

%Pseudocode for Approach 1 (3 modules of NSGA-II (green box), Objective Function (blue box) and Topology Function (red box) are coded interactively working together to generate Pareto optimal solutions)

Start ►

%.....NSGA-II Module.....

Input: Number of decision variables=5191, population size N=1000, number of generations G=10⁴1000, crossover: Blend Method, Number of objective functions=2, the percentage of population used in reproducing=1, the percentage of population used to reproduce as offspring=1, the number of random selected chromosomes used in Tournament Selection method=3, the percentage of population used for mutation=0.3, The percentage of genes of selected chromosomes used for mutilation=0.07, convergency criterion (θ)=0.01.

Output: Pareto-optimal set of rehabilitation Individuals

1: Initialize population P with N random individuals (A matrix with 1000 rows (Chromosomes) and 5191 decision variables (Genes)).

2: Evaluate objective functions for each individual in P

%.....Objective Functions Evaluations Module.....

Input: Population P, network's initial data including links' diameters, roughness, length, positions and junctions' elevations, heads, base demands, positions and enforced, desirable and minimum pressure values

Output: Hard constraints, Graph-Base Water Age and Generalized Resilience Failure Index for Individuals

%.....Setting Boundary Condition.....

1: Genes associated to the links with fixed properties must be decoded to 1 referring to the code for not changing links within the optimization process

2: Genes associated to the links in the single fed cluster connected to nodes with 0 demand must be decoded to 0 referring to the code for putting links out of design within the optimization process

3: Genes associated to the links in the single fed clusters connected to nodes with non 0 demands must be randomly decoded to 2-7 referring to the codes for setting commercial diameters on links

4: Shortest path pipes must be randomly decoded to 2-7 to not get removed within the optimization process

%.....Calculating Objectives and Constraints.....

5: parfor Individuals=1 to number of rows in P (1000)

6: Setting every Individual's diameters on pipes (5191 decoded diameters)

7: Setting Individual's roughness on pipes (5191 decoded roughness)

8: Removing every Individual's links decoded by 0

9: Removing every Individual's associated nodes connected to removed pipes

10: Running hydraulic computation and getting pressures and velocities of every Individual's new layout

11: Calculating GRF for every Individual

12: Calculating shortest paths for every new layout of Individuals

13: Calculating GWA for every Individual

14: Calculating hard constraint 1

15: Evaluate Topology Function for each individual in P

%.....Topology Function Evaluations Module.....

Input: Individuals' network layout information including links' ID and indices and junctions' ID and indices plus elevations and based demands

Output: Single fed clusters and associated root nodes and highest elevated nodes

1: parfor Individuals=1 to number of rows in P (1000)

2: Finding bridges in every layout

3: Filtering out bridges not connected to a loop

4: Filtering out bridges not connected to the secondary part of layout

5: Filtering out bridges connected to single fed clusters without demands

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6: Finding single fed clusters
7: Finding root nodes
8: Finding highest elevated node
9: end
10: Return single fed clusters; root and highest elevated nodes to the objective function module
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%.....Objective Functions Evaluations Module.....

16: Getting pressure at root nodes
17: Getting pressure at highest elevated node
18: Calculating hard constraint 2
19: end
20: Return the matrix of Z with 1000 rows and 3 columns including sum of hard constraint values, GWA, GRF for every individual to the NSGA-II module
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%.....NSGA-II Module.....

3: for generation = 1 to G do
%.....Applying Non-Dominated Sorting Box.....
4: Perform non-dominated sorting based on constraint and objective function values and assign ranks
%.....Applying Diversity Box.....
5: Compute crowding distance for diversity preservation
%.....Applying GA.....
6: Select parent Individuals using binary tournament selection
7: Apply crossover and mutation to create offspring Q
8: Evaluate objective functions for individuals in Q
9: Combine parent and offspring populations R = P U Q
10: Perform non-dominated sorting on R
11: Perform mutation
12: Evaluate the objective function
13: Select the best N individuals based on rank and crowding distance
14: Set P = new selected population
15: Check the convergency criteria
16: if hypervolume index <  $\theta$ 
17: Break the par loop
18: end
19: end

20: Return non-dominated Individuals from final population
```

%Pseudocode for Approach 2 (the differences with Approach 1 is in the objective function module where hydraulic simulation is skipped, system constraint is not calculated and therefore there is no need to run the Topology Function module; instead of GWA and GRF, cost and topology resilience objectives are calculated).

Start ►

%.....NSGA-II Module.....

Input: Number of decision variables=5191, population size N=1000, number of generations G=10⁴1000, crossover: Blend Method, Number of objective functions=2, the percentage of population used in reproducing=1, the percentage of population used to reproduce as offspring=1, the number of random selected chromosomes used in Tournament Selection method=3, the percentage of population used for mutation=0.3, The percentage of genes of selected chromosomes used for mutilation=0.07, convergency criterion (θ)=0.01.

Output: Pareto-optimal set of rehabilitation Individuals

1: Initialize population P with N random individuals (A matrix with 1000 rows (Chromosomes) and 5191 decision variables (Genes)).

2: Evaluate objective functions for each individual in P

%.....Objective Functions Evaluations Module.....

Input: Population P, network's initial data including links' diameters, roughness, length, positions and junctions' elevations, heads, base demands, positions and enforced, desirable and minimum pressure values

Output: Topology resilience Index and cost for Individuals

%.....Setting Boundary Condition.....

1: Genes associated to the links with fixed properties must be decoded to 1 referring to the code for not changing links within the optimization process

2: Genes associated to the links in the single fed cluster connected to nodes with 0 demand must be decoded to 0 referring to the code for putting links out of design within the optimization process

3: Genes associated to the links in the single fed clusters connected to nodes with non 0 demands must be randomly decoded to 2-7 referring to the codes for setting commercial diameters on links

4: Shortest path pipes must be randomly decoded to 2-7 to not get removed within the optimization process

%.....Calculating Objectives and Constraints.....

5: **parfor** Individuals=1 to number of rows in P (1000)

6: Setting every Individual's diameters on pipes (5191 decoded diameters)

7: Removing every Individual's links decoded by 0

8: Removing every Individual's associated nodes connected to removed pipes

9: Calculating topology resilience index for every Individual

10: Calculating cost for every new layout of Individuals

11: **end**

12: Return the matrix of Z with 1000 rows and 2 columns including topology resilience and cost for every individual to the NSGA-II module

%.....NSGA-II Module.....

3: **for** generation = 1 to G **do**

%.....Applying Non-Dominated Sorting Box.....

4: Perform non-dominated sorting based on constraint and objective function values and assign ranks

%.....Applying Diversity Box.....

5: Compute crowding distance for diversity preservation

%.....Applying GA.....

6: Select parent Individuals using binary tournament selection

7: Apply crossover and mutation to create offspring Q

8: Evaluate objective functions for individuals in Q

```
9: Combine parent and offspring populations  $R = P \cup Q$ 
10: Perform non-dominated sorting on R
11: Perform mutation
12: Evaluate the objective function
13: Select the best N individuals based on rank and crowding distance
14: Set  $P$  = new selected population
15: Check the convergency criteria
16: if hypervolume index <  $\theta$ 
17: Break the par loop
18: end
19: end
20: Return non-dominated Individuals from final population
```

%Pseudocode for Approach 3-Stage 1 (this is exactly the Approach 2 Pseudocode).

Start ►

%.....NSGA-II Module.....

Input: Number of decision variables=5191, population size N=1000, number of generations $G=10^4$, crossover: Blend Method, Number of objective functions=2, the percentage of population used in reproducing=1, the percentage of population used to reproduce as offspring=1, the number of random selected chromosomes used in Tournament Selection method=3, the percentage of population used for mutation=0.3, The percentage of genes of selected chromosomes used for mutilation=0.07, convergency criterion (θ)=0.01.

Output: Pareto-optimal set of rehabilitation Individuals

1: Initialize population P with N random individuals (A matrix with 1000 rows (Chromosomes) and 5191 decision variables (Genes)).

2: Evaluate objective functions for each individual in P

%.....Objective Functions Evaluations Module.....

Input: Population P, network's initial data including links' diameters, roughness, length, positions and junctions' elevations, heads, base demands, positions and enforced, desirable and minimum pressure values

Output: Topology resilience Index and cost for Individuals

%.....Setting Boundary Condition.....

1: Genes associated to the links with fixed properties must be decoded to 1 referring to the code for not changing links within the optimization process

2: Genes associated to the links in the single fed cluster connected to nodes with 0 demand must be decoded to 0 referring to the code for putting links out of design within the optimization process

3: Genes associated to the links in the single fed clusters connected to nodes with non 0 demands must be randomly decoded to 2-7 referring to the codes for setting commercial diameters on links

4: Shortest path pipes must be randomly decoded to 2-7 to not get removed within the optimization process

%.....Calculating Objectives and Constraints.....

5: parfor Individuals=1 to number of rows in P (1000)

6: Setting every Individual's diameters on pipes (5191 decoded diameters)

7: Removing every Individual's links decoded by 0

8: Removing every Individual's associated nodes connected to removed pipes

9: Calculating topology resilience index for every Individual

10: Calculating cost for every new layout of Individuals

11: end

12: Return the matrix of Z with 1000 rows and 2 columns including topology resilience and cost for every individual to the NSGA-II module

%.....NSGA-II Module.....

3: for generation = 1 to G do

%.....Applying Non-Dominated Sorting Box.....

4: Perform non-dominated sorting based on constraint and objective function values and assign ranks

%.....Applying Diversity Box.....

5: Compute crowding distance for diversity preservation

%.....Applying GA.....

6: Select parent Individuals using binary tournament selection

7: Apply crossover and mutation to create offspring Q

8: Evaluate objective functions for individuals in Q

9: Combine parent and offspring populations $R = P \cup Q$

10: Perform non-dominated sorting on R

```

11: Perform mutation
12: Evaluate the objective function
13: Select the best N individuals based on rank and crowding distance
14: Set P = new selected population
15: Check the convergency criteria
16: if hypervolume index <  $\theta$ 
17: Break the par loop
18: end
19: end
20: Return non-dominated Individuals from final population

```

%Pseudocode for Approach 3-Stage 2 (this is exactly the Approach 1 Pseudocode with a slight difference in NSGA-II Module and boundary condition of the objective function module).

Start ►

%.....NSGA-II Module.....

Input: Population obtained in stage 1 (P), Number of decision variables=5191, population size N=1000, number of generations G=10⁴1000, crossover: Blend Method, Number of objective functions=2, the percentage of population used in reproducing=1, the percentage of population used to reproduce as offspring=1, the number of random selected chromosomes used in Tournament Selection method=3, the percentage of population used for mutation=0.3, The percentage of genes of selected chromosomes used for mutilation=0.07, convergency criterion (θ)=0.01.

Output: Pareto-optimal set of rehabilitation Individuals

1: Evaluate objective functions for each individual in P

%.....Objective Functions Evaluations Module.....

Input: Population P, network's initial data including links' diameters, roughness, length, positions and junctions' elevations, heads, base demands, positions and enforced, desirable and minimum pressure values

Output: Hard constraints, Graph-Base Water Age and Generalized Resilience Failure Index for Individuals

%.....Setting Boundary Condition.....

```

1: Genes associated to the links with fixed properties must be decoded to 1 referring to the code for not
   changing links within the optimization process
2: Genes associated to the links in the single fed cluster connected to nodes with 0 demand must be decoded to
   0 referring to the code for putting links out of design within the optimization process
3: Genes associated to the links in the single fed clusters connected to nodes with non 0 demands must be
   randomly decoded to 2-7 referring to the codes for setting commercial diameters on links
4: Shortest path pipes must be randomly decoded to 2-7 to not get removed within the optimization process
5: The removed pipes obtained in the previous optimization stage must not take on diameters

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%.....Calculating Objectives and Constraints.....

```

6: parfor Individuals=1 to number of rows in P (1000)
7: Setting every Individual's diameters on pipes (5191 decoded diameters)
8: Setting Individual's roughness on pipes (5191 decoded roughness)
9: Removing every Individual's links decoded by 0
10: Removing every Individual's associated nodes connected to removed pipes
11: Running hydraulic computation and getting pressures and velocities of every Individual's new layout
12: Calculating GRF for every Individual
13: Calculating shortest paths for every new layout of Individuals
14: Calculating GWA for every Individual
15: Calculating hard constraint 1
16: Evaluate Topology Function for each individual in P

```

%.....Topology Function Evaluations Module.....

Input: Individuals' network layout information including links' ID and indices and junctions' ID and indices plus elevations and based demands

Output: Single fed clusters and associated root nodes and highest elevated nodes

```
1: parfor Individuals=1 to number of rows in P (1000)
2: Finding bridges in every layout
3: Filtering out bridges not connected to a loop
4: Filtering out bridges not connected to the secondary part of layout
5: Filtering out bridges connected to single fed clusters without demands
6: Finding single fed clusters
7: Finding root nodes
8: Finding highest elevated node
9: end
10: Return single fed clusters; root and highest elevated nodes to the objective function module
```

%.....Objective Functions Evaluations Module.....

```
17: Getting pressure at root nodes
18: Getting pressure at highest elevated node
19: Calculating hard constraint 2
20: end
21: Return the matrix of Z with 1000 rows and 3 columns including sum of hard constraint values, GWA, GRF for every individual to the NSGA-II module
```

%.....NSGA-II Module.....

```
2: for generation = 1 to G do
%.....Applying Non-Dominated Sorting Box.....
3: Perform non-dominated sorting based on constraint and objective function values and assign ranks
%.....Applying Diversity Box.....
4: Compute crowding distance for diversity preservation
%.....Applying GA.....
5: Select parent Individuals using binary tournament selection
6: Apply crossover and mutation to create offspring Q
7: Evaluate objective functions for individuals in Q
8: Combine parent and offspring populations R = P U Q
9: Perform non-dominated sorting on R
10: Perform mutation
11: Evaluate the objective function
12: Select the best N individuals based on rank and crowding distance
13: Set P = new selected population
14: Check the convergency criteria
15: if hypervolume index <  $\theta$ 
16: Break the par loop
17: end
18: end
19: Return non-dominated Individuals from final population
```

%Pseudocode for Approach 4-Stage 1 (this is exactly Approach 2 Pseudocode)

Start ►

%.....NSGA-II Module.....

Input: Number of decision variables=5191, population size N=1000, number of generations $G=10^4$, crossover: Blend Method, Number of objective functions=2, the percentage of population used in reproducing=1, the percentage of population used to reproduce as offspring=1, the number of random selected chromosomes used in Tournament Selection method=3, the percentage of population used for mutation=0.3, The percentage of genes of selected chromosomes used for mutilation=0.07, convergence criterion (θ)=0.01.

Output: Pareto-optimal set of rehabilitation Individuals

1: Initialize population P with N random individuals (A matrix with 1000 rows (Chromosomes) and 5191 decision variables (Genes)).

2: Evaluate objective functions for each individual in P

%.....Objective Functions Evaluations Module.....

Input: Population P, network's initial data including links' diameters, roughness, length, positions and junctions' elevations, heads, base demands, positions and enforced, desirable and minimum pressure values

Output: Topology resilience Index and cost for Individuals

%.....Setting Boundary Condition.....

1: Genes associated to the links with fixed properties must be decoded to 1 referring to the code for not changing links within the optimization process

2: Genes associated to the links in the single fed cluster connected to nodes with 0 demand must be decoded to 0 referring to the code for putting links out of design within the optimization process

3: Genes associated to the links in the single fed clusters connected to nodes with non 0 demands must be randomly decoded to 2-7 referring to the codes for setting commercial diameters on links

4: Shortest path pipes must be randomly decoded to 2-7 to not get removed within the optimization process

%.....Calculating Objectives and Constraints.....

5: parfor Individuals=1 to number of rows in P (1000)

6: Setting every Individual's diameters on pipes (5191 decoded diameters)

7: Removing every Individual's links decoded by 0

8: Removing every Individual's associated nodes connected to removed pipes

9: Calculating topology resilience index for every Individual

10: Calculating cost for every new layout of Individuals

11: end

12: Return the matrix of Z with 1000 rows and 2 columns including topology resilience and cost for every individual to the NSGA-II module

%.....NSGA-II Module.....

3: for generation = 1 to G do

%.....Applying Non-Dominated Sorting Box.....

4: Perform non-dominated sorting based on constraint and objective function values and assign ranks

%.....Applying Diversity Box.....

5: Compute crowding distance for diversity preservation

%.....Applying GA.....

6: Select parent Individuals using binary tournament selection

7: Apply crossover and mutation to create offspring Q

8: Evaluate objective functions for individuals in Q

9: Combine parent and offspring populations $R = P \cup Q$

10: Perform non-dominated sorting on R


```

11: Perform mutation
12: Evaluate the objective function
13: Select the best N individuals based on rank and crowding distance
14: Set P = new selected population
15: Check the convergency criteria
16: if hypervolume index <  $\theta$ 
17: Break the par loop
18: end
19: end
20: Return non-dominated Individuals from final population

```

%Pseudocode for Approach 4-Step 2 (no optimization is used in this stage. The graph-based design is performed for all the layouts achieved in the previous step)

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%.....The Demand Edge Betweenness Centrality Design Module.....

Input: Population P of Individuals obtained in the Stage 1 (1000 Individuals), Network data (Nodes and Edges
with geometry and demand), List of source nodes and their heads, Available commercial pipe diameters

Output: 301, 000 near optimal solutions (Designed pipe diameters),

%.....Setting Boundary Condition.....

1. Load all previously generated layouts from Stage 1 (GLayouts.mat)
2. Define available pipe diameters and corresponding discharge capacities using continuity equation
3. Define:
Number of sources
Source node names
Corresponding hydraulic heads
4. Generate a map for converting node names to numeric indices
5. Preallocate storage for paths, head differences, and pipe diameter assignment arrays
%..... Assigning Sources.....

6. FOR each layout i = 1 to 1000 DO
7. Assign pipe weights using edge lengths
8. FOR each source s = 1 to 4 DO
Find index of source node
Calculate distance from source to all nodes
Calculate head at each node based on head loss with distance
9. END FOR
10. For each node, assign the source providing maximum head
11. END FOR
%.....Calculating EBC.....

12. FOR each source s = 1 to 4 DO

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FOR each node n supplied by source s with non-zero demand DO

Find shortest path from source to node

Accumulate demand to all edges along the path

END FOR

Store EBC for current source

13. END FOR

14. Sum EBC values from all sources to get total design flow per edge

%.....Designing Pipe Diameters for Each Layout.....

15. FOR each velocity v from 0.5 to 3.5 m/s DO

Calculate flow capacities for all pipe diameters at current velocity

FOR each edge DO

Assign the smallest available diameter meeting flow requirement

END FOR

Store diameter assignment for this velocity

16. END FOR

18. Store all design solutions for layout i

END FOR

%Pseudocode for Approach 4-Step 2

Start ►

%.....Feasible Solutions Finding and Sorting.....

Input: Number of decision variables=5191, population size N=301,000, number of generations G=1, crossover: Blend Method, Number of objective functions=2, the percentage of population used in reproducing=1, the percentage of population used to reproduce as offspring=1, the number of random selected chromosomes used in Tournament Selection method=3, the percentage of population used for mutation=0.3, The percentage of genes of selected chromosomes used for mutilation=0.07

Output: Pareto-optimal set of rehabilitation Individuals

1: Initialize population P with 301,000 solutions generated in EBCQ-D module (A matrix with 301,000 rows (Chromosomes) and 5191 decision variables (Genes)).

2: Evaluate objective functions for each individual in P



%.....Objective Functions Evaluations Module.....

Input: Population P, network's initial data including links' diameters, roughness, length, positions and junctions' elevations, heads, base demands, positions and enforced, desirable and minimum pressure values

Output: Hard constraints, Graph-Base Water Age and Generalized Resilience Failure Index for Individuals

%.....Setting Boundary Condition.....

1: Genes associated to the links with fixed properties must be decoded to 1 referring to the code for not changing links within the optimization process

2: Genes associated to the links in the single fed cluster connected to nodes with 0 demand must be decoded to 0 referring to the code for putting links out of design within the optimization process

3: Genes associated to the links in the single fed clusters connected to nodes with non 0 demands must be randomly decoded to 2-7 referring to the codes for setting commercial diameters on links

4: Shortest path pipes must be randomly decoded to 2-7 to not get removed within the optimization process

5: The removed pipes obtained in the previous optimization stage must not take on diameters

%.....Calculating Objectives and Constraints.....

6: parfor Individuals=1 to number of rows in P (1000)

7: Setting every Individual's diameters on pipes (5191 decoded diameters)

8: Setting Individual's roughness on pipes (5191 decoded roughness)

9: Removing every Individual's links decoded by 0

10: Removing every Individual's associated nodes connected to removed pipes

11: Running hydraulic computation and getting pressures and velocities of every Individual's new layout

12: Calculating GRF for every Individual

13: Calculating shortest paths for every new layout of Individuals

14: Calculating GWA for every Individual

15: Calculating hard constraint 1

16: Evaluate Topology Function for each individual in P

%.....Topology Function Evaluations Module.....

Input: Individuals' network layout information including links' ID and indices and junctions' ID and indices plus elevations and based demands

Output: Single fed clusters and associated root nodes and highest elevated nodes

1: parfor Individuals=1 to number of rows in P (1000)

2: Finding bridges in every layout

3: Filtering out bridges not connected to a loop

4: Filtering out bridges not connected to the secondary part of layout

5: Filtering out bridges connected to single fed clusters without demands

6: Finding single fed clusters

7: Finding root nodes

8: Finding highest elevated node

9: end

10: Return single fed clusters; root and highest elevated nodes to the objective function module

%.....Objective Functions Evaluations Module.....

17: Getting pressure at root nodes

18: Getting pressure at highest elevated node

19: Calculating hard constraint 2

20: end

21: Return the matrix of Z with 1000 rows and 3 columns including sum of hard constraint values, GWA, GRF for every individual to the NSGA-II module

%..... Feasible Solutions Finding and Sorting

2: for generation = 1 to G do

%.....Applying Non-Dominated Sorting Box.....

3: Perform non-dominated sorting based on constraint and objective function values and assign ranks

%.....Applying Diversity Box.....

4: Compute crowding distance for diversity preservation

5: Select the best N individuals based on rank and crowding distance

6: Set P = new selected population

7: Set P = new selected population

8: end

9: Return non-dominated Individuals from final population

