7. Genetic Algorithms7.2 The Knapsack Problem

Fall 2010 Instructor: Dr. Masoud Yaghini

Outline

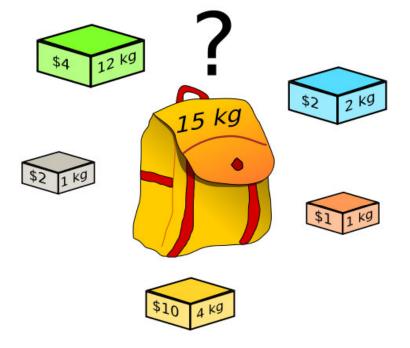
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Problem Definition

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

$$\begin{array}{ll} \max \sum_{i} v_{i} \ast x_{i} & i = 1, 2, ..., n\\ subject to & \sum_{i} w_{i} \ast x_{i} \leq W\\ & x_{i} \in \{0, 1\} \end{array}$$



Example: The Knapsack problem

• Example:

- 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:

$$\sum_{i} W_{i} \leq W$$

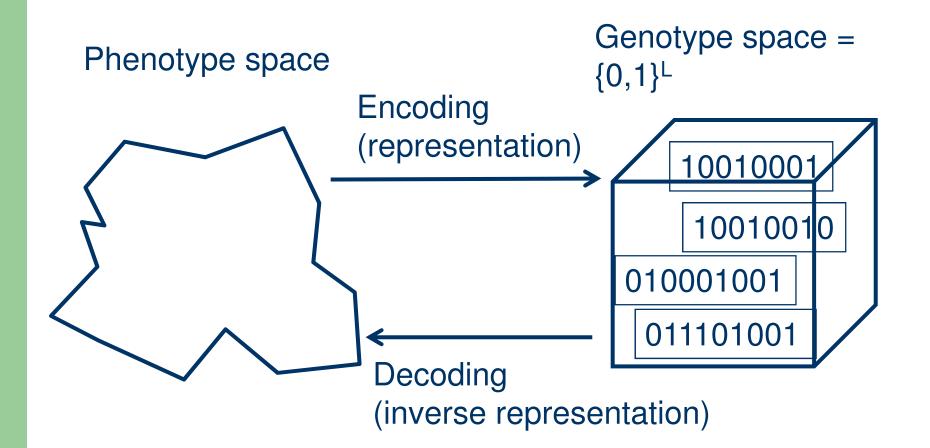
 \mathcal{V}_i

- 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 and have a value (allele)

- 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

- 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:

 $1100100 \Rightarrow \text{items } \{1,2,5\} \text{ included in sack}$ $0010000 \Rightarrow \text{items } \{3\} \text{ included in sack}$ $0001100 \Rightarrow \text{items } \{4,5\} \text{ included in sack}$ $0100001 \Rightarrow \text{items } \{2,7\} \text{ included in sack}$

• 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

$$Fitness = \sum_{i} v_i : \left(\sum_{i} w_i \le W\right)$$

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:

$$Fitness = \begin{cases} \sum_{i} v_{i} : \left(\sum_{i} w_{i} \le W\right) \\ W - \sum_{i} w_{i} : (otherwise) \end{cases}$$

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 50, but for difficult problems is can be larger
 - Too few chromosomes ⇒ 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 50
- We will create **same number of offspring** as we have members our initial population (50)

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 number of inputs:
 - number of inputs = 1 : mutation operators
 - number of inputs ≥ 2 : **Recombination operators**
 - number of inputs = 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

- Crossover is a binary variation operator (it applies to two objects as input) is called
- 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

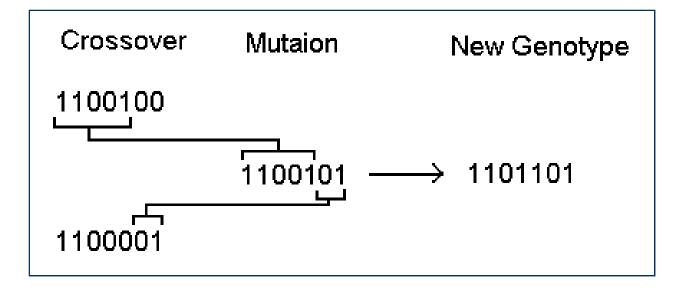
Knapsack Example: Recombination

- 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

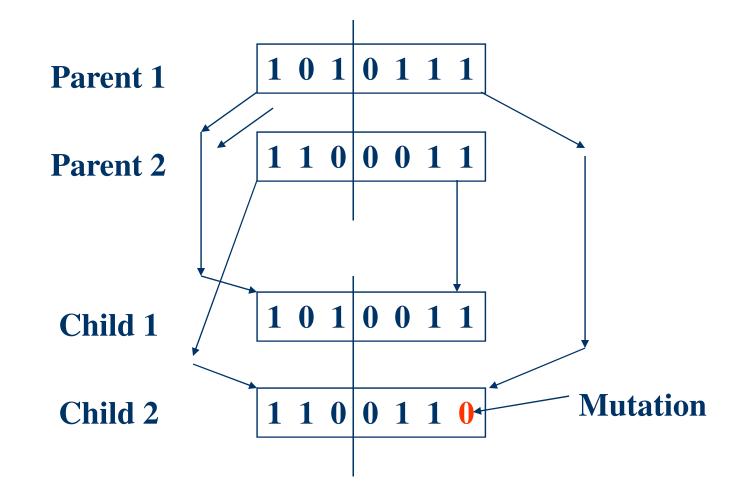
Knapsack Example: Mutation Operator

- A suitable mutation operator is so-called **bitflipping**
- 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



Knapsack Example: Crossover & Mutation Operator



Survivor Selection

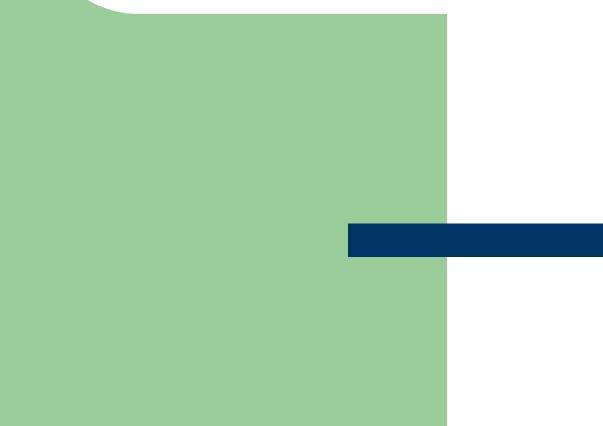
Survivor Selection (Replacement)

- 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 individuals (e.g. 95% of them) have the same value for that gene
- Chromosomes convergence:
 - When chromosomes (all genes) have converged
- Population convergence:
 - average fitness approaches best fitness

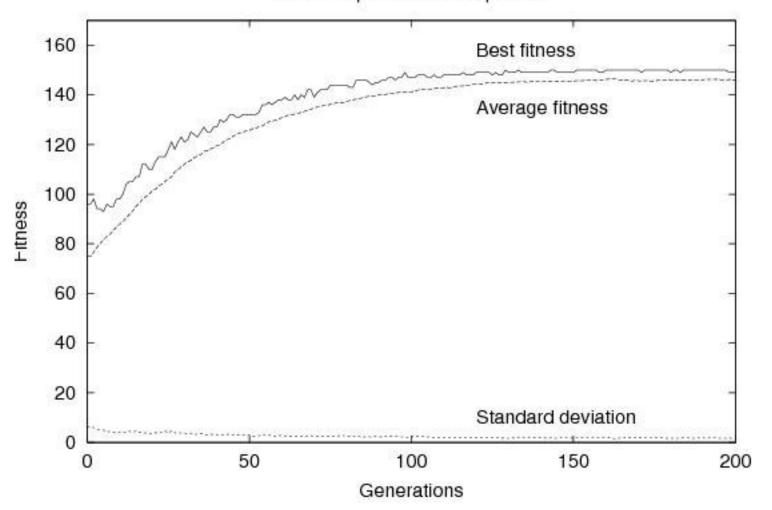
Gene & Chromosomes Convergence

- Example 1: Gene convergence
 - 100% of 4th gene is 1
- Example 2: Chromosomes 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

Population Convergence

OneMax problem: Example run



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

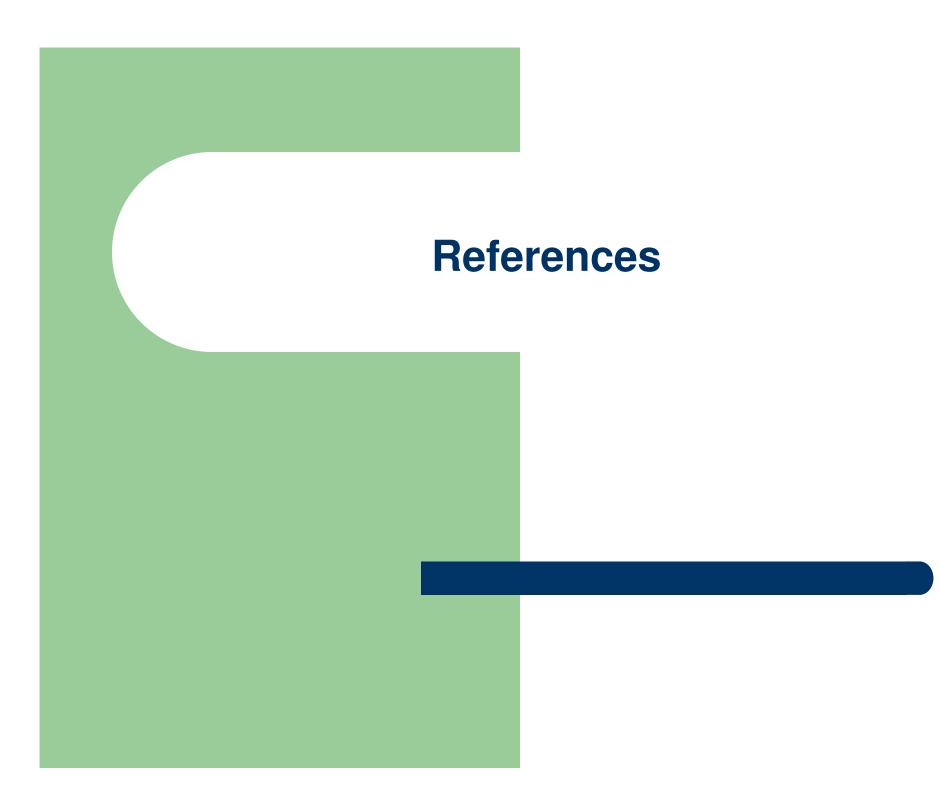
Knapsack Example: Summary

- **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:** 50
- Number of offspring: 50
- **Initialization:** Random
- **Termination Condition:** No improvement in last 25 generations
- Note: this only one possible set of operators and parameters!



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.

