

# Evolutionary Computation

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Master Artificial Intelligence

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# How does the genetic algorithm work?

A genetic algorithm is a **bio-inspired probabilistic algorithm**:

- initialize a set of individuals
- while *stopping criterium* not met
  - evaluate fitness of the individuals (in search space)
  - generate off-springs (mutation and crossover, in the encoding space)
  - generate a new generation, i.e., a subset of parents plus off-springs (selection)
- report best individual generated in the process

You'll work with this approach in the lab hours.

additional information and benchmark instances can be found at:

- <http://comopt.ifi.uni-heidelberg.de/software/TSPLIB95/> or
- <https://www.math.uwaterloo.ca/tsp/data/index.html>
- almost a counterexample of how to implement GA for TSP  
<https://jaketae.github.io/study/genetic-algorithm/>
- we use the work at  
<https://github.com/guofei9987/scikit-opt>

- Monte Carlo algorithms, and hence, evolutionary algorithms are often **quite easy to parallelize**.
- We will not talk about parallelization in this course, however, it is an important issue in order to achieve good performance on modern systems.

# the sorting problem

- **Sorting is a basic**, well known, and well studied problem.
- Given a sequence of  $n$  elements belonging to an orderable set, we have to compute a permutation of the input elements such that they are ordered (according to the underlying compare function).
- Simple example: given a sequence of integer numbers; sort ascending.
- Note that there are  $n!$  possible permutations.  
(Funny, the same number as there are tours in TSP.)

## checking a solution

- Before doing the actual sorting, let's first design an algorithm that **checks the results**, i.e., checks that the sequence is sorted.
- Remember: we require that we can **check with an algorithm** that the output/result of our initial algorithm is correct (i.e., fulfills the corresponding properties).
- Personally, I recommend that you **always** try to design and implement such a checker!
- As already stated: sometimes the properties of the output when using an evolutionary algorithm can be checked only **very weakly**.
- For TSP at least check: you got a tour, the gap lies inbetween known lower and upper bounds.

# checker for the sorting problem

Check whether a pair of elements is sorted:

```
def PairIsSorted(v, i, j):  
    return v[i] <= v[j]
```

Check whether a sequence of elements is sorted:

```
def IsSorted(v):  
    for i in range(len(v)-1):  
        if not PairIsSorted(v, i, i+1):  
            return False  
    return True
```

# the bubble sort algorithm

A **simple sorting** algorithm (bubble sort):

```
def PairSort(v, i, j): # sorts a pair
    if not PairIsSorted(v, i, j):
        v[i], v[j] = v[j], v[i]
```

```
def BubbleSort(v): # Las Vegas type
    while not IsSorted(v):
        for i in range(len(v)-1):
            PairSort(v, i, i+1)
```

Runs in quadratic time (worst case) and linear time (best case).



# Monte Carlo sorting

Let us implement a **Monte Carlo sorting** algorithm:  
we select a random pair of elements and interchange when  
necessary:

```
def MonteCarloSort (v, rounds) :  
    for j in range (rounds) :  
        i, j=RandomPair (v)  
        PairSort (v, i, j)
```

Whenever the number of rounds is sufficiently large and we are  
lucky, the sequence will become sorted.

# Las Vegas sorting

Let us implement a **Las Vegas sorting** algorithm: we select a random pair of elements, interchange when necessary, and stop when the sequence is sorted:

```
def LasVegasSort (v) :  
    while not IsSorted(v) :  
        i, j=RandomPair (v)  
        PairSort (v, i, j)
```

Maybe we need to wait a very long time, but we always get a sorted sequence. Observe: Las Vegas algorithms are easy to design, when we have a checker!



# Las Vegas Monte Carlo sorting

Whenever we have a checker, we can implement a Las Vegas algorithm on the base of a Monte Carlo algorithm, so for sorting we can do:

```
def LasVegasMonteCarloSort (v, rounds) :  
    while not IsSorted(v) :  
        MonteCarloSort (v, rounds)
```



# Monte Carlo sort with Las Vegas condition

We can improve the Monte Carlo sort introducing a Las Vegas condition to stop earlier:

```
def MonteCarloLasVegasSort (v, rounds) :  
    while not IsSorted(v) and rounds>0:  
        i, j=RandomPair (v)  
        PairSort (v, i, j)  
        rounds-=1
```

This idea reflects the **general structure of a heuristic** probabilistic algorithm: for a certain time do something maybe useful, and stop when a certain condition is met.

# Efficient sorting

An **efficient**  $O(n \log n)$  algorithm to sort is the merge-sort algorithm, here written in its iterative form (divide and conquer paradigm):

```
def Merge(v, w, left, middle, right):
    i, j = left, middle
    for k in range(left, right):
        if j >= right or (i < middle and PairIsSorted(v, i, j)):
            w[k] = v[i]; i += 1
        else:
            w[k] = v[j]; j += 1

def MergeSort(w):
    s, n = 1, len(w)
    while s < n:
        v = w[:]
        for left in range(0, n, 2*s):
            Merge(v, w, left, left+s, min(left+2*s, n))
        s *= 2
```



# sorting as an optimization problem

- In order to state the integer **sorting** problem **as** an **optimization** problem, we need to specify an objective function.
- Let  $x = (x_1, x_2, \dots, x_n)$  be the current sequence of integer values.
- We use  $f(x) = \sum_{i=1}^n i \cdot x_i$  as objective function.
- Our aim is to maximize  $f(x)$  at which point the sequence  $x$  is sorted; to minimize we take the negative value:

```
def SortObjective(v):  
    f=0  
    for i in range(len(v)):  
        f+=v[i]*(i+1)  
    return -f
```

or

```
def SortObjective(v):  
    return -sum([v[i]*(i+1) for i in range(len(v))])
```



# sorting as an optimization problem

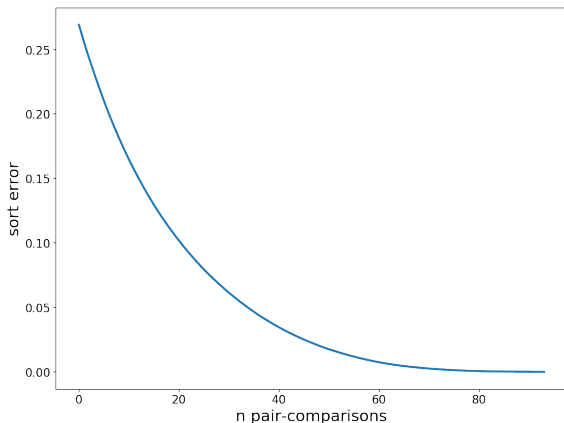
Now, we can use a **genetic algorithm** (e.g. the one we have for the TSP problem) to sort our sequence (note, we want an order on the cities, but now with our objective function for sorting and not the one for a minimal tour length).

```
def GASort (w) :  
    ga=GA_TSP (  
        func=fobj, n_dim=len(w), size_pop=100,  
        max_iter=1000, probab_mut=1  
    )  
    best_points,best_val=ga.run()  
    v=w.copy()  
    for i in range(len(best_points)) :  
        w[i]=v[int(best_points[i])]
```

More in lab hours (`fobj` will be computed on a different data structure).



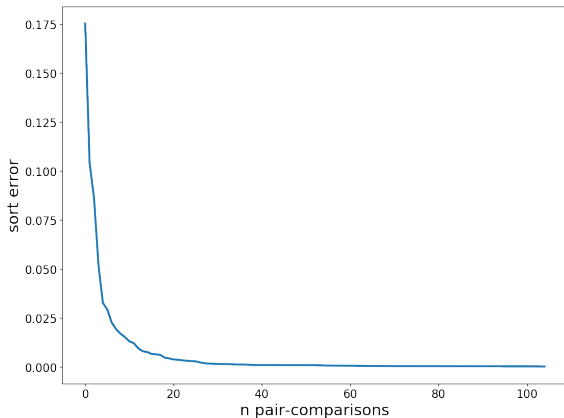
# convergence of bubble sort



Slow improvement, finds the minimum always.

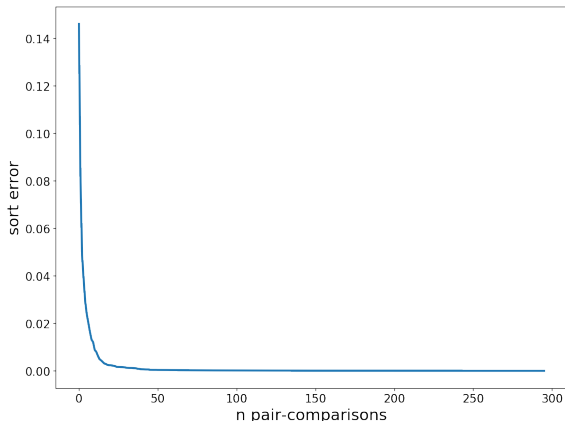


# convergence of Monte Carlo sort



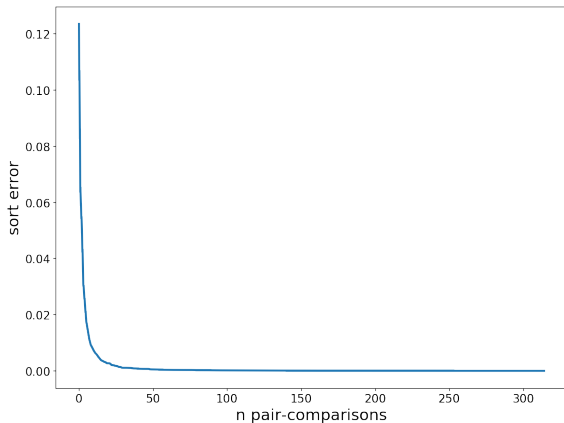
Fast improvement, fixed number of steps, might **not find** minimum.

# convergence of Las Vegas sort

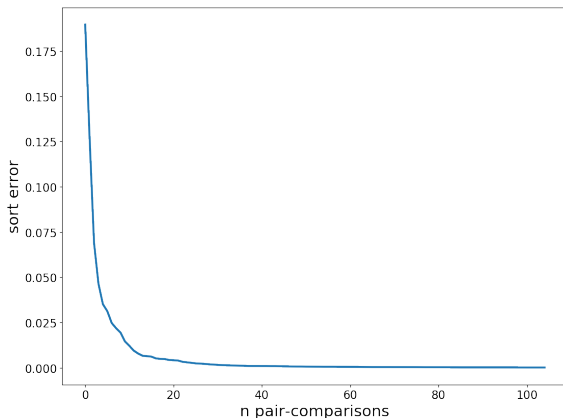


Fast improvement at the beginning, and slowly finds the minimum.

# convergence of Las Vegas with Monte Carlo sort

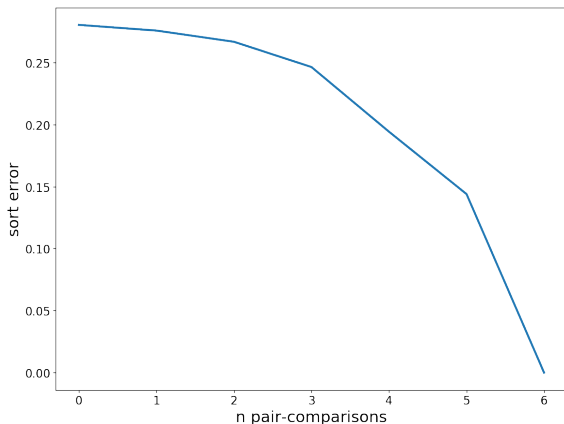


# convergence of Monte Carlo sort with Las Vegas condition



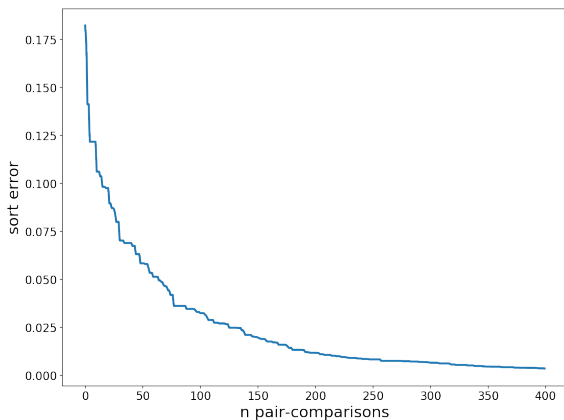
Fast improvement, but might **not find** minimum (however, stops if found).

# convergence of merge sort



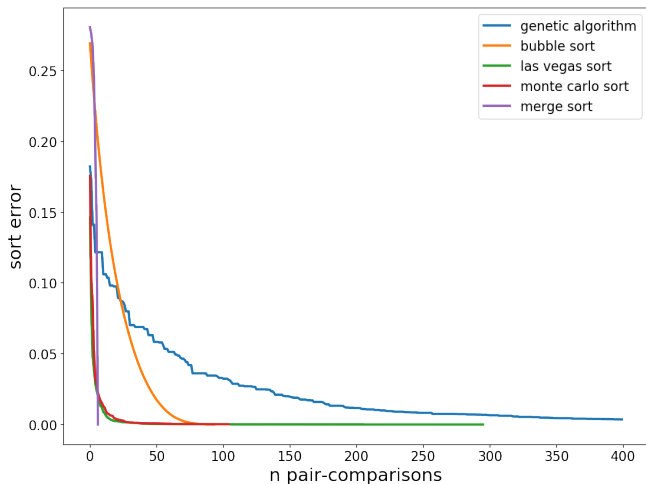
Deterministic very fast improvement, finds the minimum always!

# convergence of genetic algorithm sort



Well, works, but might **not find** the minimum.

# summary of *convergence* for sorting algorithms



Maybe the genetic algorithm is not the right choice,  
better stick to the deterministic classic one.



# Can we sort faster?

You can always ask: can we sort **faster**?

- It depends... when we have more information about the data, maybe we can sort faster!
- In the given example, we started with a random permutation of  $n$  consecutive numbers.
- So sorting them is easy: just count—starting at the minimum—up to  $n$ , hence, a linear time algorithm!
- It's always **worthwhile to analyse** the underlying data!



**Don't get betrayed** by a small number of program runs that might even *suggest* some good results (both in precision as well as in runtime).

You should always ask to see several/many runs, and to determine the variance of the results, so that you can compute the **Monte Carlo standard error**.

# The (0,1)-knapsack problem

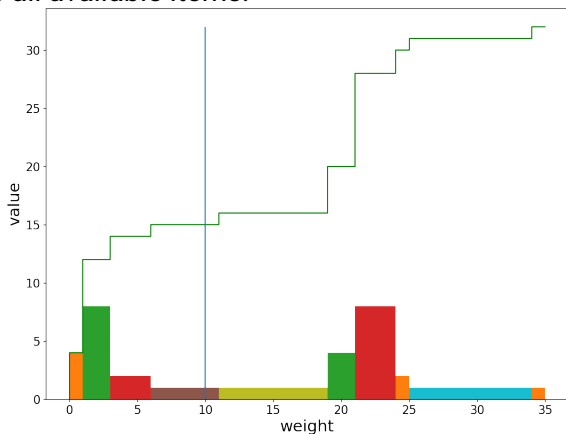
The (0,1)-knapsack problem (KSP) is another classical **combinatorial optimization** problem, where

- Given a set of items, each with a certain **weight** and **value**, and
- given a knapsack with a certain weight **capacity**,
- find the **maximum total value** you can carry with the knapsack.

Note that in this problem (in comparison to TSP or sorting) we have **infeasible** combinations (i.e., the subset might be too heavy).

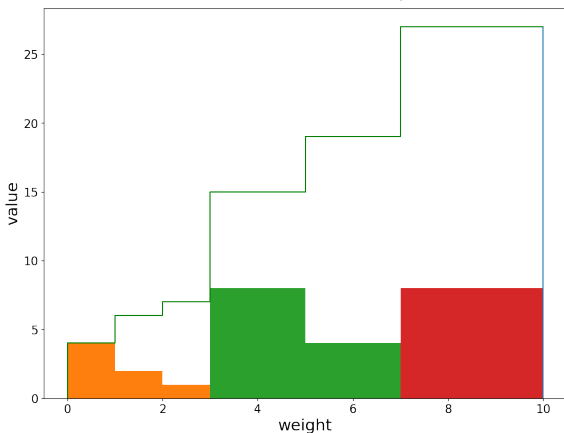
# an example knapsack problem

If we take all available items:



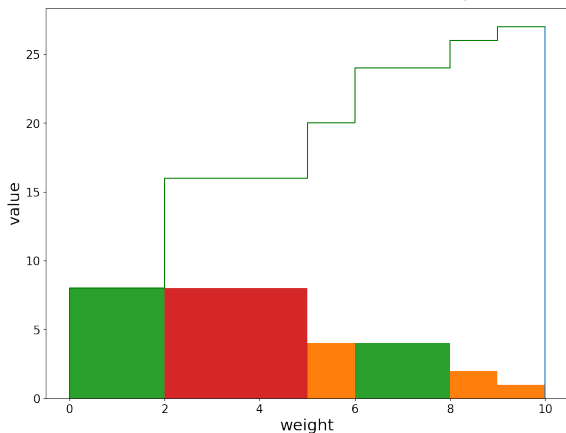
# packing the knapsack with greedy weight algorithm

We take the **lightest** items as long as they fit:



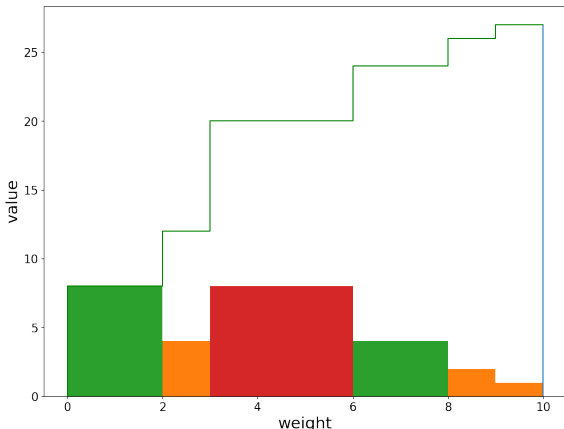
# packing the knapsack with greedy value algorithm

We take the **most valued** items as long as they fit:



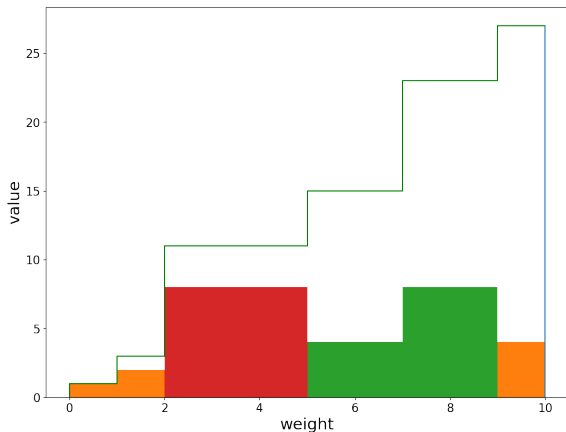
# packing the knapsack with greedy ratio algorithm

We take the **best rated** (value per weight unit) items as long as they fit:



# optimal packing the knapsack with dynamic programming

We find the **optimal** solution with dynamic programming:



# It seems all algorithms are great?

The previous algorithms all packed a value of 27 into the knapsack...

- You noticed that I have cheated?
- All algorithms found an optimal packaging!
- You know why?
- I was **lucky**.



# Evolutionary methods

- Evolutionary methods work with **populations** of individuals (or only one individual and a certain type of memory).
- There are probabilistic **modification processes** (mutation, reproduction, recombination/crossover) that change the population from one to the next generation.
- The **performance** of the individuals is based on a **fitness** which usually is the objective function (but not necessarily).
- There is a **selection process** to maintain a (more or less) stable state (size) of the population.
- Most of the algorithmic decisions are drawn **probabilistically**.

I will not give details on the history and researchers, please, take a look at the literature/bibliography.



# Genetic algorithms (GA)

- We distinguish the **genotype** (codification of the individuals) and the **phenotype** (elements of the search space).
- There must exist a **bijection** between genotype and phenotype.
- The genotype encodes the **free parameters** of an individual.
- The modifications (mutation and recombination/crossover) are carried out over the genotype.
- The fitness is evaluated over the phenotype (our objective function).
- We have to explain: codification (of the genotype), initialization, mutation, recombination/crossover, selection, and stopping.

A genetic algorithm can be summarized in the following principal loop:

```
InitializePopulation()      # initialization
EvaluateIndividuals()      # evaluation
while not Stopping():      # stopping
    DetermineParents()      # selection
    GenerateChildren()      # recombination
    MutateChildren()        # mutation
    EvaluateIndividuals()   # evaluation
    ReestablishPopulation() # selection
```

# GA: encoding of the individuals

There are many possibilities how to **encode** the free parameters of an individual to form its genotype:

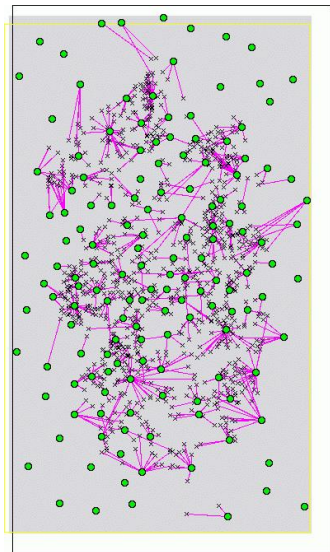
- use a binary bitstring, e.g., (101101)
- use a sequence of integer values in certain ranges, e.g.,  $(2, 6, 98, 3) \in [1 : 2] \times [1 : 10] \times [0 : 100] \times [1 : 5]$
- use a sequence of real values in certain ranges, e.g.,  $(1.23, 34.4, -2.1) \in [-50.0, 50.0]$
- use a permutation
- use a k-dimensional structure
- use a binary tree
- use a general graph
- use whatever you like (recall: do something, be happy...)

**Remember:** we need a bijection between genotype and phenotype and we need to implement crossovers and mutations that are able to explore the entire search space (or at least the region of interest).



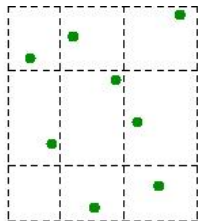
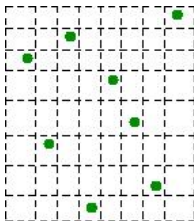
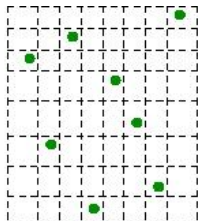
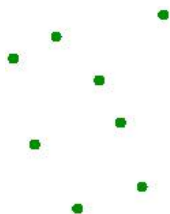
- The individual components of the sequences are called **genes**.
- The possible values of a gene are called **allele**.
- The encoding of an individual is called its **genome** or **chromosome**.

# GA: genotype an example



- green: base stations
- crosses: mobile users
- magenta: assignment
- **goal**: find the minimal subset of base stations that guarantees an assignment of all mobiles
- Note: computation of the objective function is quite complex (and will not be detailed here).

# GA: genotype an example



- initial
- $8 \times 8$  grid
- reduced to  $3 \times 3$  grid
- 4 allele (2-bit strings)
  - unusable
  - used
  - unused
  - fixed