DM841

Discrete Optimization - Heuristics

Evolutionary Algorithms

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Outline

1. Population Based Metaheuristics
    Evolutionary Algorithms

2. Multi-Objective Optimization

Evolutionary Algorithms

Key idea (Inspired by Darwinian model of biological evolution): Maintain a population of individuals that compete for survival, and generate new individuals, which in turn again compete for survival

Iteratively apply genetic operators: mutation, recombination, selection to a population of candidate solutions.

- Mutation introduces random variation in the genetic material of individuals (unary operator)
- Recombination of genetic material during reproduction produces offspring that combines features inherited from both parents (N-ary operator)
- Differences in evolutionary fitness lead selection of genetic traits (‘survival of the fittest’).

Evolutionary Algorithm (EA):

```
determine initial population sp

while termination criterion is not satisfied: do
    generate set spr of new candidate solutions
        by recombination

    generate set spm of new candidate solutions
        from spr and sp by mutation

    select new population sp from
        candidate solutions in sp, spr, and spm
```

Original Streams

- Evolutionary Programming [Fogel et al. 1966]:
  - mainly used in continuous optimization
  - typically does not make use of recombination and uses stochastic selection based on tournament mechanisms.
  - often seeks to adapt the program to the problem rather than the solutions
- Evolution Strategies [Rechenberg, 1973; Schwefel, 1981]:
  - similar to Evolutionary Programming (developed independently)
  - originally developed for (continuous) numerical optimization problems;
  - operate on more natural representations of candidate solutions;
  - use self-adaptation of perturbation strength achieved by mutation;
  - typically use elitist deterministic selection.
- Genetic Algorithms (GAs) [Holland, 1975; Goldberg, 1989]:
  - mostly for discrete optimization;
  - often encode candidate solutions as bit strings of fixed length, (which is now known to be disadvantageous for combinatorial problems such as the TSP).

Problem: Pure evolutionary algorithms often lack capability of sufficient search intensification.

Solution: Apply subsidiary local search after initialization, mutation and recombination.

Memetic Algorithms [Dawkins, 1997, Moscato, 1989]

- transmission of memes, mimicking cultural evolution which is supposed to be direct and Lamarckian
- (aka Genetic/Evolutionary Local Search, or Hybrid Evolutionary Algorithms if more involved local search including other metaheuristics, eg, tabu search)

Memetic Algorithm (MA):

```
determine initial population sp
perform subsidiary local search on sp
while termination criterion is not satisfied: do
    generate set spr of new candidate solutions
        by recombination
    perform subsidiary local search on spr
    generate set spm of new candidate solutions
        from spr and sp by mutation
    perform subsidiary local search on spm
    select new population sp from
        candidate solutions in sp, spr, and spm
```

Terminology

Individual	$\Longleftrightarrow$	Solution to a problem
Genotype space	$\Longleftrightarrow$	Set of all possible individuals determined by the solution encoding
Phenotype space	$\Longleftrightarrow$	Set of all possible individuals determined by the genotypes (ie, the variable–value themselves)
Population	$\Longleftrightarrow$	Set of candidate solutions
Chromosome	$\Longleftrightarrow$	Representation for a solution in the population
Gene and Allele	$\Longleftrightarrow$	Part and value of the representation of a solution (*e.g.*, parameter or degree of freedom)
Fitness	$\Longleftrightarrow$	Quality of a solution
Crossover Mutation	$\Longleftrightarrow$	Search Operators
Natural Selection	$\Longleftrightarrow$	Promoting the reuse of good solutions

Solution representation

Separation between solution encode/representation (genotype) from actual solution (phenotype)

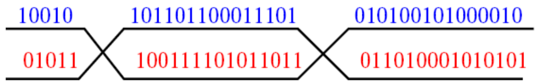
Let $\mathcal{X}$ be the search space of a problem

- genotype set made of strings of length l whose elements are symbols from an alphabet $\mathcal{A} \rightsquigarrow$ set of all individuals is $\mathcal{A}^l$
    - the elements of strings are the genes
    - the values that each element can take are the alleles
- the search space is $\mathcal{S} \subseteq \mathcal{A}^l$ (set of feasible solutions)
- if the strings are member of a population they are called chromosomes and their recombination crossover
- an expression maps individual to solutions (phenotypes) $c : \mathcal{A}^l \to \mathcal{X}$ (example, unrelated parallel machine and Steiner tree)
- strings are evaluated by $f(c(s)) = g(s)$ which gives them a fitness

Example

1001010 1101100 0111010 1010010 1000010

0101110 0111101 0110110 1101000 1010101



Which Produces the Offspring

01011101101100011101011010001010101

10010100111101011011010100101000010

Note: binary representation is appealing but not always good (in constrained problems binary crossovers might not be good)

Conjectures on the goodness of EA

Schema: subset of $\mathcal{A}^l$ where strings have a set of variables fixed.
Ex.: $S = 1 * * 1$

1. Exploit intrinsic parallelism of schemata (but epistasis)
2. Schema Theorem [Holland]:

$$E[N(S, t+1)] \geq \frac{F(S,t)}{\bar{F}(t)} N(S,t)[1 - \epsilon(S,t)]$$

$N(S,t)$ instances of a given schema S in population at generation t, $\bar{F}(t)$ av. fitness of population, $F(S,t)$ fitness schema, $\epsilon(S,t)$ destroy effect on S of operators

- a method for solving all problems $\Rightarrow$ disproved by
  No Free Lunch Theorems: no metaheuristic is better than random search; success comes from adapting the method to the problem at hand
- building block hypothesis

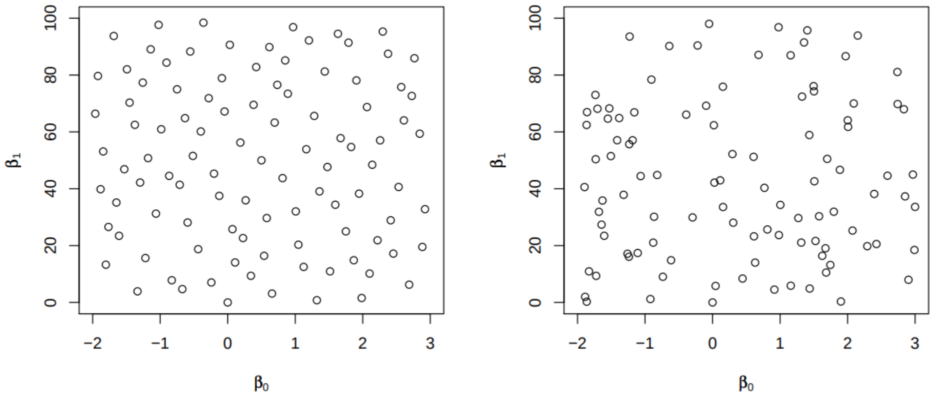
Initial Population

- Generation: often, independent, uninformed random picking from given search space.
- Which size? Trade-off
- Minimum size: connectivity by recombination is achieved if at least one instance of every allele is guaranteed to be present at each gene.
  Eg: binary repr. and uniform sampling with replacement:

  $$\Pr\{\text{presence of allele in M strings of length } l\} = (1 - (0.5)^M)^l$$

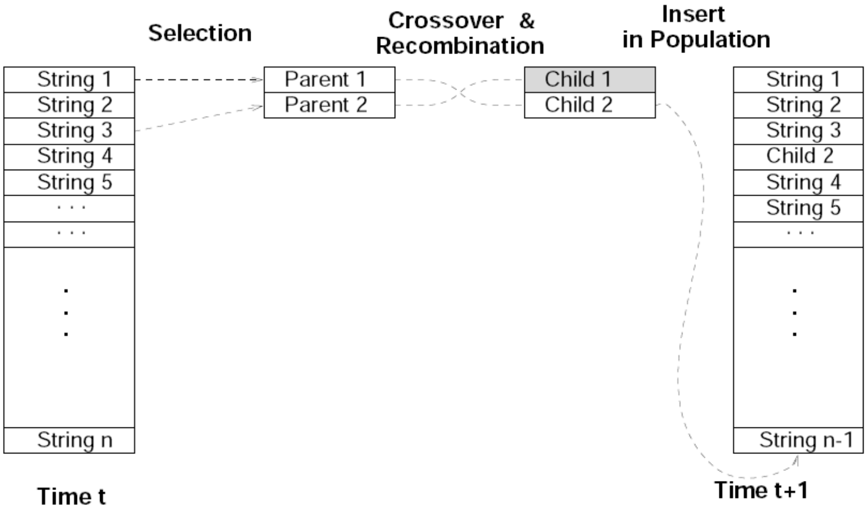
  for $l = 50$, it is sufficient $M = 17$ to guarantee $P_2^* > 99.9\%$.
- Attempt to cover at best the search space, eg, Latin hypercube, Quasi-random (low-discrepancy) methods (Quasi-Monte Carlo method).
- But: can also use multiple runs of randomized construction heuristic.

Quasi-Monte Carlo sampling



Left, quasi Monte Carlo sampling method based on low-discrepancy sequences. [Bratley, P., Fox, B.L., Niederreiter, H.: Algorithm-738 - programs to generate niederreiters low-discrepancy sequences. ACM Transactions On Mathematical Software 20(4), 494–495]
Right, uniformly at random.

Selection


Selection
Crossover &
Recombination
Insert
in Population
String 1
String 2
String 3
String 4
String 5
. . .
. . .
String n
Parent 1
Parent 2
Child 1
Child 2
String 1
String 2
String 3
Child 2
String 4
String 5
. . .
String n-1
Time t
Time t+1

Selection

Main idea: selection should be related to fitness

- Fitness proportionate selection (roulette-wheel method)

$$p_i = \frac{f_i}{\sum_j f_j}$$

- Tournament selection: a set of chromosomes is chosen and compared and the best chromosomes chosen.

- Rank based and selection pressure

- Fitness sharing (aka niching): probability of selection proportional to the number of other individuals in the same region of the search space.

Selection pressure:
$p_k = \alpha + \beta k$ probability for individual ranked kth (linear function)

$$\begin{cases} \sum_{k=1}^{M} (\alpha + \beta k) = 1 \\ \phi = \frac{\Pr[\text{selecting the best}]}{\Pr[\text{selecting the median}]} \end{cases} \qquad \text{selection pressure}$$

$\Pr[\text{selecting the best}] = \alpha + \beta M$; $\Pr[\text{selecting the median}] = \alpha + \beta(\frac{M+1}{2})$
Solving the system of equations

$$\alpha = \frac{2M - \phi(M+1)}{M(M-1)} \qquad \beta = \frac{2(\phi - 1)}{M(M-1)} \qquad 1 \leq \phi \leq 2$$

Then for a pseudo-random number the selected individual k from the cumulative probability is found in $O(1)$ solving the quadratic equation:

$$\sum_{i=1}^{k} \alpha + \sum_{i=1}^{k} \beta i = \alpha k + \beta \frac{(k+1)k}{2} = r$$

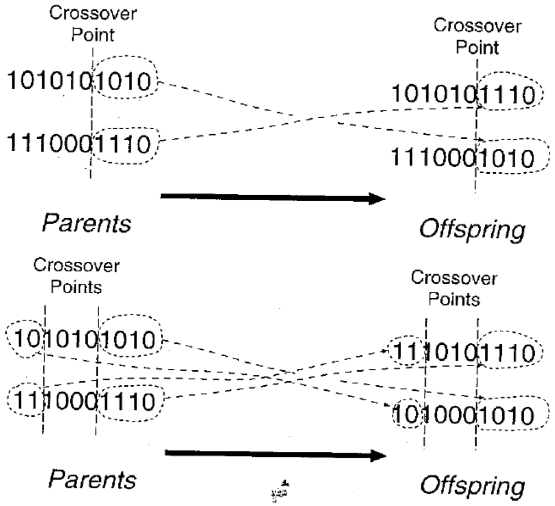
Crossovers

Recombination operator (Crossover)

- Binary or assignment representations
  - one-point, two-point, m-point (preference to positional bias w.r.t. distributional bias)
  - uniform cross over
    (through a mask controlled by a Bernoulli parameter p)
- Permutations
  - Partially mapped crossover (PMX)
  - Order crossover (OX)
  - Mask based crossover
  - Cycle crossover (CX)
- Sets
  - greedy partition crossover (GPX)
- Real vectors
  - arithmetic crossovers
  - k-point crossover

Assignments

Example: crossovers for binary representations



Assignments

Uniform (mask):

```
s1:   1010101010
s2:   1110001110

mask: 1101011110

o1:   1010001010
o2:   1110101110
```

Permutations

Permutations: relations of interest: adjacency, relative position, absolute position
Partially mapped crossover (PMX): defines interchanges

```
s1:   16 345 2
s2:   43 126 5

o1:   __ 126 _
o2:   __ 345 _
```

in o1: 3 is mapped to 1, 4 is mapped to 2, 5 is mapped to 6 in o2: viceversa

```
o1:   35 126 4
o2:   21 345 6
```

Permutations

Order crossovers:

One point crossover: $q \in \{1..n\}$ at random

$$\begin{array}{ll} \pi_\lambda^{o_1} := \pi_\lambda^{s_2} & \lambda = 1..q \\ \pi_\lambda^{o_1} := \pi_k^{s_1} & k \text{ smallest with } \pi_k^{s_1} \notin \{\pi_1^{o_1}..\pi_\lambda^{o_1}\} \end{array}$$

```
s1:   7132 58469
s2:   1426 39875

o1:   1426 73589
o2:   7132 46985
```

preserves relative positions

Permutations

Order crossovers:

Two point crossover: $q_1, q_2 \in \{1..n\}$, $q_1 < q_2$ at random

$$\begin{array}{ll} \pi^{o_1}_\lambda := \pi^{s_2}_\lambda & \lambda = 1..q_1, q_2..k \\ \pi^{o_1}_\lambda := \pi^{s_1}_k & k \text{ smallest with } \pi^{s_1}_k \notin \{\pi^{o_1}_1..\pi^{o_1}_\lambda\} \end{array}$$

```
s1:   71 3258 469
s2:   14 2639 875

o1:   14 ____ 875
o2:   71 ____ 469

o1:   14 ____ 875
o2:   71 2385 469
```

preserves relative positions

Permutations

Order crossovers, mask based crossover:
Uniform crossover: $\lambda = \{1..n\}$, $\xi_\lambda \in \{0,1\}$

$$\begin{array}{llll} \mathit{if}\, \xi_\lambda = 1 & \pi^{o_1}_\lambda := \pi^{s_2}_k & & k \text{ smallest with } \pi^{s_2}_k \notin \{\pi^{o_1}_1 .. \pi^{o_1}_\lambda\} \\ \mathit{if}\, \xi_\lambda = 0 & \pi^{o_1}_\lambda := \pi^{s_1}_k & & k \text{ smallest with } \pi^{s_1}_k \notin \{\pi^{o_1}_1 .. \pi^{o_1}_\lambda\} \end{array}$$

Permutations

Cycle crossover:

- divide elements into cycles
- select randomly cycles from parents

Positions:	1	2	3	4	5	6	7	8	9	10	11	12
Parent 1:	A	B	C	D	E	F	G	H	I	J	K	L
Parent 2:	h	k	c	e	f	d	b	l	a	i	g	j
Cycle label:	1	2	3	4	4	4	2	1	1	1	2	1
Offspring:	A	k	C	e	f	d	b	H	I	J	g	L

Sets

Partitions:
Greedy partitioning crossover

```
s1={{1,2,3,4},{5,6,7},{8,9,10}}
s2={{4,6,7,8},{1,2,10},{3,5,9}}
```

choose the largest set left alternating parent selection

```
s1={{ , , , }{5, , }{ , ,  }}
s2={{ , , , },{ , ,  },{ ,5, }}
```

```
o1={{1,2,3,4},{6,7,8},{9,10}}
```

reassign randomly left elements

```
o1={{1,2,3,4},{6,7,8,5},{9,10}}
```

- Crossovers appear to be a crucial feature of success
- Therefore, more commonly: ad hoc crossovers
- Two off-springs are generally generated
- Crossover rate controls the application of the crossover. May be adaptive: high at the start and low when convergence

Mutation

- Goal: Introduce relatively small perturbations in candidate solutions in current population + offsprings obtained from recombination
- Typically, perturbations are applied stochastically and independently to each candidate solution
- Mutation rate controls the application of bit-wise mutations.
  It may be adaptive: low at the start and high when convergence
- Possible implementation through Poisson variable which determines the m genes which are likely to change allele.
- Can also use subsidiary selection function to determine subset of candidate solutions to which mutation is applied.
- With real vector representation: Gaussian mutation

Subsidiary local search

- Often useful and necessary for obtaining high-quality candidate solutions.
- Typically consists of selecting some or all individuals in
  the given population and applying an iterative improvement procedure to each element of this set independently.

New Population

- Determines population for next cycle (generation) of the algorithm by selecting individual candidate solutions from
  - current population +
  - new candidate solutions from recombination, mutation (and subsidiary local search).
- Generational Replacement (λ, μ): $\lambda \leftarrow \mu$
- Elitist strategy $(\lambda + \mu)$ the best candidates are always selected
- Steady state (most common) only a small number of least fit individuals is replaced
- Goal: Obtain population of high-quality solutions while maintaining population diversity.

  Survival of the fittest and maintenance of diversity (duplicates avoided)

Example

A memetic algorithm for TSP

- **Search space:** set of Hamiltonian cycles
  Tours represented as permutations of vertex indexes.
- **Initialization:** by randomized greedy heuristic (partial tour of $n/4$ vertices constructed randomly before completing with greedy).
- **Recombination:** greedy recombination operator GX applied to $n/2$ pairs of tours chosen randomly:
  1) copy common edges (param. p_e)
  2) add new short edges (param. p_n)
  3) copy edges from parents ordered by increasing length (param. p_c)
  4) complete using randomized greedy.
- **Subsidiary local search:** LK variant.
- **Mutation:** apply double-bridge to tours chosen uniformly at random.
- **Selection:** Selects the μ best tours from current population of $\mu + \lambda$ tours (=simple elitist selection mechanism).
- **Restart operator:** whenever average bond distance in the population falls below 10.

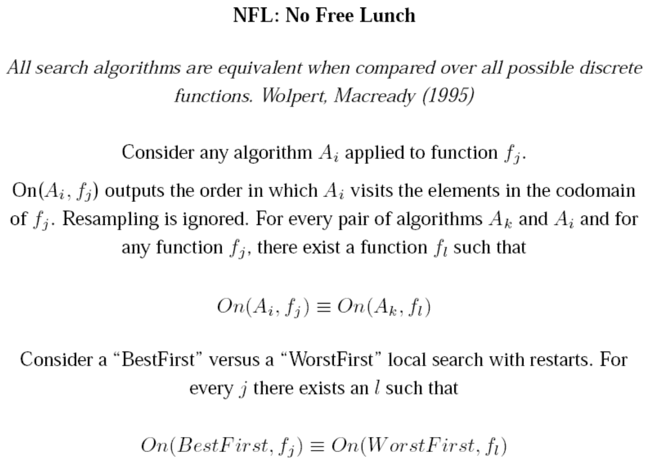
Theoretical studies

- Through Markov chains modelling some versions of evolutionary algorithms can be made to converge with probability 1 to the best possible solutions in the limit [Fogel, 1992; Rudolph, 1994].
- Convergence rates on mathematically tractable functions or with local approximations [Bäck and Hoffmeister, 2004; Beyer, 2001].
- "No Free Lunch Theorem" [Wolpert and Macready, 1997]. On average, within some assumptions, blind random search is as good at finding the minimum of all functions as is hill climbing.

However:

- These theoretical findings are not very practical.
- EAs are made to produce useful solutions rather than perfect solutions.

No Free Lunch Theorem



NFL: No Free Lunch

All search algorithms are equivalent when compared over all possible discrete functions. Wolpert, Macready (1995)

Consider any algorithm A_i applied to function f_j.

On(A_i, f_j) outputs the order in which A_i visits the elements in the codomain of f_j. Resampling is ignored. For every pair of algorithms A_k and A_i and for any function f_j, there exist a function f_l such that

$$On(A_i, f_j) \equiv On(A_k, f_l)$$

Consider a "BestFirst" versus a "WorstFirst" local search with restarts. For every j there exists an l such that

$$On(BestFirst, f_j) \equiv On(WorstFirst, f_l)$$

Research Goals

- Analyzing classes of optimization problems and determining experimentally the best components for evolutionary algorithms.

- Applying evolutionary algorithms to problems that are dynamically changing.

- Gaining theoretical insights for the choice of components.

- Prove bounds on the runtime that such algorithms have in order to obtain optimal or nearly optimal solutions.
  Bio-inspired algorithms are
  - general-purpose algorithms
  - randomized algorithms = stochastic search algorithms

  computational complexity analysis is achieved by bounding the expected runtime to achieve good solutions for a certain problem

References

Moraglio A. and Poli R. (2011). **Topological crossover for the permutation representation**. *Intelligenza Artificiale*, 5(1), pp. 49–70.

Neumann F., Witt C., Neumann F., and Witt C. (2010). **Bioinspired Computation in Combinatorial Optimization**. Natural Computing Series. Springer Berlin Heidelberg.

Reeves C. (2002). **Genetic algorithms**. In *Handbook of Metaheuristics*, edited by F. Glover and G. Kochenberger, vol. 57 of **International Series in Operations Research & Management Science**, pp. 55–82. Kluwer Academic Publishers, Norwell, MA, USA.

Parallel Implementations

- Population based heuristics lends theselves naturally to parallel implementations
- Trajectory based heuristics are less prone to parallelizations: parallelize the neighborhood exploration by delegating move evaluations to child processes.
  keep move generation and move selection at the parent (master) level

Other Nature Inspired Algorithms

A literature search on the Unit Commitment Problem (a mixed discrete continuous opt. problem) unveiled at least the following attempts:

- Harmony search
- Differential evolution algorithm
- Quantum-inspired evolutionary algorithm
- Particle swarm optimization
- Bee colony algorithm
- Bacterial foraging-based solution
- Coyote optimization algorithm
- Firefly algorithm
- Imperialistic competition algorithm
- Flower pollination algorithm
- Mine blast algorithm
- Binary grasshopper optimization algorithm
- Binary grey wolf optimizer
- Binary fireworks algorithm
- Binary cuckoo search algorithm
- Binary fish swarm algorithm
- Binary shuffled frog leaping algorithm
- Hopfield neural network

See also:

- Evolutionary Computation Bestiary: `https://github.com/fcampelo/EC-Bestiary`
- "Metaheuristics—the metaphor exposed", Kenneth Sörensen, 2013
  `https://doi.org/10.1111/itor.12001`

Outline

1. Population Based Metaheuristics
    Evolutionary Algorithms

2. Multi-Objective Optimization

Multi-Objective Optimization: Basics

- Objective vector $\boldsymbol{f} = [f_1, \dots, f_Q]$
- We want to minimize $\boldsymbol{f}$ but what does it mean?
  - Weighted sum
  - Lexicographic
  - Pareto optimality (without previous knwoledge on component importance)

Basic Notions

Let $\boldsymbol{u}$ and $\boldsymbol{v}$ be vectors in $\mathbb{R}^Q$:

weak component-wise order	$\boldsymbol{u} \leqq \boldsymbol{v}$	$u_i \leq v_i,\ i = 1, \dots, Q$;
component-wise order	$\boldsymbol{u} \leq \boldsymbol{v}$	$u_i \leq v_i,\ i = 1, \dots, Q$ and $\boldsymbol{u} \neq \boldsymbol{v}$;
strict component-wise order	$\boldsymbol{u} < \boldsymbol{v}$	$u_i < v_i,\ i = 1, \dots, Q$

Let s and s' be two solutions to a problem $\mathcal{P}$ with objective function $\boldsymbol{f}$:

$\boldsymbol{f}(s)$ weakly dominates $\boldsymbol{f}(s')$	iff $\boldsymbol{f}(s) \leqq \boldsymbol{f}(s')$
$\boldsymbol{f}(s)$ dominates $\boldsymbol{f}(s')$	iff $\boldsymbol{f}(s) \leq \boldsymbol{f}(s')$
$\boldsymbol{f}(s)$ strictly dominates $\boldsymbol{f}(s')$	iff $\boldsymbol{f}(s) < \boldsymbol{f}(s')$

- $\boldsymbol{f}(s)$ and $\boldsymbol{f}(s')$ are non-dominated if $\boldsymbol{f}(s) \not\leq \boldsymbol{f}(s')$ and $\boldsymbol{f}(s') \not\leq \boldsymbol{f}(s)$
- $\boldsymbol{f}(s)$ and $\boldsymbol{f}(s')$ are non-weakly dominated if $\boldsymbol{f}(s) \not\leqq \boldsymbol{f}(s')$ and $\boldsymbol{f}(s') \not\leqq \boldsymbol{f}(s)$

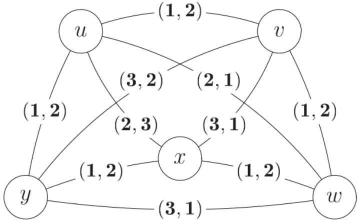
- A solution s is a Pareto global optimum solution iff there is no $s' \in S$ such that $\boldsymbol{f}(s') \leq \boldsymbol{f}(s)$
- A set of solutions S is a Pareto global optimum set iff it contains only and all Pareto global optimum solutions.

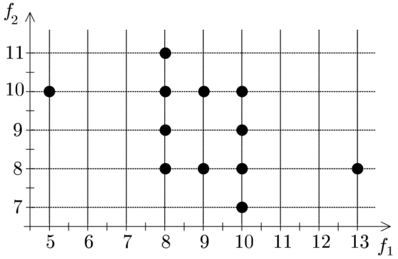
Basic Notions

- Efficient set (or Pareto frontier) is the image of the Pareto global optimum set in the objective space.

- $S' \subseteq S$ is strict Pareto global optimum set iff:
    - it contains only Pareto global optimum solutions
    - the corresponding set of objective function value vectors coincides with the efficient set and its elements are unique.

Example – Multi-objective TSP





Pareto global optimum set:

π	$f(\pi)$
$\pi = [u, v, w, x, y]$	$[5, 10]$
$\pi = [u, w, v, x, y]$	$[8, 8]$
$\pi = [u, v, w, x, y]$	$[10, 7]$

strict Pareto global optimum set

if all edges had weights, eg, $(3, 3)$, then all $\binom{5}{2}$ solutions would have cost $[5 \cdot 3, 5 \cdot 3]$ and would be in the Pareto global optimum set. However, both the efficient set and the strict Pareto global optimum set would have one single solution, which is any of the feasible ones.

Basic Notions

Computational class #P: concerned with counting the number of solutions.

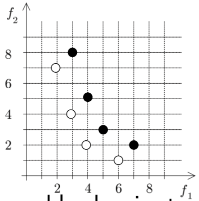
A counting problem belongs to #P if there is a polynomial nondeterministic algorithm such that for any instance of the problem, it computes a number of yes-answers that is equal to the number of distinct solutions of that instance.

Class #P-complete: a problem $\mathcal{P}_1$ is #P-complete if it belongs to #P and for all problems $\mathcal{P}_2$ in #P there exists a polynomial transformation from $\mathcal{P}_1$ to $\mathcal{P}_2$ such that any instance of $\mathcal{P}_1$ is mapped into an instance of $\mathcal{P}_2$ with the same number of yes-answers as the instance of $\mathcal{P}_1$.

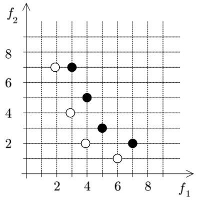
Basic Notions

Given two arbitrary sets of objective function value vectors in a Q-dimensional objective space, $A = \{\boldsymbol{a}^1, \dots \boldsymbol{a}^m\}$ and $B = \{\boldsymbol{b}^1, \dots \boldsymbol{b}^n\}$

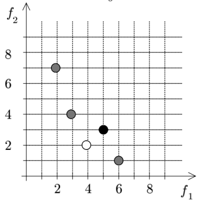
strictly dominates



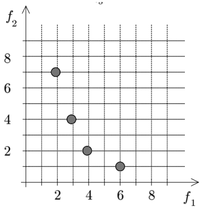
dominates



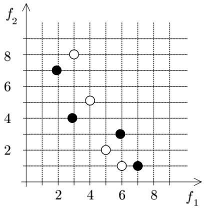
better than



weakly dominates



incomparable



Evolutionary Algorithms Approaches

- strength Pareto EA (SPEA) [Zitzler and Thiele, 1998]
  maintain an external population at every generation storing all non-dominated solutions discovered so far beginning from the initial population. This external population participates in genetic operations. At each generation, a combined population with the external and the current population is first constructed. All non-dominated solutions in the combined population are assigned a fitness based on the number of solutions they dominate and dominated solutions are assigned fitness worse than the worst fitness of any non-dominated solution. A deterministic clustering technique is used to ensure diversity among non-dominated solutions.

- Pareto-archived evolution strategy (PAES) [Knowles and Gome, 1999]
  one parent and one child, the child is compared with respect to the parent. If the child dominates the parent, the child is accepted as the next parent and the iteration continues. If the parent dominates the child, the child is discarded and a new mutated solution (a new child) is found. If the child and the parent do not dominate each other, the choice between the child and the parent is made by comparing them with an archive of best solutions found so far. Both domination and diversity are considered.

Evolutionary Algorithms Approaches

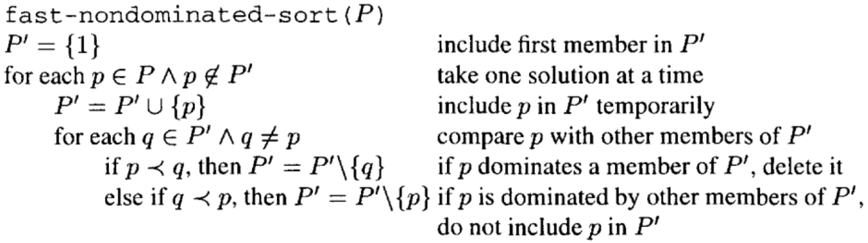
- elitist GA [Rudolph, 1999]
  systematic comparison of individuals from parent and offspring populations.
  The non-dominated solutions of the offspring population are compared with parent solutions to form an overall non-dominated set of solutions, which becomes the parent population of the next iteration.
  If the size of this set is not greater than the desired population size, other individuals from the offspring population are included.

- Fast Elitist Non-dominated Sorting Genetic Algorithm for Multi-objective Optimization: NSGA-II [Deb, Agrawal, Pratap, Meyarivan, 2000]

NSGA-II: Main Components

Systematic comparison between solutions to find the non-dominated fronts.
It requires $O(MN^3)$ if only one solution in each front. (M number of objectives, N population size)

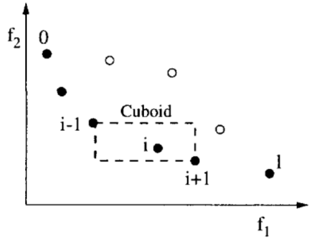
Fast non-dominated sorting approach in $O(MN^2)$



```
fast-nondominated-sort($P$)
$P' = \{1\}$                                      include first member in $P'$
for each $p \in P \wedge p \notin P'$                    take one solution at a time
    $P' = P' \cup \{p\}$                              include $p$ in $P'$ temporarily
    for each $q \in P' \wedge q \neq p$                   compare $p$ with other members of $P'$
        if $p \prec q$, then $P' = P' \backslash \{q\}$         if $p$ dominates a member of $P'$, delete it
        else if $q \prec p$, then $P' = P' \backslash \{p\}$    if $p$ is dominated by other members of $P'$,
                                                  do not include $p$ in $P'$
```

NSGA-II: Main Components

Density estimation (crowding distance) of a particular point in the population: average distance of the two points on either side of this point along each of the objectives



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crowding-distance-assignment($\mathcal{I}$)
$l = |\mathcal{I}|$                                          number of solutions in $\mathcal{I}$
for each $i$, set $\mathcal{I}[i]_{distance} = 0$            initialize distance
for each objective $m$
    $\mathcal{I} = \text{sort}(\mathcal{I}, m)$                          sort using each objective value
    $\mathcal{I}[1]_{distance} = \mathcal{I}[l]_{distance} = \infty$        so that boundary points are always selected
    for $i = 2$ to $(l - 1)$                             for all other points
        $\mathcal{I}[i]_{distance} = \mathcal{I}[i]_{distance} + (\mathcal{I}[i+1].m - \mathcal{I}[i-1].m)$
```

NSGA-II: Main Components

The crowded comparison operator $\prec_n$ guides the selection process towards a uniformly spread-out Pareto-optimal front.

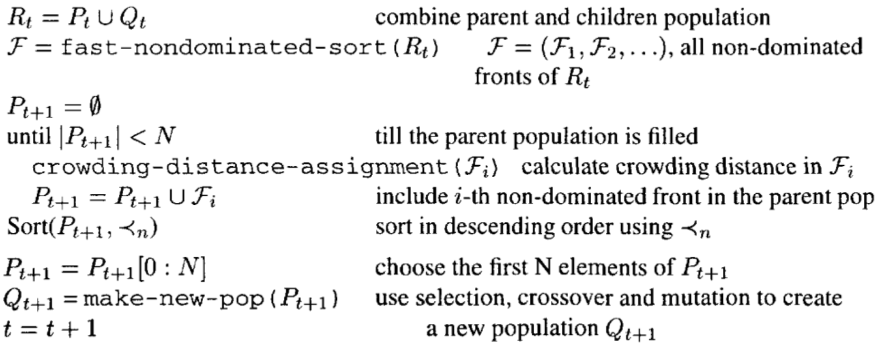
Let us assume that every individual i in the population has two attributes.

1. Non-domination rank (s_{rank})
2. Local crowding distance (s_{distance})

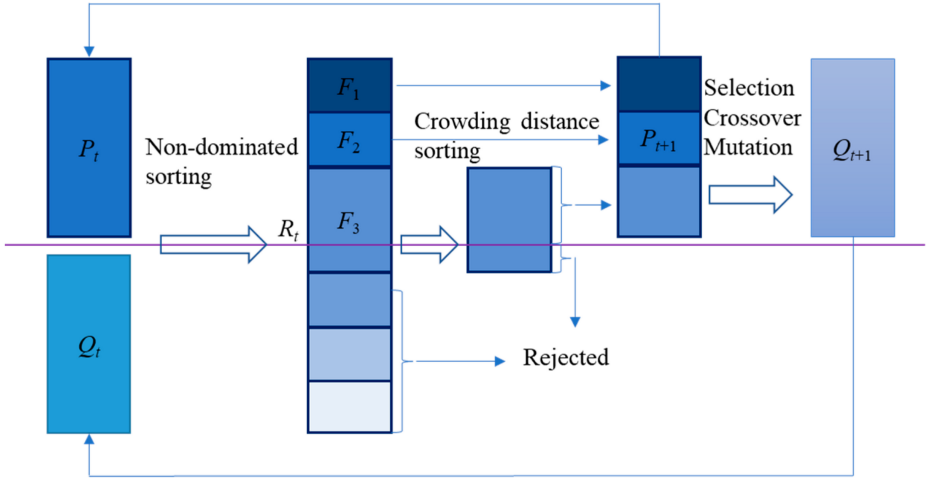
Partial order $\prec_n$:
$s \prec_n s'$ if $(s_{\text{rank}} < s'_{\text{rank}})$ or $((s_{\text{rank}} = s'_{\text{rank}}) \wedge (s_{\text{distance}} > s'_{\text{distance}}))$

NSGA-II: Algorithm

- Initially, a random parent population P_0 is created. The population is sorted based on the non-domination. Each solution is assigned a fitness equal to its non-domination level (1 is the best level). Thus, minimization of fitness is assumed.
- Binary tournament selection, recombination, and mutation operators are used to create a child population Q_0 of size N.
- At each iteration $t > 1$ and for a particular generation an elitism procedure is used:



```
$R_t = P_t \cup Q_t$                                   combine parent and children population
$\mathcal{F} =$ fast-nondominated-sort($R_t$)          $\mathcal{F} = (\mathcal{F}_1, \mathcal{F}_2, \ldots)$, all non-dominated
                                                           fronts of $R_t$
$P_{t+1} = \emptyset$
until $|P_{t+1}| < N$                                  till the parent population is filled
    crowding-distance-assignment($\mathcal{F}_i$)      calculate crowding distance in $\mathcal{F}_i$
    $P_{t+1} = P_{t+1} \cup \mathcal{F}_i$             include $i$-th non-dominated front in the parent pop
Sort($P_{t+1}, \prec_n$)                               sort in descending order using $\prec_n$
$P_{t+1} = P_{t+1}[0 : N]$                             choose the first N elements of $P_{t+1}$
$Q_{t+1} =$ make-new-pop($P_{t+1}$)                    use selection, crossover and mutation to create
$t = t + 1$                                                a new population $Q_{t+1}$
```



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Iteration Complexity

At each generation, the basic operations being performed and the worst case complexities associated with it are as follows:

1. Non-dominated sort is $O(MN^2)$,
2. Crowding distance assignment is $O(MN \log N)$
3. Sort on $\prec_n$ is $O(2N \log(2N))$

The overall complexity of the single iteration is $O(MN^2)$.