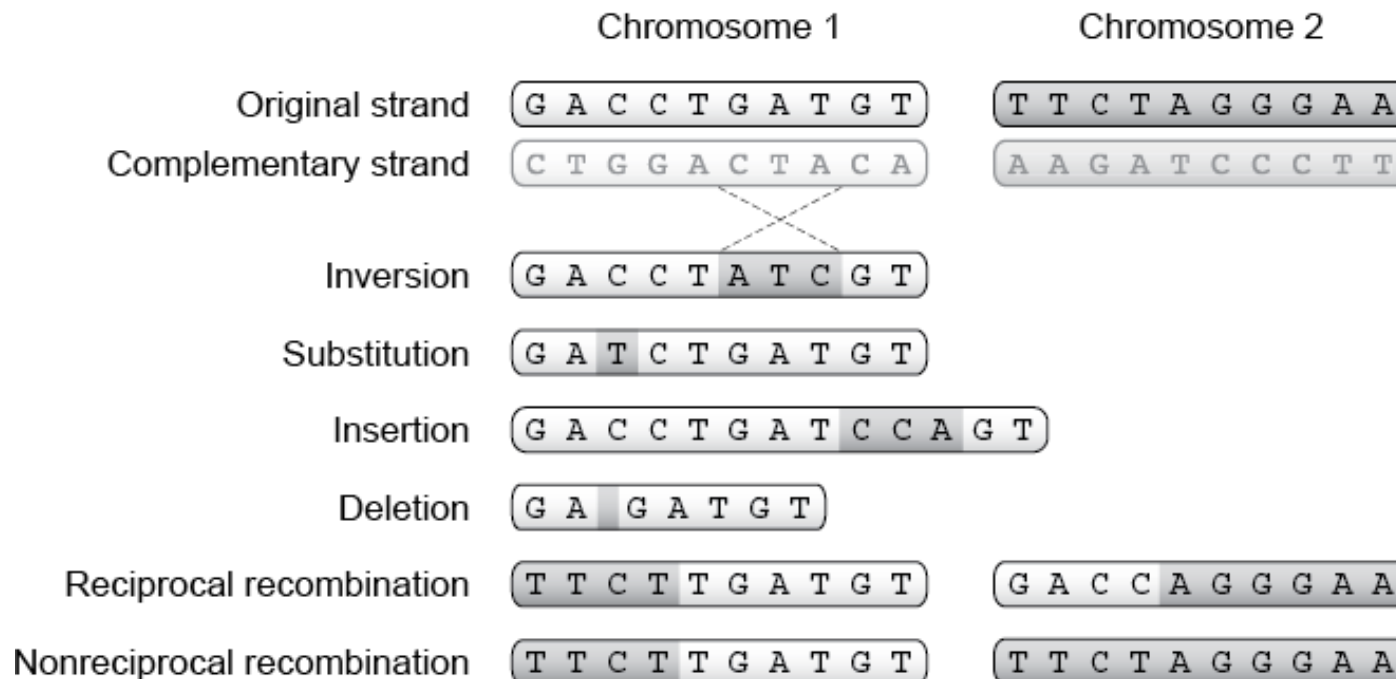
The coding region is translated into a protein if another protein binds onto the regulatory region. Regulation can also be negative (i.e., inhibition of protein production).

Genome is a self-regulatory code



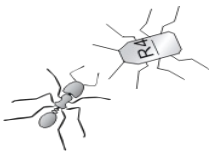
# Genetic Mutations

- Genetic mutations occur during cell replication ( $4^{-10}$  per nucleotide per year)
- Those that occur in sex cells can affect evolution
- Sexual recombination is a mutation that affects two homologous chromosomes




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# Genome Size

Genome size within a species is constant (C-value, expressed in Mega bases), but it greatly varies across species [www.genomesize.com](http://www.genomesize.com) for comparisons

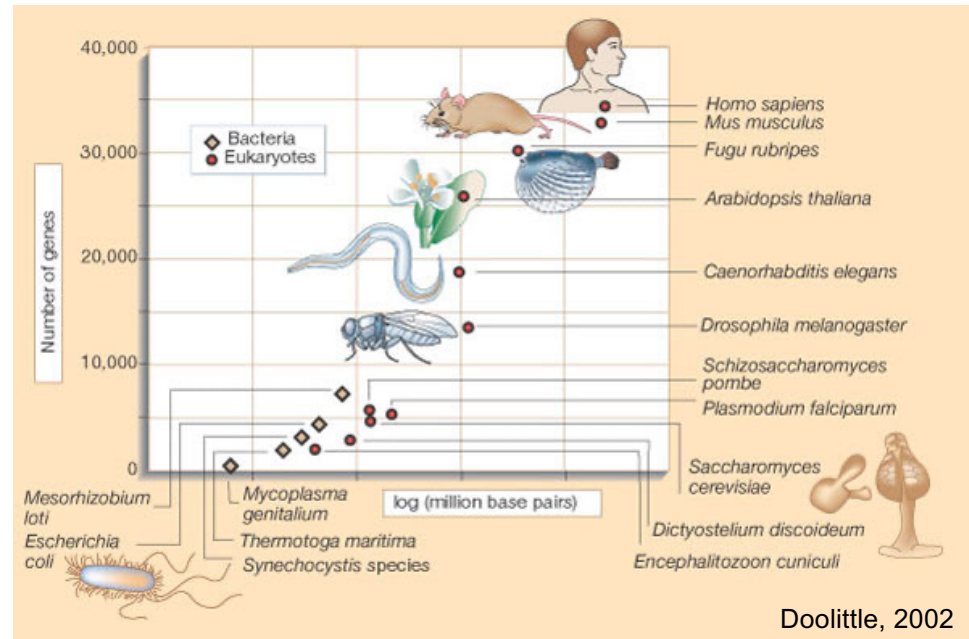
Genome size is not related to complexity of phenotype

Genome contains:

- **Genic DNA**
- **Nongenic DNA**

Nongenic DNA **arises** from:

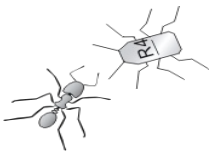
- insertion/deletion mutations
- gene duplication



Nongenic DNA may have an **adaptive value**:

- pseudogenes may be re-activated
- pseudogenes may transform into new genes by several neutral mutations

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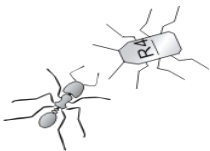
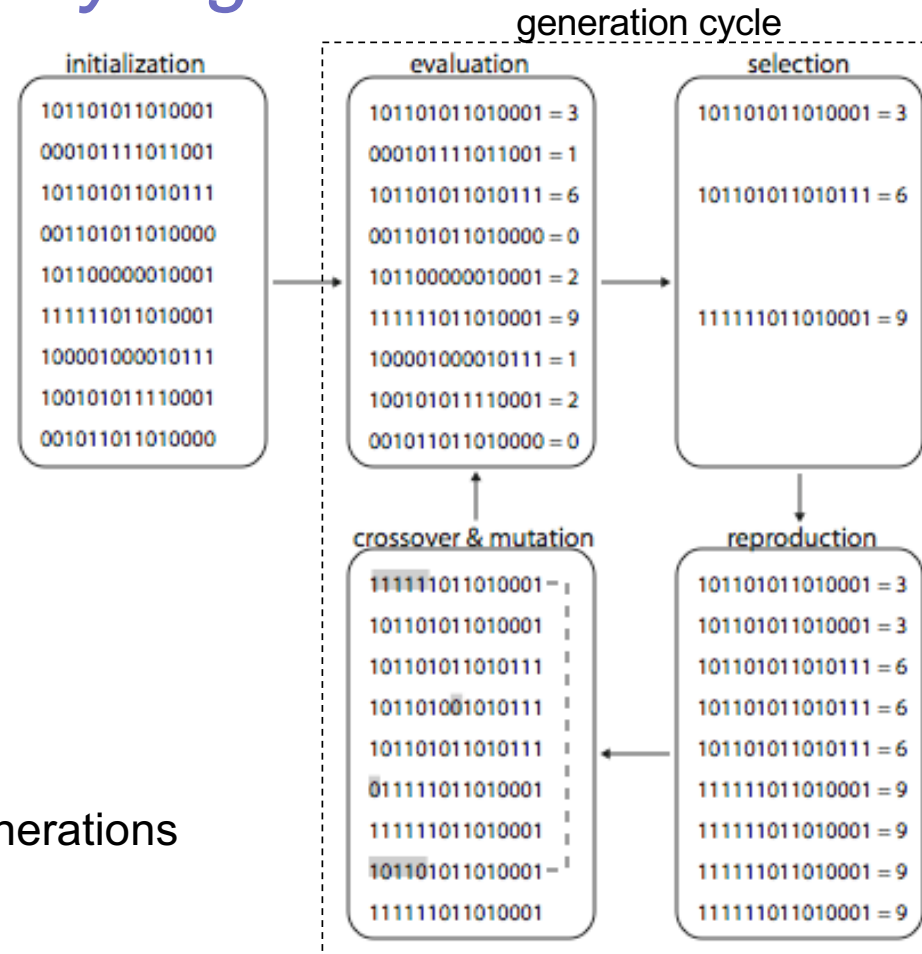


# Elements of an evolutionary algorithm

- Devise genetic representation
- Build a population
- Design a fitness function
- Choose selection method
- Choose crossover & mutation
- Choose data analysis method

Repeat generation cycle until:

- maximum fitness value is found
- solution found is good enough
- no fitness improvement for several generations



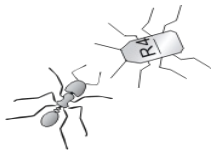
# Artificial and Natural Evolution

## Similarities between natural and artificial evolution:

- Phenotype (computer program, object shape, electronic circuit, robot, etc.)
- Genotype (genetic representation of the phenotype)
- Population
- Diversity
- Selection
- Inheritance

## Differences between natural and artificial evolution:

- Fitness is measure of performance of the individual solution to the problem
- Selection of the best according to performance criterion (fitness function)
- Expected improvement between initial and final solution

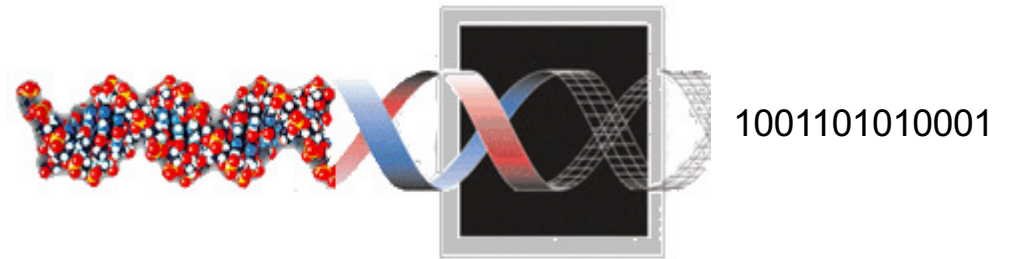


# Genetic Representation

Coding of the phenotype (function variables, network weights, body parts, etc.) into a string

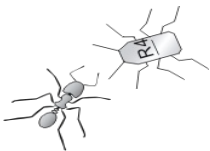
## Simplification of biology:

- Single stranded sequence of elements
- Fixed length along generations, only genic
- Haploid structure and one chromosome
- Often one-to-one direct correspondence between genotype and phenotype



## Types of representations:

- Discrete
- Real-valued
- Sequence
- Tree-based

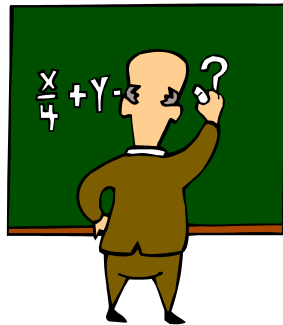


# Discrete Representations

A sequence of  $l$  discrete values drawn from alphabet with cardinality  $k$

- E.g., binary string of 8 positions ( $l=8, k=2$ ): 01010100
- Can be mapped into several phenotypes:

to integer  $i$  using binary code



to real value  $r$  in range  $[min, max]$ :  
 $r = min + (i/255)(max-min)$

to configuration string of FPGA electronic circuits

01010100

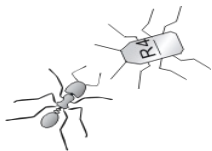
84

0.328125

Job	A.M.	P.M.
1	x	
2		x
3	x	
4		x
5	x	
6		x
7	x	
8	x	



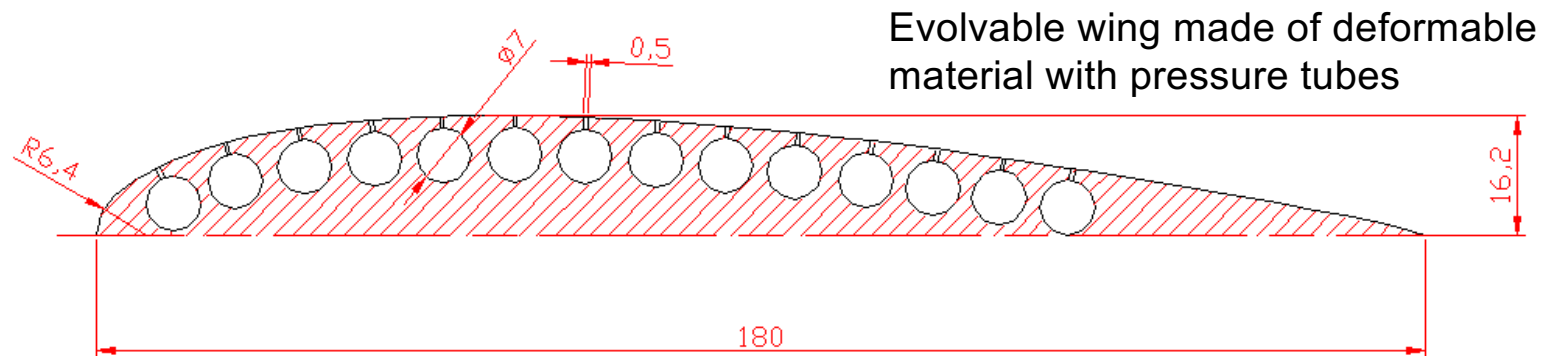
to job schedule:  
 • job=gene position  
 • time=gene value



# Real-Valued Representation

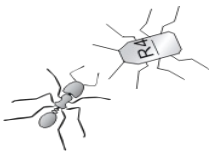
A vector of real values that represent parameters of a function, e.g.: [0.6, -0.01, 0.87, ...]

- This representation is used when high-precision parameter optimization is required, e.g.:
  - Variables of multi-dimensional function
  - Connection weights of neural networks
  - Parameters defining a shape
- Example: representation of wing profile for shape optimization



Evolvable wing made of deformable material with pressure tubes

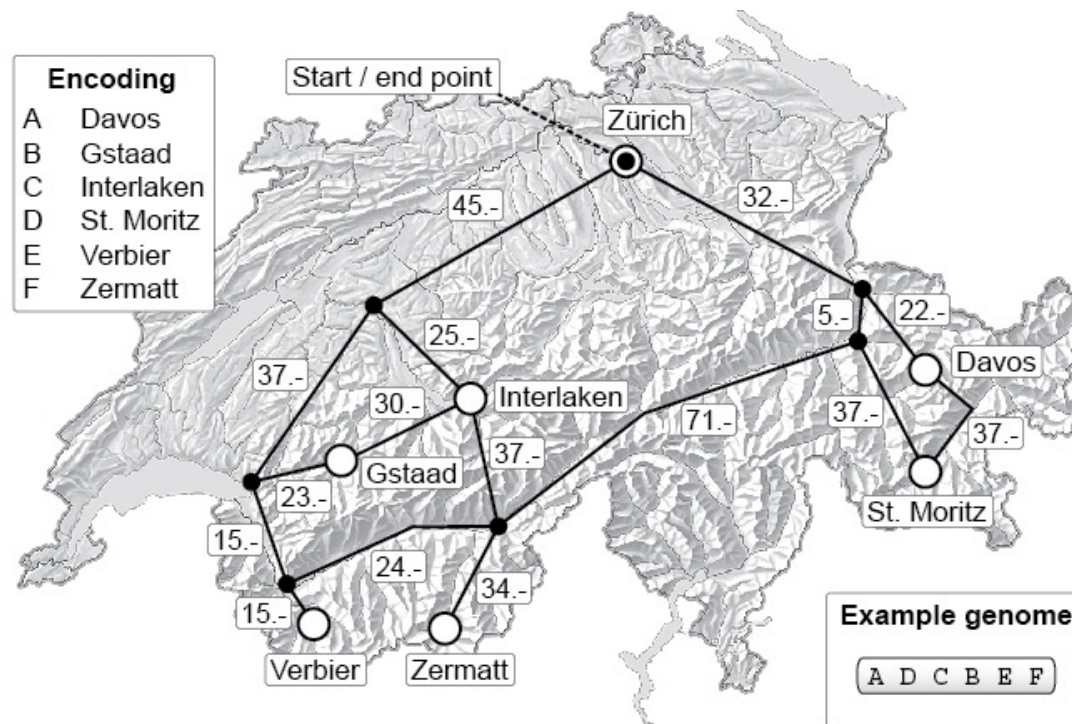
Genotype= 14 pressure values of the 14 tubes



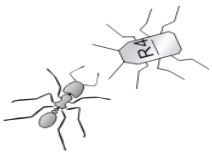


# Sequence Representation

A specific case of discrete representations used for Traveling Salesman Problems (plan a path to visit n cities under some constraints). E.g., planning ski holidays with lowest transportation costs



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# Tree-based Representation

A nested list describing a tree with branching points and terminals

Suitable for encoding hierarchical structures, such as computer programs and robot body plans

For example, a computer program is made of:

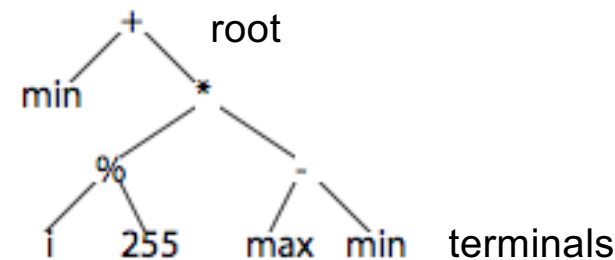
- Function set: multiplication, If-Then, Log, etc.
- Terminal set: constants, variables, sensor readings, etc.

Expression

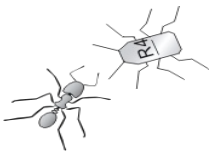
$r = \min + (i / 255)(\max - \min)$

Nested list

$(+, \min, (*, (/, i, 255), (-, \max, \min)))$



- Closure: all functions must accept all terminals in Terminal set and outputs of all functions in Function set (e.g., protected division %)
- Sufficiency: elements in Function and Terminal sets must be sufficient to generate program that solves the problem



# Build Initial Population

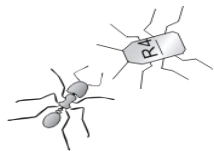
How large? Sufficiently large to cover problem space (!), but sufficiently small for evaluation costs (typical size found in the literature: between 10s and 1000s individuals)

## Uniform sampling of search space:

- Binary strings: 0 or 1 with probability 0.5
- Real-valued representations: uniform on a given interval if bounded phenotype (e.g., +2.0, -2.0); otherwise best guess
- Sequence: position all elements at random locations of each string
- Trees are built recursively starting from root:
  - root is randomly picked from function set
  - set maximum depth of tree
  - for every branch, randomly pick from all elements of function set and of terminal set
  - if a terminal is picked, it becomes a leaf (end of the branch)

Clone and mutate previously evolved genotype or hand-designed genotype; possible dangers:

- Small genetic diversity
- Unrecoverable bias



# Fitness Function

Evaluates **performance** of phenotype with a numerical score

- Choice of components; e.g., lift and drag of wing
- Combination of components; e.g. (lift + 1/drag) or (lift - drag)
- Extensive test of each phenotype
- Warning! You Get What You Evaluate (example in application, later)

**Subjective fitness:** select phenotype by visual inspection

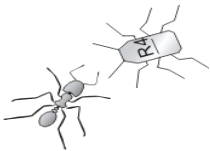
- Used when aesthetic properties cannot be quantified objectively
- Can be combined with objective fitness function



"A-Volve", Sommerer and Mignonneau,  
NTT ICC Tokyo Opera House, [www.ntticc.or.jp](http://www.ntticc.or.jp)

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# Selection



A method to make sure that better individuals make comparatively more offspring

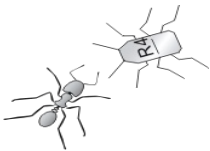
Some methods:

- Proportionate selection
- Rank-based selection
- Truncated rank-based selection
- Tournament selection

- Selection pressure is inversely proportional to percentage of selected individuals
- High selection pressure = rapid loss of diversity and premature convergence
- Make sure that also less performing individuals have a chance to reproduce

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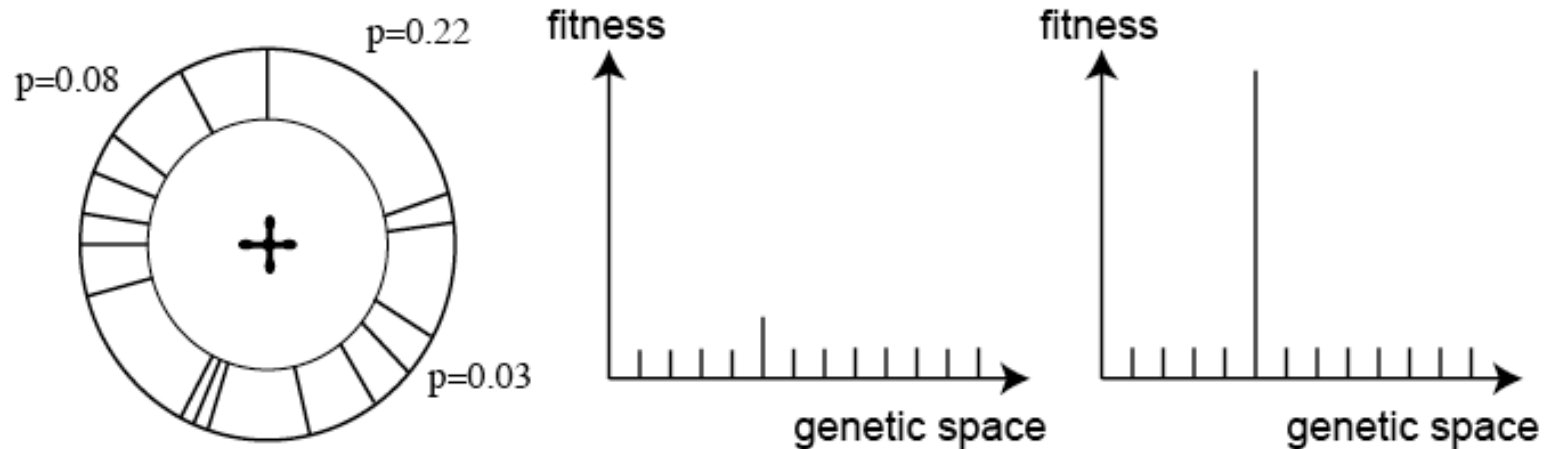
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# Proportionate Selection

The probability that an individual makes an offspring is proportional to how good its fitness is with respect to the population fitness:  $p(i) = f(i)/\sum f(i)$

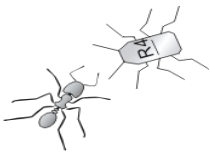
Also known as Roulette Wheel selection



## Problems:

Uniform fitness values = random search

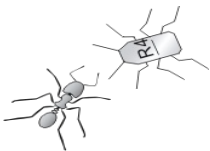
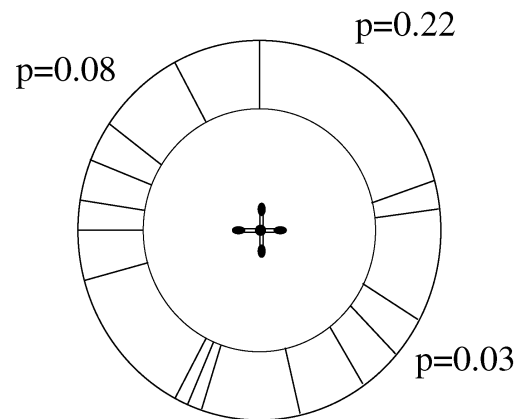
Few high-fitness individuals = high selection pressure



# Rank-based Selection

- Individuals are sorted on their fitness value from best to worse. The place in this sorted list is called the **rank r**.
- Instead of using the fitness value of an individual, the rank is used to select individuals:  $p(i) = 1 - r(i)/\sum r(i)$
- Use roulette wheel

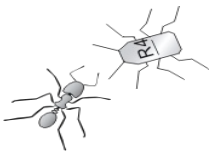
individual	fitness	rank
A	5	5
B	7	3
C	8	2
D	2	8
E	3	7
F	9	1
G	7	4
H	4	6



# Truncated Rank-based Selection

- Only the best  $x$  individuals are allowed to make offspring and each of them makes the same number of offspring:  $N/x$ , where  $N$  is the population size.
- E.g., in population of 100 individuals, make 5 copies of 20 best individuals

individual	fitness	rank	list
A	5	5	F
B	7	3	C
C	8	2	B
D	2	8	G
E	3	7	A
F	9	1	H
G	7	4	E
H	4	6	D

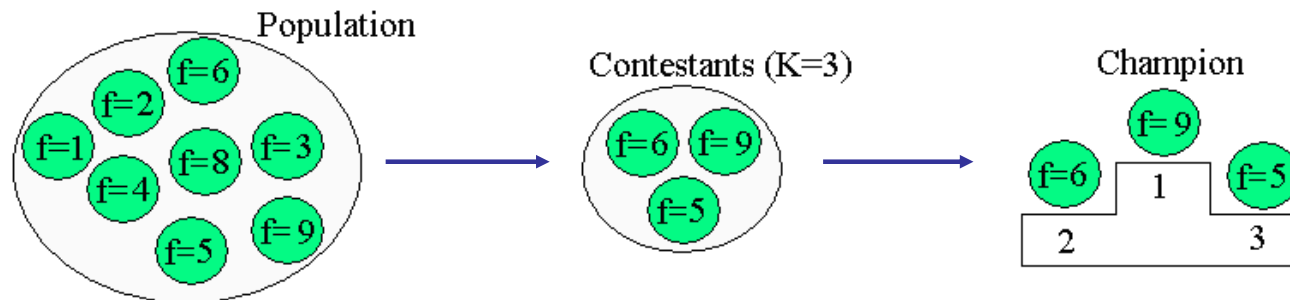




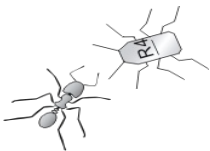
# Tournament Selection

For every offspring to be generated:

- Pick randomly  $k$  individuals from the population
- Choose the individual with the highest fitness and make a copy
- Put all individuals back in the population



$k$  is the tournament size (larger size = larger selection pressure)



# Generational Replacement

All individuals are replaced by their offspring in the new generation

Gen x individuals



Offspring (Gen x+1)



Best individual of Gen x



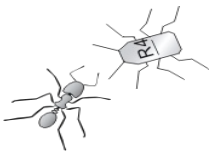
**Population size:** constant over generations

**Problem:** mutations or poor fitness assessment may lead to loss of good individuals

**Elitism:** insert  $n$  best individuals from previous generation and randomly remove  $n$  individuals

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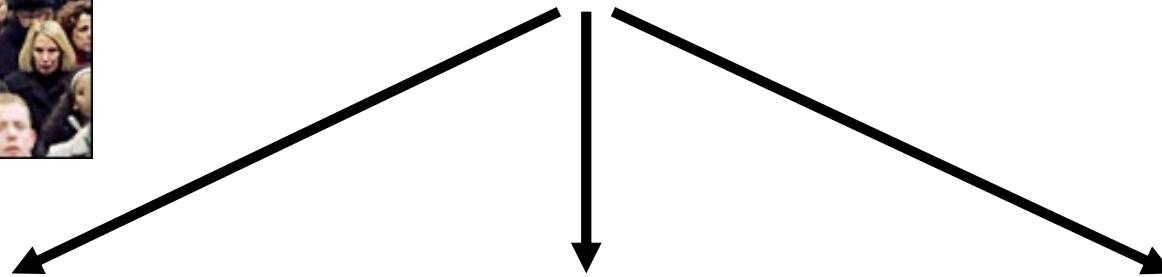


# Generational rollover

Generate and insert one offspring at a time in the population and let it compete with other individuals



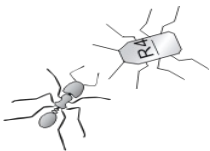
Methods to maintain population size



Remove individual at random

Remove oldest individual

Remove worst individual



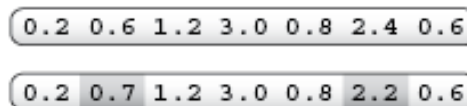
# Mutation

Applied to each gene in the genetic string with probability  $p_m$

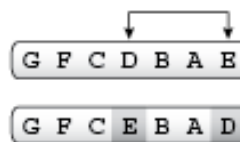
Binary genotypes



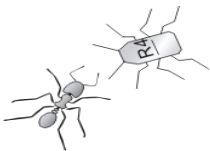
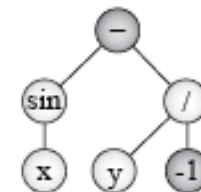
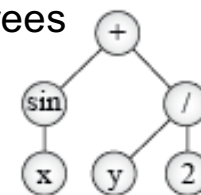
Real-valued genotypes  
(uniform mutation)



Sequence genotypes

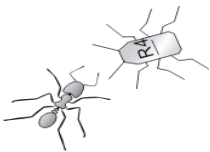
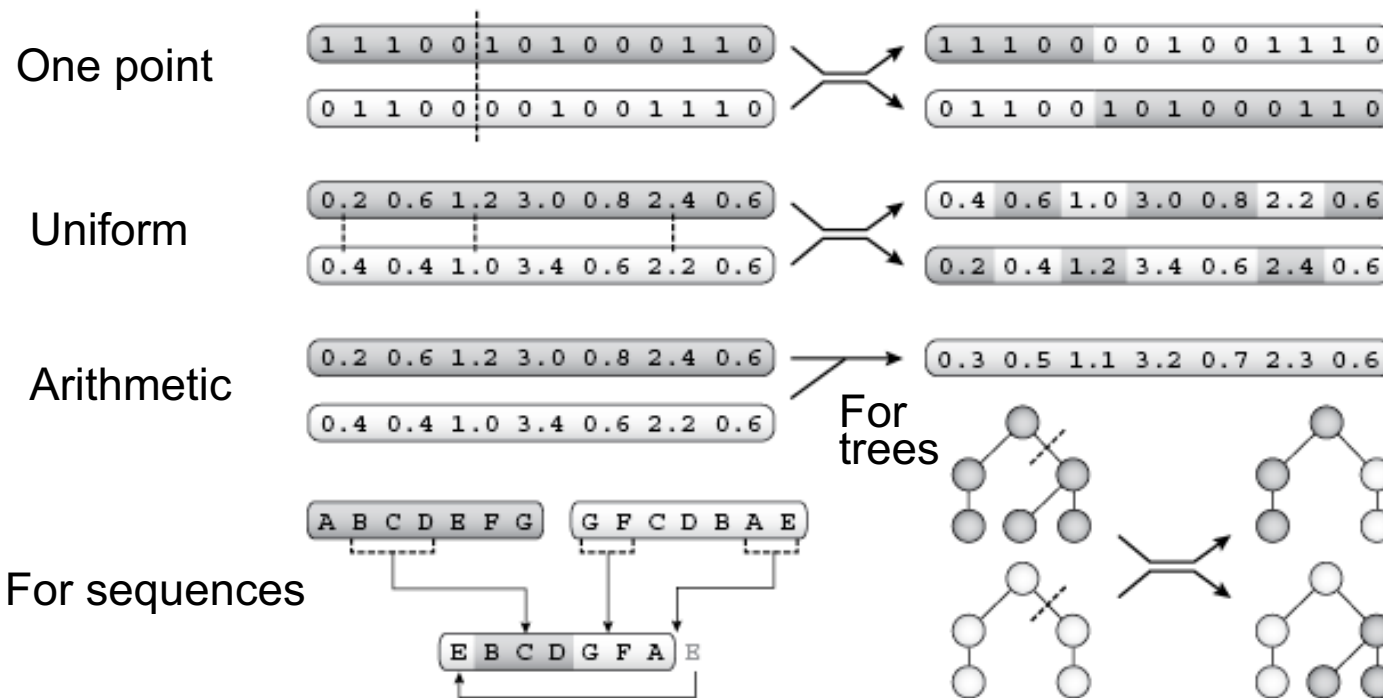


For trees



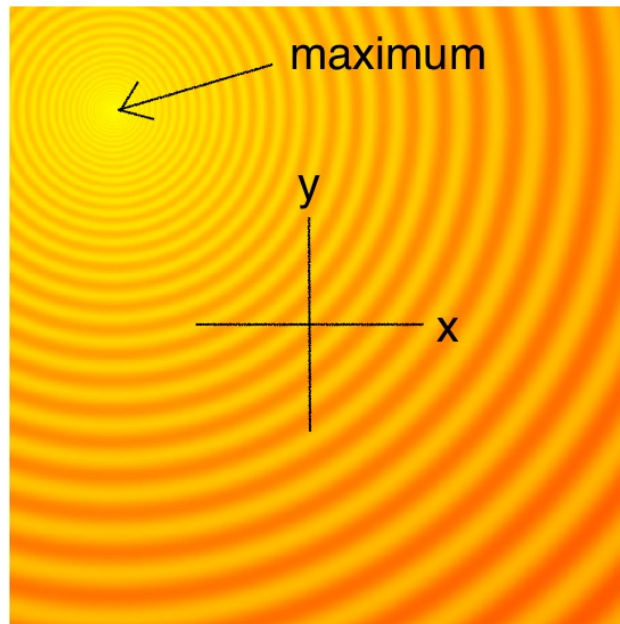
# Crossover

Emulates recombination of genetic material from two parents during meiosis  
 Exploitation of synergy of sub-solutions (building blocks) from parents  
 Applied to randomly paired offspring with probability  $p_c$ (pair)

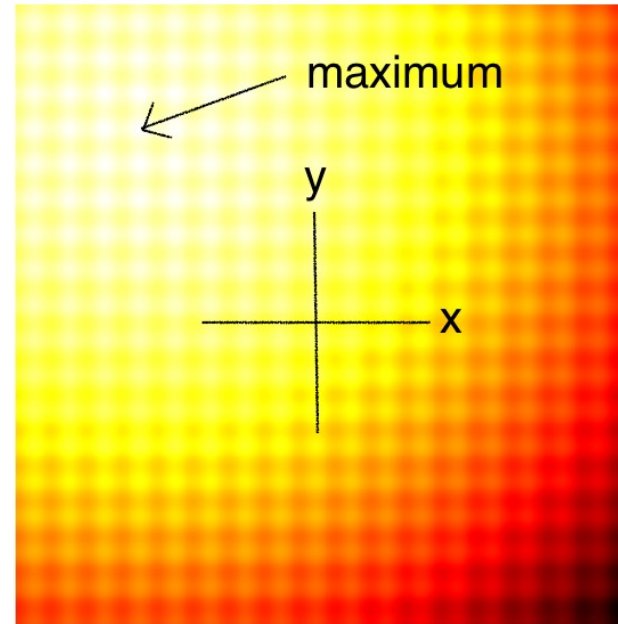


# Artificial landscapes

Shifted Schaffer-2D function



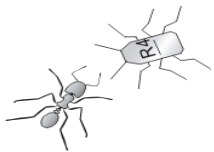
Shifted Rastrigin-2D function



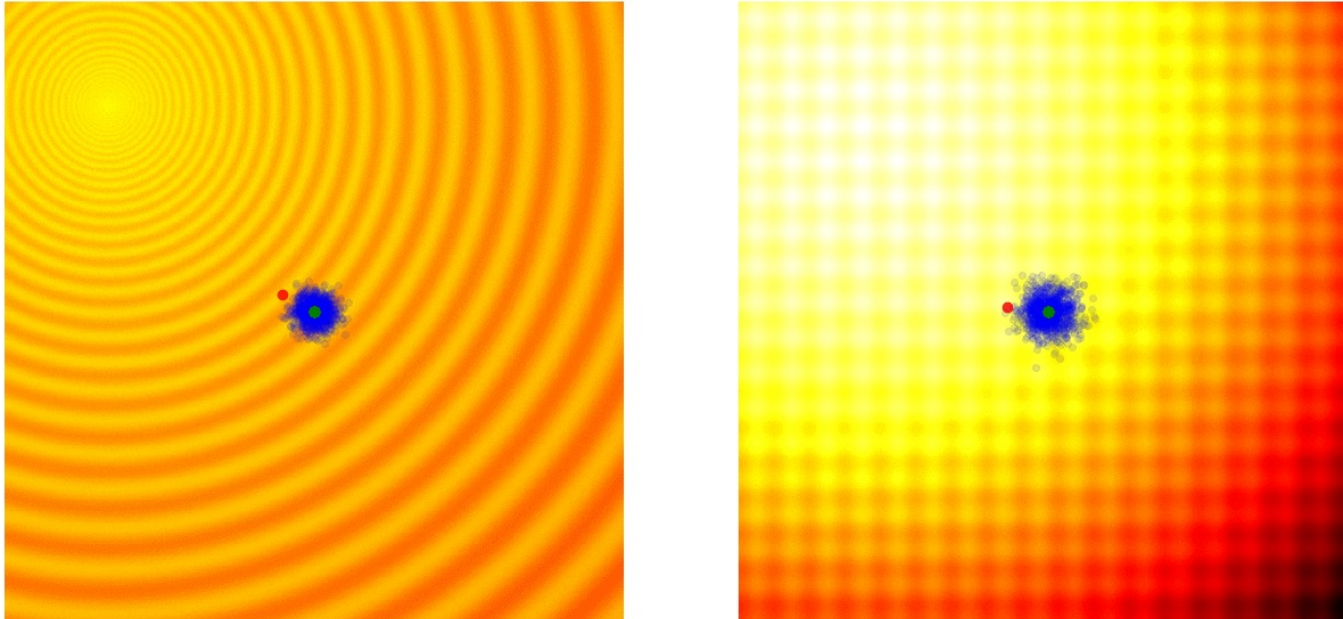
Goal: find a set of *parameters*  $(x,y)$ ,  
such that  $F(x,y)$  is as close as possible to the global maximum

More test functions: [https://en.wikipedia.org/wiki/Test\\_functions\\_for\\_optimization](https://en.wikipedia.org/wiki/Test_functions_for_optimization)

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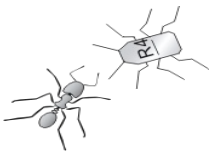
# A Simple Evolutionary Algorithm



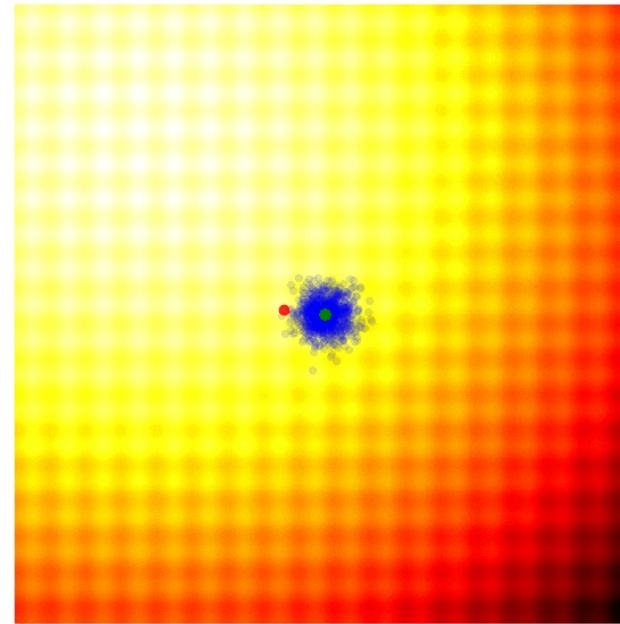
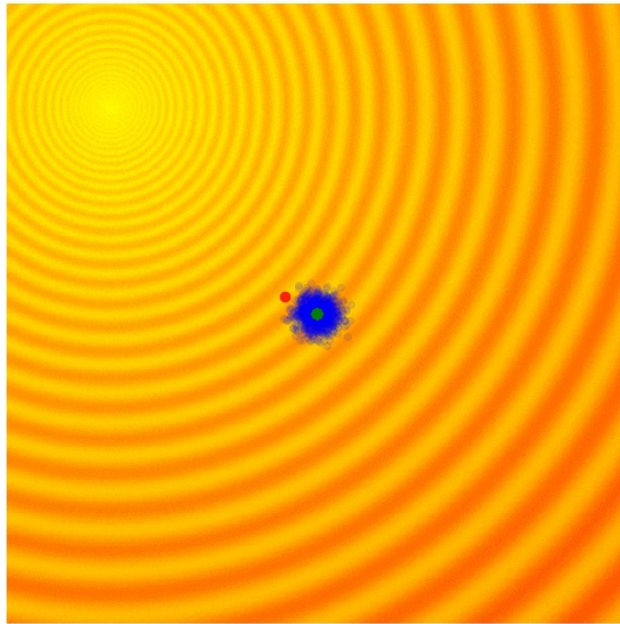
1. Sample initial population from Normal distribution, with mean  $\mu=(\mu_x,\mu_y)$  and standard deviation  $\sigma=(\sigma_x,\sigma_y)$  set at the axis origin
2. Select best 10% and make copies to create new population
3. Crossover and mutate by adding Gaussian noise with fixed  $\sigma$
4. Repeat steps 2&3 until satisfactory solution is found

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## 20 generations



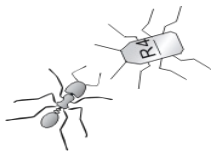
Blue dots show the individuals of the current generation

Red dot shows the best individual of the current generation

Green dots show the selected parents of the previous generation

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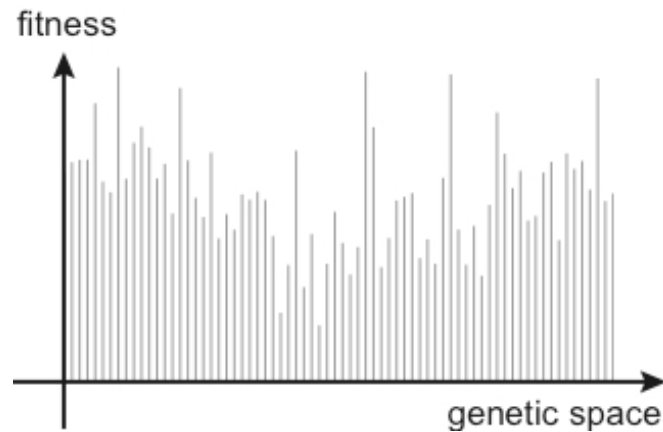


# Measuring evolvability: Fitness Landscape

Fitness landscape is a theoretical plot of fitness values associated to all genotypes

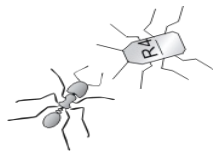
Landscape ruggedness helps identify population size, selection pressure, mutation

Notion of landscape can be deceptive



Estimating ruggedness of real landscape:

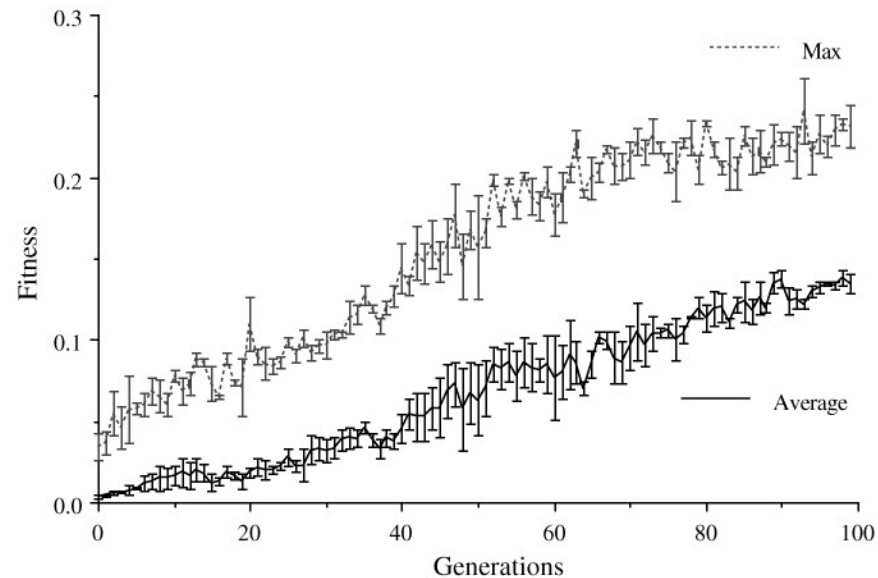
- Sample random genotypes: if flat, use large populations
- Explore surroundings of individual by applying genetic operators in sequence for fixed number of times: the larger the fitness improvement, the smaller the population size



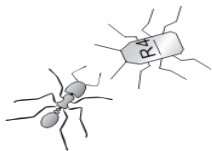
# Measuring Performance: Fitness Graph

Track best and population average fitness of each generation

Multiple runs are necessary: plot average data and standard error



- Fitness graphs are meaningful only if the problem is stationary
- Stagnation of fitness function may mean best solution found or premature convergence



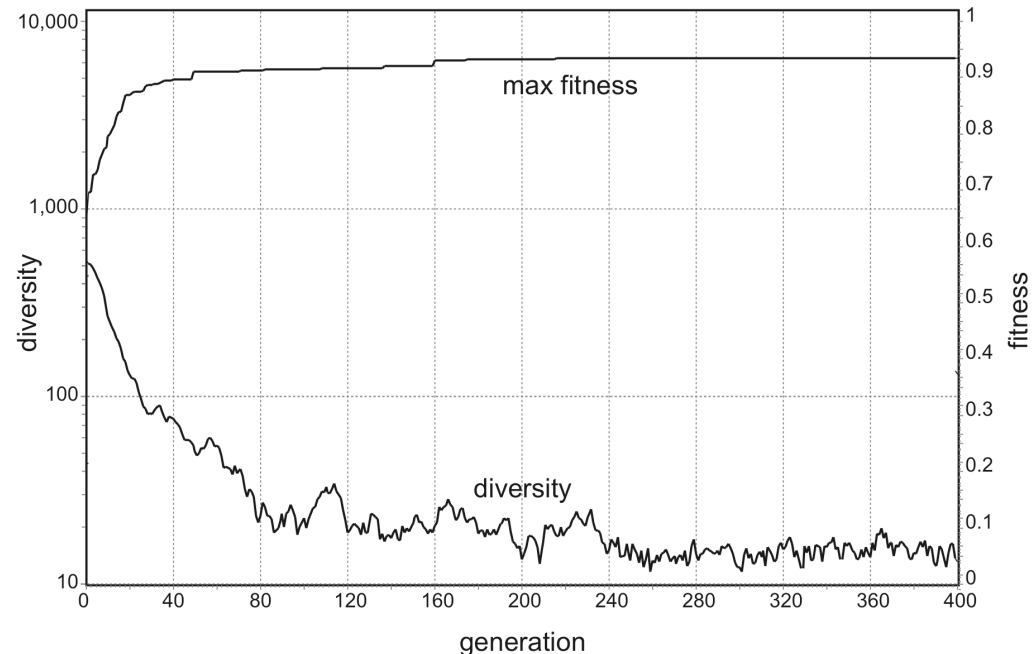
# Measuring Diversity: Genotype distance

Diversity tells whether the population has potential for further evolution

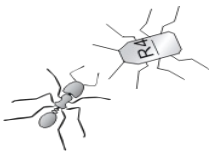
Measures of diversity depend on genetic representation

E.g., for binary and real valued, use sum of Euclidean or Hamming distances

$$D_a(P) = \sum_{i,j \in P} d(g_i, g_j)$$

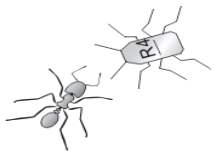
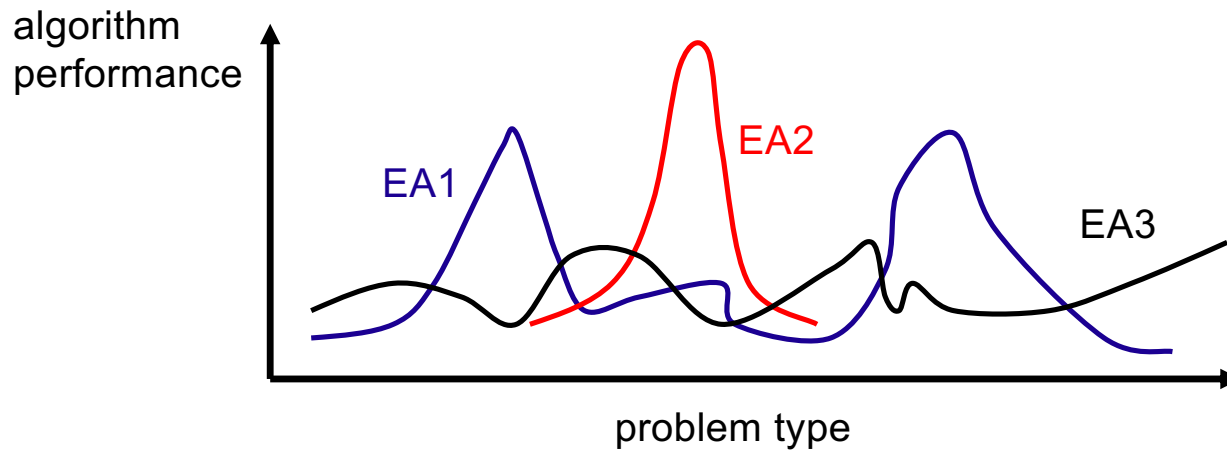


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# Applicability

- Evolutionary algorithms can be used for any problem
- Different problems may require different algorithms
- Knowledge of problem domain can help to choose best algorithm



# Examples of Evolutionary Algorithms

**Genetic Algorithms (GA)** - Holland, 1975

Binary genotypes, crossover and mutation

**Genetic Programming (GP)** - Koza, 1992

Tree-based genotypes, crossover and mutations

**Steady-State GA (SSGA)** – Whitley et al., 1988

Gradual replacement: Best individuals replace worst individuals

**Differential Evolution (DE)** – Storn & Prince, 1996

As SSGA, but with differential factor

**Evolutionary Strategies (ES)** - Rechenberg, 1973

Real-valued genotypes, mutation step(s) encoded in genotype

**Covariance Matrix Adaptation ES (CMA-ES)** – Hansen & Ostermeier, 2001

Evolutionary Strategies with correlated and adaptive mutations

**Non-dominated Sorting GA (NSGA)**– Srinivas, Deb, 1998

Multi-objective evolutionary optimization

**Viability Evolution (ViE)**– Maesani, Mattiussi, Floreano, 2014

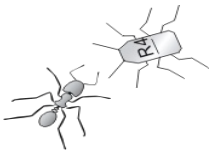
Evolution without fitness ranking and diversity preservation

**MAP Elites** – Mouret and Clune, 2015

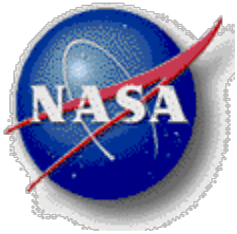
Preserve diversity by making similar solutions compete with each other

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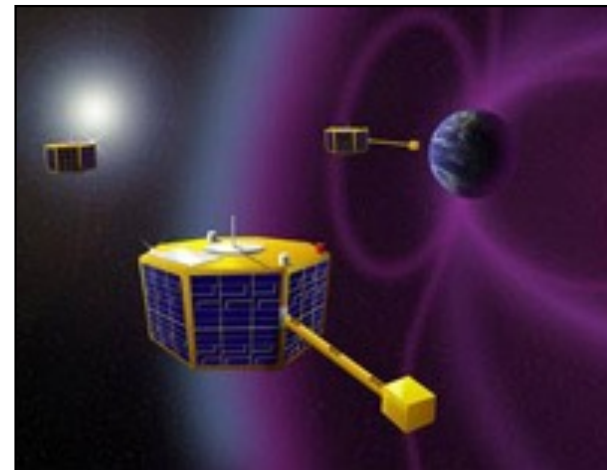
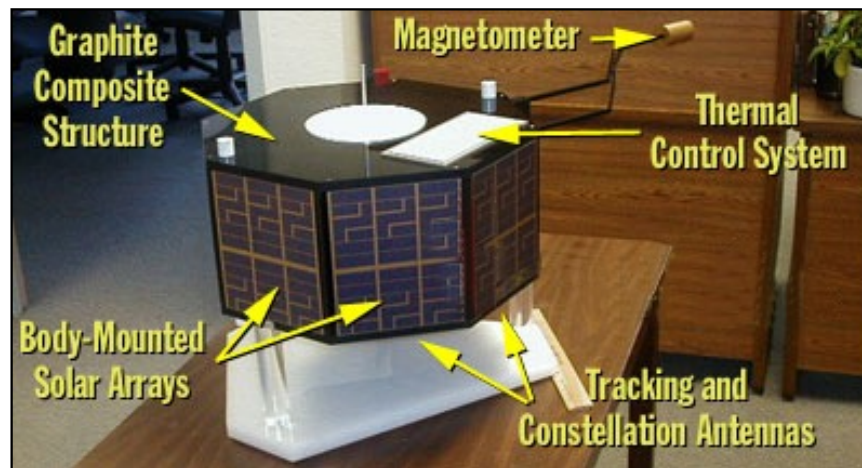


# Evolutionary Design of Nanosatellite Antenna

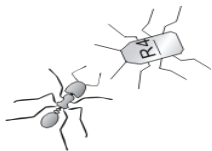


ST5 mission: Measure effect of solar activity on the Earth's magnetosphere  
3 nanosatellites (50 cm)  
Design of antenna to send data to ground station

[Lohn, Hornby, Linden, 2004]



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# Genetic Programming of Antenna Fabrication

Tree-based Encoding with Genetic Programming

Evaluate fitness in simulation

Build best and test in anechoic chamber

## Function Set

f = forward (length, radius)

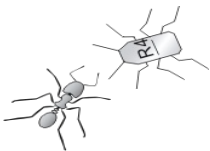
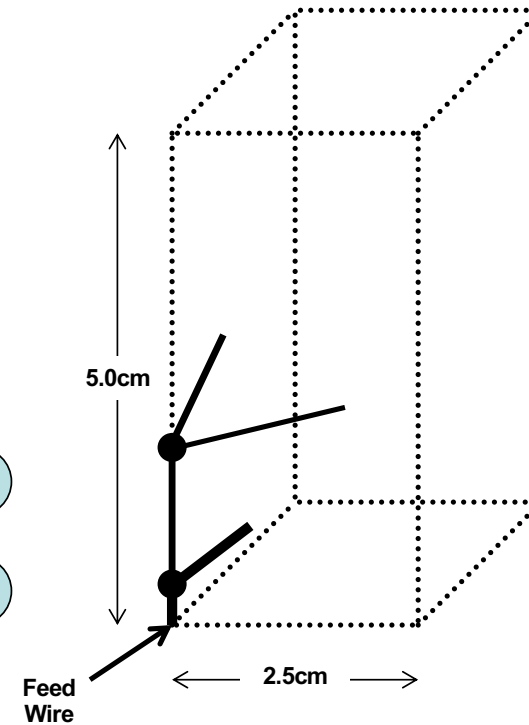
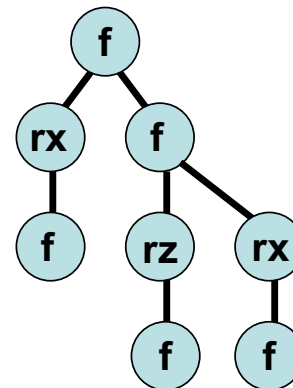
r x/y/z = rotate x/y/z

## Terminal Set

Length, radius, x, y, z

## Constraint:

max. 3 branches for each f node

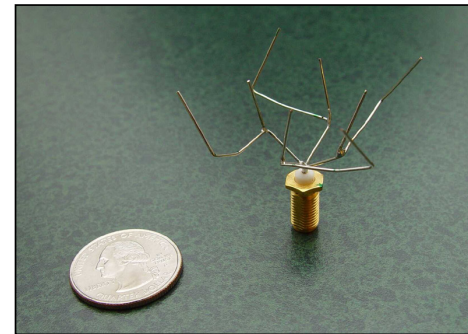


# Comparison human/evolved

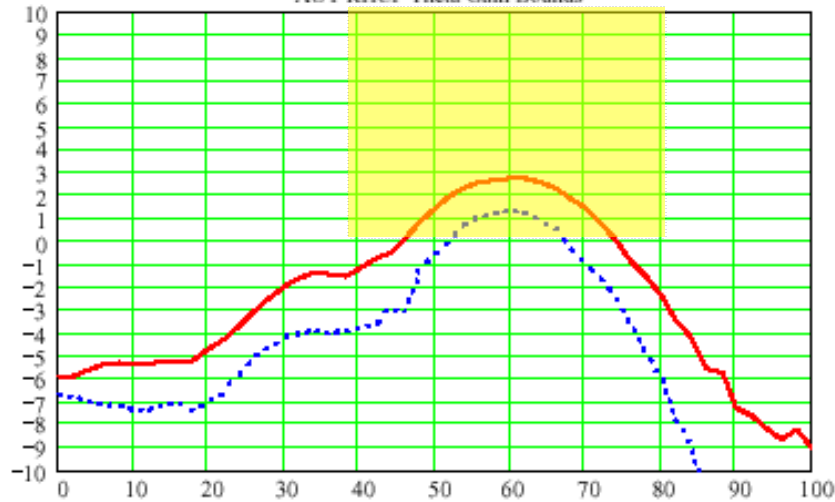
Human



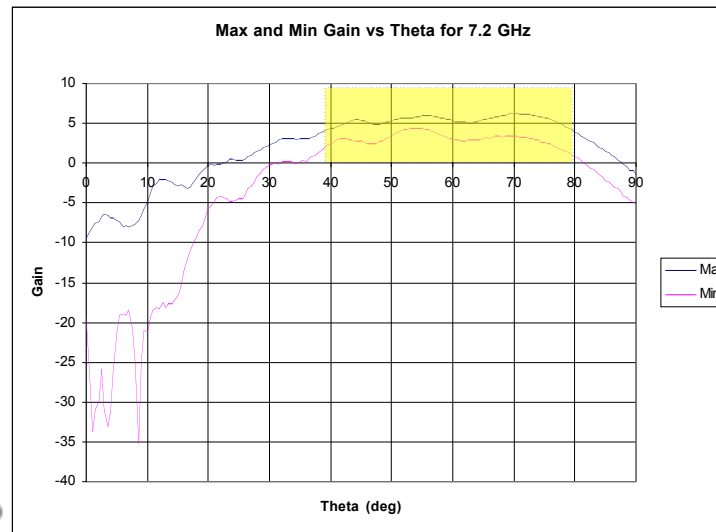
Evolved



AUT RHCP Theta Gain Bounds



Max and Min Gain vs Theta for 7.2 GHz



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