Evolutionary Multi-Objective Optimisation: part 2

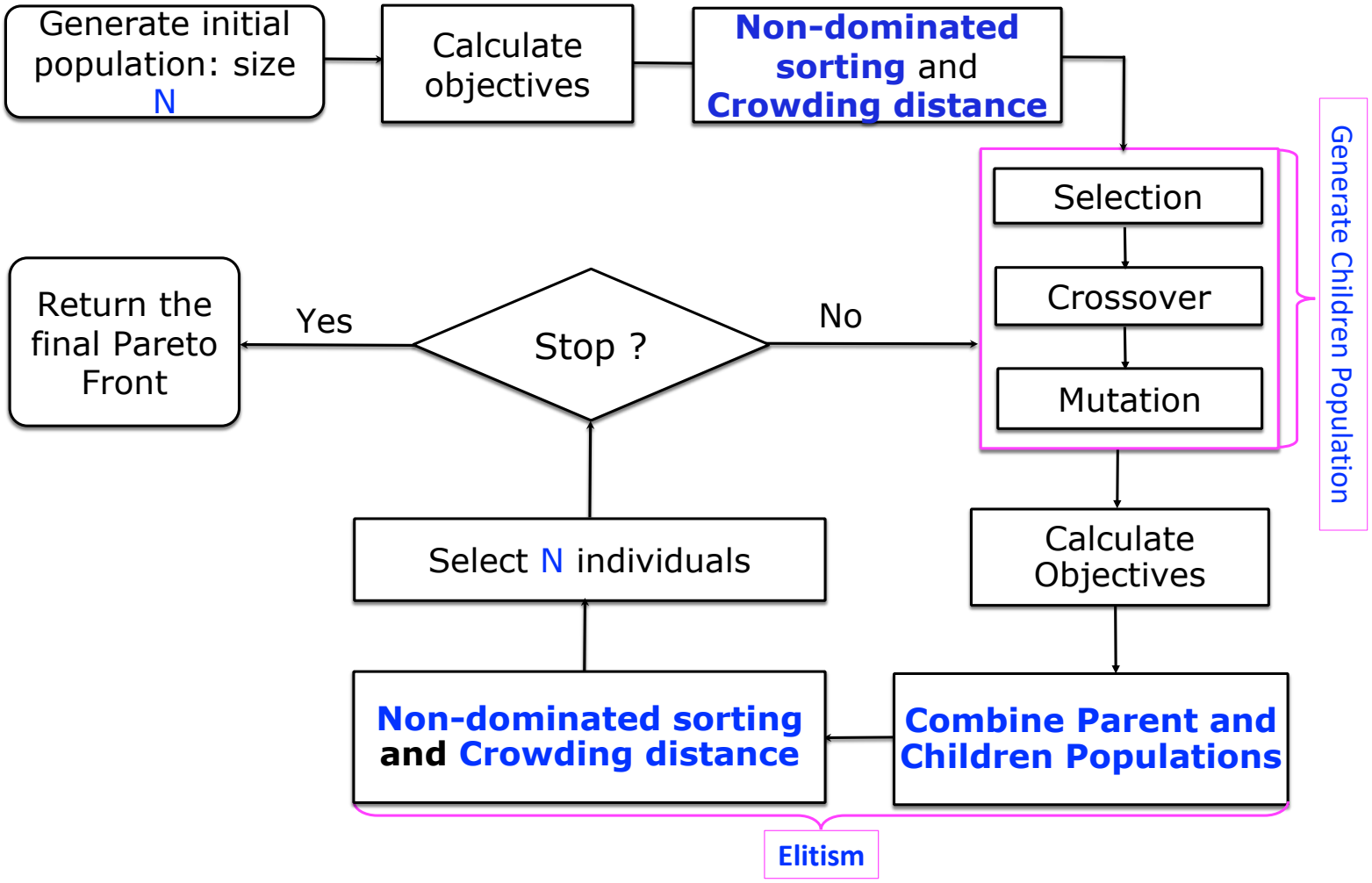
By: DR. Vahid Ghasemi

Outline

- Non-dominated Sorting Genetic Algorithm II
  - Fitness Assignment (non-dominated sorting)
  - Diversity (crowding distance)
  - Elitism (population combination and truncation)
- Strength Pareto Evolutionary Algorithm 2
  - Fitness Assignment (score based on #dominating and #dominated)
  - Diversity (density measure)
  - Elitism (population + archive)

NSGA-II

- A genetic algorithm based on non-dominated sorting
  - Version II (the most well-known version)

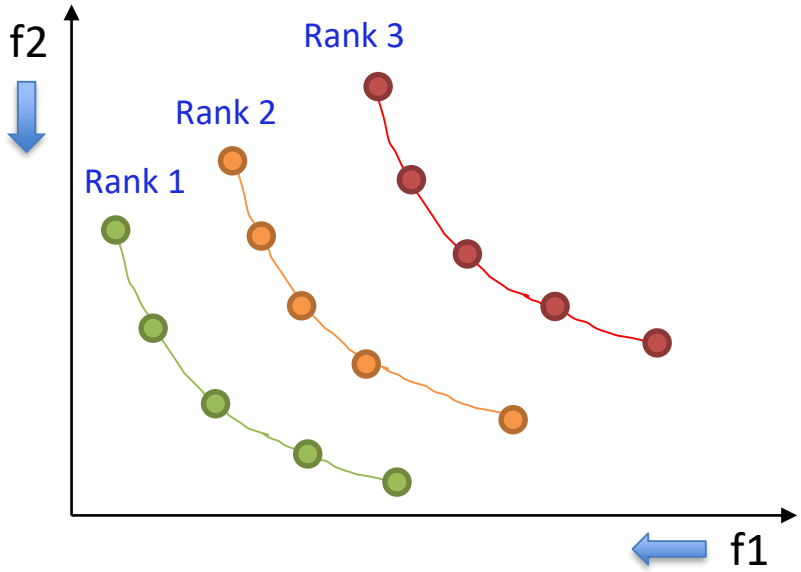


NSGA-II

- Similar to traditional GA
  - Individual representation
  - Crossover and mutation
- Different in Fitness Assignment
  - Non-dominated ranks and crowding distance
  - Used in both parent selection and environmental selection
- Crowding distance preserves the population diversity
- Combine parent and offspring population to achieve elitism

Non-dominated Sorting

- Calculate the dominance relation of each pair of the individuals in the population
  - **Rank 1**: the individuals with no individuals in the population dominating them
  - **Rank 2**: the individuals with no individuals in the population except the rank-1 individuals dominating them
  - **Rank N**: the individuals with no individuals in the population except the previously ranked individuals dominating them
- **Time complexity**: $O(N^2M)$, N is the number of individuals, M is the number of objectives



Non-dominated Sorting

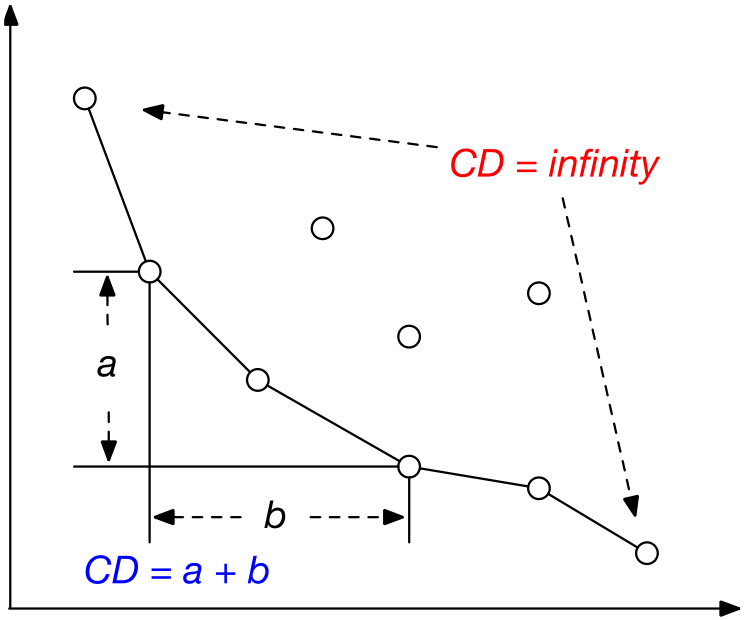
- How to get each rank?
  - Rank ≠ Number of individuals dominating it
- Need to store extra information
  - The list of individuals it dominates


```
For each ind in population:
    numDom[ind] = 0, dominates[indi] = {}
For each A in population:
    For each B ≠ A in population:
        If A dominates B:
            Add B into dominates[A]
        else if B dominates A:
            numDom[A] = numDom[A] + 1

Set front[0] = {all individuals with numDom[ind] = 0}, r = 0

While front[r] is not empty:
    For each ind in front[r]:
        For each B in dominates[ind]:
            numDom[B] = numDom[B] - 1
            If numDom[B] = 0:
                Add B into front[r+1]
    r = r + 1
```

Crowding Distance

- For the individuals with the same rank (in the same front)
  - For each objective, sort the individuals in ascending order of this objective
  - Calculate the normalised objective distance of the two adjacent individuals (extreme points have infinite distance)
  - Sum up the distances for all the objectives
  - $O(MN \log N)$ complexity, N is number of individuals, M is number of objectives

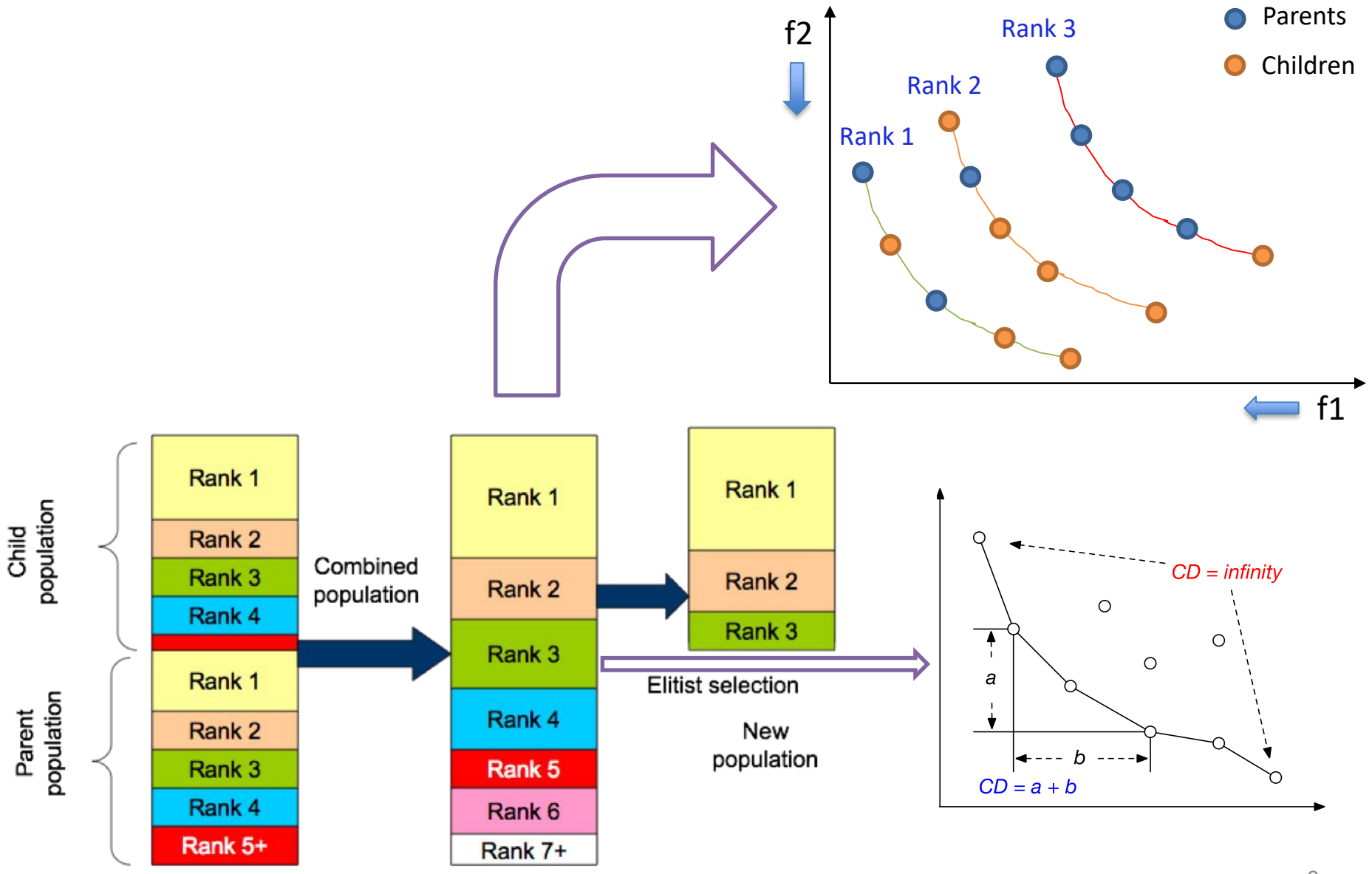
Larger CD ->
In less crowded area ->
Better Diversity



NSGA-II Selection

- Parent selection
  - **Random selection**: the same as traditional GA
  - **Tournament selection**: A is better than B if
    - A has a smaller rank, or
    - A and B have the same rank, and A has a larger CD
- Environmental Selection
  - Merge population and offspring (2N individuals)
  - Non-dominated sorting and crowding distance for the 2N individuals
  - Set an empty population for the next generation
  - Fill in the next population based on rank until it is full
  - If the last front exceed the population size, use crowding distance to select a partial last front (the individuals with largest crowding distance)

NSGA-II Selection



NSGA-II

- Advantages of NSGA-II
  - Flexible, robust to the shape of the true Pareto front
  - Fast if not too many objectives
    - $O(N^2M)$ for non-dominated sorting
    - $O(MN \log N)$ for crowding distance
  - Performance is reasonably good, no need to tune much
  - **The most used EMO algorithm**
- Disadvantages of NSGA-II
  - Not perfect performance
  - Sometimes not uniform enough

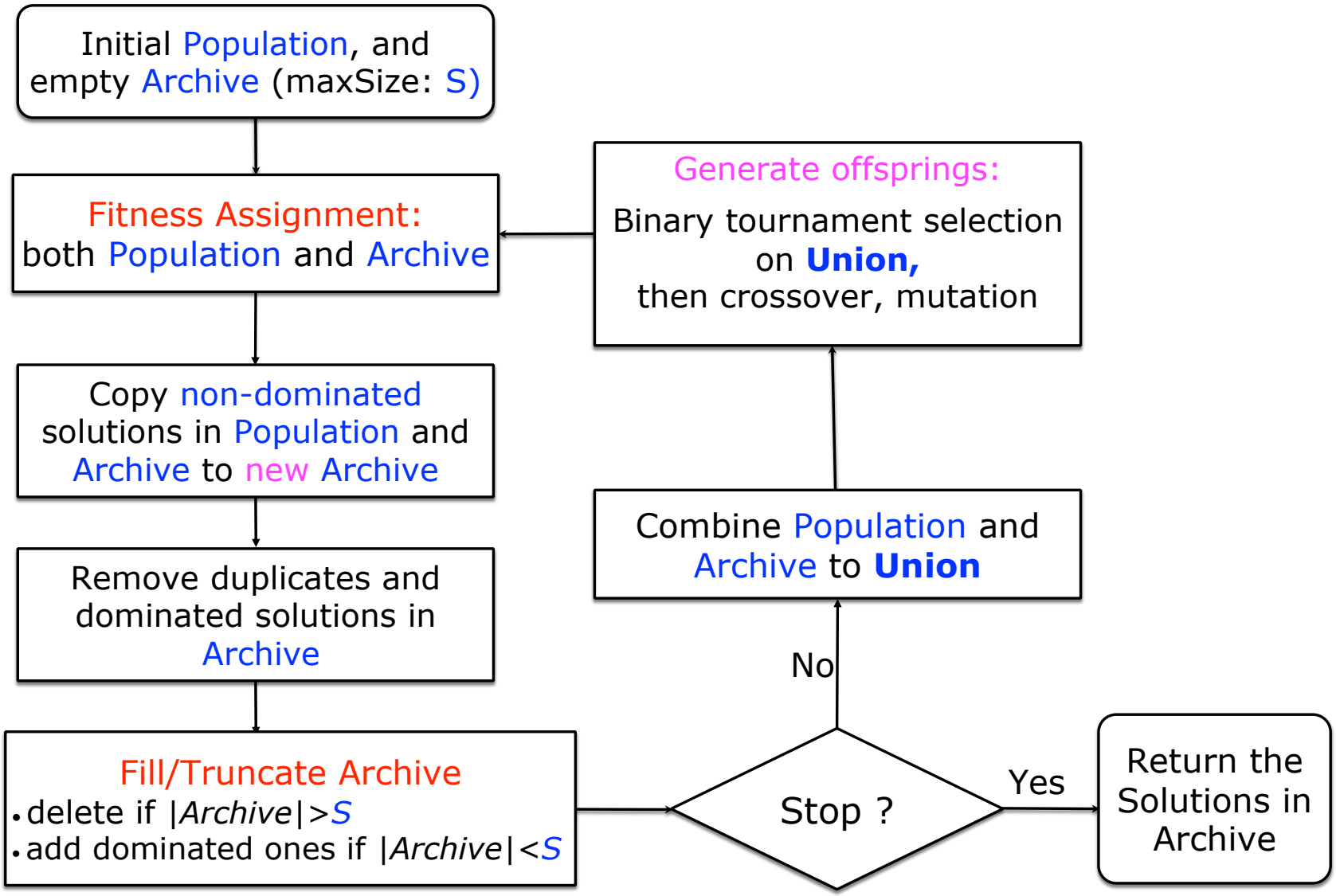
A fast and elitist multiobjective genetic algorithm: NSGA-II

K Deb, A Pratap, S Agarwal… - IEEE transactions on …, 2002 - ieeexplore.ieee.org

… **NSGA**, which we call **NSGA-II**. From the simulation results on a number of difficult test problems, we find that **NSGA-II** … constraint-handling strategy with **NSGA-II** that suits well for any EA. …

★ Save 99 Cite Cited by 41774 Related articles All 44 versions

Strength Pareto Evolutionary Algorithm 2



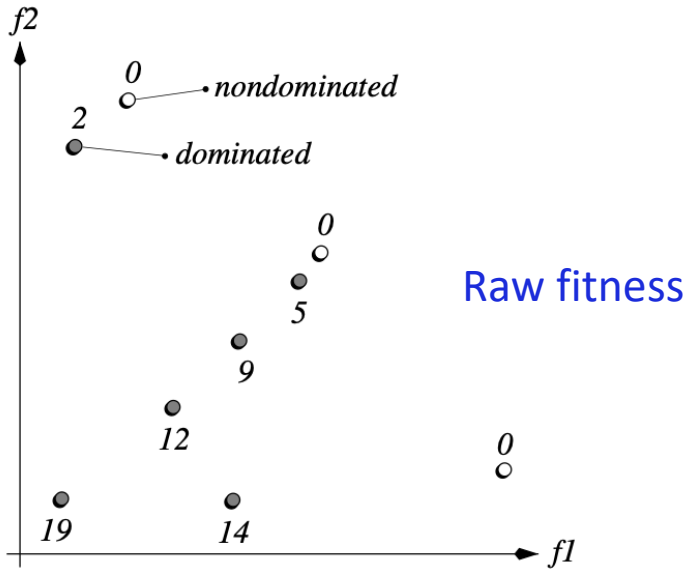
SPEA2

- Fitness assignment of SPEA2 (a single fitness value for each individual)
  - Convergence (depending on dominating and dominated solutions)
  - Diversity (density measure)

$$Fitness(X) = RawF(X) + Density(X)$$

$$RawF(X) = \sum_{\substack{X' \in Pop \cup Arch, \\ X' \ dominates \ X}} S(X')$$

- Strength value: $S(X) = |X' \in Pop \cup Arch \mid X \ dominates \ X'|$
  - How many solutions dominated by X



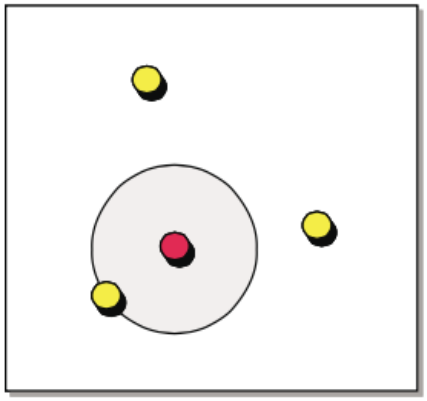
Raw fitness

SPEA2

- Density: the inverse of the distance (*in the objective space*) $d_k(X)$ to the k-th nearest neighbour in $Pop \cup Arch$
- $Density(X) = \frac{1}{d_k(X)+2}, k = \sqrt{|Pop| + |Arch|}$
  - $0 < Density(X) \leq \frac{1}{2} < 1$
  - $RawF(X)$ takes priority to $Density(X)$

Nearest neighbor

SPEA2



SPEA2

- Fill/Truncate archive
  - At the beginning, all are non-dominated solutions
  - If $|Arch| < S$, add dominated solutions based on their fitness
  - If $|Arch| > S$, delete crowded solutions based on the distance to the other individuals in the archive
    - **Remember**, this can change after each removal

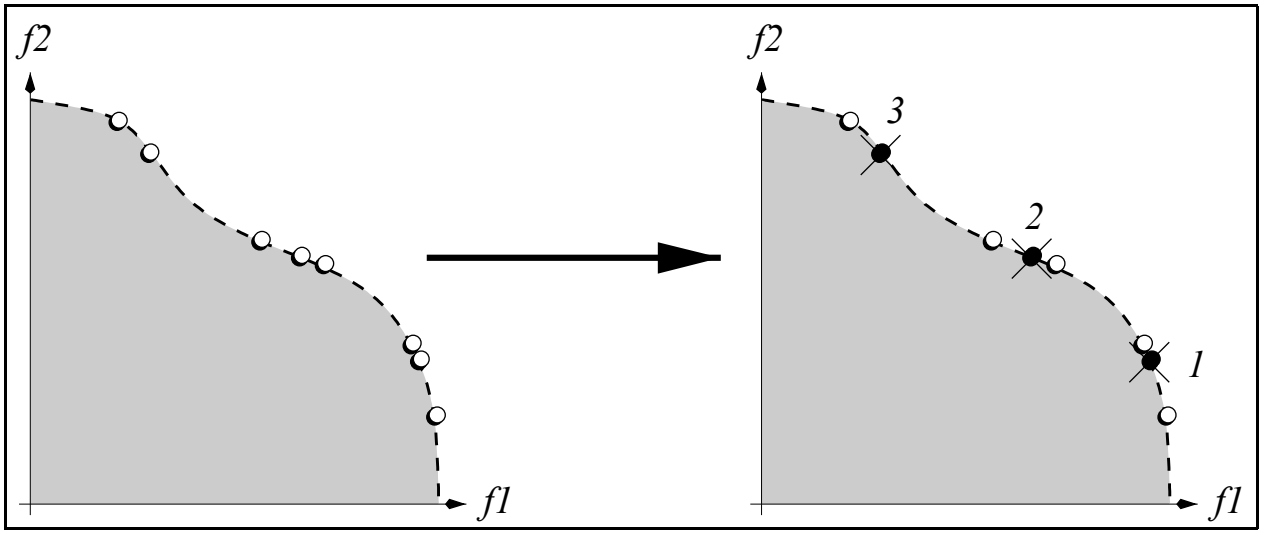


Figure 2: Illustration of the archive truncation method used in SPEA2. On the right, a nondominated set is shown. On the left, it is depicted which solutions are removed in which order by the truncate operator (assuming that $\overline{N} = 5$).

SPEA2

- Similar to NSGA-II in the sense that it is also based on dominance relation
- **Fitness Assignment**
  - Raw fitness based on dominating and dominated solutions
  - Density measure
- **Diversity preservation**
  - Add dominating solutions to archive based on density
  - Truncate the archive based on density / distance
- **Elitism**
  - The archive stores the non-dominated solutions so far
  - Archive size should not be too small (the same as population size)

SPEA2 vs NSGA-II

- Ideas are similar
- Dominance relation + Density/Crowdedness measure
- Both are very widely used in many applications

- Cannot say one is always better than the other – case by case, although in practice NSGA-II usually outperforms SPEA2…
- Try both and compare them

[PDF] **SPEA2**: Improving the strength Pareto evolutionary algorithm

E Zitzler, M Laumanns, L Thiele - TIK-report, 2001 - research-collection.ethz.ch

… In this paper, **SPEA2** is presented, for which we tried to eliminate the potential weaknesses of its predecessor and to … The main differences of **SPEA2** in comparison to SPEA are: …

★ Save 99 Cite Cited by 9024 Related articles All 20 versions »

Summary

- Two well known MOEAs introduced
- NSGA-II and SPEA2 are both based on dominance relation and some kind of density/crowdedness measures
  - Dominance primary
  - Density secondary
- Elitism is based on merging parents and children, and truncate selection
  - NSGA-II: merging parent and offspring populations
  - SPEA2: population + archive
- Very widely used, and easy to implement, first algorithms to try when solving a problem