

A Tutorial on Evolutionary Multiobjective Optimization

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ETH

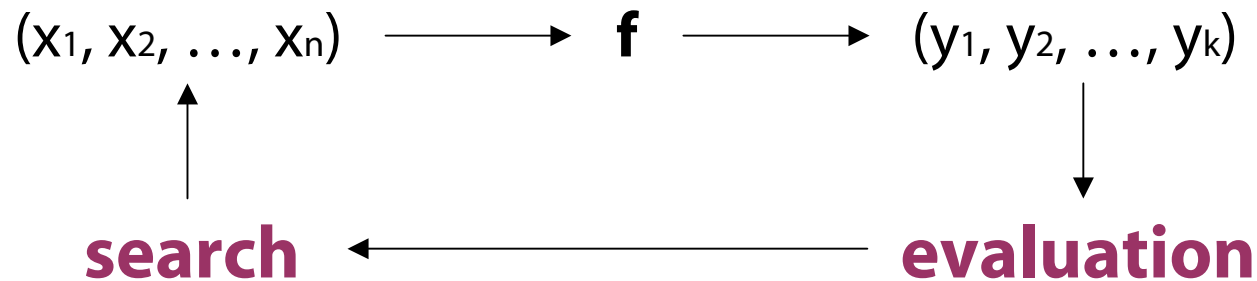
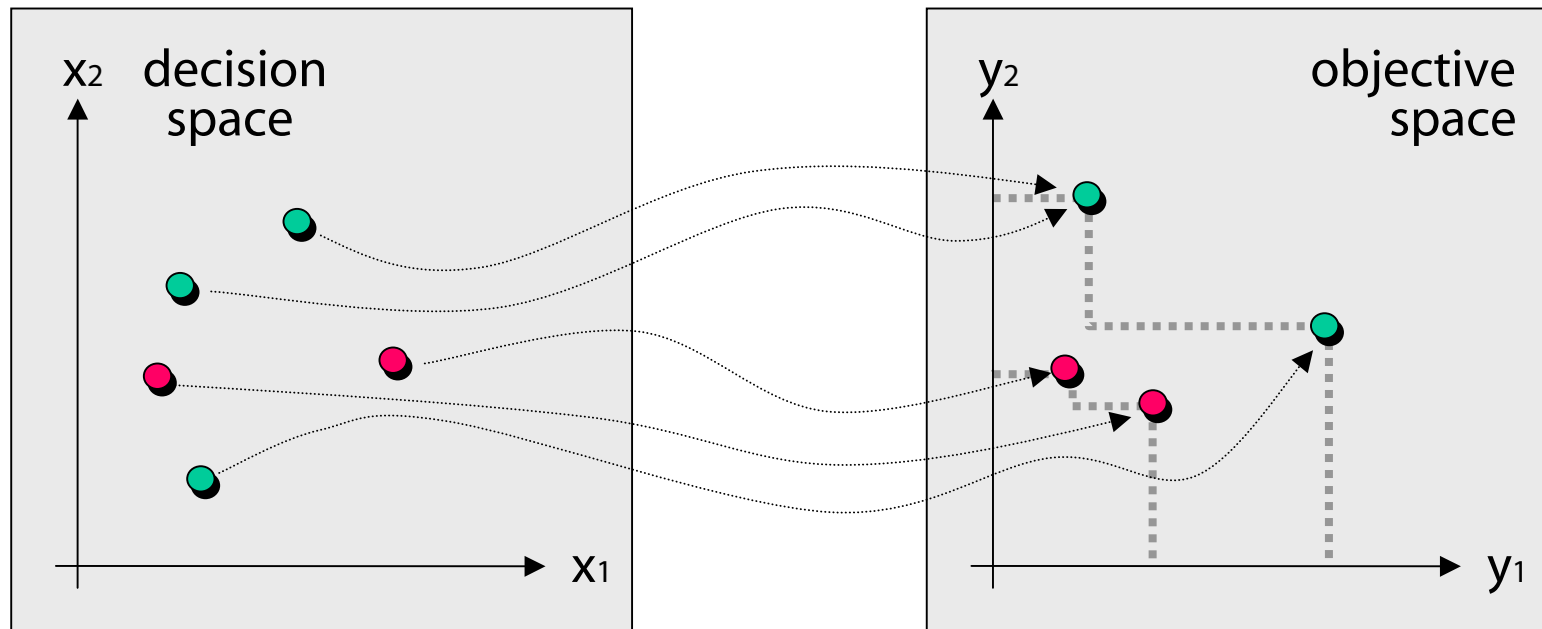
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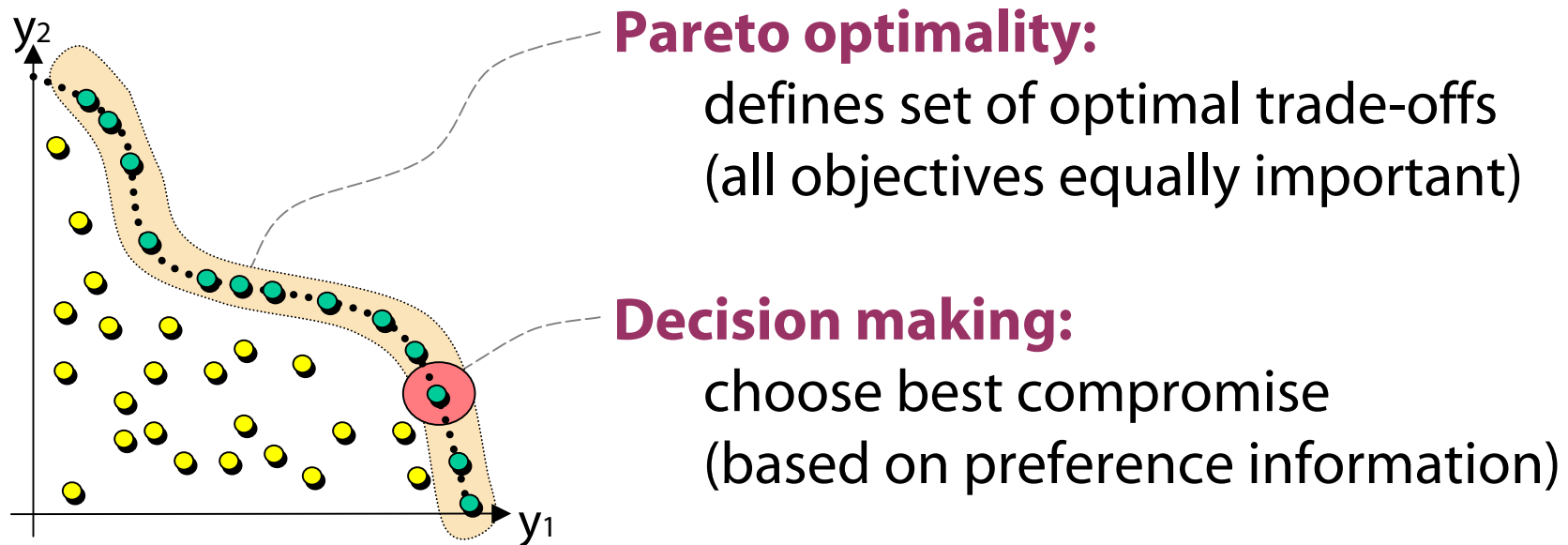
TIK

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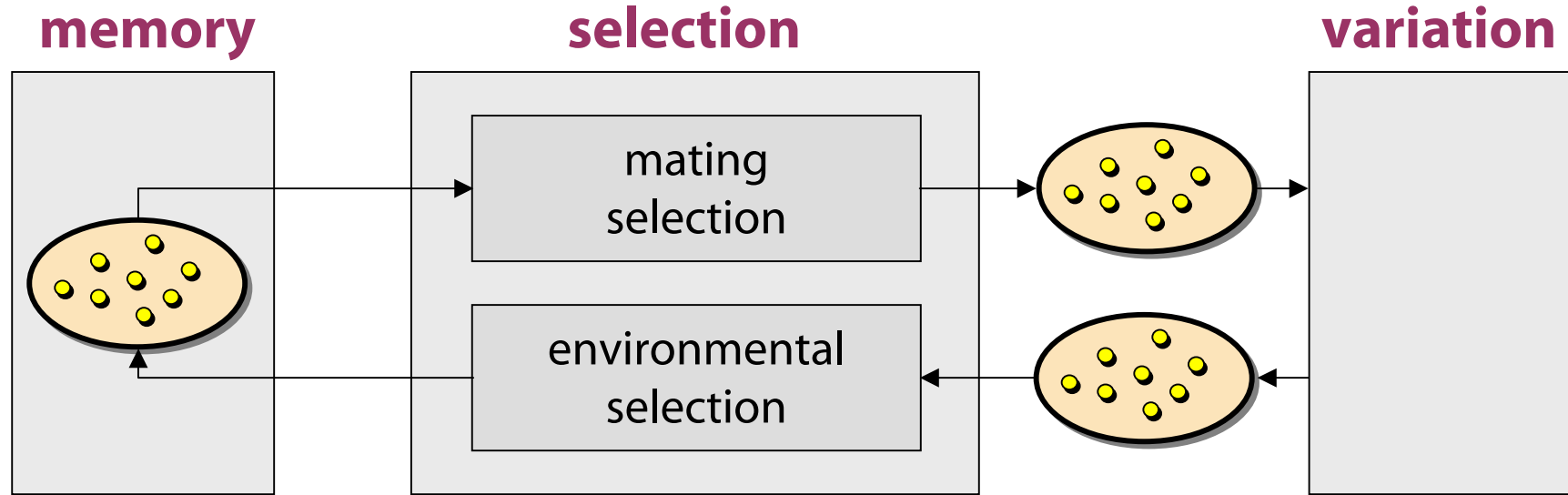
- ① **The Big Picture:**
Optimization and evolutionary computation
- ② **The Construction Kit:**
Design issues and algorithmic concepts
- ③ **The Pieces Put Together:**
Example of an algorithm variant
- ④ **The Big Question:**
Performance of evolutionary algorithms
- ⑤ **The Challenge:**
Standard interface for search algorithms
- ⑥ **The End:**
Conclusions and outlook

Pareto set ● Pareto front
Pareto set approximation ● Pareto front approximation



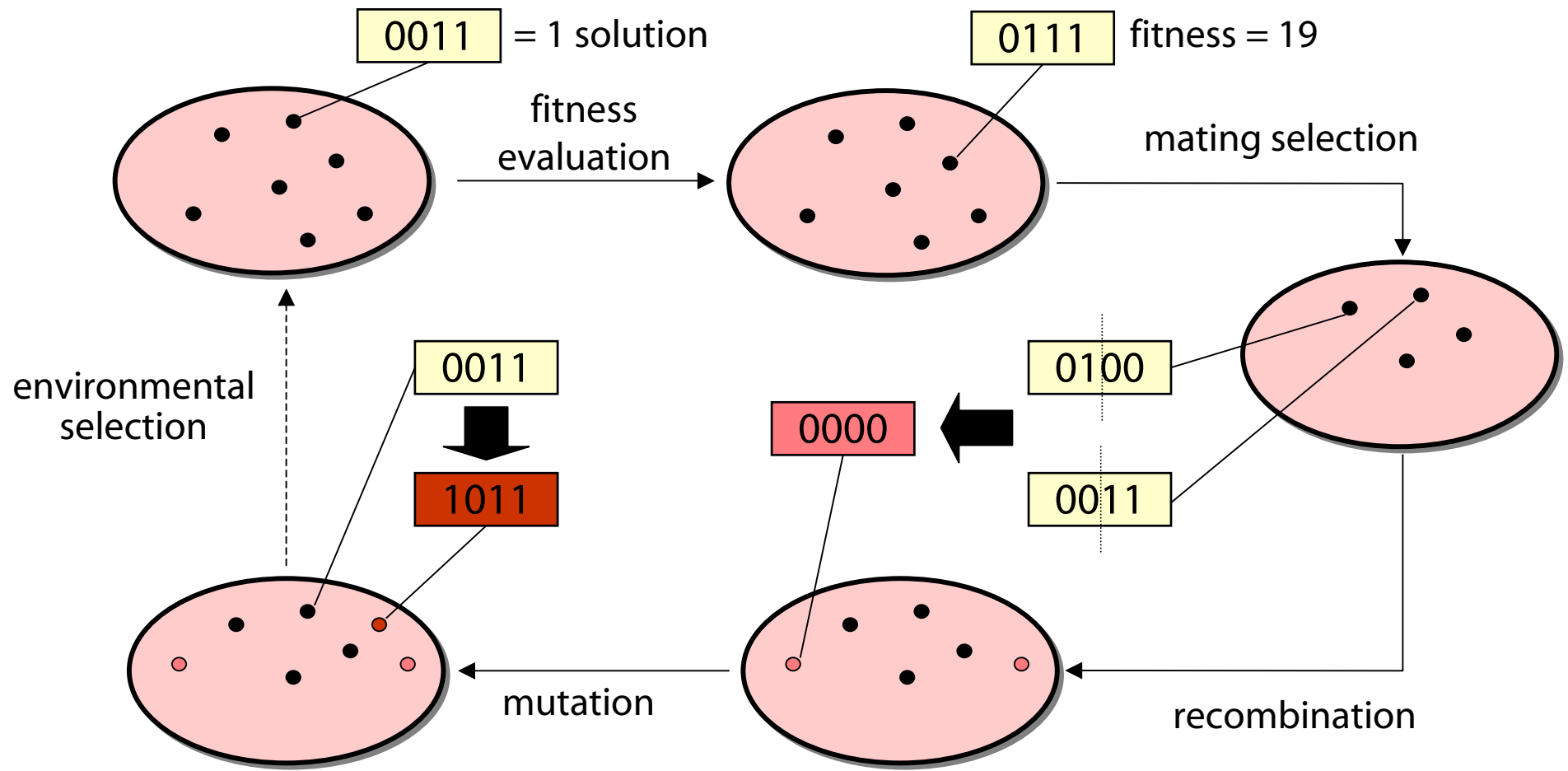


- 1 Decision making before search (define single objective)
- 2 Decision making after search (find/approximate Pareto set first)
- 3 Decision making during search (guide search interactively)
- 4 Combinations of the above

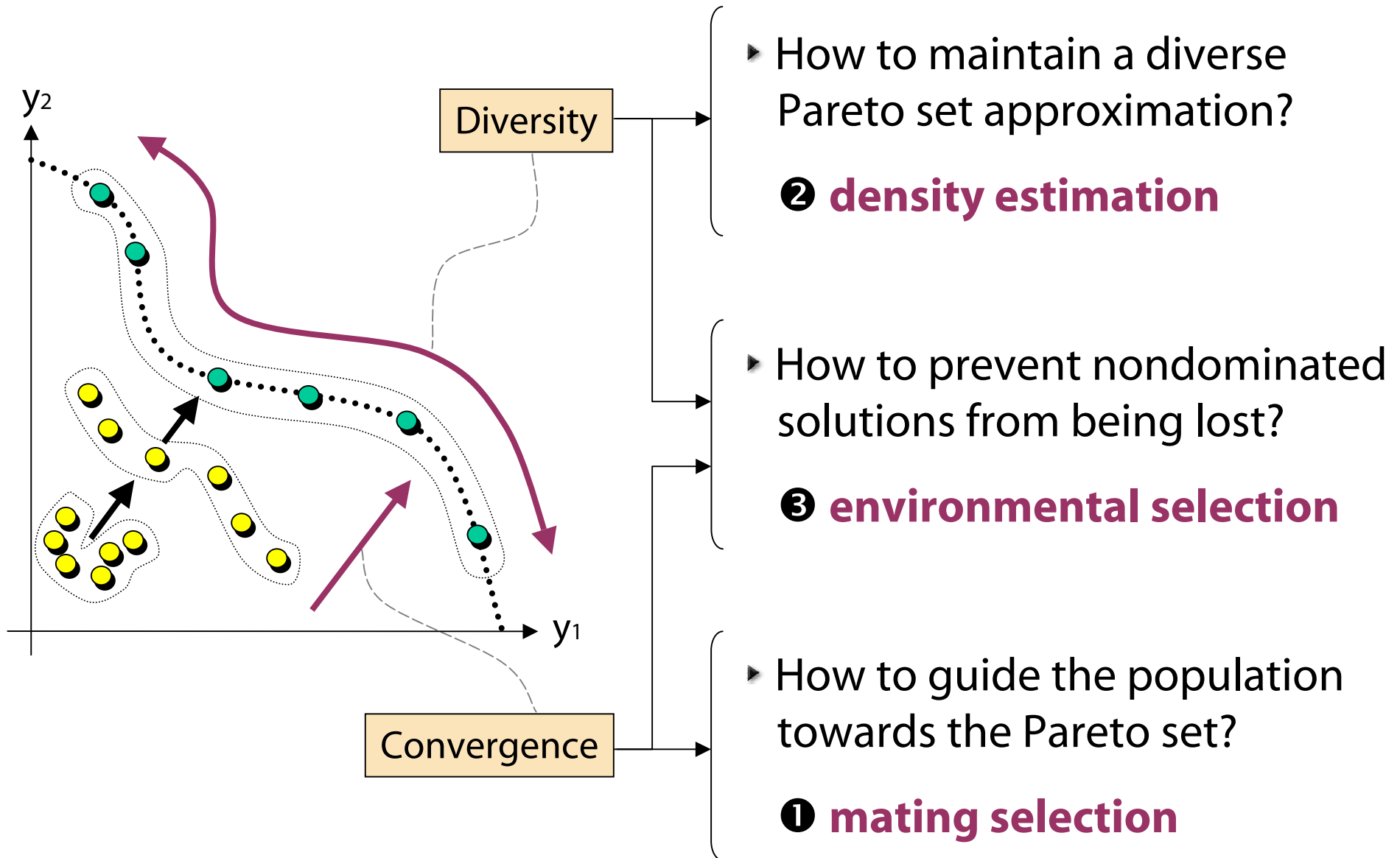


EA	≥ 1	both	≥ 1 ≥ 1	$N : M$ randomized
TS	1	no mating selection	1 ≥ 1	1 : M deterministic
SA	1	no mating selection	1 ≥ 1	1 : M randomized
ACO	1	neither	1 1	1 : 1 randomized

Outline of a Simple Evolutionary Algorithm



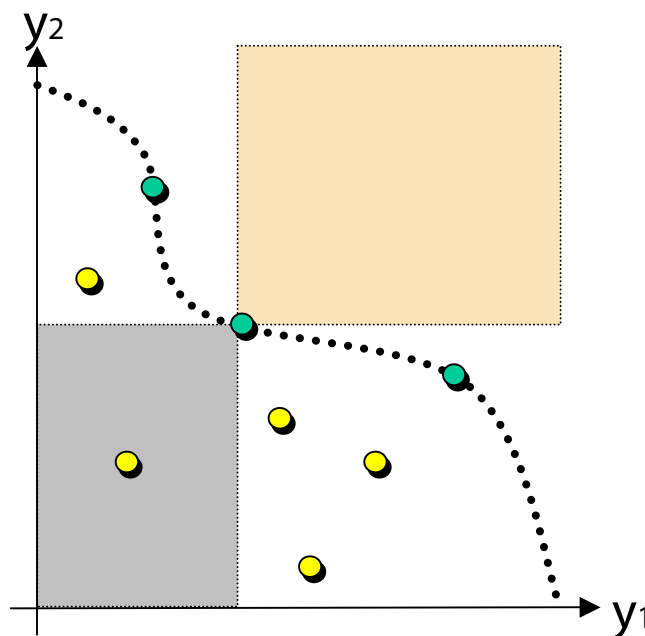
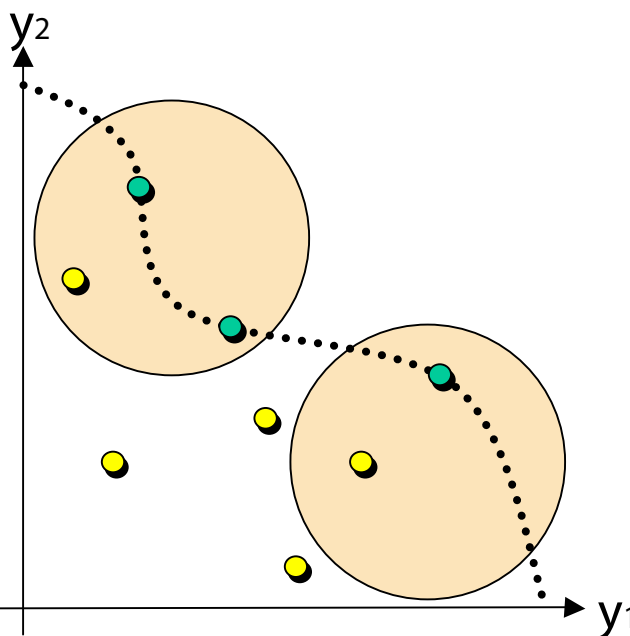
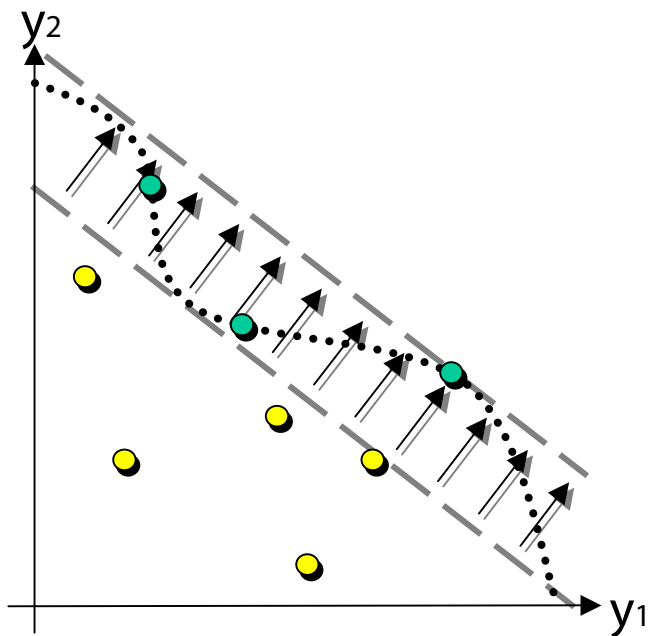
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aggregation-based *weighted sum*

criterion-based *VEGA*

dominance-based *SPEA2*



parameter-oriented
scaling-dependent



set-oriented
scaling-independent

Types of information:

- **dominance rank** by how many individuals is an individual dominated?
- **dominance count** how many individuals does an individual dominate?
- **dominance depth** at which front is an individual located?

Examples:

- *MOGA, NPGA* dominance rank
- *NSGA/NSGA-II* dominance depth
- *SPEA/SPEA2* dominance count + rank

Density estimation techniques: [Silverman: 1986]

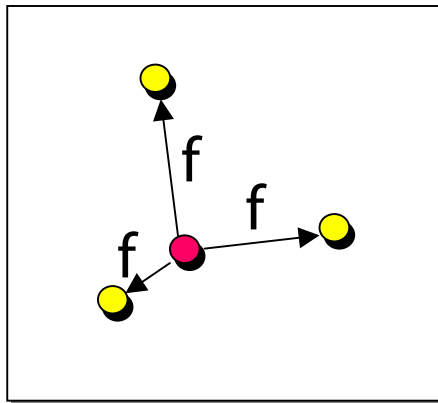
Kernel

MOGA

density estimate

=

sum of f values
where f is a
function of the
distance



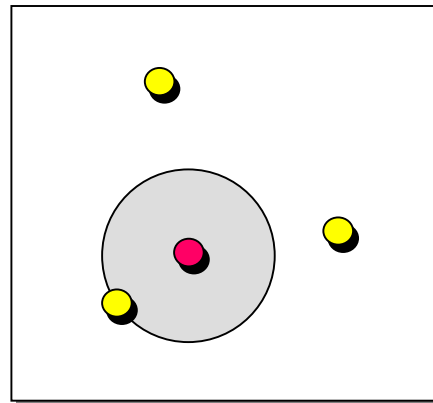
Nearest neighbor

SPEA2

density estimate

=

volume of the
sphere defined by
the nearest
neighbor



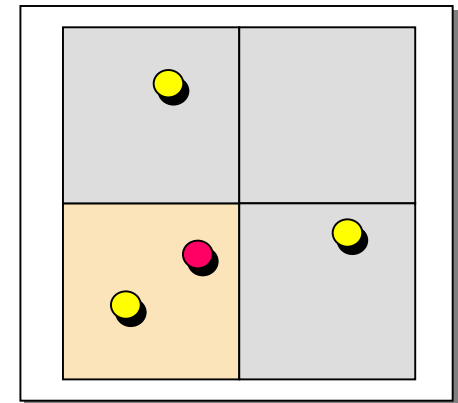
Histogram

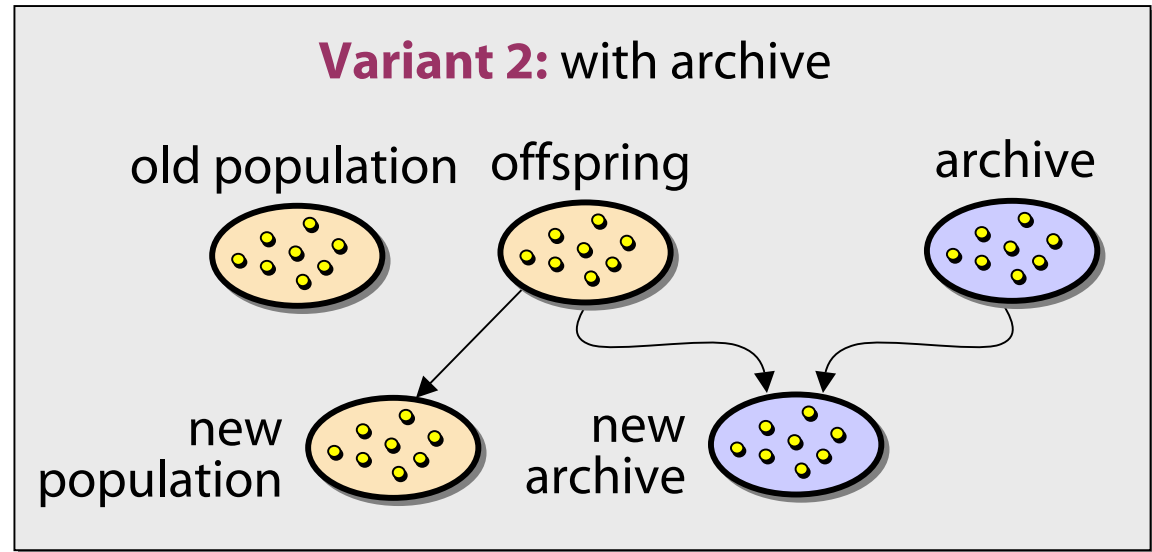
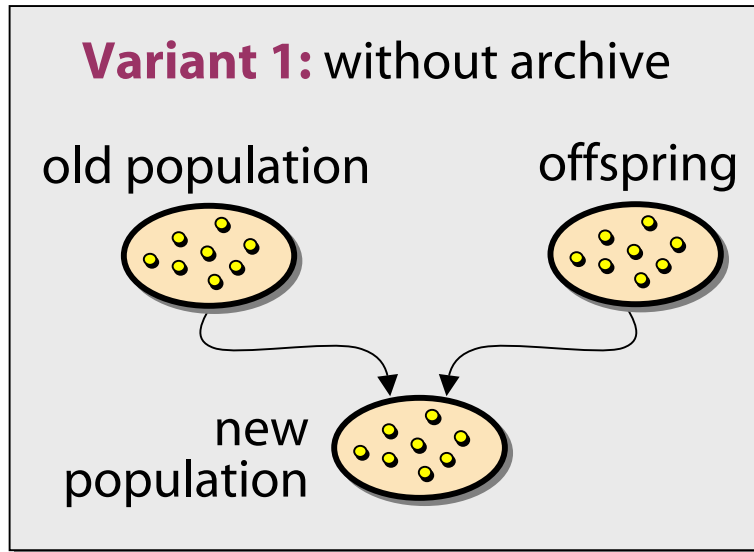
PAES

density estimate

=

number of
solutions in the
same box



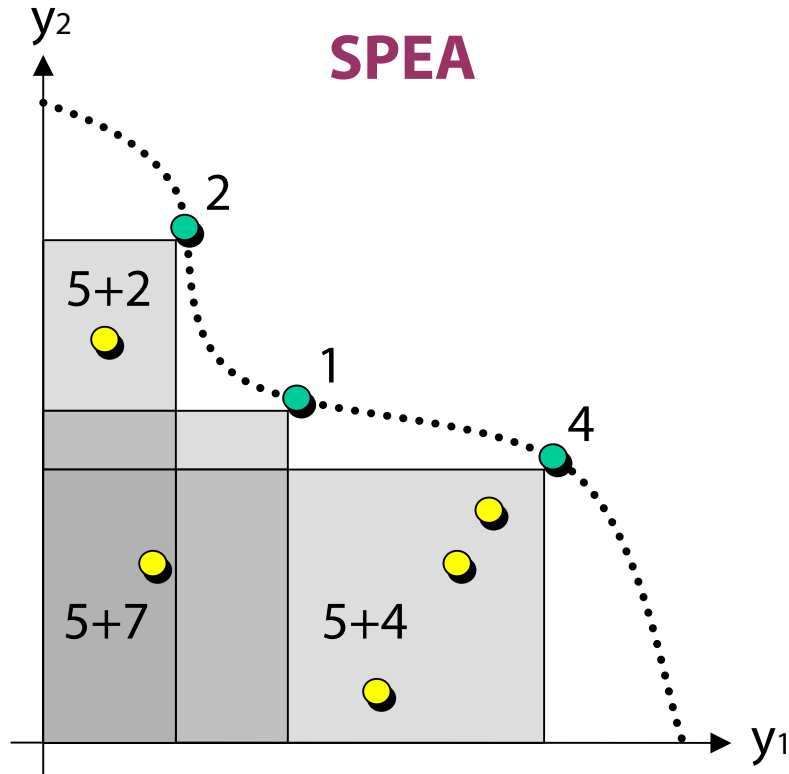


Selection criteria:

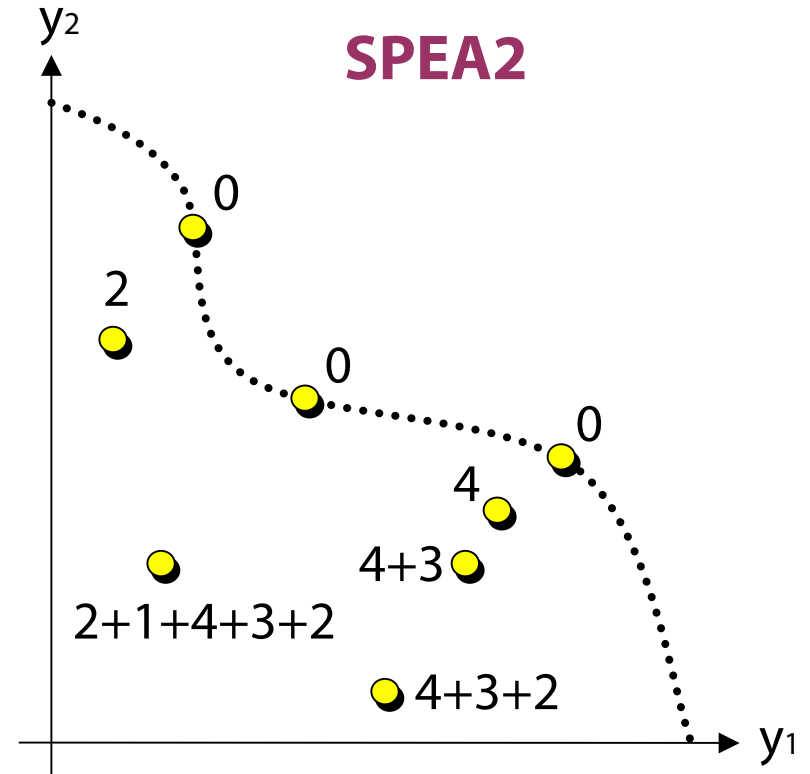
- **Dominance:** only nondominated solutions are kept
- **Density:** less crowded regions are preferred to crowded regions
- **Time:** old archive members are preferred to new solutions
- **Chance:** each solution has the same probability to enter the archive

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<i>Step 1:</i>	Generate initial population P_0 and empty archive (external set) A_0 . Set $t = 0$.
<i>Step 2:</i>	Calculate fitness values of individuals in P_t and A_t .
<i>Step 3:</i>	A_{t+1} = nondominated individuals in P_t and A_t . If size of $A_{t+1} > N$ then reduce A_{t+1} , else if size of $A_{t+1} < N$ then fill A_{t+1} with dominated individuals in P_t and A_t .
<i>Step 4:</i>	If $t > T$ then output the nondominated set of A_{t+1} . Stop.
<i>Step 5:</i>	Fill mating pool by binary tournament selection with replacement on A_{t+1} .
<i>Step 6:</i>	Apply recombination and mutation operators to the mating pool and set P_{t+1} to the resulting population. Set $t = t + 1$ and go to Step 2.



- S (strength) = #dominated solutions ●
- R (raw fitness) = $N + \sum$ strengths of dominators ●



- S (strength) = #dominated solutions ●
- R (raw fitness) = \sum strengths of dominators ●

Density Estimation

k-th nearest neighbor method:

- $$\text{Fitness} = R + \underbrace{1 / (2 + D_k)}_{< 1}$$
- D_k = distance to the k-th nearest individual
- $k = \sqrt{\text{popsize} + \text{archivesize}}$

Truncation

Incremental approach:

- Remove individual A for which $A <_d B$ for all individuals B
- $B <_d A$ iff:
 - ▶ D_k identical for A and B for all k
 - ▶ D_k of A greater than D_k of B for a particular k and identical for smaller k

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① **Theoretically (by analysis):** difficult

- Limit behavior

“Is the Pareto set found, if there are unlimited run-time resources?”

- Run-time analysis

“How long does it take to generate the Pareto set with high probability?”

② **Empirically (by simulation):** standard

Basic assumptions:

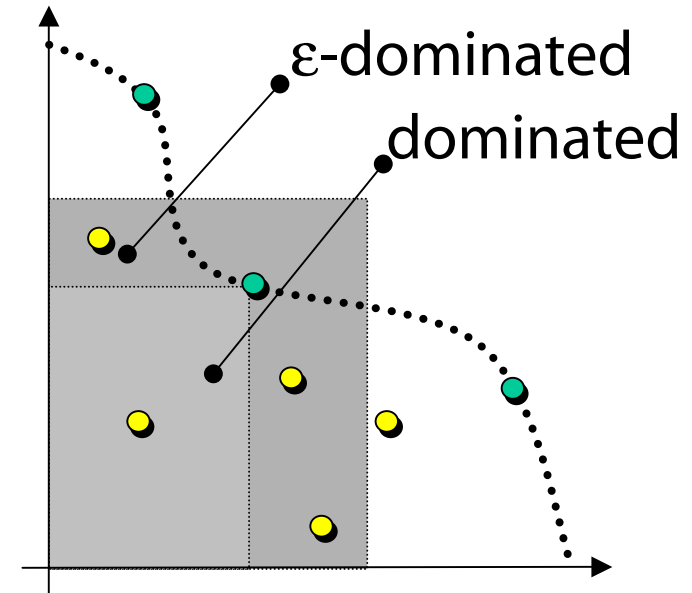
- Every solution can be generated from every other solution by mutation
- The number of iterations t goes to infinity ($t \rightarrow \infty$)

Studies:

- Convergence: *[Hanne: 1999][Rudolph, Agapie: 2000]*
- Diversity: e.g., *[Knowles, Corne: 2000][Deb et al.: 2001]*
- Convergence + diversity:
 - ▶ Unlimited memory resources *[Rudolph and Agapie: 2000]*
 - ▶ Limited memory resources *[Laumanns et al.: 2002]*

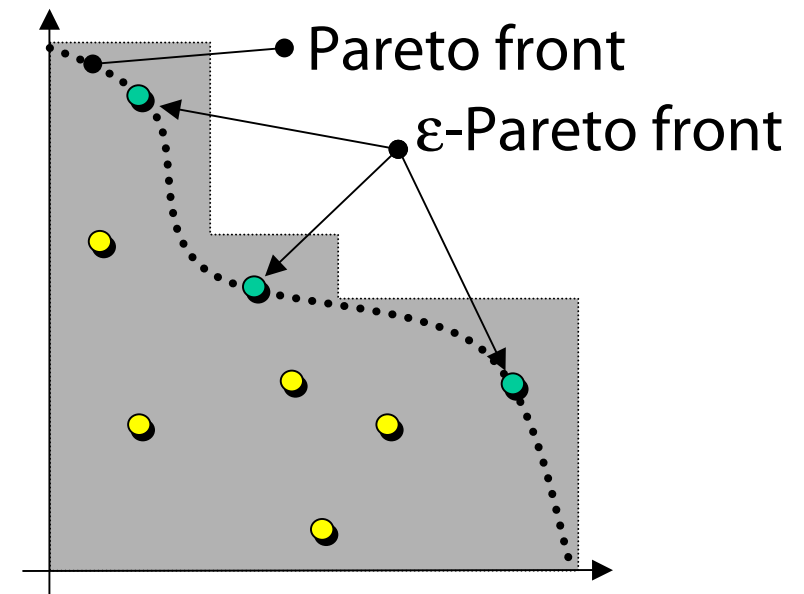
Definition 1: ϵ -Dominance

A ϵ -dominates B iff $\epsilon \cdot f(A) \geq f(B)$
(known since 1987)



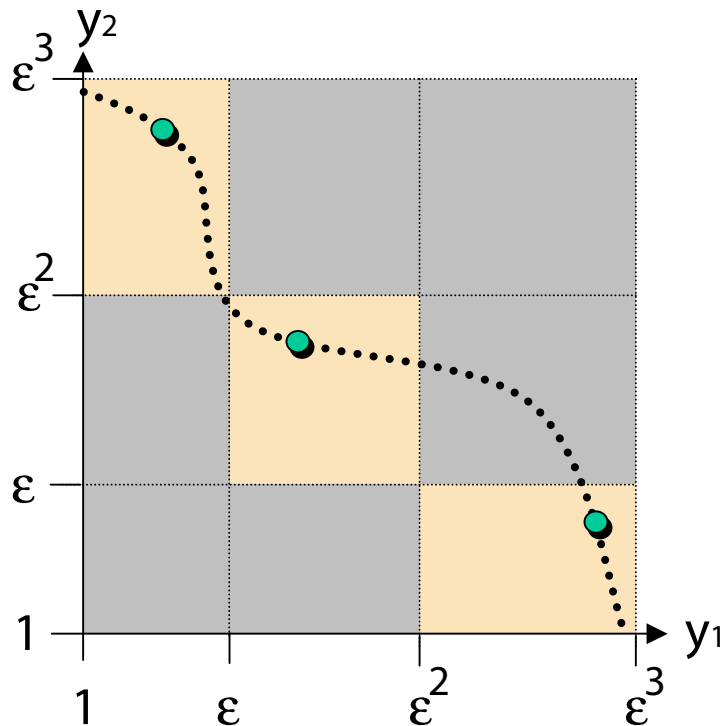
Definition 2: ϵ -Pareto set

subset of the Pareto set
which ϵ -dominates all Pareto-optimal solutions



Goal: Maintain ε -Pareto set

Idea: ε -grid, i.e. maintain a set of nondominated boxes (one solution per box)



Algorithm: (ε -update)

Accept a child if

- 1 the corresponding box is not dominated by any box that contains an individual

AND

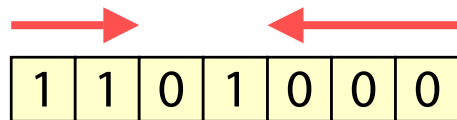
- 2 any other individual in the same box is dominated by the new solution

Basic question: [Laumanns et al.: 2002]

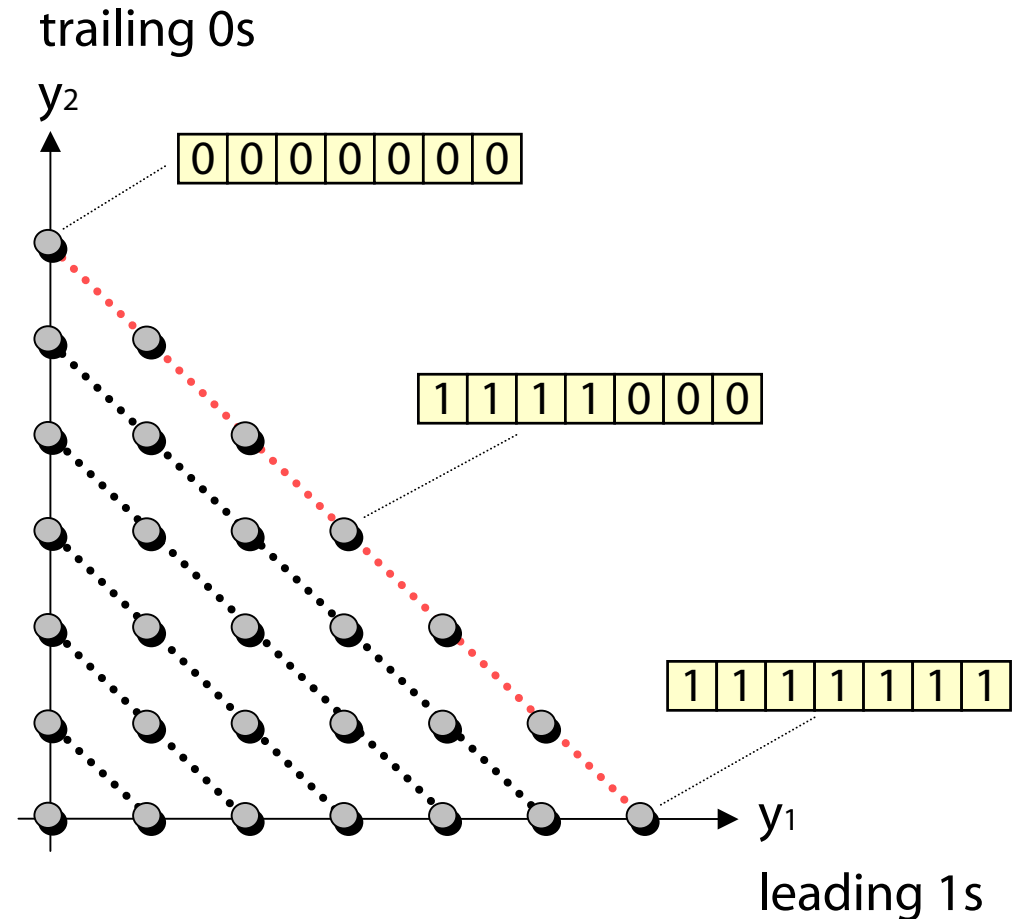
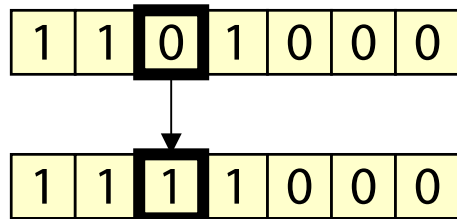
What is the worst case run-time of a multiobjective EA to find the Pareto set with high probability?

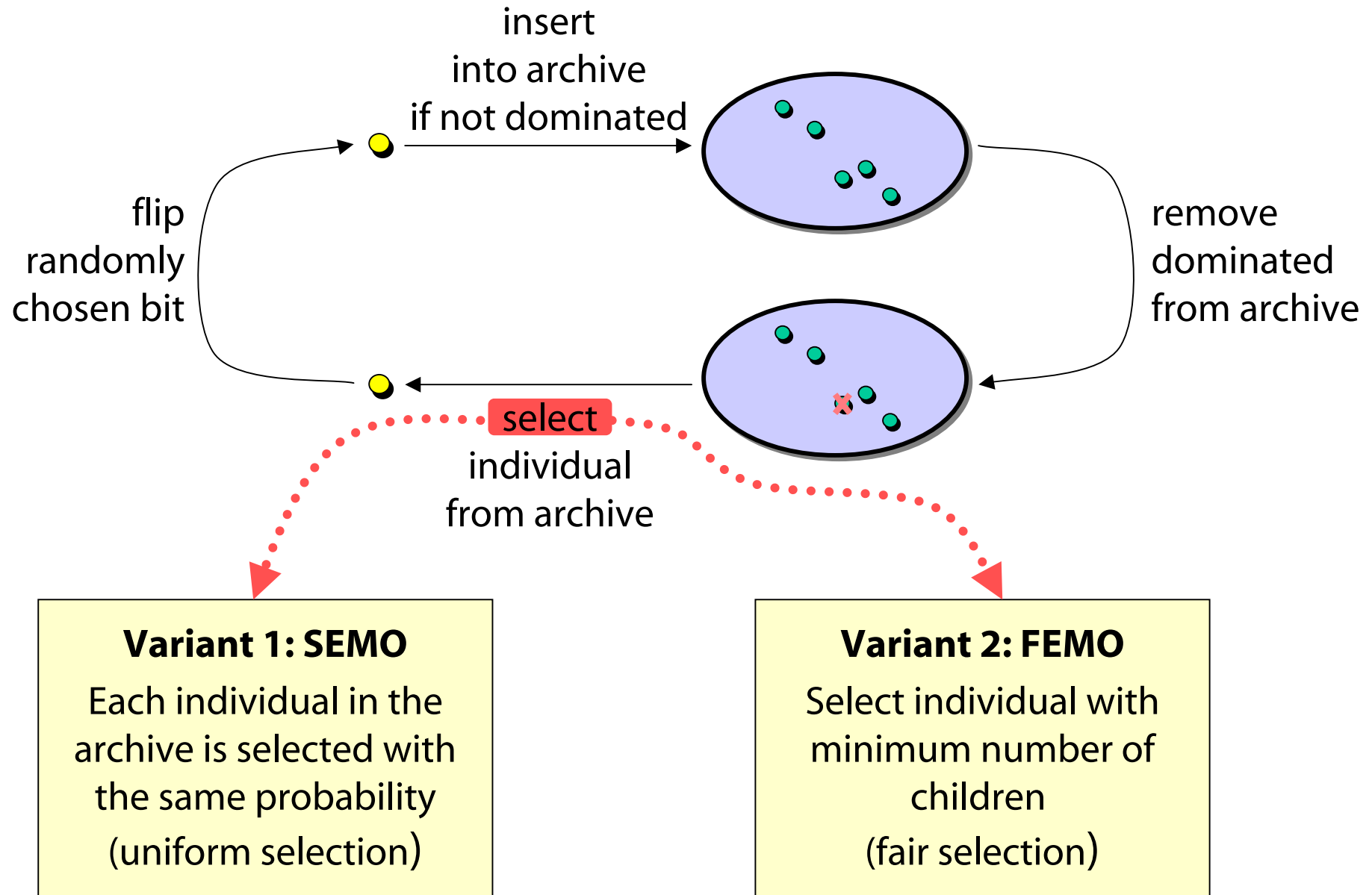
Scenario:

- **Problem:** leading ones, trailing zeros (LOTZ)



- **Variation:** single point mutation



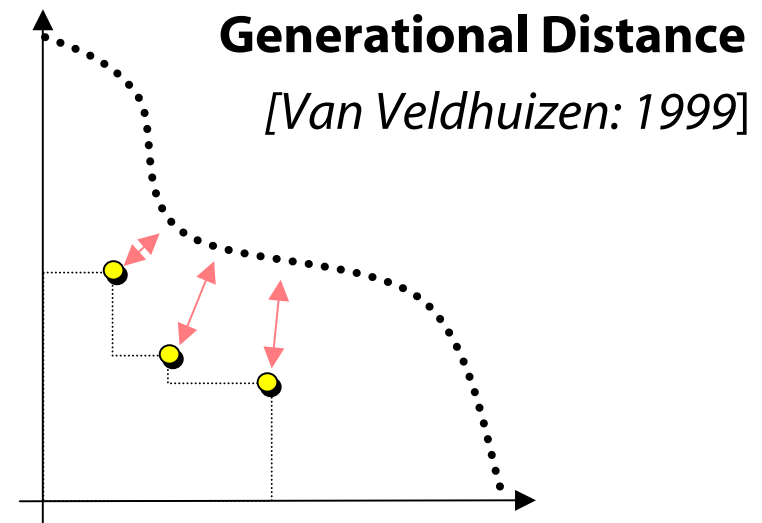
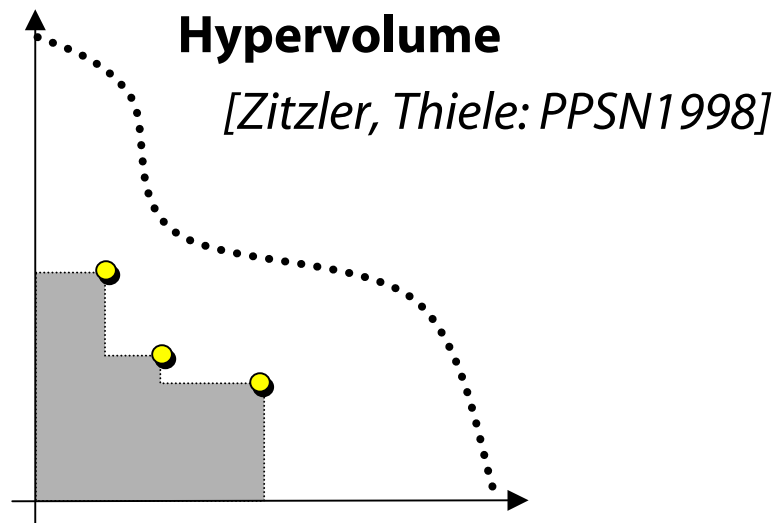


- Simple multiobjective EA with uniform selection (SEMO): $\Theta(n^3)$
 - ▶ To get to the Pareto front requires n^2 steps
 - ▶ To cover the entire front needs n^3 steps
- Simple multiobjective EA with fair selection (FEMO): $\Theta(n^2 \log n)$
 - ▶ Fair selection helps to spread over the Pareto front
- Multistart single-objective optimizer: $\Omega(n^3)$
 - ▶ In average, one out of n mutations successful
 - ▶ To get to the Pareto front, n successful mutations needed
 - ▶ Overall n Pareto-optimal solutions have to be found

multiobjective EA faster than multistart strategy

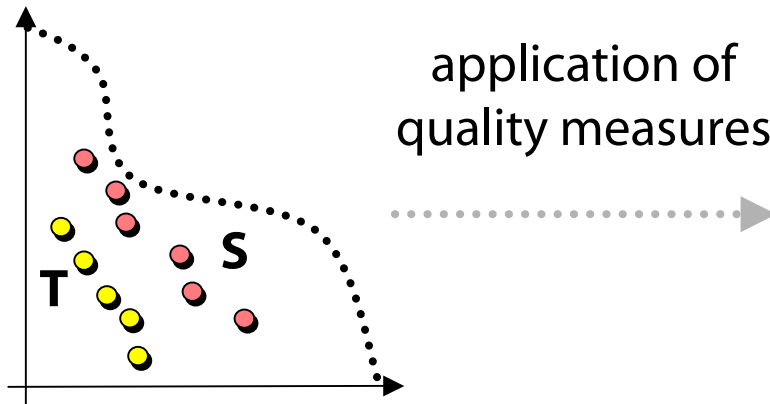
Issues: quality measures, statistical testing, benchmark problems, visualization, ...

Popular approach: unary quality measures



- Assign each outcome a *real number*
- Outcomes are compared by comparing the corresponding *values*

Basic question: Can we say on the basis of the quality measures *whether* or *that* an algorithm outperforms another?



	S	T
hypervolume	432.34	420.13
distance	0.3308	0.4532
diversity	0.3637	0.3463
spread	0.3622	0.3601
cardinality	6	5

There is no combination of unary quality measures such that **S** is better than **T** in all criteria is equivalent to **S** dominates **T**

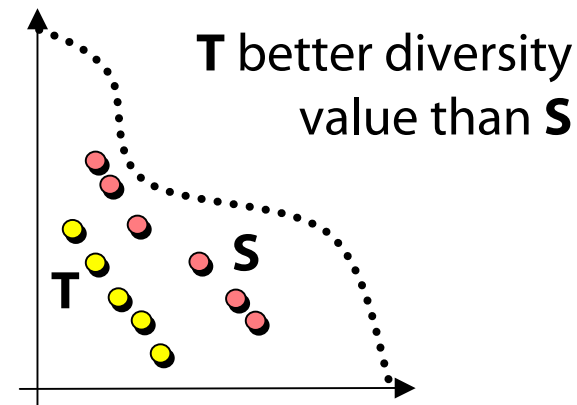
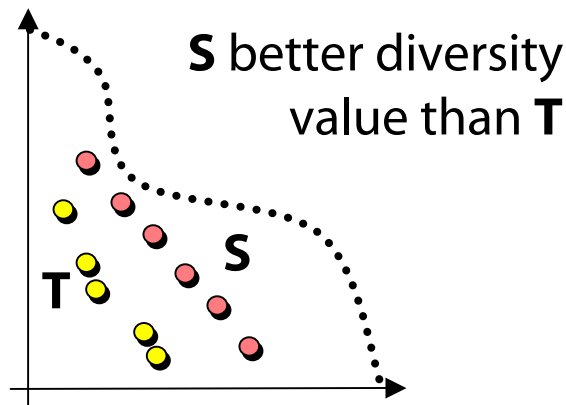
Unary quality measures usually do not tell that **S** dominates **T**; at maximum that **S** does not dominate **T**

[Zitzler et al.: 2002]

Many popular quality measures are not compliant with the dominance relation

[Hansen, Jaszkiwicz: 1998][Knowles, Corne: 2002][Zitzler et al.: 2002]

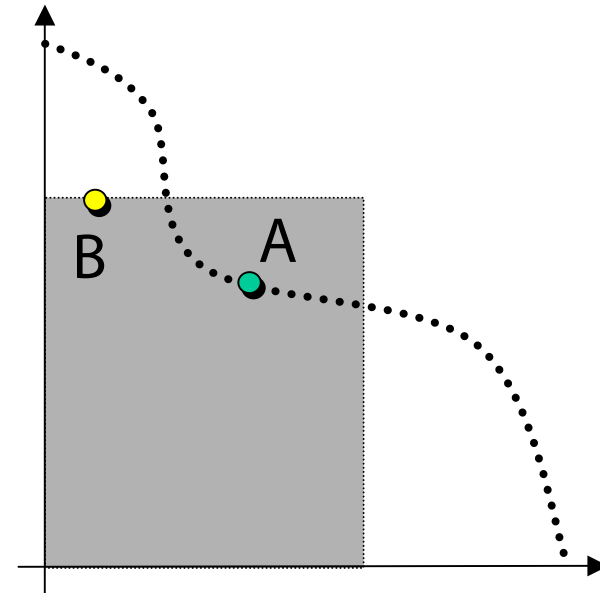
Example: diversity measures



Needed: appropriate binary quality measures that indicate *whether* an outcome dominates another, e.g., ϵ -measure

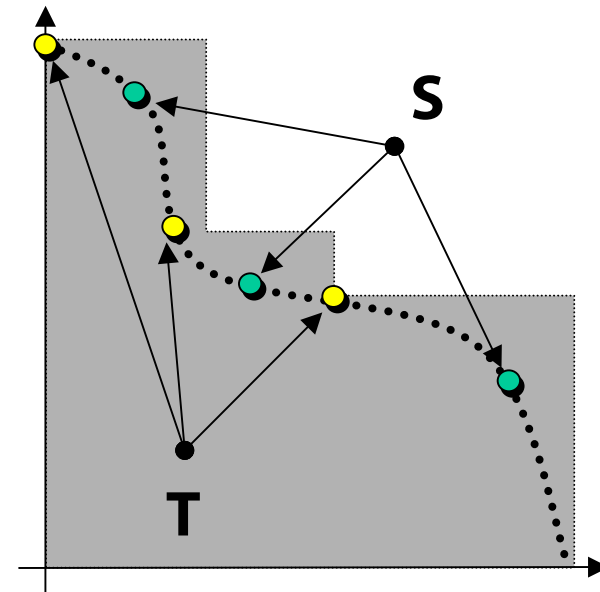
Definition 3: single solutions

$l_\varepsilon(A,B)$ = minimum ε such that
A ε -dominates B



Definition 4: sets of solutions

$l_\varepsilon(\mathbf{S},\mathbf{T})$ = minimum ε such that
each solution in \mathbf{T} is
 ε -dominated by at least
one solution in \mathbf{S}



[Zitzler et al.: 2002]

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Application engineer

- knowledge in the algorithm domain necessary
- state-of-the-art algorithms get more and more complex
- many algorithms

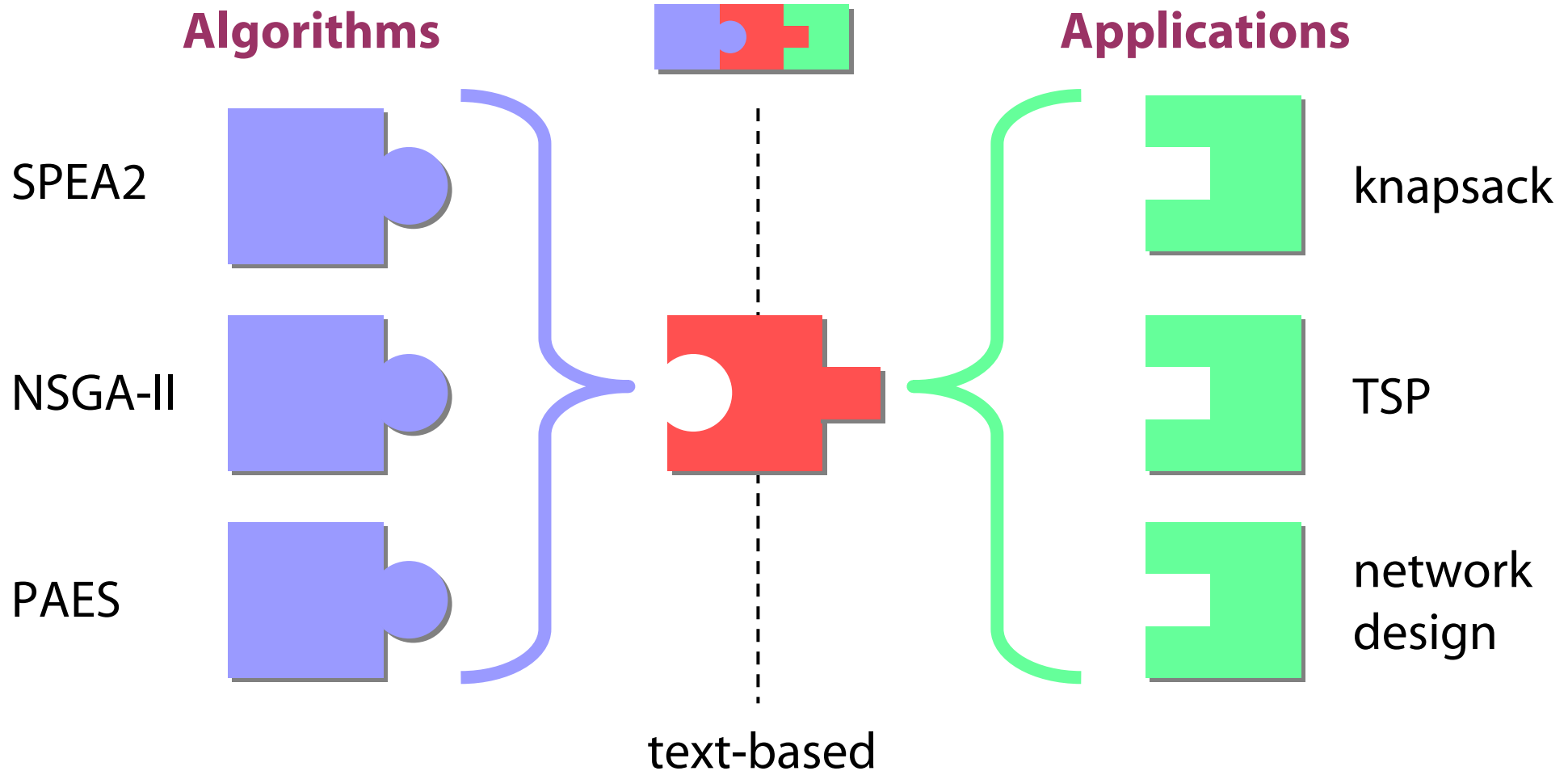
Algorithm designer

- comparison to competing algorithms mandatory
- tests on various benchmark problems necessary
- algorithms and applications become increasingly complex

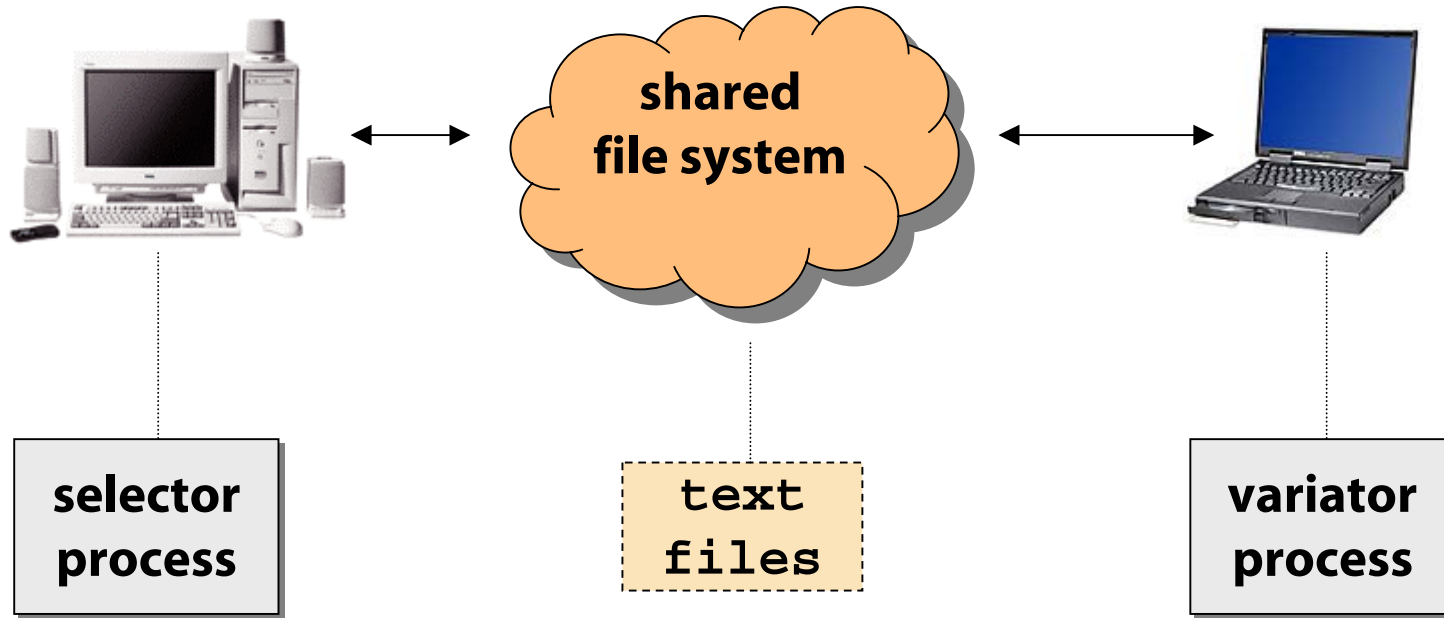
high implementation effort / risk of implementation errors

Programming libraries:

- ⊕ valuable tools to tailor a particular technique to a specific application
- ⊖ exchange of optimization algorithm or application still difficult



Platform and programming language independent **I**nterface
for **S**earch **A**lgorithms [Bleuler et al.: 2002]



application independent:

- mating / environmental selection
- individuals are described by IDs and objective vectors

handshake protocol:

- state / action
- individual IDs
- objective vectors
- parameters

application dependent:

- variation operators
- stores and manages individuals

Why using an evolutionary algorithm?

- **Flexibility:** problem formulation can be easily modified / extended (minimum requirements)
- **Multiple objectives:** the solution space can be explored in a single optimization run
- **Feasibility:** EAs are applicable to complex and huge search spaces

Why multiobjective optimization?

- **Robustness:** aggregation of several objectives into a single one requires setting of parameters
- **Confidence:** it is easier to select a solution if alternatives are known

Main application of EMO: design space exploration

Links:

- EMO mailing list:
<http://w3.ualg.pt/lists/emo-list/>
- EMO bibliography:
<http://www.lania.mx/~ccoello/EMOO/>
- PISA website:
<http://www.tik.ee.ethz.ch/pisa/>

Events:

- Conference on Evolutionary Multi-Criterion Optimization (EMO 2003),
April 8-11, 2003, Algarve, Portugal:
<http://conferences.ptrede.com/emo03/>

Acknowledgments:

- Stefan Bleuler, Marco Laumanns, Lothar Thiele