Genetic Algorithms

Part 3: The Knapsack Problem

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Outline

Problem Definition

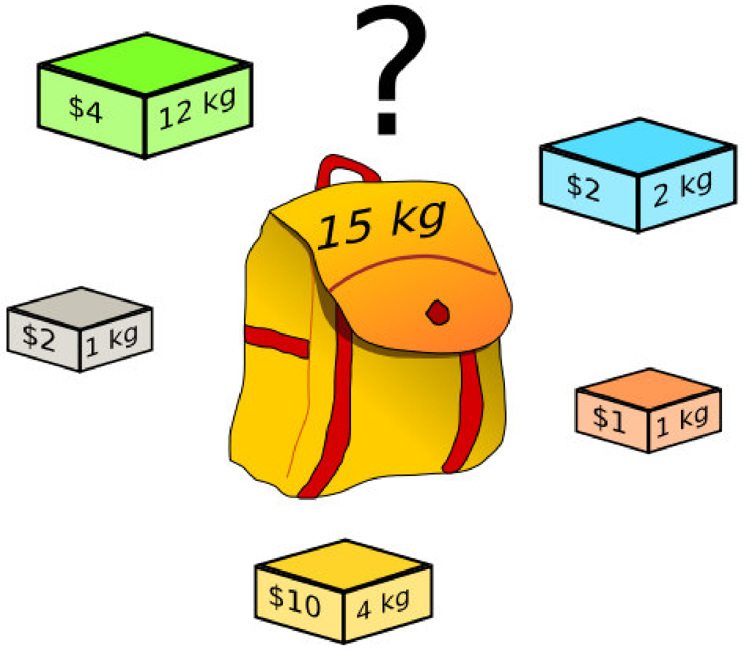
Example: The Knapsack problem

- There are *n* items:
  - Each item *i* has a weight w_i
  - Each item *i* has a value v_i
- The knapsack has a limited capacity of W units.
- We can take one of each item at most

$$\max \sum_i v_i * x_i \qquad i = 1,2,\ldots,n$$

$$\textit{subject to} \ \sum_i w_i * x_i \leq W$$

$$x_i \in \{0,1\}$$



Example: The Knapsack problem

Item:	**1**	**2**	**3**	**4**	**5**	**6**	**7**
Benefit:	**5**	**8**	**3**	**2**	**7**	**9**	**4**
Weight:	**7**	**8**	**4**	**10**	**4**	**6**	**4**

- **Knapsack holds a maximum of 22 pounds**
- **Fill it to get the maximum benefit**
- The problem description:
  - Maximize $\sum_i v_i$
  - While $\sum_i w_i \leq W$

Representations

Representations

- Candidate solutions (individuals) exist in phenotype space
- They are encoded in chromosomes, which exist in genotype space
- Chromosomes contain genes, which are usually in fixed positions called (loci / locus) and have a value (allele)

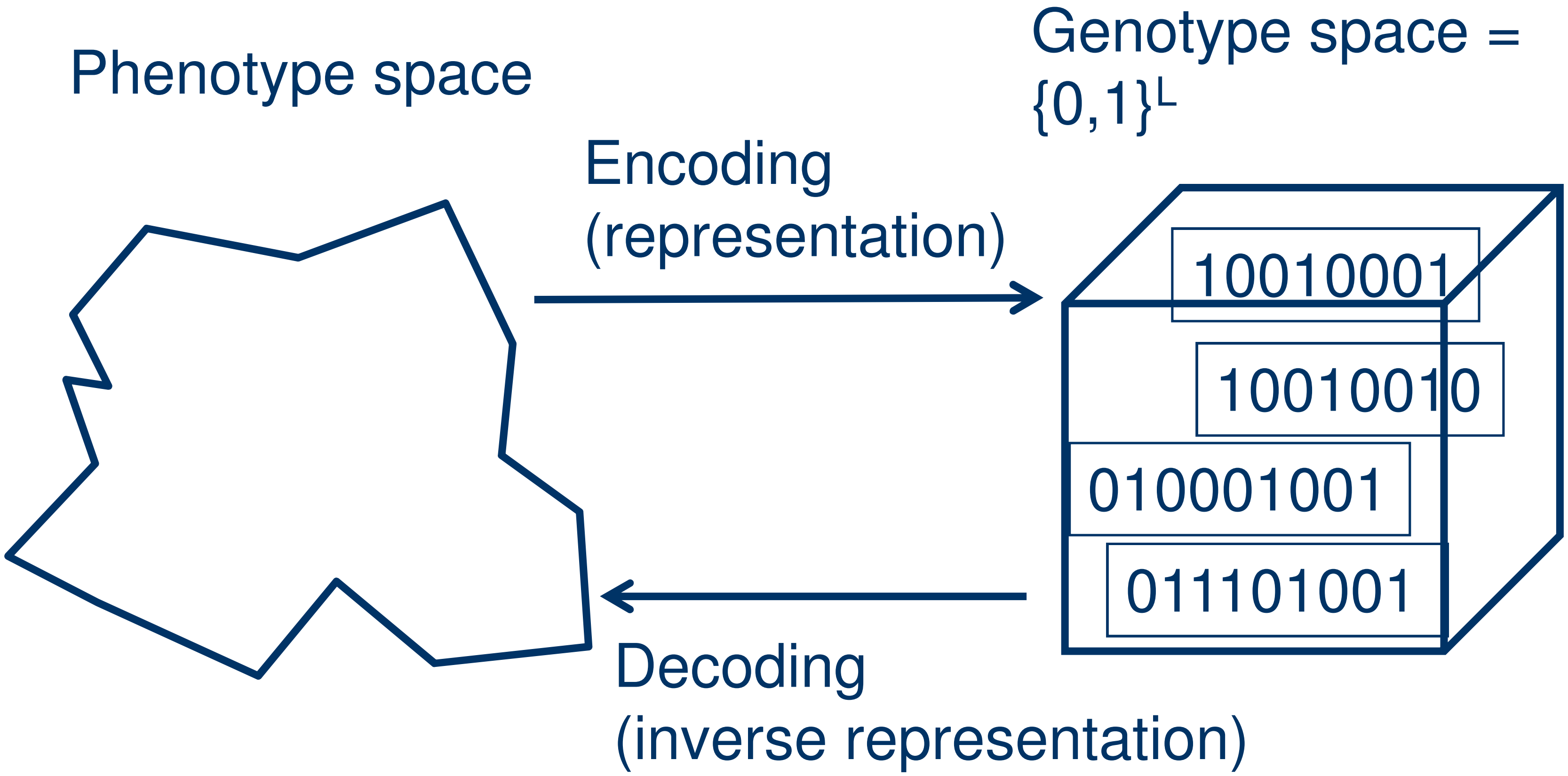
Representations

- For example, given an optimization problem on integers:
  - The given **set of integers** would form the set of phenotypes
  - They can be represented by binary code
  - **18** would be seen as a phenotype, and 10010 as a genotype representing it
- In order to find the **global optimum**, every feasible solution must be represented in genotype space

Representations

- A solution (**a good phenotype**) is obtained by decoding the best genotype after **termination**
- Coding can be done in two different ways:
  - **Encoding**:
    - the mapping from the phenotype to the genotype space
    - phenotype=> genotype
  - **Decoding**:
    - the inverse mapping from genotypes to phenotypes
    - genotype=> phenotype

Binary Representation



Knapsack Example: Representations

- Solutions take the form of a string of 1's and 0's
- Where

  0 = don't take the item in a given positions

  1 = take the item in a given positions
- Solutions: Also known as strings of genes called Chromosomes
- Example chromosomes:

  1100100 $\Rightarrow$ items {1,2,5} included in sack

  0010000 $\Rightarrow$ items {3} included in sack

  0001100 $\Rightarrow$ items {4,5} included in sack

  0100001 $\Rightarrow$ items {2,7} included in sack
- The genotype space *G* is the set of all strings with size 2^n

Fitness Function

Fitness Function

- **Fitness function** represents the requirements that the population should adapt to
- It defines what improvement means
  - i.e, **quality function** or **objective function**
- Assigns a single real-valued fitness to each phenotype which forms the basis for selection
- Typically we talk about fitness being maximised
  - Some problems may be best posed as minimisation problems, but conversion is easy

Knapsack Example: Fitness Function

- The fitness function as the total benefit, which is the sum of
  - the gene values in a string solution **x** their representative benefit coefficient

$$Fitness = \sum_i v_i : \left(\sum_i w_i \leq W \right)$$

Knapsack Example: Solution 1

Item	1	2	3	4	5	6	7
Solution	**1**	**1**	**0**	**0**	**1**	**0**	**0**
Benefit	5	8	3	2	7	9	4
Weight	7	8	4	10	4	6	4

- Fitness: 5 + 8 + 7 = 20
- Weight: 7 + 8 + 4 = 19 <= 22

Handling of Constraints

Knapsack Example: Solution 2 overweighted

Item	1	2	3	4	5	6	7
Solution	**0**	**1**	**0**	**1**	**0**	**1**	**0**
Benefit	5	8	3	2	7	9	4
Weight	7	8	4	10	4	6	4

- Weight: 8 + 10 + 6 = 24 > 22

The trouble with constraints and EAs

- Standard reproduction operators are **blind** to constraints.
- **Recombining** two feasible individuals can result in infeasible new individuals.
- **Mutating** a feasible individual can result in an infeasible new individual.

Handling of Constraints

- **Constraint handling**:
  - Eliminating infeasible candidates
  - Penalizing functions
  - Repairing infeasible candidates

Eliminating of Infeasible Candidates

- Additional version of penalty approach (i.e., the most severe penalty: death penalty
- Disadvantages:
  1. For some problems the probability of generating a feasible solution is relatively small and the algorithm spends a significant amount of time evaluating illegal individuals.
  2. In this approach non-feasible solutions do not contribute to the gene-pool of any population

Penalizing Functions

- Generating potential solutions without considering the constraints and then to penalize them by decreasing the "goodness" of the evaluation function.
- A variety of possible penalty functions which can be applied
  - assign a constant as a penalty measure
  - assign a penalty measure depend on the degree of violation: the larger violation is, the greater penalty is imposed
  - the growth of the penalty can be logarithmic, linear, quadratic, exponential, etc.

Knapsack Example: if overweight

- Penalize:

$$Fitness = \begin{cases} \sum_i v_i : \left(\sum_i w_i \leq W \right) \\ W - \sum_i w_i : (otherwise) \end{cases}$$

Knapsack Example: Solution 2 overweighted

Item	1	2	3	4	5	6	7
Solution	**0**	**1**	**0**	**1**	**0**	**1**	**0**
Benefit	5	8	3	2	7	9	4
Weight	7	8	4	10	4	6	4

- Fitness (Benefit): 22 – (8 + 10 + 6) = -2
- Weight: 8 + 10 + 6 = 24 > 22

Repair Algorithms

- Special **repair algorithms** to "correct" any infeasible solutions so generated.
- **Disadvantages:**
  1. Such repair algorithms might be computationally intensive to run and the resulting algorithm must be tailored to the particular application.
  2. Moreover, for some problems the process of correcting a solution may be as difficult as solving the original problem.

Knapsack Example: if overweight

- Repair:
  - When creating solution we read from left to right along binary string,
  - We first check to see if including the item would break our capacity constraint
  - We interpret it as meaning include this item, IF it does not take us over the weight constraint
  - We do not add the right of the current position to the solution
  - This makes the mapping from genotype to phenotype space many-to-one.

Population

Population

- Population holds (representations of) **possible solutions**
- Usually has a fixed size and is a **multiset** of genotypes
- Selection operators usually take whole population into account
  - i.e., parent selection mechanisms are relative to current generation

Population

- **Diversity of a population** refers to the difference solutions
  - The number of fitness's / phenotypes / genotypes present
- **Population size** may be around 500, but for difficult problems is can be larger
  - Too few chromosomes $\Rightarrow$ the GA won’t have the diversity needed to find a good solution
  - Too many $\Rightarrow$ the GA will be much slower, without much improvement in the quality of the solution

Knapsack Example: Population

- We will work with a **population size of 500**
- We will create **same number of offspring** as we have members our initial population (500)

Parent Selection Mechanism

Parent Selection Mechanism

- An individual is a **parent** if it has been selected to create offspring
- In GA, **parent selection** is usually probabilistic:
  - high quality individuals (solutions) more likely to become parents than low quality
  - but not guaranteed
  - worst in current population usually has non-zero probability of becoming a parent
- This stochastic nature can aid escape from local optima

Knapsack Example: Parents Selection

- We will use a **tournament** for selecting the parents
  - where each time we pick two members of the population at random (with replacement), and the one with the highest fitness value

Variation Operators

Variation Operators

- **Variation operators** are to generate new candidate solutions
- Usually divided into two types according to their **arity** (number of inputs):
  - Arity = 1 : **mutation operators**
  - Arity ≥ 2 : **Recombination operators** (e.g. Arity = 2 typically called **crossover**)
- There has been much debate about relative importance of recombination and mutation
  - Nowadays most GAs use both
  - Choice of particular variation operators depends upon genotype representation used.

Mutation

- **Mutation** is **unary variation operator** (it applies to one object as input)
- Acts on one genotype and delivers another, the child or offspring of it
- A mutation operator is **stochastic**
- Nature of the mutation operator depends upon the genotype representation
  - For example: flipping one or several bits with a given (small) probability.

Recombination

- A **binary variation operator** (it applies to **two objects** as input) is called **recombination** or **crossover**
- It merges information from **two parent** genotypes into one or two offspring genotypes
- Similar to mutation recombination is a **stochastic** operator
  - Choice of what information to merge is stochastic

Recombination

- The principle behind recombination is simple,
  - by mating two individuals with different but desirable features, we can produce an offspring that combines both of two features
- Most offspring may be worse, or the same as the parents
- Hope is that some are better by combining elements of genotypes that lead to good traits
- Principle has been used for millennia by breeders of plants and livestock

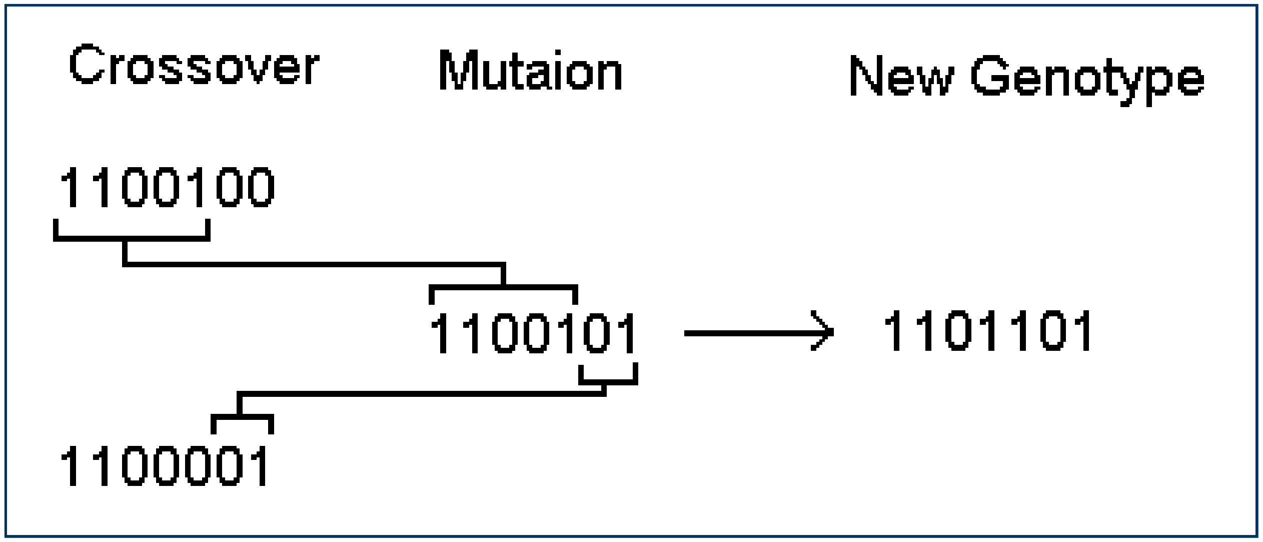
Knapsack Example: Recombination

- A suitable recombination operator is **one-point crossover**
- We will apply crossover
  - with 70% probability and
  - for other 30% we will make copies of the parents
- We align two parents for crossing over and pick a random point along their length
- The two offspring are created by exchanging the tails of the parents at that point

Knapsack Example: Mutation Operator

- A suitable mutation operator is so-called **bit-flipping**
- **Mutation rate:**
  - In each position we invert the value with a small probability [0, 1)
- We define a **mutation rate** of $P_m = 1/n$,
  - i.e. that on average 1 gene per recombination mutated
  - n: number of genes in a chromosome

Knapsack Example: Crossover & Mutation Operator



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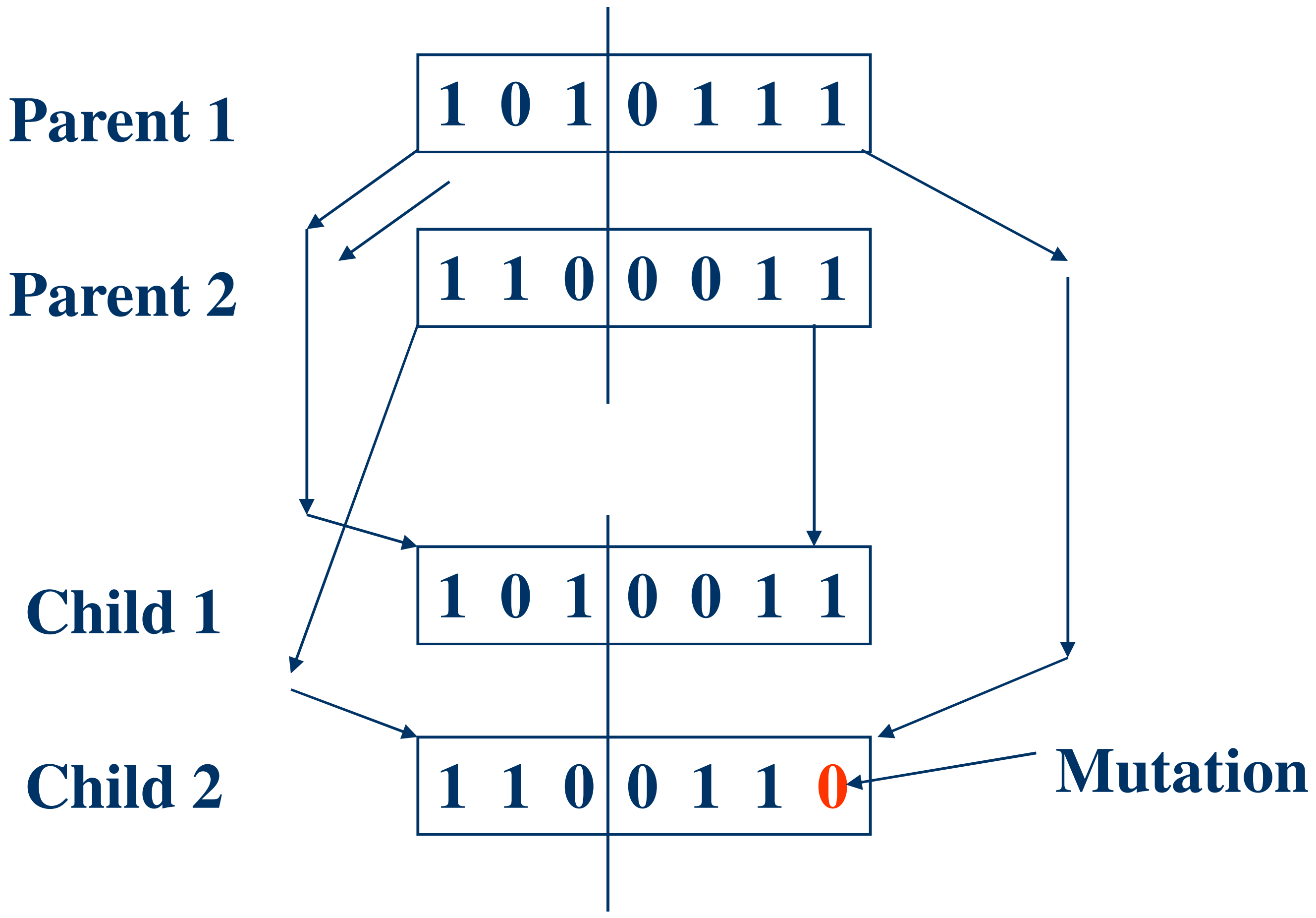
Knapsack Example: Crossover & Mutation Operator



Survivor Selection

Survivor Selection (Replacement)

- **Survivor selection mechanism** (**replacement**) is called after created the offspring of the selected parents
- Most GAs use fixed population size so need a way of going from (parents + offspring) to next generation
- Survivor selection often is **deterministic**
  - **Fitness based**: e.g., rank parents+offspring and take best
  - **Age based**: make as many offspring as parents and delete all parents

Knapsack Example: Survivor Selection

- We will use a **generational scheme** for survivor selection
  - In this scheme, all the population in each iteration are discarded and replaced by their offspring

Initialization and Termination

Initialization

- **Initialization** usually done at **random**
- The first population is created by randomly generated individuals
- We can use problem-specific heuristics, to seed an initial population with higher fitness
- Need to ensure even spread and mixture of possible allele values

Termination

- **Termination condition** checked every generation
- Reaching some (known/hoped for) fitness
  - GAs are stochastic and there are no guarantees to reach an specific fitness
- Therefore we need another condition

Termination

- Options for certainly stops:
  - Reaching maximum allowed **CPU time** elapses
  - Reaching some maximum allowed **number of generations**
  - Reaching some specified **number of generations without fitness improvement**
  - Reaching **population convergence**

Convergence

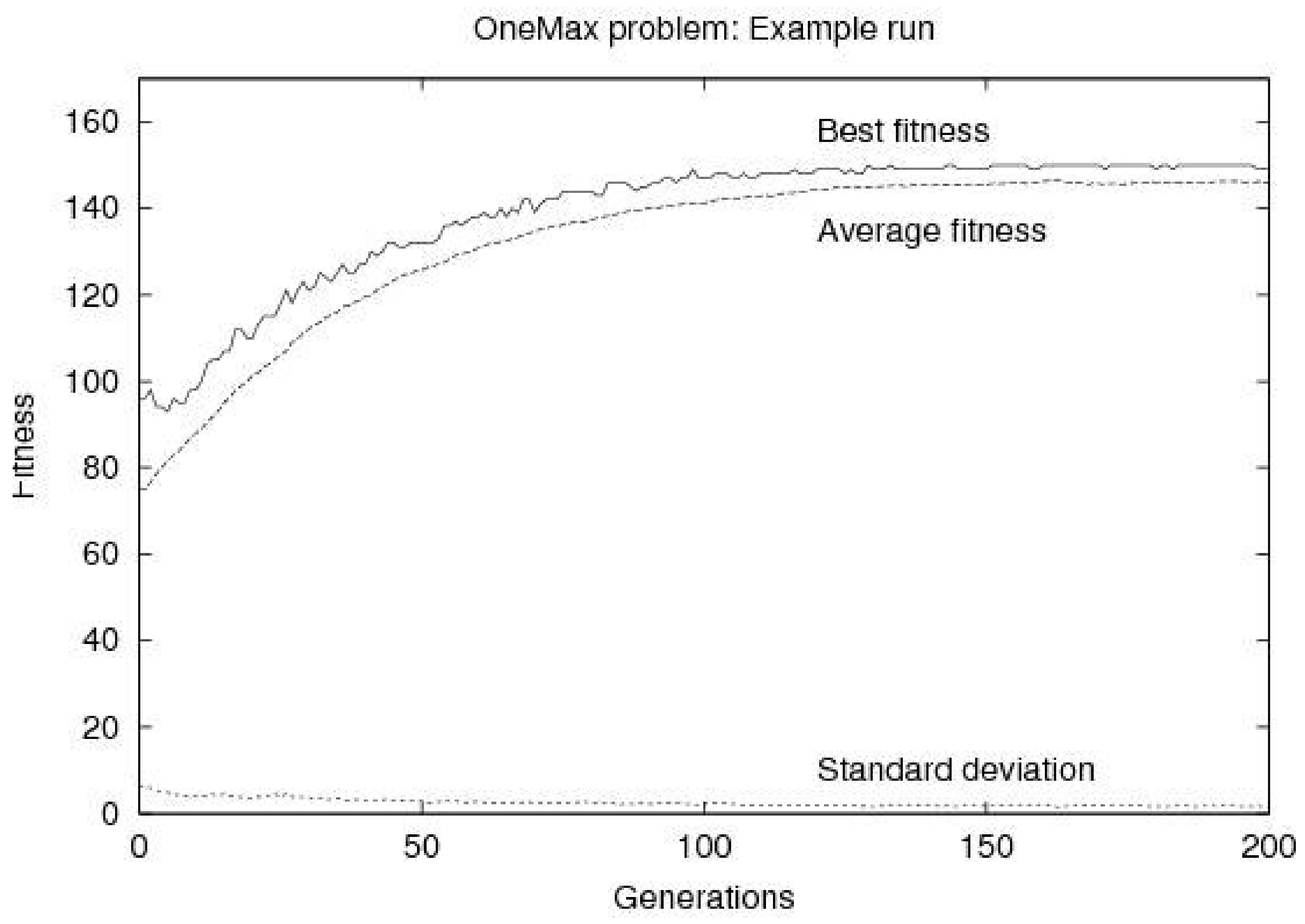
- **Gene convergence**:
  - when 95% of the individuals have the same value for that gene
- **Population convergence**:
  - when **all genes** (**chromosomes**) have converged
  - average fitness approaches best

Convergence

- Example 1: Gene convergence
  - 100% of 4th gene is 1
- Example 2: Population convergence
  - 75% of genes is same

Example 1:	Example 2:
i1: 01010	i1: 11111
i2: 10010	i2: 11111
i3: 00010	i3: 11010
i4: 11010	i4: 11111

Convergence



Knapsack Example: Initialization & Termination

- **Initialization:**
  - We all do initialization by random choice of 0 and 1 in each position of our initial population
- **Termination:**
  - We will run our algorithm until no improvement in the fitness of the best number of the population has been observed for **25 generations**

Knapsack Example: Summary

Representation: Binary strings of length n

Recombination: One-point crossover

Recombination probability: 70%

Mutation: Each value inverted with independent probability P_m

Mutation probability P_m: $1/n$ (Average 1 gene per recombination mutated)

Parent Selection: Best out of random 2 (Tournament)

Knapsack Example: Summary

Survivor Selection: Replace all (Generational)

Population Size: 500

Number of offspring: 500

Initialization: Random

Termination Condition: No improvement in last 25 generations

Note: this **only one possible** set of operators and parameters!

References

References

- Eiben and Smith. **Introduction to Evolutionary Computing**, Springer-Verlag, New York, 2003.
- J. Dreo A. Petrowski, P. Siarry E. Taillard, **Metaheuristics for Hard Optimization**, Springer-Verlag, 2006.

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