



Optimal design of laminated composite structures with ply drops using stacking sequence tables



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ABSTRACT

This article introduces the concept of stacking sequence table (SST) for the optimal design of laminated composite structures with ply drops. The SST describes the sequence of ply-drops ensuring the transition between a thick guide laminate and a thinner one. A blended design is represented by a SST combined with a thickness distribution over the regions of the structure. An evolutionary algorithm is specialized for SST-based blending optimization. Optimization of the sequence of ply-drops with the proposed algorithm enables satisfying design guidelines that could not have been considered in previous studies. An extensive set of design guidelines representative of the actual industrial requirements is introduced. The method is applied to an 18-panel benchmark problem from the literature with convincing results. In particular, the present results show that strength-related guidelines can be enforced without significantly penalizing the stiffness behavior and consequently the mass of the structure.

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1. Introduction

Over the last decade, design and manufacturing of large scale one-shot structures using straight-fiber laminated composite materials have attracted increasing attention from structural designers. The mass of such structures can be minimized by progressively reducing the thickness away from the load introduction zones while allowing for oriented laminates to obtain locally optimized design. Detailed design of large composite structure is usually based on the subdivision of the global problem into local panel design problems. The subdivision results from higher design levels and is not meant to be called into question at lower design levels. Stiffness variations between panels are obtained by modifying the ply orientations and by adding or terminating plies. Continuity of the plies has to be preserved to obtain one-shot manufacturable structures and avoid stacking sequence mismatch between adjacent panels. The ply-drops form taper sections between adjacent panels. Ply-drops cause out-of-plane stress concentrations in tapers that can initiate in-plane matrix cracking and delamination.

In their literature survey on tapered composite structures, He et al. [1] bring out two major categories of studies. The first category aims at understanding the damage mechanisms at ply-drop locations and study the propagation of delamination in the structure. The second category aims at identifying and investigating

the influent parameters on the strength of the taper section and propose design guidelines to reduce damage initiation at ply-drops. Since then a third category of related studies has developed that deals with the optimal design of composite structures with ply-drops. Review about the topic can be found in [2]. Designing laminated structures with ply-drops is commonly referred to as blending. There are few if any links between laminate blending optimization and the first two categories of studies. In particular, no design guidelines for the taper sections are considered in the optimization. Thus, there is no guarantee for the optimized designs that damages initiated at ply-drops could not propagate and lead to failure under the design loads. The present work intends to bridge the gap and introduce a complete set of relevant design guidelines into the optimization.

Industrial design guidelines for composite structures with ply-drops are summarized in Section 2. Section 3 provides background on blending and introduces the concept of stacking sequence tables (SSTs). Next, an evolutionary algorithm (EA) is specialized for SST-blending optimization in Section 4. Finally, the results obtained for an 18-panel benchmark from the literature are compared and discussed in Section 5.

2. Design guidelines

Laminate design starts by selecting the set of ply angles relevant to a given application. Due to manufacturing constraints, the allowed ply orientations are reduced to a discrete set of angles such

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as $\{0^\circ, \pm 15^\circ, \pm 30^\circ, \pm 45^\circ, \pm 60^\circ, \pm 75^\circ, 90^\circ\}$. Once the angles are selected, the total number of plies and proportion of each orientation in the laminate are set and a stacking sequence is chosen. Additionally, when designing structures comprising several zones of different thicknesses, thickness variations are obtained by dropping plies at specific locations. For both laminate stacking sequence design and ply-drop design, numerous guidelines apply, based on industry past experience from test and analysis. A more detailed discussion about design guidelines and their justification is provided in [3,4].

Six *laminate design guidelines* are considered as a basis for the design of the stacking sequences of most composite structures in aerospace industry.

1. *Symmetry*. Whenever possible, stacking sequences should be symmetric about the mid-plane.
2. *Balance*. Whenever possible, stacking sequences should be balanced, with the same number of $+\theta^\circ$ and $-\theta^\circ$ plies ($\theta \neq 0$ and $\theta \neq 90$).
3. *Contiguity*. No more than a given number of plies of the same orientation should be stacked together. The limit is set here to two plies.
4. *Disorientation*. The difference between the orientations of two consecutive plies should not exceed 45° .
5. *10%-rule*. A minimum of 10% of plies in each of the 0° , $\pm 45^\circ$ and 90° directions is required. Here, to allow for other ply orientations, this rule is transposed in terms of a minimal in-plane stiffness requirement in all directions, as proposed by Abdalla et al. [5].
6. *Damtol*. No 0° -ply should be placed on the lower and upper surfaces of the laminate.

Symmetry and balance guidelines aim at avoiding respectively shear-extension and membrane-bending coupled behaviors. The other rules are beneficial to the strength of the structure. They aim at avoiding matrix dominated behaviors (10%-rule) and possible strength problem due to unwanted failure modes such as free-edge delamination (disorientation) or propagation of transverse matrix cracking (contiguity). With primary load carrying plies shielded from the exposed surface of the laminates (damtol), the effect on strength of exterior scratches or surface ply delamination is reduced.

The *ply-drop design guidelines* aim on the one hand at avoiding delamination at ply-drop location and, on the other hand, at obtaining ply layouts that can actually be manufactured.

7. *Covering*. Covering plies on the lower and upper surfaces of the laminate should not be dropped.
8. *Maximum taper slope*. The taper angle should not exceed 7° , i.e. the minimal stagger distance (the length of the increment of thickness) is about eight times the thickness of the dropped plies.
9. *Max-stopping*. No more than two plies should be stopped at the same increment of thickness.
10. *Internal continuity*. A continuous ply should be kept every three consecutive dropped plies.
11. *Ply-drop alternation*. As far as possible, ply-drops should be located alternately close and far from the mid-surface of the laminate.
12. *Taper guidelines*. All laminates in the taper section should respect to the maximum possible extend the laminate design guidelines.

The schematic of a 4 ply-drop transition zone is shown in Fig. 1.

All the above guidelines are local in the sense that they apply to the design of each individual panel of the structure, or

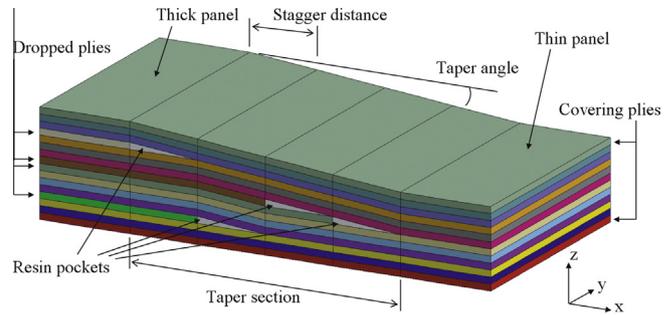


Fig. 1. Schematic of a taper section with four internal ply-drops.

each ply-drop. However, the design of a variable-thickness composite structure also has to fulfill two *global requirements*.

13. *Continuity*. This requirement aims at ensuring structural integrity and manufacturability of the structure. All plies from the thinner panel must cover the whole structure. Ply orientation mismatches between adjacent panels are not allowed, i.e. cutting plies between two panels to change their orientations is not allowed.
14. *Δn -rule*. The second requirement specifies a maximum number of ply-drops Δn between adjacent zones. Indeed, constraining the thickness variation between adjacent zones can help to smooth the load distribution over the structure and avoid high stress concentrations at dropped plies, especially interlaminar stresses.

3. Blending of laminates and stacking sequence tables

3.1. Blending definitions

The continuity requirement is commonly referred to as the blending constraint in the composite optimization literature. The term *blending* was first introduced by Kristinsdottir et al. in 2001 [6]. In their work, each ply emanates from a key region and may cover any number of adjacent regions. Once a ply is dropped, it is not allowed to be added back in the structure. The authors named this way of consistently dropping plies from the most loaded region the *greater-than-or-equal-to* blending rule. The method leads to highly constrained problems with many variables. Liu and Haftka [7] investigated the use of inequality constraints to enforce stacking sequence continuity, thus obtaining trade-offs between structural continuity and mass. Much smaller weight penalty for perfectly blended solutions were obtained by Soremekun et al. [8] using an approach based on sublaminates.

The most successful definition up to now originates from Adams et al. [9] in which the authors introduce the concept of *guide-based blending*. A guiding stack is defined from which all laminates in the structure are obtained by deleting contiguous series of plies. In case of *inner blending*, the innermost plies are dropped whereas in case of *outer blending*, the outermost plies are dropped. The main asset of the method is that blending is enforced without adding any constraint into the optimization problem while adding only one variable per region of the structure, representing the number of plies dropped from the guide. However continuity of the deletions narrows the design space (see [10,11]).

Another worth mentioning approach is the *patch concept* proposed by Zehnder and Ermanni [12] and further used and developed in [13,14]. In this approach, a patch is a layer of arbitrary shape that can be positioned anywhere over the structure. At any

point of the structure, the stacking sequence is defined by the order and orientations of the patches. The patch concept is very appealing in the sense that the parameterization directly derives from the physical composition of laminated structures and does not narrow the design space. However the large number of degrees of freedom offered by the method makes engineering problems difficult to solve.

3.2. Stacking sequence tables

In all the studies mentioned above, the set of design guidelines handled is restricted to the continuity, symmetry and balance guidelines. In this paper, we introduce the stacking sequence table (SST) as a convenient tool to handle the full set of guidelines listed in Section 2. The SST originates in composite panels manufacturing practice from aeronautical industry [15]. A SST describes a unique laminate for each number of plies between a lower bound n_{min} and an upper bound n_{max} . Fig. 2 shows a SST ranging from a 12-ply laminate ($n_{min} = 12$) to a 16-ply laminate ($n_{max} = 16$). Plies are added one by one from the thinner laminate to the thicker one (in the right-hand column of the table). Thus, plies from the thinner laminate spread over the whole structure and ensure its continuity. For a given structure and a given distribution of numbers of plies over its constitutive regions, the laminate associated to each region can be read in the SST based on its number of plies. The laminates in the transition zone between two regions of different thicknesses are also described in the SST. The SST describes general thickness distributions, not only monotonously varying thicknesses: once the thickness of a region is fixed, the associated laminate is read from the SST which can therefore be read in any order.

Compared to the guide-based blending as proposed by Adams et al. [9], the SST contains additional information consisting in the order of the ply-drops. Thus, the notion of SST encompasses the classical guide-based blending by providing a more detailed description of the layout of the plies over the structure and affording more freedom to define which plies to drop. Additionally, satisfaction of the ply-drop design guidelines can be assessed based

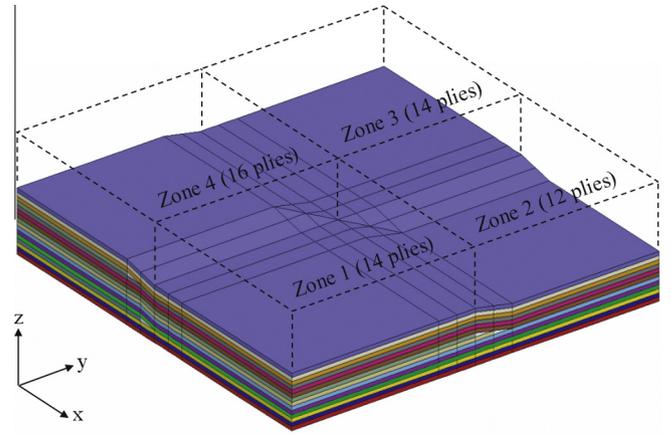


Fig. 3. Schematic of a four-region panel with thickness variations along the x- and y-directions ($n_{min} = 12$ and $n_{max} = 16$).

on the SST. The SST of Fig. 2 is compatible with the unidirectional taper zone presented in Fig. 1. Fig. 3 shows a four-region panel with bidirectional thickness variations compatible with the SST of Fig. 2.

4. Evolutionary optimization of stacking sequence tables

Evolutionary Algorithms (EA) are stochastic optimization algorithms that sample the design space by iteratively creating sets (populations) of solution points using stochastic operations. It is handy to describe these algorithms through the metaphor of evolution in nature, so we will use this metaphor in the text while providing its optimization meaning. EA iterations are made of selection and replacement phases, and stochastic variations of the current population of points. The stochastic variations aim at exploring the design space in a way which is determined by the

	12	13	14	15	16	
	45	45	45	45	45	Plies added
	90	90	90	90	90	
	-45	-45	-45	-45	-45	
					0	
	-45	-45	-45	-45	-45	
	0	0	0	0	0	
Mid-plane of the SST	45	45	45	45	45	
			90	90	90	
		90	90	90	90	
	45	45	45	45	45	
	0	0	0	0	0	
	-45	-45	-45	-45	-45	
					0	
	-45	-45	-45	-45	-45	
	90	90	90	90	90	
	45	45	45	45	45	

	12	14	16
	45	45	45
	90	90	90
	-45	-45	-45
			0
	-45	-45	-45
	0	0	0
	45	45	45
		90	90

Condensed view of the SST using symmetry

Fig. 2. Stacking sequence table with four internal ply drops ($n_{min} = 12$ and $n_{max} = 16$). Full view and condensed view using symmetry. The number of plies of the laminates are indicated over the corresponding columns.

current population of points. Mutation and recombination operators are the two main stochastic variations. Mutations locally perturb solution points. Recombinations explore subregions of the design space described by two or more solution points. The selection and replacement operators are progressively limiting the population to the best performing individuals, where performance is measured by a fitness function f to maximize. The goal of the selection and replacement is to focus the search in high performing regions. Solution points are encoded in a way that is specific to the application at hand, and which will be detailed in the rest of the article. The variation operators, as well as the initialization, work in the space of the codings of the solutions. It can be considered that, through the encoding and variation operators, evolutionary algorithms implicitly define a probability density of sampling a given part of the design space. The selection and replacement phases update this density. Some versions of evolutionary algorithms, such as CMA-ES in continuous spaces [17] or Estimation of Density Algorithms [16] handle the sampling density explicitly in generic optimization cases, but the design of composite structures calls for specific operations. For a particular application, the efficiency of the evolutionary search depends on the coupled choices of encoding and variation operators.

Reviews about the use of EA for stacking sequence optimization of composite structures can be found in [18,19,2]. The Pareto multiobjective EA used in the present study is based on previous work by Irisarri et al. [20,21]. The algorithm is adapted for SST-based blending optimization in the following.

4.1. Encoding

The algorithm is specialized for combined thickness and laminate blending optimization, using an encoding based on stacking sequence tables (SST). Applying the metaphorical terminology of EAs to the laminate blending problem, the *phenotype* is a decoded design which consists of the set of r laminates corresponding to the r regions of the panel. Additionally, the complete phenotype must also define the ply-drops between zones of different thickness. The phenotype of a blended solution can be conveniently represented by a SST and the distribution of the numbers of plies over the structure. Figs. 2 and 3 show a possible phenotype for a 4-region square panel. The thickness of the ply, the number r of regions of the panel, their numbering and connectivity are fixed parameters of the problem.

The *genotype* encodes the solution in vectors called *chromosomes*. In this work, a three-chromosome genotype is proposed. Two chromosomes are devoted to the SST, and one to the thickness distribution over the structure.

- i. Chromosome SST_{lam} represents the stacking sequence of the thickest laminate of the SST. SST_{lam} is an integer vector of length n_{max} .
- ii. Chromosome SST_{ins} contains the rank of insertion of the plies from the thinner laminate to the thicker one. SST_{ins} is an integer vector of length n_{max} . The first ply introduced is given rank 1, the second ply rank 2 and so on. Plies from the thinner laminate are given rank 0. Thus, the vector contains n_{min} zero values.
- iii. Chromosome N_{str} represents the distribution of the numbers of plies over the structure. It is an integer vector of length r .

Table 1 shows the genotype of the 4-region square panel described in Figs. 2 and 3 for $n_{max} = 16$ and $n_{min} = 12$. The symmetry guideline allows to encode half of the SST only.

It is most likely that during the optimization a solution is generated such that the values contained in N_{str} cover only a part of the interval $[n_{min}, n_{max}]$. For such a solution, part of the genotype is

Table 1

Genotype corresponding to the 4-region square panel described in Fig. C.2 for $n_{min} = 12$ and $n_{max} = 16$.

Chromosome N_{str}	[14	12	14	16]				
Chromosome SST_{lam}	[45	90	-45	0	-45	0	45	90]
Chromosome SST_{ins}	[0	0	0	2	0	0	0	1]

non-coding. Thus, several genotypes can exist that encode the same phenotype. Non-coding genes are not a common feature for composite structure optimization algorithms. Nevertheless they have been extensively studied in the field of evolutionary computing. Wu and Lindsay [22] show that including non-coding segments in a GA can improve its performance and stability. In the present work however, the proposed EA significantly differs from their binary GA so that extension of their conclusions to this work is questionable. Nonetheless, numerical experiments and the results presented in next section show the efficiency of the method.

4.2. Constraint and design guideline handling

4.2.1. Direct versus indirect constraints handling

On a conceptual level, Eiben [23] distinguishes direct from indirect constraints handling strategies. *Indirect constraint handling* consists in circumventing the problem of satisfying the constraints by incorporating them in the fitness function f , generally through penalty functions. This means that the constraints are transformed into optimization objectives, thus creating a new optimization problem such that optimality of the penalized f implies that the constraints are satisfied. With *direct constraint handling* the EA is modified at the chromosome level to enforce the constraints. Violating the constraints is not reflected in the fitness function. Therefore the population will not become increasingly feasible as it is expected with indirect constraint handling methods. This means that feasible solutions have to be created and maintained in the population. Specific operators able to preserve feasibility are required. They can be compared to projections into the feasible domain.

In this work, both direct and indirect approaches are used. The constraints handled with an indirect approach are related to the global mechanical performance of the structure (e.g., buckling, see Section 5) and are referred to as the *constraints*. The required computational cost to evaluate these constraints is typically the main computational expense. The constraints usually delineate a

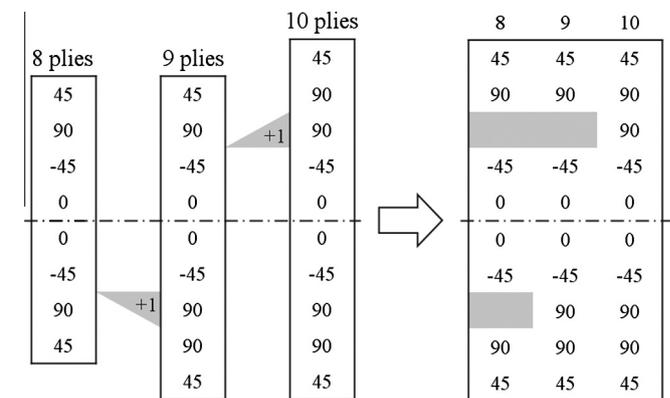


Fig. 4. Creation of a SST. Plies are added one by one to create the SST on the right-hand side of the figure. The orientation of the first ply added is chosen in the set $\{0^\circ, \pm 45^\circ, 90^\circ\}$. 0° and $+45^\circ$ are forbidden by the disorientation guideline. A 90° -ply is drawn in the set of the remaining admissible values. A second 90° -ply is then added to recover symmetry.

feasible domain made of one or few islands. In the following, the modified binary tournament selection scheme proposed by Deb and Gupta [24] is used.

The constraints handled with a direct approach are referred to as the *guidelines*. The *guidelines* are formulated on the stacking sequences of the laminates and, as such, they are of negligible computational cost. The *guidelines* are satisfied in disconnected regions of the decision space organized in a complex pattern. Thus, finding a feasible solution with respect to the *guidelines* offers little help to find another feasible solution. Therefore penalty methods fail to guide the search towards feasible solutions. All the design *guidelines* listed in Section 2 are considered as *guidelines* in the following, with the notable exception of the 10%-rule. Indeed, the 10%-rule defines a convex feasible region in the in-plane stiffness space of the laminate (see [5]). Hence, the 10%-rule is handled with an indirect approach. We now explain how a direct approach to design *guidelines* satisfaction can be implemented in an EA.

4.2.2. General principle for making an EA satisfy design guidelines

The evolutionary algorithm is implemented so that, at each of its step, the encoded solutions, i.e., the chromosomes, satisfy the design *guidelines*. The operations of the EA that affect the design chromosomes are the initialization of the population and the variation operators. These operators are all devised according to the same general principle. The following steps are repeated, sometimes in a recurrent way, until the initialization or variation is complete.

- (a) *Selection of a subset of the optimization variables.* For example, it can be a one angle component of SST_{lam} , or more generally it can be any subset of any chromosomes.
- (b) *Enumeration of guidelines compatible values.* Enumerate and store all possible values of the optimization variables within this subset that satisfy the purpose of the operator and all the *guidelines*.
- (c) *Random choice.* Choose at random, with uniform probability, one of the feasible subset of optimization variables values and assign it to the chromosome.

Application specific expertise enters in step (a). It will soon be seen in the detailed presentation of the EA operators how subset of variables are chosen within the SST_{lam} , SST_{ins} and N_{str} chromosomes for each EA operation. A general principle underlying the design of our algorithm is that the stacking sequence table (chromosomes SST_{lam} and SST_{ins}) is handled before the thickness

distribution (N_{str}). In the following, SSTs operations are presented in Section 4.3 and thickness distribution operations in Section 4.4.

4.3. Evolutionary operations for stacking sequence tables

4.3.1. SST Initialization: creation of SB-cycles

Creation of a feasible SST starts from the thinner laminate. The procedure for the creation of laminates satisfying the laminate design *guidelines* has already been published in [21]. The procedure follows the general principle presented in Section 4.2.2. It consists of the following steps. (a) *Optimization variables subset order.* Symmetrical laminates are created ply-by-ply from the surface to the mid-plane of the laminate. (b) *Enumeration.* Feasible ply orientations satisfy the following *guidelines* for the plies chosen so far: symmetry and damtol, contiguity, disorientation, and balance. (c) *Random choice* within the above set of admissible ply orientations. The balance *guideline* is handled at the overall level of the laminate, taking into account that any created θ^o -ply ($\theta \neq 0$ and $\theta \neq 90$) has to be balanced by a $-\theta^o$ -ply before the end of the stack.

Once the thinner laminate is chosen, the SST is built as follows. The method is illustrated in Fig. 4. (i) *Variables subset order.* Plies are added one-by-one until the maximum number of plies in the SST n_{max} is reached, thus building the SST column by column from the thinner laminate to the thicker one. First SST_{ins} is considered, then SST_{lam} . (ii) *Enumeration.* For each added ply, the set of admissible positions and the set of admissible angles are enumerated. The following *guidelines* are applied: covering, internal continuity and taper *guidelines* (i.e. symmetry, balance, contiguity and disorientation, see Section 2). The covering *guideline* implies that no ply can be added to the surface of the laminates. The internal continuity *guideline* requires a continuous ply every three consecutive ply-drops in the SST. The taper *guidelines* define the set of admissible angles corresponding to a given position of insertion. If the set is empty, the position is considered unfeasible. (iii) *Random choice.* The position of the added ply is drawn in the set of admissible positions. Roulette wheel selection is used to handle the ply-drop alternation *guideline*. The probability associated to a position is proportional to the distance to the surface of the laminate or to its mid-plane, depending on whether the last position drawn is closer to the mid-plane than to the surface of the laminate or not. The k th ply added is attributed value k in chromosome SST_{ins} . The orientation of the ply is drawn with uniform probability in the set of admissible angles and added to chromosome SST_{lam} .

Eight *guidelines* are explicitly handled in the process. The remaining *guidelines* are either satisfied or not relevant at this step. The continuity requirement is satisfied by construction of

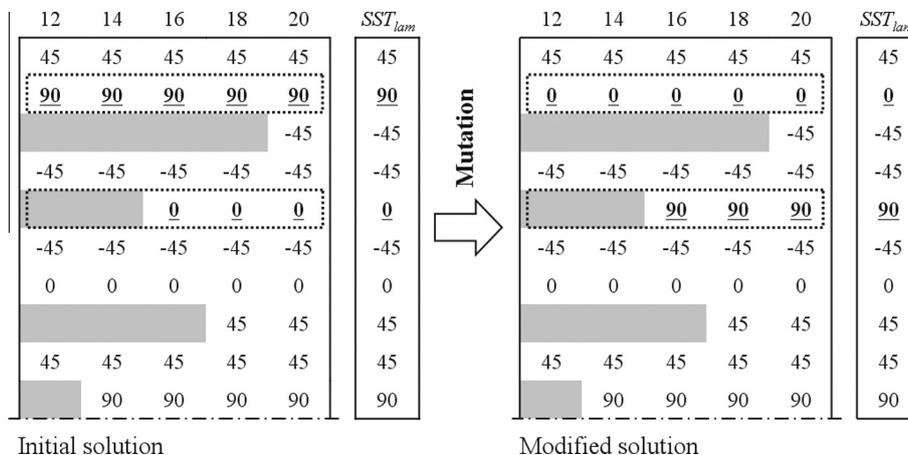


Fig. 5. Mutation of chromosome SST_{lam} and corresponding variation of the SST.

the SST. The damtol guideline is enforced for the whole SST through the covering rule. Indeed, the thinner laminate of the SST satisfies the damtol guideline by construction and the covering rule entails that no plies are added to the surface of the SST. The maximum taper slope rule and the max-stopping rule apply to the detailed representation of the solutions rather than the optimization process and are not taken into account here. The Δn -rule applies to chromosome N_{str} and will be handled later with the appropriate operators (see Section 4.4).

Adding plies one by one in the SST necessarily generates unsymmetrical and/or unbalanced laminates. If a 0° -ply or a 90° -ply is added to a symmetrical laminate, the next ply added reestablishes symmetry. If θ is different from 0 and 90, symmetry is restored first, then balance. In the first case, a cycle of length 2 is formed, in the second case, a cycle of length 4. Such cycles are called symmetry and balance cycles, or *SB-cycles*, and used to modify SSTs as further explained in the following.

4.3.2. SST mutation

The mutation operator for SSTs modifies chromosome SST_{lam} or SST_{ins} with equal probability. The mutation operator for SST_{lam} modifies the orientation of a pair of $\pm\theta^\circ$ -plies or a couple of plies of orientation 0° or 90° . The new orientation is randomly chosen in a set of feasible orientations that depends on the orientations of the neighboring plies in the SST and the contiguity and disorientation guidelines. Fig. 5 shows an example of mutation of chromosome SST_{lam} and the corresponding variation of the SST.

The mutation operator for chromosome SST_{ins} permutes the order of insertion of two SB-cycles. The permutation is illustrated in Fig. 6. In the figure, SB-cycles are identified with Roman numerals. Cycles I and II are permuted to generate a new solution. The corresponding variation of SST_{ins} is shown in the figure. The operator is applied to the same SST example as in Fig. 5.

4.3.3. SST recombination

The recombination operator developed in this work consists of a crossover operation followed by a repair operation. The crossover operator exchanges same-length balanced sublaminates between the thinner laminates of the parent solutions. The respective position of the two sublaminates within chromosome SST_{lam} can differ, as shown in Fig. 7. Offspring SSTs are scanned from the thinner laminate to the thicker one for violation of the contiguity and disorientation guidelines. Unfeasible SSTs are cut before their first unfeasible column. The remaining columns are regenerated using the procedure described in Section 4.3.1.

4.4. Evolutionary operations for thickness distribution

The only guideline applying to chromosome N_{str} is the Δn -rule which defines a maximum difference Δn between the number of plies of contiguous zones. Contiguity between zones is defined by a r -by- r array of connectivity which is a fixed parameter of the problem. Feasible instances of N_{str} are created by random generation of uniform distributions of number of plies over the structure.

The mutation operator modifies the number of plies associated to a region i . The new number of plies in region i is randomly selected in the set of admissible values which are defined by n_{min} , n_{max} , Δn and the number of plies of the regions connected to region i . A 2-point crossover is used to exchange sequences of genes between the two parent chromosomes. A preliminary scan is performed to identify which genes can be exchanged with respect to the Δn -rule. Contiguous sequences formed of these genes are exchanged only.

The proposed encoding and the corresponding operator maintain a complete separation between the thickness distribution and the SST. Nevertheless, the notion of SB-cycles calls for a comment. Allowing the number of plies per panel to take any value in the range n_{min} - n_{max} would result in designs composed of unsymmetrical or unbalanced laminates or both. Forcing the optimizer to drop full SB-cycles restricts the search to designs composed of symmetrical and balanced panels only.

In order to preserve separation between the thickness distribution and the SST, Chromosome N_{str} is interpreted and repaired prior to the evaluation of the solution. The chromosome is not altered by this process which does not penalize the overall mass of the population of designs. The method is inspired by the recessive gene like repair strategy proposed by Todoroki and Haftka [25]. The SST is scanned for symmetrical and balanced laminates resulting in a set of admissible ply numbers. The genes of N_{str} are interpreted to the nearest admissible ply number. In case of violation of the Δn -rule due to the decoding process, the new thickness distribution is repaired by iteratively forcing the number of plies of the thinnest non-feasible region to the upper admissible number of plies until a satisfactory distribution is obtained. The overall process is deterministic so that a chromosome can only be interpreted in a single way.

5. Results

The test problem consists of 18 panels in a horseshoe configuration ($r = 18$), as shown in Fig. 8. The problem was proposed by

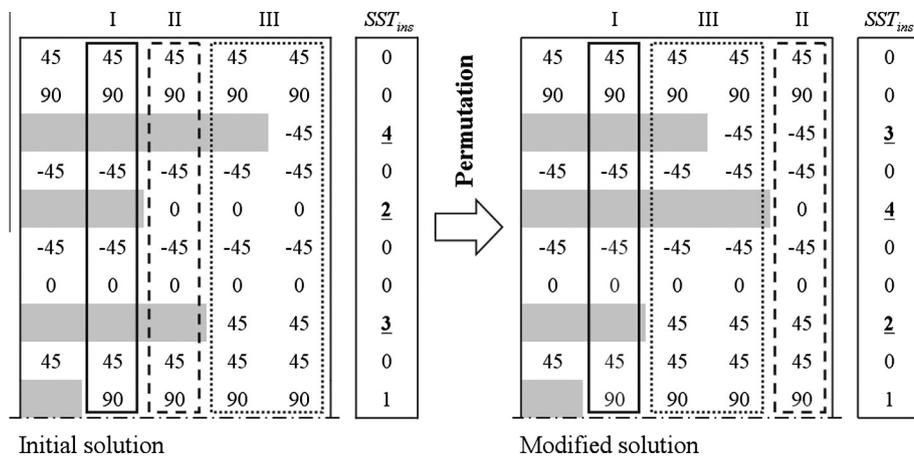


Fig. 6. Permutation within chromosome SST_{ins} and corresponding variation of the SST. SB-cycles are numbered with Roman numerals. Cycles II and III are permuted.

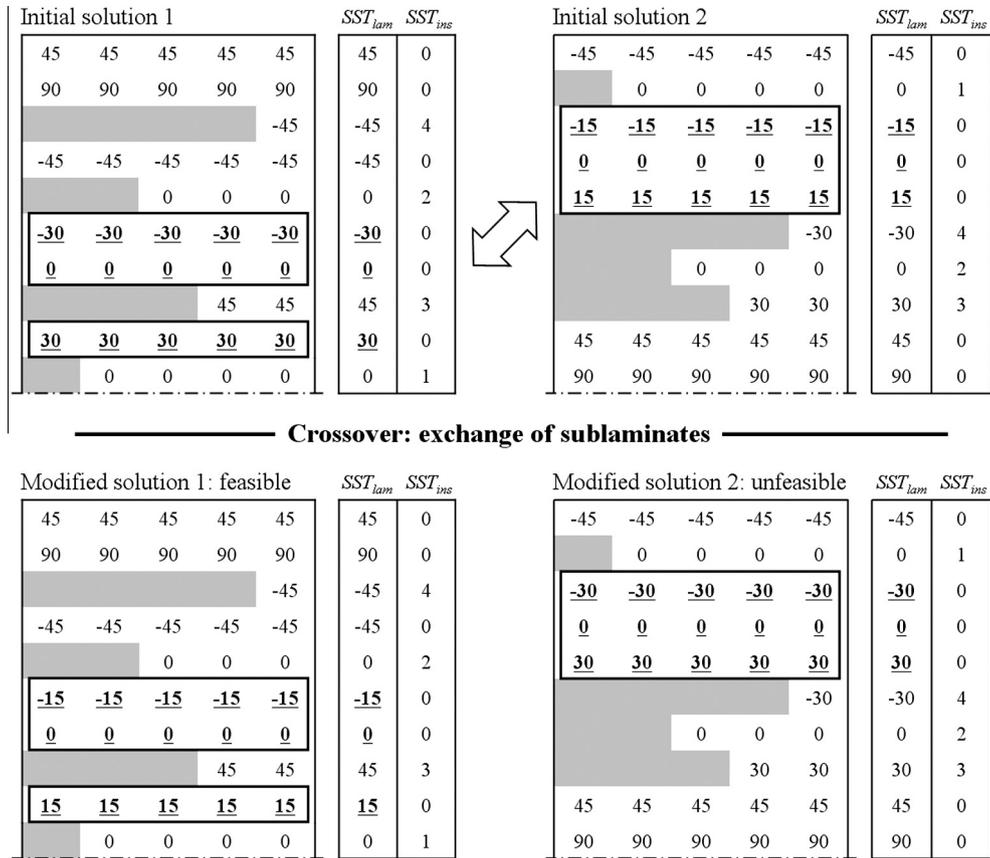


Fig. 7. Crossover operator. Same length balanced sublaminate are exchanged between the thinner laminates of the parent solutions. Plies 5 and 6 of modified Solution 2 do not satisfy the disorientation guidelines.

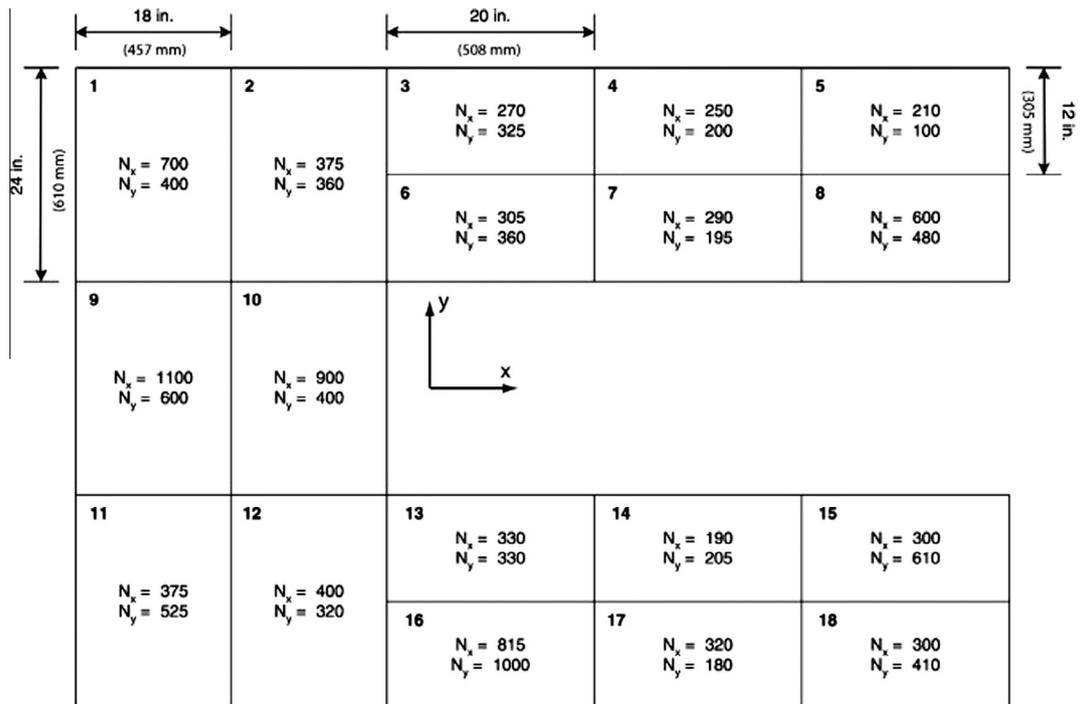


Fig. 8. Eighteen-panel test problem [8,26], all loads in lbf/in (×175.1 for N/m).

Table 2
Parameters of the evolutionary algorithm.

Parameter	Value
Initial population size	150
Current population size	30
Archive population size	120
Number of generations	8000
Probability of crossover (per solution) P_c	0.3
Probability of mutation (per solution) P_m	0.9

Soremekun et al. [8] and subsequently examined in [9,26,11]. The dimensions of the panels and the local loadings are given in the figure. The array of connectivity of the panels is given in A. The loads are assumed to be fixed. All panels are assumed to be simply supported on their four edges. As in [8], n_{min} is set to 14 and n_{max} is set to 48. A Graphite/Epoxy IM7/8552 material is used with $E_1 = 141$ GPa (20.5 Msi), $E_2 = 9.03$ GPa (1.31 Msi), $G_{12} = 4.27$ GPa (0.62 Msi) and $\nu_{12} = 0.32$. Ply thickness is 0.191 mm (0.0075 in.). Ply orientations are restricted to 0, ± 15 , ± 30 , ± 45 , ± 60 , ± 75 and 90° . The objective is to find a fully blended design that minimizes the mass of the structure without individual panel failure under buckling. The minimal buckling factor over the individual panels is called *Reserve Factor* and noted RF in the following. Buckling analysis is detailed in B.

In the present work, the problem is stated as follows: minimize the total mass of the structure and maximize the reserve factor under the constraint that no individual panel fails under buckling ($RF > 1$). Ply-drop design guidelines and global design guidelines (see Section 2) are enforced. The problem is first solved for symmetrical laminates, then with all laminate design guidelines enforced. The parameters of the EA are given in Table 2. The algorithm is implemented in MATLAB. The termination criterion corresponds to a maximum number of generations.

It should be pointed out that, although load redistribution is not taken into account here, the proposed method presents no intrinsic limitation in that regard. FE modeling is required to assess load redistributions in complex structures which raises the problem of the calculation costs. A two-step design method, as in [26], or

response surface methods, as in [27], may be needed to circumvent the difficulty.

5.1. Case 1: symmetrical laminates

Fig. 9a presents the solutions obtained during a single optimization run. The x-axis corresponds to the reserve factor of the structure and the y-axis to its normalized mass. The reference mass m_0 is 28.63 kg and corresponds to the lightest blended design found by Adams et al. in [9] using symmetrical laminates but no forced balanced condition. The buckling margin of this solution is null. To allow for a fair comparison with the results obtained by Adams, the only laminate design guidelines enforced here are symmetry and balance. However, the solutions are not repaired for the balanced guideline, thus the laminates can present up to 2 unbalanced plies. Δn is set to 20, so that the corresponding constraint is inactive along the obtained non-dominated front. Initial solutions are marked with a green square. Feasible and unfeasible solutions are identified in the figure, depending on whether they satisfy or not the constraint $RF > 1$. The obtained non-dominated solutions are shown in red in the figure. These solutions correspond to the best trade-offs between the objectives of the problem. It is interesting to note that the corresponding front is roughly linear with 0.25 slope. Thus, a 10% increase of the RF of the structure is approximately counter-balanced by a 2.5% increase in mass.

Fig. 9b shows the evolution of the mass of the lightest feasible solution during the search for 5 runs of the EA. The computational time for a single run on a regular laptop is about 40 min. After 2000 generations, all 5 runs return solutions weighting less than 30 kg (about $1.05 \times m_0$). Convergence to the lightest solution is achieved after 4000 generations with very good reproducibility. All 5 curves are less than 29 kg (about $1.015 \times m_0$). The lightest feasible design encountered (Solution 0) outperforms the reference solution with a slightly lower total mass of 28.55 kg but clearly superior buckling margin of 2.9%. The performances of Solution 0 are detailed in Table 3 and compared with the reference design from [9]. The genotype of the solution is given in Table 4.

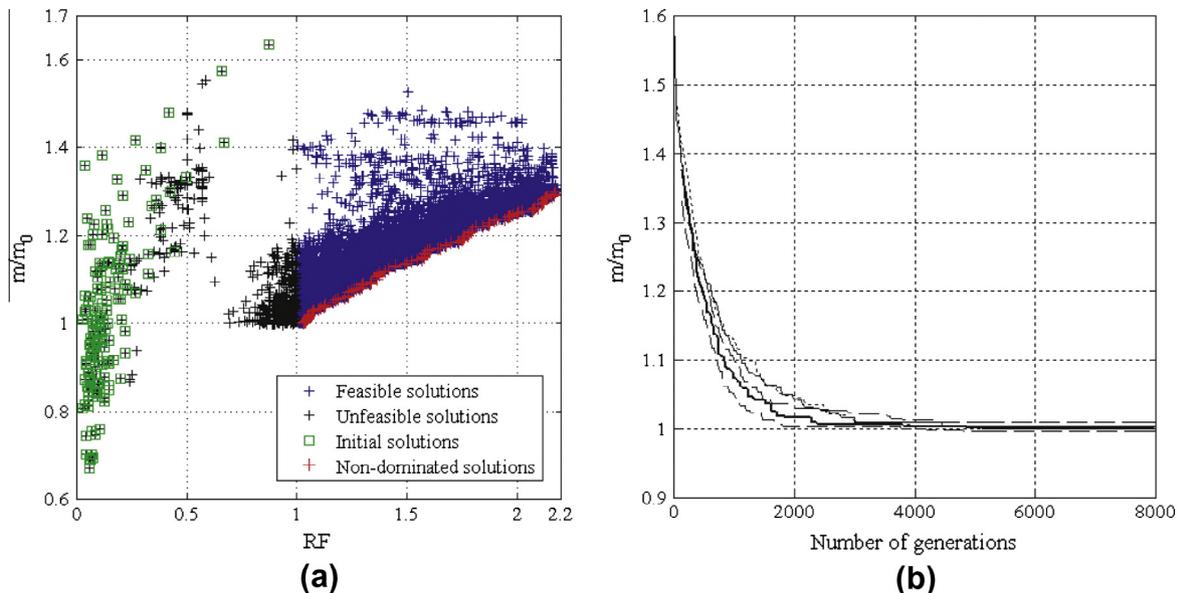


Fig. 9. Results of the optimization of the 18-panel test problem using symmetrical laminates. (a) Solutions obtained during a single optimization run (1 generation every 20 is represented only). (b) Convergence of the EA over 5 runs. The curve represented with a thick continuous line corresponds to (a).

Table 3

Result comparison for symmetrical laminates only. Difference of numbers of plies per panels are marked between brackets. The buckling margin is equal to $100 \times (\lambda - 1)$ in percents. Negative buckling margin indicates failed panel.

Panel	Solution 0		Adams et al. [9]	
	Number of plies	Margin (%)	Number of plies	Margin (%)
1	34	(0)	34	15.3
2	28	(0)	28	0.5
3	22	(0)	22	21.8
4	19	(1)	18	3.8
5	16	(0)	16	20.4
6	22	(0)	22	9.5
7	19	(1)	18	0.5
8	26	(0)	26	11.0
9	38	(0)	38	4.2
10	35	(-1)	36	12.9
11	30	(0)	30	8.2
12	28	(0)	28	0.0
13	22	(0)	22	14.6
14	19	(1)	18	10.1
15	26	(0)	26	7.6
16	32	(-6)	38	78.1
17	19	(1)	18	2.0
18	24	(2)	22	-0.7

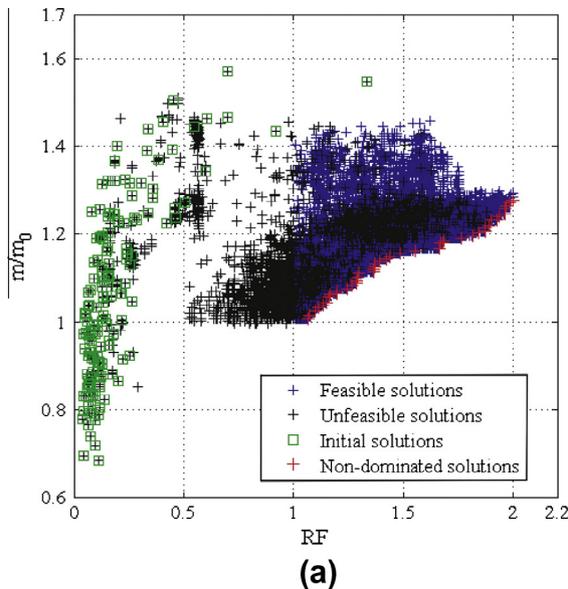
5.2. Case 2: all laminate design guidelines

Fig. 10 presents the results obtained in the case that all laminate design guidelines are enforced. The solutions are repaired for both symmetry and balanced guidelines. Fig. 10a presents the solutions of a single optimization run. Feasible and unfeasible solutions are identified in the figure, depending on whether they satisfy or not the two constraints (10%-rule and $RF > 1$). The computational time

Table 4

Genotype of Solution 0. Chromosome N_{str} is repaired for symmetry. Performances of the solution are computed based on repaired chromosome N_{str} .

Solution 0. Mass: 28.55 kg. $RF = 1.029$ (panel 16)	
Chromosome N_{str}	[34 28 22 19 16 22 19 26 38 35 30 28 22 19 26 32 19 24]
Repaired N_{str}	[34 28 22 19 16 22 19 26 38 35 30 28 22 19 26 32 19 24]
Chromosome SST_{lam}^*	[-45 30 45 45 -30 45 -45 60 30 30 -30 45 45 -45 -30 -45 -30 30 -45 -60 15 0 0 -15]
Chromosome SST_{ins}^*	[0 15 5 0 6 9 8 0 12 7 14 0 2 4 13 0 16 17 1 0 10 3 0 11]



for a single run on a regular laptop is about 1 h in this case, due to the increased complexity of the constraints and guidelines. Convergence to the lightest solution is examined in Fig. 10b over 5 runs. After 2000 generations, all 5 curves are less than 30 kg (about $1.05 \times m_0$). After 4000 generations, the lightest feasible solutions are reached for 4 runs over 5. All curves are less than 29.3 kg (about $1.023 \times m_0$). Compared to the results shown in Fig. 9 the EA behaves similarly. Analysis of the whole non-dominated fronts shows that, for each run, the front after 2000 generations is already very close to the final non-dominated set. The EA achieves very good exploration of the decision space during the first part of the search. During the next generations, it is mostly the density of the distribution of the solutions along the non-dominated front that are improved.

The lightest feasible solution obtained compares very well with the best designs published by other authors. Seresta et al. [11] report an innerly blended design composed of symmetrical and balanced laminates with a mass of 28.82 kg and a 1% buckling margin. The lightest solution (Solution 1) found in the present work weighs 28.85 kg and presents a buckling margin of 6.8%. The performances of the solution are detailed in Table 5. The genotype of Solution 1 is given in Table 6. The corresponding SST is detailed in Fig. 11.

6. Conclusions

This paper introduces the concept of stacking sequence table (SST) for the optimal design of laminated composite structures with ply drops. The SST describes the sequence of ply-drops ensuring the transition between a thick guide laminate and a thinner one. A blended design is represented by a SST combined with a

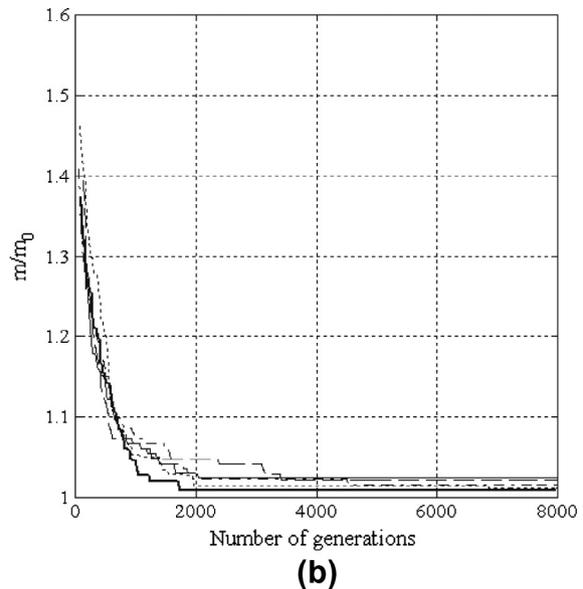


Fig. 10. Results of the optimization of the 18-panel test problem all guidelines are enforced. (a) Solutions obtained during a single optimization run (1 generation every 20 is represented only). (b) Convergence of the EA over 5 runs. The curve represented with a thick continuous line corresponds to (a).

Table 5
Result comparison for symmetrical and balanced laminates. Difference of numbers of plies per panels are marked between brackets.

Panel	Solution 1			Seresta et al. [11]	
	Number of plies	Margin (%)		Number of plies	Margin (%)
1	34	(0)	17.2	34	13.1
2	30	(2)	15.9	28	2.3
3	22	(0)	36.4	22	12.5
4	18	(-2)	13.3	20	23.1
5	18	(2)	59.3	16	3.7
6	22	(0)	22.6	22	1.1
7	18	(-2)	9.8	20	19.2
8	26	(0)	31.9	26	12.3
9	38	(0)	6.9	38	1.0
10	38	(2)	25.6	36	10.1
11	30	(0)	10.0	30	30.6
12	30	(2)	27.1	28	1.9
13	22	(0)	28.3	22	5.8
14	18	(-2)	20.2	20	30.6
15	26	(0)	27.8	26	8.9
16	30	(0)	6.8	30	11.4
17	18	(-2)	11.3	20	20.9
18	22	(-4)	11.2	26	51.1

thickness distribution over the regions of the structure. An evolutionary algorithm is specialized to operate on that representation of the solutions.

SST-based blending encompasses the classical guide-based blending while affording more freedom to define which ply to drop. Optimization of the position and order of the ply-drops enables satisfying design guidelines that were discarded in previous studies. An extensive set of design guidelines representative of the actual industrial requirements has been introduced. The *laminates design guidelines* aim at preventing unwanted coupled behaviors, matrix dominated behaviors or premature failure modes in the panels. The *ply-drop design guidelines* aim at avoiding delamination at ply-drop location and obtaining ply layouts that can actually be manufactured. The *global requirements* aim at ensuring ply continuity and smooth load redistribution over the structure. Accounting for the guidelines in the optimization is possible by devising specific evolutionary operators. A clear distinction is made between *guidelines* and other *constraints* such as buckling. Guidelines are enforced by construction of the solutions whereas constraints are incorporated to the objectives of the optimization.

The method is applied to a benchmark problem from the literature with convincing results. The EA shows satisfactory convergence rate and very good reproducibility over successive runs. The lightest designs obtained outperform all published solutions while satisfying many more design guidelines. In particular, the present results show that strength-related guidelines can be enforced without significantly penalizing the stiffness behavior and consequently the mass of the structure.

Table 6
Genotype of Solution 1. Chromosome N_{str} is repaired for symmetry and balance. Performances of the solution are computed based on repaired chromosome N_{str} .

Solution 1. Mass: 28.85 kg. $RF = 1.068$ (panel 16)	
Chromosome N_{str}	[35 30 23 19 18 23 19 27 39 38 31 31 23 19 27 31 19 23]
Repaired N_{str}	[34 30 22 18 18 22 18 26 38 38 30 30 22 18 26 30 18 22]
Chromosome SST_{lum}	[45 45 60 30 45 30 30 45 90 -45 -30 -45 90 90 -45 -45 90 -60 -30 -45 0 -30 0 45]
Chromosome SST_{ins}	[0 5 2 12 0 10 13 7 0 8 11 6 0 15 3 0 16 1 14 0 17 9 0 4]

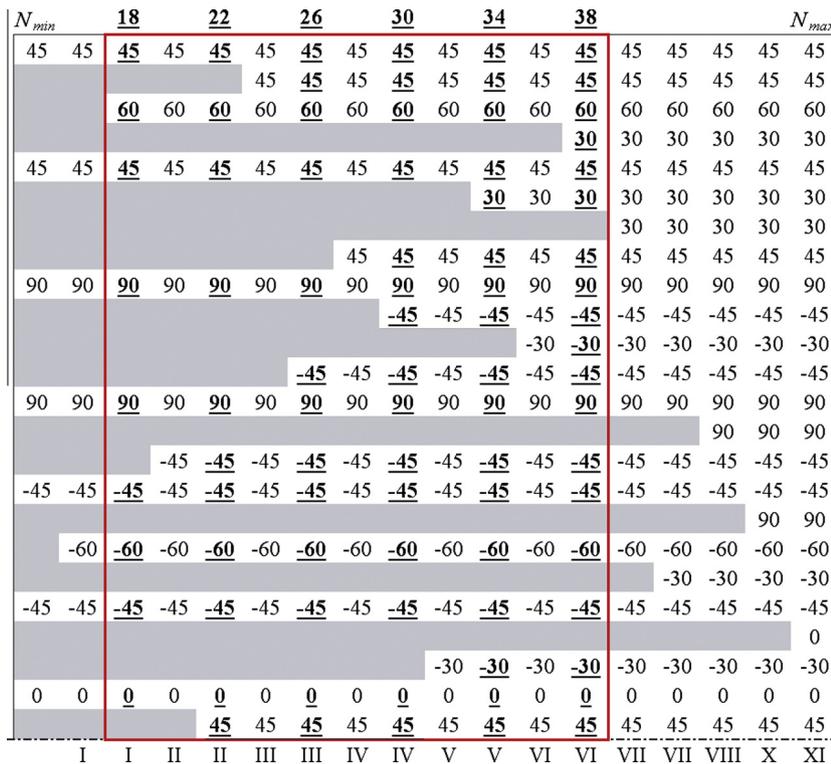


Fig. 11. SST of Solution 1 in Table 6. Columns corresponding to the laminates of the panels are marked in bold letters. SB-cycles are numbered with Roman numerals.

Appendix A. Connectivity between panels

Connectivity between panels is defined by a r -by- r binary array. Row and column numbers correspond to the panel numbers in the structure. In the present work, two panels are considered connected if they share a common edge or vertex. Nevertheless panels 6 and 10 and 13 in Fig. 8 are considered disconnected. The array of connectivity χ is given below ($r = 18$).

$$\chi = \begin{bmatrix} 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 1 \end{bmatrix} \quad (A.1)$$

Appendix B. Buckling analysis

The buckling factor $\lambda_{(m,n)}$ for each buckling mode, defined by the number of half-waves (m, n) in the longitudinal (x) and transverse (y) directions, is given by:

$$\lambda_{(m,n)} = \frac{\pi^2 [D_{11}(m/a)^4 + 2(D_{12} + 2D_{66})(m/a)^2(n/b)^2 + D_{22}(n/b)^4]}{(m/a)^2 N_x + (n/b)^2 N_y}, \quad (B.1)$$

where N_x and N_y are the stress resultants in the longitudinal and transverse directions respectively. a and b are the corresponding dimensions of the panel. m and n are the number of half wavelengths along the x and y directions respectively. D_{11} , D_{12} , D_{66} and D_{22} are bending stiffness terms of the laminate. The same formulation is used in [8,9,26,11]. The critical buckling mode is the mode of minimal buckling factor λ .

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