Co-Operative Co-Evolutionary Genetic Algorithms
for Multi-Objective Topology Design

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ABSTRACT

This paper studies the effectiveness of incorporating co-operative co-evolutionary strategy into 4 evolutionary multi-objective optimisation algorithms – MOGA, NPGA, NSGA and CNSGA – for continuum topology design. Apart from the co-operative co-evolutionary concept, the algorithms employ the elitism and crowding distance techniques to promote the diversity within the set of preserved non-dominated solutions. Three-related 2D heat conduction problems with two design objectives are used as the case studies. The proposed co-operative co-evolution is found to improve the optimisation effectiveness significantly. The species arrangements and sizes have some impacts; the use of moderately small species barely improves the search performances due to the interference from species coupling. As these effects depend on physical meanings of problems, it is more expedient to estimate the parameters in practice.

Keywords: Topology design, co-operative co-evolution, multiple objectives, genetic algorithm

1. INTRODUCTION

The genetic algorithm (GA) and computational mechanics have been combined for continuum structural topology optimisation. The topology design may be divided into 3 main categories – the discrete truss design, unit cell properties, e.g. orientation and porosity in composite materials, and the continuum structural design, which allows the creation of new boundaries [1]. The space that contains the structure is specified and divided into rectangular grids. By selective filling these grids or leaving spaces empty, different configurations are obtained. GA randomly generates a population within the solution space set which is evolved repeatedly toward structures that can perform superlatively.

Since most design problems involve balancing functions and restrictions, the multi-objective optimisation is needed. As it is very rare that a single point in the solution space simultaneously optimises all objective functions f_j, the concept of Pareto ranking is used instead. It gives a set of non-dominated solutions or the Pareto optimal set by comparing the domination of an individual against others. Given a set of possible solutions, an individual is said to be Pareto optimal if there are no other solutions in the set that can dominate the individual. In other words, the optimised solutions must be non-dominated and can be displayed together in the Pareto front in the objective function space.

As in the single-objective optimisations, performances of algorithms usually degrade as the search space or problem size increases. Hence, the non-dominated solutions may deviate from the true Pareto front. Many strategies have been used to counter this problem including the elitism [2-3], diversity control [4] and co-evolution, that can be further divided into competitive and co-operative approaches in which sub-population can either compete or co-operate during the evolution [5]. It is the co-operative co-evolutionary strategy that is utilised in this paper.

The resulting non-dominated solutions can be qualitatively measured and compared. Due to the randomly directed nature of GA, the comparison uses the averaged values of many runs. A solution set may be measured against another by the coverage C, which quantifies the domination of the solution set contents over the other. If the true Pareto front can be obtained, the quality of the solution set can be much better judged through parameters M_1, M_2 and M'_3 which respectively represents the average distance between the non-dominated solutions to the true Pareto optimal set, the distribution of the non-dominated solutions and the normalised absolute difference between the extent of the front described by the non-dominated solutions and the true Pareto optimal solutions [6-7].

As various evolutionary multi-objective optimisation algorithms (EMOAs) have been proposed with their strengths and weaknesses, it is necessary to study the effects of the co-operative co-evolutionary strategy upon several EMOAs. In a

previous study [7], 4 popular algorithms – the multi-objective genetic algorithm (MOGA) [8], the niched Pareto genetic algorithm (NPGA) [9], the non-dominated sorting genetic algorithm (NSGA) [10] and the controlled elitist non-dominated sorting genetic algorithm (CNSGA) [11] – are chosen. The resulting procedures – CCMOGA, CCNPGA, CCNSGA and CCCNSGA – are collectively called the co-operative co-evolutionary multi-objective optimisation algorithms or CCMOAs.

As the topology design are highly non-linear, discontinuous and the structure performances can be greatly affected be even a single well-placed connection, the true Pareto fronts may be generated only by exhaustive searches, an immersed feat even for a midsize two-dimensional problems, making the topology design not useful in the study of co-operative co-evolutionary effects upon the EMOAs. Hence, ZDT benchmarks, consisting of 6 two-objective minimisation problems by Zitzler et al. [6], are instead used to test effectiveness of the co-operative co-evolution. ZDT1 is a 30-dimensional problem with a continuous and uniformly distributed, convex Pareto front. The 30-dimensional ZDT2 has a non-convex Pareto front. ZDT3 is a 30-dimensional problem with five discrete Pareto fronts. The 10-dimensional ZDT4 has 21^9 local fronts and is used to test the algorithm's ability to deal with multi-modality. ZDT5 with deceptive Pareto fronts is an 11-dimensional problem. The 10-dimensional ZDT6 has a non-uniform search space.

It has been conclusively shown that the CCMOAs significantly outperform the EMOAs [7]. It is clear that the solutions from CCMOAs are superior to the corresponding EMOAs' non-dominated solution set at the end of runs. Major solution improvements from EMOAs are observed for all ZDT test cases, making the strategy problem independent. For a given equivalent solutions, the CCMOAs can find them generations before EMOAs and hence distinctive accelerated findings of better solutions are observed [18]. The CCMOAs can capture the true Pareto fronts with the exception for ZDT5. In ZDT5, the incorporation of the co-operative co-evolutionary strategy appears to produce only a marginal improvement. The CCNPGA, CCNSGA and CCCNSGA are still unable to locate the true Pareto optimal solutions of the test problem ZDT5; nonetheless, it is enough to push the solutions from the best deceptive front to the true Pareto front in CCMOGA. It should be noted that the ZDT5 have probably proved to be so problematic such that some discard it when the ZDT test series are used [12-13].

With this assurance of co-operative co-evolution effectiveness, two-dimensional heat transfer problems with midsize grid division are used to test the topology design optimisation with EMOAs and CCMOAs for 3 related problems with 2 design objectives. In this paper, the finite volume (FV) method is used to calculate the performance values of the evolving structures. Apart from the performance comparison between the EMOAs and CCMOAs, the effects of species arrangements and sizes in CCMOAs are also considered.

In short, this paper is structured as follows. In the next section, the genetic algorithm integration and additional genetic operators for the co-operative co-evolutionary strategy is discussed. Then, the topology design test cases are described, the FV main procedures outlined. The results and its non-dominated solution fronts are shown; solution sets from EMOAs and CCMOAs and the effects of the species characteristics (arrangement and size) are compared through the coverage C. Finally, the conclusions of the effectiveness of the proposed CCMOAs are drawn.

2. GENETIC ALGORITHMS
The co-operative co-evolution is integrated into the following 4 EMOAs. Firstly, brief descriptions of the algorithms are given, and then the integration with co-operative co-evolution and relevant operators are outlined.

2.1 Evolutionary Multi-Objective Optimisation Algorithms (EMOAs)
2.1.1 Multi-Objective Genetic Algorithm (MOGA)
MOGA [8] seeks to optimise components of the objective function vector. Each solution in the solution set is optimal if no improvement can be achieved in any component of the objective vector that does not lead to degradation of one or more remaining components.

Assuming a minimisation problem, an n-dimensional objective vector $\mathbf{p}$ is said to be dominating another n-dimensional objective vector $\mathbf{q}$ if, and only if, $\mathbf{p}$ is partially less than $\mathbf{q}$ ($\mathbf{p}\, p < \mathbf{q}$), i.e.

$$\mathbf{p}\, p < \mathbf{q} \leftrightarrow \forall i = 1,...,n : p_i \leq q_i \wedge \exists i = 1,...,n : p_i < q_i. \tag{1}$$

By identifying the number of solutions in the solution set that dominates the solution of interest, a rank value can be assigned to the solution. The rank of an individual is the number of solutions in the solution set that dominates the individual. After a rank has been assigned to each solution, a fitness value can be interpolated onto the solution where GA is applied in the optimisation procedure. The description of the MOGA, including goal attainment and priority assignment strategies, can be found in [15].

2.1.2 Niched Pareto Genetic Algorithm (NPGA)

NPGA [9] employs a tournament selection without an actual fitness assignment. Two randomly selected individuals are compared against one another in a comparison set, which is randomly extracted from the population. If one candidate is dominated by the comparison set while the other is not, the latter is selected for reproduction. Otherwise, the winner is the individual with less niche count, which measures the distance between two individuals in the objective space and is obtained from the fitness sharing [16]. A higher value of niche count indicates the lower diversity, and vice versa.

2.1.3 Non-dominated Sorting Genetic Algorithm (NSGA)

NSGA [10] is derived from the concept of normal Pareto ranking [16]. In MOGA, the rank is used to determine the fitness of each individual by the domination of all members. In NSGA, the ranking procedure first identifies the non-dominated individuals in the population. These individuals are given the first rank and subsequently removed from the population. The non-dominated members among the remaining individuals in contention are then identified and given the next rank. The process is repeated until all members are ranked. Then, fitness value is assigned to the individual such that a higher-rank individual is fitter than another with a lower rank.

2.1.4 Controlled Elitist Non-dominated Sorting Genetic Algorithm (CNSGA)

The CNSGA [11] is the most recent version of the NSGA which includes elitism and the controlled propagation of individuals of all ranks from one generation to the next. The elitist strategy merges the parent and offspring populations; fittest individuals are then extracted from the merged population, ensuring elitism across generations by comparing parents and their offspring together. The extracted individuals are selected from individuals of all ranks such that the ratios between the numbers of selected individuals across the ranks are kept constant. If the number of individuals in one rank is higher than the allowed survival number, individuals are chosen by the crowding distance selection to ensure that the individual with higher diversity has more chances of being selected.

2.2 Integration of Co-Operative Co-Evolution

The concept of co-operative co-evolution is integrated into the 4 EMOAs. The co-operative co-evolutionary concept is outlined and the two additional genetic operators – the crowding distance selection and the elitism – are described

2.2.1 Co-Operative Co-Evolutionary Concept

A co-operative, co-evolutionary search involves the evolution of multiple species together by the standard GA where population is split into a number of sub-populations or species, each representing a decision variable or a part of solution [17-18]. By partitioning the population into species in this manner, the search space that each sub-population has to cover is significantly reduced.

Although the co-operative, co-evolutionary strategy is developed for single-objective optimisations, it has also been successfully embedded into an MOGA and is found to outperform the original algorithm using benchmark GA problems [19]. Later, the protocol is modified with crowding distance diversity control into 4 EMOAs [7]. In addition, the incorporation of co-operative co-evolution significantly increases the efficiency of optimisation search for maximised heat dissipation porous fin-structures [7], in contrast with the vague improvements from incorporating the physical meanings into the crossover operators [20].

With co-operative co-evolution (Fig. 1), the chromosome is divided into species which are initialised randomly. The preserved non-dominated solution set (PNSS) is originally created by combining different species together randomly and non-dominated solutions are selected into the set. Then, each species evolves one after another through generations. The objective vector of a species member is obtained by substituting the species into its location in an individual that is randomly extracted from the PNSS. If the complete chromosome obtained after combining the species of interest with other species is neither dominated by any solutions in the preserved set nor a duplicate of a solution in the preserved set, this complete solution is added to the preserved set and the dominated solutions in the set is expunged. It is noted that if the number of non-duplicated non-dominated individuals exceeds a prescribed number, the crowding distance strategy will be used to limit the PNSS size by eliminate the least diverse individuals from the elite individual set. After objective values have been assigned to every individual in all sub-populations, the evolution of every species is then commenced by one of the 4 EMOAs with main genetic operators summarised in Tab. 1. The resulting co-operative co-evolutionary multi-objective optimisation algorithms (CCMOAs) are uniquely referred with co-operative co-evolutionary (CC) prefix as CCMOGA, CCNPGA, CCNSGA and CCCNSGA, respectively.
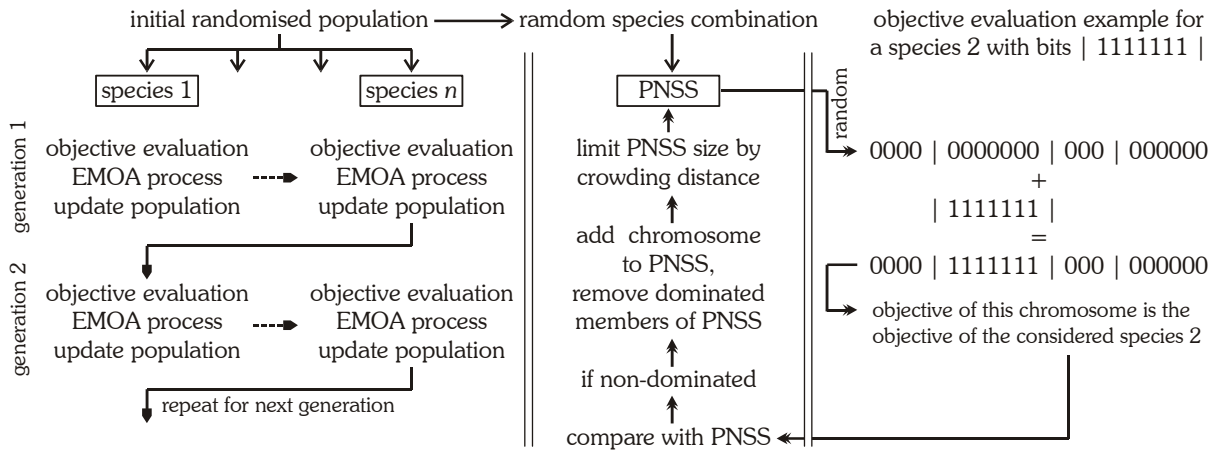
initial randomised population ⟶ ramdom species combination

objective evaluation example for
a species 2 with bits | 1111111 |

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species 1          species n              PNSS
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generation 1

objective evaluation   objective evaluation
EMOA process ----> EMOA process
update population   update population

generation 2

objective evaluation   objective evaluation
EMOA process ----> EMOA process
update population   update population

repeat for next generation

limit PNSS size by
crowding distance

add chromosome
to PNSS,
remove dominated
members of PNSS

if non-dominated

compare with PNSS ◄

random

0000 | 0000000 | 000 | 000000
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objective of this chromosome is the
objective of the considered species 2

Fig. 1. Overall procedure of the co-operative co-evolutionary genetic algorithms.

Parameter	EMOAs	CCMOAs
Chromosome representation	Binary chromosome	
Fitness sharing	Triangular sharing with the sharing radius estimated in the objective space [8]	
Selection operator	Stochastic universal sampling or tournament selection (NPGA and CCNPGA)	
Crossover operator	Uniform crossover with probability = 1.0	
Mutation operator	Bit-flip mutation with probability = 0.025	
Chromosome length	100	100 with 20 or 10-bit species
Population/Sub-population size	200	200
Maximum size of PNSS	-	50
Maximum number of elite members	50	50
Number of generations	250	Equal number of objective evaluations 50 (20-bit species) or 25 (10-bit species)
Number of repeated runs	30 (case 1,2) and 10 (case 3)	

Tab. 1. EMOAs and CCMOAs parameters. The fitness sharing, selection and elitist strategy are not used in CNSGA and CCCNSGA.

2.2.2 Diversity Control by Crowding Distance Strategy
In order to maintain the diversity within the PNSS, the crowding distance selection [3-4] is used to regulate the size of the preserved set. For every objective evaluation of species, the complete chromosome is compared with the PNSS. If it is non-dominated, the chromosome is added into the PNSS. The PNSS members are compared and those found dominated are expunged from the preserved set. However, this may lead to more individuals in the PNSS than the prescribed numbers since the new chromosome and the existing members of PNSS may be all non-dominated. This problem is substantially increased with enlarged search space or problem sizes. The crowding distance selection eliminates the extra chromosome with highest niche count. As the PNSS check after each objective evaluation, only one chromosome is eliminated at one time. Therefore, the procedure does not experience the difficulties where a large portion of the set needs to be removed.

2.2.3 Elitism Strategy
Elitism is important for the success of GA in multi-objective optimisation [3],[11] even though it is not used in the original propositions of MOGA, NPGA and NSGA. As in single-objective GA, the elitist strategy passes a number of individuals (of the same species) from one generation to the next with neither crossover nor mutation if the members under consideration are non-duplicated non-dominated. The prevention of using duplicated individuals as elite individuals promotes genetic diversity [21-22]. The main difference between this study and a previous study [7] is the elitism. During the normal EMOA evolution of each species in the CCMOAs, whole population of species extracted

from the PNSS is considered elite and, thus, passes through to the next generation unchanged by crossover or mutation. It is noted that this strong elitism is unsuitable for the ZDT5 problem with the deceptive front.

3. TOPOLOGY DESIGN PROBLEMS
3.1 Problem Descriptions of Test Cases
2D heat transfer problems with convective boundary are used as the case studies. The unit-thick structure within a square domain is used to transport heat from a point source Q at the bottom left corner to a thin heating plate placing over the domain such that the temperature in the plate is evenly distributed as shown in Fig. 2a. It is also assumed that the air circulation is so good that the ambient temperature in close proximity to the structure remains unchanged.
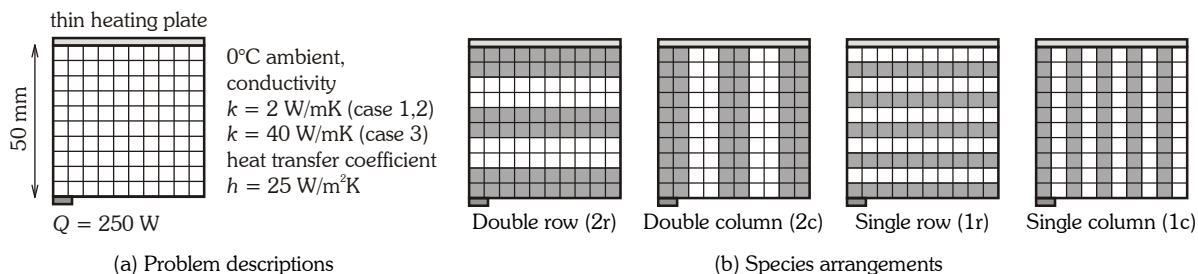

Fig. 2. Problem descriptions and species arrangements of the test cases.

The available spaces are divided into 10×10 grids of equal size. The problem is encoded using a 100-bit binary representation in the on-off style; the block insertion on a grid is represented by '1' whilst '0' signifies a void. As the chromosome has to be divided into species for the CCMOAs, the domains are simply divided by rows or columns as there are no distinct groups for each decision variables. In all, 4 different types of species are employed – double row or column, each with 20-bit species, and single row or column with 10-bit species, as shown in Fig. 2b. In CCMOAs, the numbers of evolved generations are calculated from those of the EMOAs such that both algorithms require the same number of chromosome objective evaluations, which use up such remarkable computational efforts that the objective evaluation becomes the bottle neck of the whole computational process.

3.1.1 $[\overline{T}, \mathrm{SD}_T]$ Test Case
In the first test case, two design objectives are maximised average temperature $\overline{T}$ and minimised the standard deviation SD_T in the heating plate. The value of conductivity k of 2 W/mK is used.

3.1.2 $[\overline{T}, \mathrm{SD}_T/\overline{T}]$ Test Case
This test is similar to the first but the second design objective of SD_T minimisation is slightly modified to the quotient of the standard deviation SD_T and the average temperature in the plate or $\mathrm{SD}_T/\overline{T}$. Here, $k = 2$ W/mK.

3.1.3 $[\overline{T}, \mathrm{SD}_T, \text{high } k]$ Test Case
This test is similar to the first test case but with a higher value of conductivity $k = 40$ W/mK.

3.2 Objective Evaluation by the Finite Volume Method
The heat conduction of configurations is evaluated by a custom-made finite volume (FV) method [14] with the energy conservation with the Fourier's law as the governing equation. The employed boundary conditions are prescribed heat flux and surface convection by the Newton's law of cooling. The mathematical model is discretised by a cell-centred FV technique for arbitrarily shaped control volumes with future uses in shape and size optimisations in mind. The FV method is straightforward and does not require the finite element connectivity analysis [1] due to its superlative physical representation as control volumes with only one shared corner vertex are not physically attached [14].

4. RESULTS AND DISCUSSIONS
For each of the test case, 4 different EMOAs and their CCMOAs with 4 sets of species search for optimised solution sets using 30 or 10 runs (Tab. 1). For comparisons between EMOAs and CCMOAs, the same numbers of objective values are evaluated in each run instead of specifying the total CPU time for the runs. There are 2 reasons behind this

decision. Firstly, the time required for structural performance evaluations are problem dependent. For instance, in the given test cases, better solutions takes more computational efforts to evaluate, hence CCMOA runs takes more time as the accelerated findings yield better solutions much faster in the same number of generations. However, if the optimised objectives are reversed, the opposite situation occurs, making the comparison not universally applicable. Secondly, as GA is characterised by the evolutionary nature, the consideration of quality improvements should be measured across generations or have some equivalent measurement of evolutionary period. Besides, the frequent uses of random in GA operators cause each run to yield dissimilar searches and solutions. The use of equivalent run time may cut short the optimisation during the evolution between generations, rendering the comparisons less meaningful while the use of equal evaluation numbers forces the appearance of the same numbers of evolving members.

Examples of non-dominated solutions from first 5 EMOA and CCOMA runs for the test cases are shown in Fig. 3 and are used to illustrate the results of practical design processes in which few runs are performed. It is clearly shown that for the same generation numbers, the CCMOAs, represented here by CCCNSGA, find significantly better solutions than EMOAs.

All resulting sets of non-dominated solutions are then combined to produce the superset of results as shown in Fig. 4. For better visualisation of results, structures of selected individuals across the fronts of non-dominated solutions are displayed in Fig. 5.
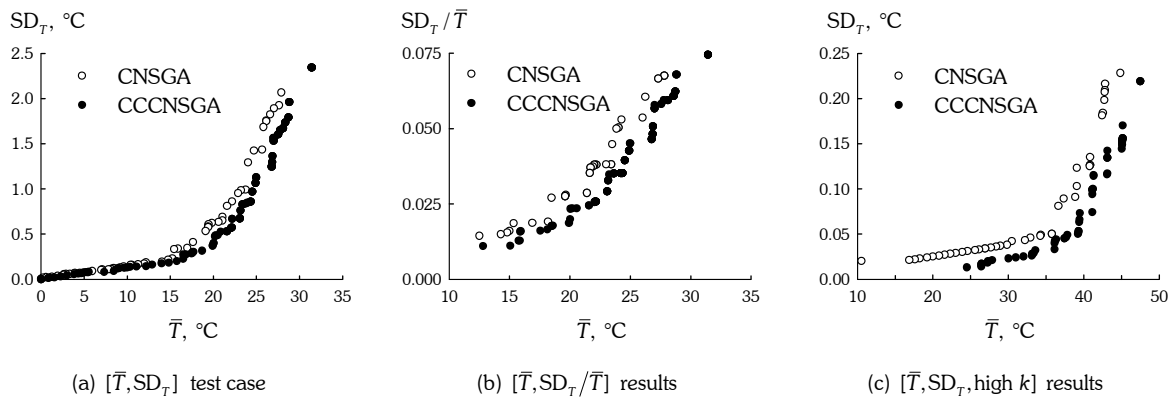

(a) $[\overline{T}, SD_T]$ test case   (b) $[\overline{T}, SD_T/\overline{T}]$ results   (c) $[\overline{T}, SD_T, \text{high } k]$ results

Fig. 3.Comparison of merged non-dominated solutions from the first 5 runs using CNSGA and CCCNSGA with single row species.

(a) Superset of $[\overline{T}, SD_T]$ (129 solutions).   (b) Superset of $[\overline{T}, SD_T/\overline{T}]$ (72 solutions).   (c) $[\overline{T}, SD_T, \text{high } k]$ (54 solutions).
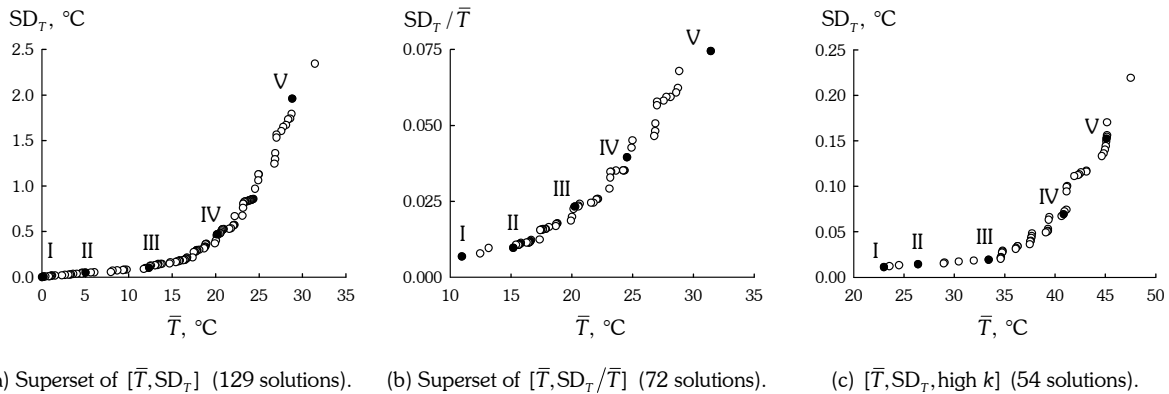
Fig. 4. Resulting superset non-dominated solution for topology design problems.

The PNSS superset of first test case $[\overline{T}, SD_T]$ shows a large front of non-dominated solutions with two competing optimisation characteristics (Fig. 4a and Fig. 5a). At the maximised $\overline{T}$ end on the right, the optimised structures maximise the $\overline{T}$ by entirely filling the available spaces in order to minimised the convective heat loss to the surrounding by limiting the surface area and ensuring the lowest possible temperature profiles at the boundary. These solutions, however, have relatively high SD_T due to the unequal distances from the heat source to different positions of

the heating plate. On the other hand, the evolution minimises the SD_T by evolving tortuous structures that direct towards the domain centre before separating into branches, all heading towards various locations of the heating plate. This strategy indeed lowers the SD_T by dissipating as much energy as possible into the environment in order to hold the temperature, and subsequently its standard deviation, down. This phenomenon indicates that the use of absolute values of SD_T as an objective is not appropriate and the design procedure is absolutely free of human bias such that any ingenious or ludicrous designs are equally possible.

As the objective SD_T is modified into the normalised $SD_T/\bar{T}$ in the second test case, the average temperature $\bar{T}$ are given prominence and the high values of $\bar{T}$ are desirable in both objective functions. Hence, the PNSS front becomes much shorter as shown in Fig. 4b. From Fig. 5b, the available space is still entirely filled to minimise the heat loss to the surrounding at the maximised $\bar{T}$ end as in the first test case. However, holes are less desirable in this problem as their presences facilitate heat loss and reduces the $\bar{T}$. Therefore, in order to smooth the temperature profiles across the heating plate, only few small holes are placed in the top left corner to hinder the direct vertical heat flow from the heat source so the temperature on the left side of the plate drops and get closer to that of the right side. Some structures also show the trimming of the bottom right corner as the secondary trait. In short, the evolution overwhelmingly favours densely packed structures while the temperature profile is levelled by tactfully inserting few gaps that disrupts the heat flow and disperse heat flux out of the domain.

The test case 3 is identical to the first except for the material properties. As the value of the conductivity k is increased 20 folds, the heat can travel in the structure much easier. Hence, the temperature distributions in the structures and planes are of higher value and more even. At the maximised $\bar{T}$ end on the right of Fig. 4c and Fig. 5c, the optimised structures still maximise the $\bar{T}$ by entirely filling the available spaces. But for minimised SD_T, the left end of the non-dominated solution set are truncated such that the structures occupy a lot of the available space as the heat dissipation strategy is not as effective for the given 10×10 grid as in test case 1 due to the higher heat conduction rate.

I [0.040°C, 0.000°C]   II [5.030°C, 0.048°C]   III [12.348°C, 0.101°C]   IV [20.167°C, 0.467°C]   V [28.837°C, 1.956°C]

(a) selected $[\bar{T}, SD_T]$ results which are denoted by block circles in Fig. 4a.

I [10.974°C, 0.0067]   II [15.191°C, 0.0096]   III [20.225°C, 0.0231]   IV [24.542°C, 0.0395]   V [31.428°C, 0.0744]

(b) selected $[\bar{T}, SD_T/\bar{T}]$ results which are denoted by block circles in Fig. 4b.

I [23.01°C, 0.011°C]   II [26.41°C, 0.014°C]   III [33.42°C, 0.019°C]   IV [40.84°C, 0.069°C]   V [45.12°C, 0.152°C]

(c) selected $[\bar{T}, SD_T, \text{high } k]$ results which are denoted by block circles in Fig. 4c.
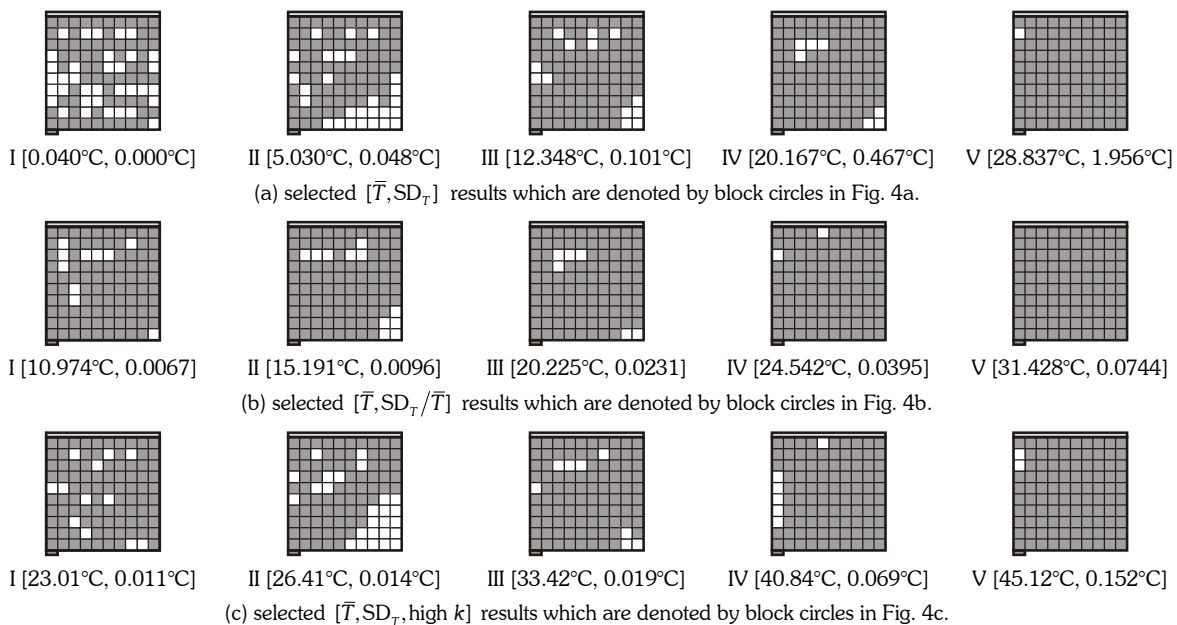
Fig. 5. Selected non-dominated structures of test cases which are denoted by block circles in Fig. 4.

Without the true Pareto fronts, which may be obtained only by exhaustive searches, the coverage C is used to compare quality of dominance between two sets of results. Given two decision vectors X and Y, X covers Y if and only if X dominates Y or the objective vector of X is identical to that of Y. The function $C(X, Y)$ computes the percentage of decision vectors in Y that is covered by solutions of X such that $0 \le C \le 1$. Hence, if the value of $C(X, Y)$ is higher than $C(Y, X)$, the solutions in set X is considered more valuable than Y.

The EMOAs and CCMOAs are compared by the coverage distributions in Fig. 6 which clearly shows that the solution sets obtained from the EMOAs coverage over CCMOAs (top row) is lower while the sets of non-dominated solutions

obtained from the CCMOAs cover the solution sets generated from the corresponding EMOAs (bottom row) quite well in all test cases. These results lead to the conclusion that search performances of the EMOAs is worse than those of the proposed CCMOAs as the CCMOAs can find more valuable solution sets with the same number of objective evaluations (Fig. 3), an important advantage in the topology design problems in which most of the CPU time are spent on the numerical simulations. The much better coverage in test case 2 is due to the less difficult nature of the search problem in which a single parameter $\bar{T}$ is influential to both objectives.

In addition, the much better coverage in test case 2 may be further aided by the shorter non-dominated solution front since the number of solutions in the superset is merely 44% more than the prescribed number of PNSS maximum size. Meanwhile, the size of superset solutions of the first $[\bar{T}, \mathrm{SD}_T]$ test case is more than 2.5 times the prescribed PNSS sizes, making the full domination between two solution sets much less likely due to the inability of the PNSS to contain all non-dominated solutions. However, the coverage of CCMOAs over EMOAs of the third $[\bar{T}, \mathrm{SD}_T, \mathrm{high}\ k]$ test case is slightly better than the first even though the solution superset contain only 54 results. This is due to the search difficulty taking the precedence and the scarcity of the solutions during the runs that the preserved set of non-dominated solutions, PNSS, can not be fully filled to the prescribed value during the runs. Besides, the lesser number of runs further aggravates the comparison; the overall solution trend is more susceptible to few, or even one, freak runs with bad solutions.

It may be noted that for the comparison between CNSGA and CCCNSGA for the third $[\bar{T}, \mathrm{SD}_T, \mathrm{high}\ k]$ case in Fig. 6, the superiority of the CCCNSGA is not be as good as other pairs. This is due to the much improved effectiveness of the latest version of the NSGA series as well as the lower number of runs that are used for comparisons.
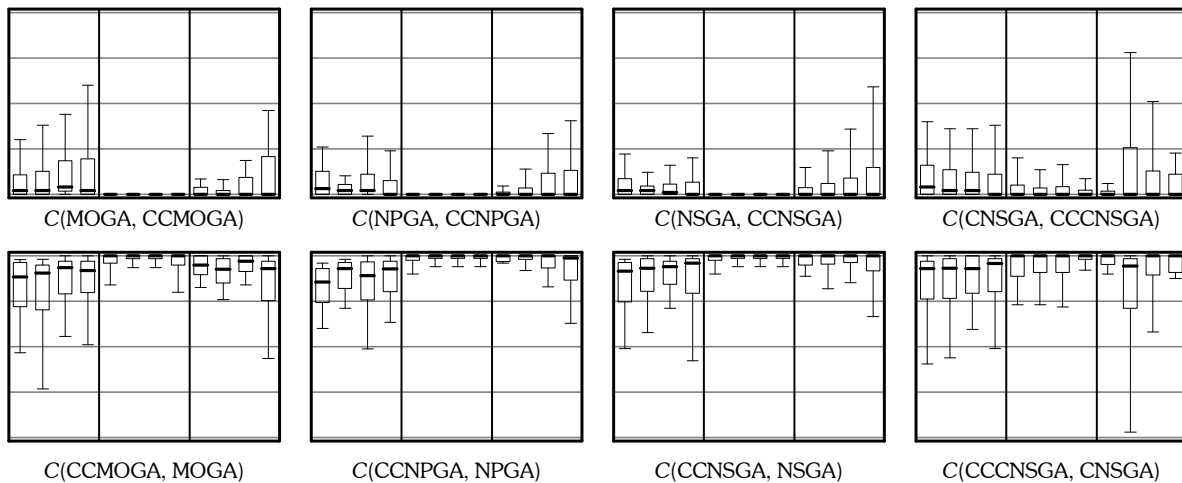

Fig. 6. Box plots of coverage $C(X, Y$ which is covered by X) indices for each pair of EMOA and CCMOA. The scale is 0 (no coverage) at the bottom and 1 (total coverage) at the top. Left-side plot sets show $[\bar{T}, \mathrm{SD}_T]$ test case, the middle plots the $[\bar{T}, \mathrm{SD}_T / \bar{T}]$ and the right plot sets the $[\bar{T}, \mathrm{SD}_T, \mathrm{high}\ k]$. For each test case, plots from left to right are double row (2r), double column (2c), single row (1r) and single column (1c).

For the study of species effects on performances of CCMOAs, Fig. 7 shows the coverage comparison between different species. The species are arranged by rows or columns which show up perpendicular to each others in Fig. 2b, presenting different coupling characteristics. The upper plots, from left to right, show the coverage functions of $C(2r, 2c)$, $C(1r, 1c)$, $C(2r, 1r)$ and $C(2c, 1c)$ while the lower plots exhibit the reversed coverage of $C(2c, 2r)$, $C(1c, 1r)$, $C(1r, 2r)$ and $C(1c, 2c)$. In short, the effects on search performances by horizontally and vertically arranged species are first compared, followed by the species sizes. When coverage plots from the solution sets from horizontal and vertical species – $C(2r, 2c)$, $C(1r, 1c)$, $C(2c, 2r)$ and $C(1c, 1r)$ – are compared, the overall performances are not that much different. There is almost no difference for the second $[\bar{T}, \mathrm{SD}_T / \bar{T}]$ and third $[\bar{T}, \mathrm{SD}_T, \mathrm{high}\ k]$ test cases as the problem favours comparatively packed structures with few gaps. If the domain is totally filled, there are no differences between the choices of row or columns species at all.

For the first test case, the use of row species shows slightly improved results, probably due to the physical natures of heat flows from the heat source on the bottom left corners in the left fronts where $\bar{T}$ approaches zero. The solutions

exhibit complicate structures at the bottom half, whose main function is to dissipate as much heat as possible, aided by the relatively high temperature gradient between the structure and the surrounding environment from proximity with the heat source. Hence, the heat flows in the horizontal direction is marginally more important and the horizontally arranged species gain a small edge over the vertical ones. Perhaps, the optimisation performances may be slightly improved by capturing heat flows through the structures.

The effects of different sizes of species on the search performances are also investigated. In this paper, lengths of species are simply chosen to be 20 or 10-bit, equivalent to each chromosome comprising of 5 or 10 species, respectively. If there is no coupling between species at all, the search space in CCMOAs would be drastically reduced from $2^{100} \approx 1.27 \times 10^{30}$ to $5 \times 2^{20} \approx 5.24 \times 10^6$ and $10 \times 2^{10} \approx 1.02 \times 10^4$ for 20-bit and 10-bit species, respectively. The use of species produces best performances when there is no coupling between different species at all. However, if there are coupling between species, the search performances of the CCMOAs would be deteriorated with the coupling strength.

In topology designs, it is clear that coupling between species are inevitable as each control volume connects with the 4 adjacent blocks and each species has at least one, usually 2, adjacent species. Shorter species may have a much lower search space, but the interferences from adjacent species become stronger as the species can not contain a physically meaningful features in the short data string and vice versa. Fig. 7's coverage plots – $C(2r, 1r)$, $C(2c, 1c)$, $C(1r, 2r)$ and $C(1c, 2c)$ – show that results from chromosomes with smaller 10-bit species are marginally better than those of 20-bit for the first two cases in most comparisons, i.e. the specific reduction in search space somewhat outweighs the interference/coupling effects of adjacent species. The situations for test 3 are reversed except for CCCNSGA runs.
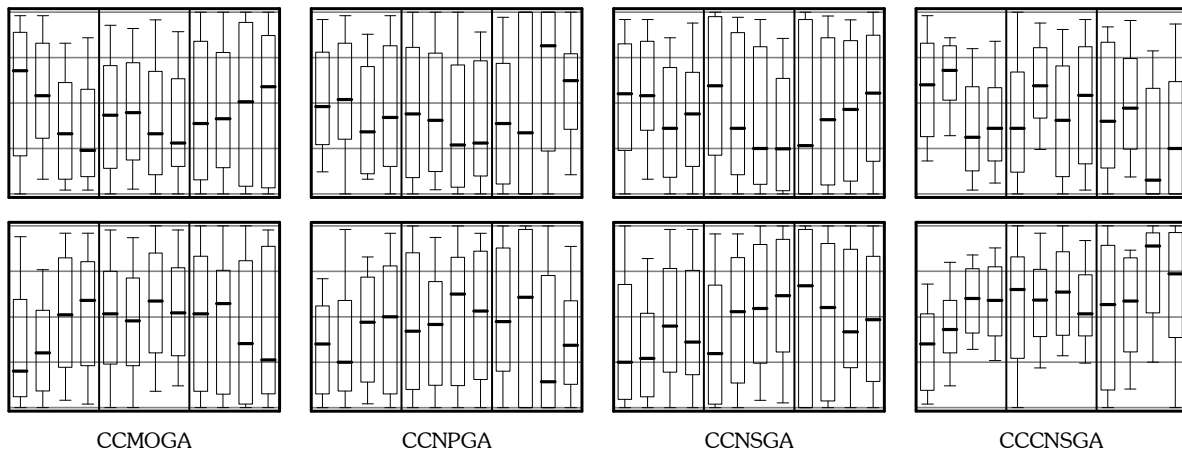

| CCMOGA | CCNPGA | CCNSGA | CCCNSGA |

Fig. 7. Box plots of coverage distribution $C(X, Y$ which is covered by $X)$ indices for different pairs species types. The scale is 0 (no coverage) at the bottom and 1 (total coverage) at the top. Left-side plot sets show $[\overline{T}, SD_T]$ test case, the middle plots the $[\overline{T}, SD_T/\overline{T}]$ and the right plot sets the $[\overline{T}, SD_T, \text{high } k]$. For top rows, plots from left to right are $C(2r, 2c)$, $C(1r, 1c)$, $C(2r, 1r)$ and $C(2c, 1c)$ while plots on bottom rows are reversed coverage or $C(2c, 2r)$, $C(1c, 1r)$, $C(1r, 2r)$ and $C(1c, 2c)$.

5. CONCLUSIONS

This paper describes the incorporation of co-operative, co-evolution into 4 EMOAs – MOGA, NPGA, NSGA and CNAGA – becoming CCMOGA, CCNPGA, CCNSGA and CCCNAGA for continuum topology designs of heat transfer structures. The non-dominated solution set gives a series of solutions for designers to choose for further shape and sizing optimisations. The resulting non-dominated solution sets help understanding and interpreting the physical phenomena underlying the performances of the structures as well as identifying key characteristics that confer superior functionalities. In stead of a single field of bitmap-type chromosomes in EMOAs, the division of chromosomes into smaller species reduces the search problems into a combination of smaller ones.

Three related test cases with slightly different objective functions are studied. It is clear that even with slight adjustments on the objective and parameters, the resulting solutions sets greatly differ in terms of favourable design characteristics. For the same number of objective evaluations, the CCMOAs accelerate the searches significantly for all 4 different algorithms. The arrangements and sizes of the species in CCMOAs also affect the search efficiency; comparatively small species and alignment to the heat flows help improving the search performances. However, these two factors show the characteristics of problem dependency; the alignment requires a prior insight into the physical meanings of the to-be-

identified optimised structures while the choice of species length depends upon an even more elusive quantity, the strength of coupling and interferences between species. Even though these effects may be investigated numerically for specific problems, the results do not directly translate to others, making the efforts counterproductive in practices such that it may be more effective to simply guesstimate both parameters instead.

6. ACKNOWLEDGEMENTS

7. REFERENCES

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