Flowchart of NSGAII

1. Generate initial population: size $N$
2. Evaluate fitness
3. Non-dominated Ranking
   - Selection
   - Crossover
   - Mutation
4. Evaluate fitness
   - Combine Parent and Children Populations
5. Non-dominated Ranking and Crowding distance
6. Select $N$ individuals
7. Stop?
   - Yes: Return the final Pareto Front
   - No: Go back to step 2
NSGAII — Elitism

- Elitism: Keep the best Parent Child individuals from the parent and child population.
NSGAII — Elitism

Child population

Parent population

Combined population

Elitist selection

New population

Rank 1

Rank 2

Rank 3

Rank 4

Rank 5+

Rank 1

Rank 2

Rank 3

Rank 4

Rank 5

Rank 6

Rank 7+

Rank 1

Rank 2

Rank 3
Crowding distance

- $c = a + b$
- Ends have infinite crowding distance
SPEA2

- SPEA2: Improving the Strength Pareto Evolutionary Algorithm
- Compared to SPEA:
  - **Fitness assignment** scheme is used, which takes for each individual into account how many individuals it dominates and it is dominated by.
  - Fitness is **NOT** based on objective function values
  - Objective function values determine **dominance** relation
  - A **nearest neighbour density estimation** technique is incorporated which allows a more precise guidance of the search process.
  - A new **archive truncation method** guarantees the preservation of boundary solutions.
Flowchart of SPEA2

1. Initial **Population**, and empty **Archive** (maxSize: S)
2. **Fitness Assignment**: both **Population** and **Archive**
3. Copy non-dominated solutions in **Population** and **Archive** to **new Archive**
4. Remove duplicates and dominated solutions in **Archive**
5. **Archive Truncation**
   - delete if |Archive| > S
   - add dominated ones if |Archive| < S
6. **Generate offsprings**: Binary tournament selection on **Union**, then crossover, mutation
7. Combine **Population** and **Archive** to **Union**
8. **Stop**?
   - Yes: Return the Solutions in **Archive**
   - No: Environmental selection
9. **Fitness Assignment**:
   - both **Population** and **Archive**
Fitness Assignment

- Each individual both dominating and dominated solutions are taken into account
- \( \text{Fitness } F(i) = \text{Raw fitness } R(i) + \text{Density } D(i) \)
  - Nondominated: \( F(i) < 1 \); dominated: \( F(i) \geq 1 \)
- Raw fitness \( R(i) \):
  - Strength value \( S(i) \), representing the number of solutions (in both Population and Archive) \( i \) dominates:
    \[
    S(i) = |j| j \in (Pop + Arch) \land i \succ j |
    \]
  - Raw fitness \( R(i) \): is determined by the strengths of its dominators in both archive and population:
    \[
    R(i) = \sum_{j \in (Pop + Arch), j \succ i} S(j)
    \]
- Density \( D(i) \):
  - Additional density information is incorporated to discriminate between individuals having identical raw fitness values.
  - \( k \)-th nearest neighbour method: the inverse of the distance \( \sigma_{ik} \) (in objective space) to the \( k \)-th nearest neighbour (in both archive and population) as the density estimate:
    \[
    D(i) = \frac{1}{\sigma_{ik}^k + 2} \quad k = \sqrt{|Pop| + |Arch|}
    \]
Archive Truncation

- if $|\text{Archive}| < S$, add dominated ones based on the fitness values
- if $|\text{Archive}| > S$, delete crowded ones based on density measure

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 $N = 5$).