# Structural Optimization under Topological Constraint Represented by Homology Groups*
## (Topological Constraint on One-Dimensional Complex by Use of Zero- and One-Dimensional Homology Groups)

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Topology of any one-dimensional complex can be represented by zero- and one-dimensional homology groups, which are isomorphic to the direct sum of additive groups. In this paper, a method is proposed to impose constraint on the topology of a frame treated as a one-dimensional complex by use of homology groups in the field of structural optimization. As the numerical examples, the total strain energy of the frame is minimized under topological constraints and constant weight. Useless members are eliminated from a ground structure by use of genetic algorithm. Any number of additive groups can be freely set up as a topological constraint because of generalized inverse matrices, and a rule of coding in the genetic algorithm is prescribed so that all strings (corresponding to chromosomes in biological systems) generated in the optimization process could satisfy the topological constraints. As the result it is found that loops in the topology of the optimum structure adjoin each other. The proposed method is also applied to the topology optimization of a square, flat panel board fixed on a rigid wall and loaded vertically on points distant from the wall.

***Key Words***: Optimum Design, Computational Mechanics, Framed Structure, Homology Group, Group of Cycles, Genetic Algorithm, Generalized Inverse Matrix, Topology

### 1. Introduction

Several distinguished methods proposed for topology optimization in recent years have been employed in industries[1]. For instance, the homogenization method has been developed well and is especially remarkable[2]. It has been extended into not only structural optimization but also other fields such as stress analysis of composite materials. There are very few methods which directly and explicitly deal with topology of a structure from mathematical point of view, however. Most of benefits of algebraic topology to structural optimization remain yet unknown, but expression of topological constraints can be cited as an example of the benefits. Topological constraint conditions of a structure can be explicitly expressed by algebraic topology. It was shown that boundary cycles in the algebraic topology are useful for representation of the necessary condition which topology of the optimum frame or truss must satisfy, and that optimum structures can be searched efficiently by them[3],[4]. The boundary cycles cannot deal with all topological constraints. The boundary cycles play an important role in calculation of homology groups in the algebraic topology[5],[6], but they do not yield any information about topology of a structure. Therefore, we attempt to utilize homology groups which can represent complicated topology for formulation of topological constraints in this paper. Structures are treated as a simplicial complex consisting of simplexes in the homology theory, so that the homology theory can be easily involved in structural optimization for which finite element method has been used usually. The authors purpose to construct a general-

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ized method using homology theory which can deal with various topology optimization problems in a unified way and is able to impose arbitrary topological constraints on structures of any dimension. As the first step to this purpose, a method is proposed for imposing topological constraints using zero- and one-dimensional homology groups on a structure represented by one-dimensional complex such as frame or truss. Homology groups of a one-dimensional complex are isomorphic to the direct sum of additive groups of integers. Then it is able to control topology of a structure by assigning the number of additive groups to one-dimensional homology group using generalized inverse matrices[7]. Additive groups of zero-dimensional homology group can be also restricted to any number, as is proved mathematically later, and the number is always set equal to unity in this paper. Topological constraints on homology groups of two or more dimensions are not necessary, because such homology groups are always isomorphic to zero. As numerical examples, the total strain energy of a frame is minimized by the use of the genetic algorithm (abbreviated to GA)[8] under topological constraints. The code between a string (a chromosome) and a structure is decided so that all structures made from an arbitrary string could satisfy topological constraints. The proposed method is also applied to topology optimization of a flat panel in the end of this paper.

## 2. Description of Problem

It is aimed at that the total strain energy of a frame is minimized under a certain loading and the constraints of both weight and topology. It is assumed that only the frame topology can be changed to optimize a frame, and that all the frame members remain the same each other in weight and in size. The cross section of the members is circular, and the diameter is adjusted so that the weight of a structure could be equal to a given value as a weight constraint. Useless members are eliminated from a ground structure by means of the GA to obtain an optimum structure. Structures (a) and (b) shown in Fig. 1 are employed as ground structure in the optimization. The solid lines in the figure are members, and connecting point of members is called node. The hexagonal planar

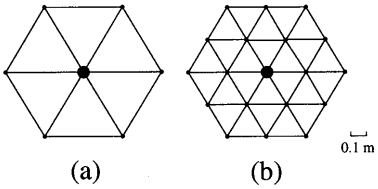



Fig. 1 Ground structures (a) and (b)

domain in Fig. 1 is subjected to uniform lateral (vertical to the sheet) load acting to each node. The solid circle at the center of the structures (a) and (b) indicates the frame support which has no degree of freedom of deformation. The fitness value of each string in the GA is the total strain energy of a structure made from the string. The strain in the members is calculated by the finite element method on the assumption that the frame deformation is elastic and infinitesimal, the axial strain being neglected. The topological constraints are written as follows,

$$H_0(K)\cong Z \tag{1}$$

$$H_1(K)\cong Z\oplus Z\oplus\cdots\oplus Z \quad \text{(the number of } Z \text{ is } N) \tag{2}$$

where $K$ denotes a complex obtained by eliminating unnecessary members from a ground structure. Equation (1) means that the number of connected components is unity, that is, the complex $K$ is not split into pieces. All nodes contained in a ground structure must be joined together to satisfy Eq. (1), because all the nodes remain as independent component even after the elimination of members. Equation (2) means that the complex $K$ has $N$ loops consisting of several members.

## 3. Method to Identify Removable Members

A ground structure can be treated as a one-dimensional complex when nodes and members are recognized as 0-simplexes and 1-simplexes, respectively. Zero-dimensional homology group $H_0(K_0)$ of a ground structure $K_0$ (a structure (a) or (b) in Fig. 1) is isomorphic to an additive group of integers $Z$, and one-dimensional homology group $H_1(K_0)$ is also isomorphic to the direct sum of $N_0$ additive groups, for $N_0=1-\chi(K_0)$, $\chi(K_0)$ being Euler number. Thus a method to keep $H_0(K)$ constant throughout the optimization process and to decrease the number of $Z$ of a one-dimensional homology group from $N_0$ to $N$ can be devised to satisfy Eqs. (1) and (2). Such a method is convenient, because satisfaction of either of Eqs. (1) and (2) implies automatic satisfaction of the other. In the other words, if elimination of a member surely causes reduction of the number of $Z$ in $H_1(K)$ by unity, $H_0(K)$ never changes, and vice versa. This can be proved by the Mayer-Vietoris theorem for reduced homology groups as follows[5),9].

Let $K_3$ be a complex and $K_1$, $K_2$ be its subcomplexes with $K_3=K_1\cup K_2$. The following exact sequence holds,

$$\cdots\longrightarrow \tilde{H}_r(K_1\cap K_2)\xrightarrow{i_*} \tilde{H}_r(K_1)\oplus\tilde{H}_r(K_2) \xrightarrow{j_*} \tilde{H}_r(K_3)\xrightarrow{\partial_*} \tilde{H}_{r-1}(K_1\cap K_2)\longrightarrow\cdots \tag{3}$$

where $i_*[z]=([z],-[z])$, $j_*([z_1],[z_2])=[z_1]+[z_2]$ and $\partial_*[z_3]=[\partial c_1]$ with $[z]\in\tilde{H}_r(K_1\cap K_2)$, $[z_1]\in\tilde{H}_r(K_1)$, $[z_2]\in\tilde{H}_r(K_2)$, $[z_3]\in\tilde{H}_r(K_3)$ and $c_1\in C_r(K_1)$. $[z]$ is

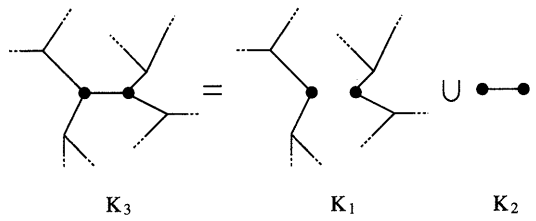



Fig. 2 Complex $K_3$ and its subcomplexes $K_1$, $K_2$

homology class of $z$. The relation between homology groups and reduced homology is written as

$$H_r(K)=\tilde{H}_r(K),\ r\neq 0$$
$$H_0(K)\cong\tilde{H}_0(K)\oplus Z. \quad (4)$$

If $Im\ f_{n+1}=Ker\ f_n$ exists for all $n$, a sequence

$$\cdots\longrightarrow G_{n+1}\xrightarrow{f_{n+1}}G_n\xrightarrow{f_n}G_{n-1}\xrightarrow{f_{n-1}}\cdots$$

is called the exact sequence.

Figure 2 shows an example of $K_1$, $K_2$ and $K_3$. $K_1$ is a complex made from $K_3$ by elimination of 1-simplex $K_2$. The broken lines indicate that a part of structures $K_3$ and $K_1$ are shown in this figure, instead of the entire ones. The solid circles are $K_1\cap K_2$, that is, $K_2$ is connected with $K_1$ by two 0-simplexes. The case that $K_1\cap K_2$ is one 0-simplex need not be considered, because elimination of such 1-simplex is obviously against a topological constraint of Eq.(1). Consequently only the case shown in Fig. 2 is discussed in this chapter. When the number of the connected components of both $K_1$ and $K_3$ is unity (i.e. $\tilde{H}_0(K_1)=\tilde{H}_0(K_3)=0$), the exact sequence of Eq.(3) becomes

$$0\longrightarrow\tilde{H}_1(K_1)\oplus 0\xrightarrow{j_*}\tilde{H}_1(K_3)\xrightarrow{\partial_*}Z\xrightarrow{i_*}0\oplus 0. \quad (5)$$

If a sequence of Abelian group $0\longrightarrow A\xrightarrow{i}B\xrightarrow{j}Z\longrightarrow 0$ is the exact sequence, then there is $B\cong A\oplus Z$. Therefore, the following formula holds.

$$\tilde{H}_1(K_3)\cong\tilde{H}_1(K_1)\oplus Z \quad (6)$$

The above equations (5) and (6) prove that the number of $Z$ in $H_1(K)$ is always decreased by unity, if elimination of a 1-simplex $K_2$ does not make any change in the number of the connected components. This means that Eq.(2) is automatically satisfied, if Eq.(1) is satisfied throughout the elimination process of $N-N_0$ 1-simplexes.

The reverse process is proved as follows. If the connected components of $K_1$ is unknown and $K_3$ satisfies Eq.(6), the following sequence is obtained by the Mayer-Vietoris theorem.

$$0\longrightarrow\tilde{H}_1(K_1)\oplus 0\xrightarrow{j_*}\tilde{H}_1(K_1)\oplus Z\xrightarrow{\partial_*}Z\xrightarrow{i_*}\tilde{H}_0(K_1)\oplus 0\longrightarrow 0 \quad (7)$$

Exactness of this diagram results in the following four equations.

$$Ker\ j_*=0 \quad (8)$$
$$Im\ j_*=Ker\ \partial_* \quad (9)$$
$$Im\ \partial_*=Ker\ i_* \quad (10)$$
$$Im\ i_*=\tilde{H}_0(K_1) \quad (11)$$

Furthermore, the following relation is assured by the theorem of homomorphism.

$$\tilde{H}_1(K_1)/Ker\ j_*\cong Im\ j_* \quad (12)$$
$$(\tilde{H}_1(K_1)\oplus Z)/Ker\ \partial_*\cong Im\ \partial_* \quad (13)$$
$$Z/Ker\ i_*\cong Im\ i_* \quad (14)$$

When it can be assumed that homology groups of one-dimensional complex do not include any torsion coefficient, Eq.(15) is derived from Eqs.(8)-(14).

$$\tilde{H}_0(K_1)=0 \quad (15)$$

This proves that $H_0(K)$ never change, if the number of $Z$ in $H_1(K)$ is decreased by unity by removal of a 1-simplex.

In this study, only the number of $Z$ in $H_1(K)$ in Eq.(2) is controlled and Eq.(1) is neglected (both of the constraints are satisfied, however). Identification of removable members must be repeated whenever a certain member is eliminated, because elimination of even a member may change topology of a complex. The process of identifying removable members is as follows.

$H_1(K)$ of any one-dimensional complex is equal to group of cycles $Z_1(K)$. Let $[A]$ be a matrix decided by the ground structure $K_0$ and boundary homomorphism $\partial_1$, and $\{n\}$ be a vector of which ingredients are coefficient of 1-simplexes. 1-cycle $z$ ($z\in Z_1(K_0)$) must satisfy the following equation corresponding to $\partial_1 z=0$.

$$[A]\{n\}=\{0_m\} \quad (16)$$

$\{0_m\}$ is null vector which has $m$ ingredients, and $m$ is the number of 0-simplexes in $K_0$. Ingredients in $[A]$ are any of 1, 0, $-1$. Let $k$ be the number of 1-simplexes. $[A]$ is a matrix of order $m\times k$. For computing time sawing, it is desirable that $[A]$ is a matrix of full rank. The reason is described in the subsequent chapter. Let $\alpha_r$, $\gamma_r$, $\beta_r$ and $b_r$ be rank of group of $r$-dimensional chains $C_r(K)$, cycles $Z_r(K)$, boundary cycles $B_r(K)$ and homology group $H_r(K)$, respectively. The following equations hold in general.

$$b_r=\gamma_r-\beta_r,\ \beta_{r-1}=\alpha_r-\gamma_r \quad (17)$$

As the result, Eq.(18) is obtained when the relation of $C_0(K)=Z_0(K)$ is taken into account.

$$\gamma_1=\alpha_1-\beta_0=\alpha_1-(\alpha_0-b_0) \quad (18)$$

As for the ground structures in Fig. 1, the formula of $\gamma_1=k-(m-1)$ is derived from $\alpha_0=m$, $\alpha_1=k$ and $b_0=1$ ($k>m$). $\gamma_1$ is equal to $1-\chi(K_0)$, namely, the rank of $H_1(K_0)$. On the other hand, the solution of $\{n\}$ in Eq. (16) consists of $k-rank([A])$ linear independent vectors when rank of a matrix $[A]$ is denoted by $rank([A])$[10]. As is aforementioned, $H_1(K_0)$ is equal to $Z_1(K_0)$, and then $\gamma_1=k-rank([A])$ holds. Hence, $rank([A])$ is found to be $m-1$. $[A]$ has a feature that the sum of the ingredients of each column is zero. It means that $[A]$ can be changed to a matrix of full rank by deletion of an arbitrary row. In this study

such row is deleted that the number of zero ingredients is the least. When $[A^0]$ is the matrix of full rank obtained from $[A]$ by deletion of the row, Eq.(16) is rewritten by use of $[A^0]$ as given below.

$$[A^0]\{n\}=\{0_{m-1}\} \tag{19}$$

The matrix $[A^0]$ must be defined newly when a member is eliminated from the ground structure. Using a superscript to indicate the number of eliminated members, such as $[A^0]$, $[A^1]$, $[A^2]$, $\cdots$, Eq.(19) is rewritten in the following form when $s+1$ members are removed,

$$[A^{s+1}]\{n\}=\{0_{m+s}\} \tag{20}$$

where $[A^{s+1}]$ is defined as given below.

$$[A^{s+1}]=\begin{bmatrix} [A^s] \\ 0 \cdots\cdots 0 \underset{i}{1} 0 \cdots\cdots 0 \end{bmatrix}=\begin{bmatrix} [A^s] \\ \{b\}^T \end{bmatrix} \tag{21}$$

Superscript $T$ indicates transpose of vector or matrix. By denoting the number to be eliminated by $i$, the vector $\{b\}$ in the right hand side of Eq.(21) is so defined that the $i$-th ingredient is 1 and others are 0, that is, elimination of the $i$-th member is represented by fixing the $i$-th ingredient of $\{n\}$ as zero. A member to be eliminated is selected in the manner that topological constraints could be satisfied. When the Moor-Penrose generalized inverse matrix[7] of $[A^s]$ is denoted by $[A^s]^-$, the following equations are obtained,

$$[A^s]\{n\}=\{0_{m+s-1}\}$$
$$\{n\}=([I_k]-[A^s]^-[A^s])\{h\} \tag{22}$$

where $[I_k]$ is the identity matrix of order $k\times k$, and $\{h\}$ is an arbitrary vector. If some ingredients of $\{n\}$ are equal to zero, the members corresponding to such ingredients of $\{n\}$ are not components of 1-cycle, whatsoever value the vector $\{h\}$ takes. In the other words, if all the ingredients in the $j$-th row of the matrix $[I_k]-[A^s]^-[A^s]$ are equal to zero, the $j$-th member cannot be removed. Whenever a member is eliminated, this operation by use of the matrix $[I_k]-[A^s]^-[A^s]$ must be carried out to all members before selecting another member eliminated by the GA. It means that the operation is to be repeated $N-N_0$ times.

The following is an example of $[A]$ corresponding to Fig. 3. Let $(a_0, a_1, a_2, \cdots, a_r)$ be $r$-simplex $x^r$, then

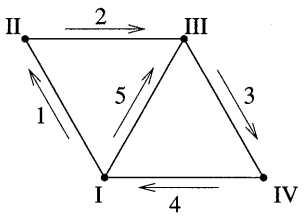



Fig. 3 Example of simplicial complex

$\partial_r x^r$ is represented in the following form,

$$\partial_r x^r=\sum_{i=0}^{r}(-1)^i(a_0, \cdots, \hat{a}_i, \cdots, a_r) \tag{23}$$

where $a_i$ $(i=1, \cdots, r)$ is an independent point (0-simplex), and $\hat{a}_i$ means lack of a point $a_i$. $r$-chain denoted by $c^r$ of a complex which has $u$ $r$-simplexes is written as given below,

$$c^r=n_1x_1^r+n_2x_2^r+\cdots+n_ux_u^r \tag{24}$$

where $n_i$ is a coefficient. A suffix of $x^r$ is a number assigned to each $x^r$. When the boundary homomorphism $\partial_r$ is operated to the $r$-chain $c^r$, the following is resulted.

$$\partial_r c^r=n_1\partial_r x_1^r+n_2\partial_r x_2^r+\cdots+n_u\partial_r x_u^r \tag{25}$$

In the case of $r=1$, $n_i$ is a coefficient of 1-simplex and corresponds to the $i$-th ingredient of $\{n\}$ in Eq.(16). Numbers from 1 to 5 and from I to IV in Fig. 3 indicate those of 1-simplex and 0-simplex, respectively, and the arrows show the orientation of 1-simplexes, that is, the order of 0-simplexes. A vector whose ingredients are coefficient of 0-simplex is denoted by $\{p\}$. Then Eqs.(23), (24) and (25) enable us to express the relation between $\{n\}$ and $\{p\}$ as follows in the case of Fig. 3.

$$[A]\{n\}=\begin{bmatrix} -1 & 0 & 0 & 1 & -1 \\ 1 & -1 & 0 & 0 & 0 \\ 0 & 1 & -1 & 0 & 1 \\ 0 & 0 & 1 & -1 & 0 \end{bmatrix}\{n\}=\{p\} \tag{26}$$

Equations (16) and (26) stand for that 1-cycle is special 1-chain whose $\{p\}$ is equal to $\{0_m\}$.

## 4. Reduction of Computing Time

It is necessary for the proposed formulation to compute the Moor-Penrose generalized inverse matrix $[A^s]^-$ repeatedly whenever a member is removed for each string and generation in the GA. It probably takes long to compute the generalized inverse when one of such complicated methods as singular value decomposition is employed. The matrix $[I_k]-[A^{s+1}]^-[A^{s+1}]$ can be computed easily when $[I_k]-[A^s]^-[A^s]$ is computed once, because the difference between $[A^{s+1}]$ and $[A^s]$ is only one row.

The Moor-Penrose generalized inverse $[B]^-$ of a fully-ranked rectangular $[B]$ (the rank is equal to the number of rows) can be obtained by Eq.(27) by use of the regular inverse matrix $([B][B]^T)^{-1}$[10].

$$[B]^-=[B]^T([B][B]^T)^{-1} \tag{27}$$

$[A^{s+1}]$ is fully-ranked, because $[A^0]$ is fully-ranked and $rank([A^{s+1}])=rank([A^s])+1$, and the number of columns is greater than that of the rows. Equation (27) can be utilized to obtain $[A^{s+1}]^-$ as follows. The following abbreviation is used for $\alpha$, $\{q\}$ and $[P]$.

$$\alpha=\{b\}^T([I_k]-[A^s]^-[A^s])\{b\} \tag{28}$$

$$\{q\}^T=-\frac{1}{\alpha}\{b\}^T[A^s]^- \tag{29}$$

$$[P]=([A^s][A^s]^T)^{-1}+\frac{1}{\alpha}([A^s]^-)^T\{b\}\{b\}^T[A^s]^- \tag{30}$$

Then the regular inverse matrix $([A^{s+1}][A^{s+1}]^T)^{-1}$ can be partitioned in the following form.

$$([A^{s+1}][A^{s+1}]^T)^{-1}=\begin{bmatrix}[P] & \{q\}\\ \{q\}^T & \frac{1}{\alpha}\end{bmatrix} \tag{31}$$

In addition, by use of the matrix $[F]$ and vector $\{g\}$ as defined below,

$$[F]=[A^s]^- -\frac{1}{\alpha}([I_k]-[A^s]^-[A^s])\{b\}\{b\}^T[A^s]^- \tag{32}$$

$$\{g\}=\frac{1}{\alpha}([I_k]-[A^s]^-[A^s])\{b\} \tag{33}$$

the generalized inverse matrix $[A^{s+1}]^-$ is obtained by Eqs. (27) and (31) in the following form.

$$[A^{s+1}]^-=[[F]\{g\}] \tag{34}$$

Furthermore, $[I_k]-[A^{s+1}]^-[A^{s+1}]$ is rewritten as follows.

$$[I_k]-[A^{s+1}]^-[A^{s+1}]=[I_k]-[A^s]^-[A^s] -\frac{1}{\alpha}([I_k]-[A^s]^-[A^s])\{b\}\{b\}^T([I_k]-[A^s]^-[A^s]) \tag{35}$$

Equation (35) shows that it takes only short time to compute $[I_k]-[A^{s+1}]^-[A^{s+1}]$, because $[I_k]-[A^s]^-[A^s]$ is computed already, and $\alpha$, $([I_k]-[A^s]^-[A^s])\{b\}$ and $\{b\}^T([I_k]-[A^s]^-[A^s])$ are scalar $(i, i)$, the $i$-th column and $i$-th row of $[I_k]-[A^s]^-[A^s]$, respectively.

## 5. Coding in the GA to Always Satisfy Topological Constraints

Coding to relate a structured frame with a string is the first step of the GA applied to minimization of the total strain energy of the frame. In this study, coding is so defined that any strings can satisfy topological constraints expressed by Eqs. (1) and (2). A string has different features (corresponding to genes in biological systems) in the first half from those in the second half as described in the following.

It is possible to assign string positions (loci) in the first half of a string to $1-\chi(K_0)$ independent loops in a ground structure $K_0$, because there are one or more removable 1-simplexes in each independent loop. Feature values (alleles) are number assigned to 1-simplexes in each independent loop (not consecutive numbers to all 1-simplexes, as Fig. 3). 1-simplexes corresponding to feature values are eliminated in the decoding process of a string. If a certain 1-simplex is judged unremovable, 1-simplex of the subsequent number is tried to be removed. If the subsequent 1-simplex is also unremovable, 1-simplex of larger number is to be removed. This process is repeated until a removable one is found. In the case that no removable 1-simplex exists in a loop, the string position is skipped over and decoding process is tried again from the top of a string. This skip can be interpreted as a shift among string positions.

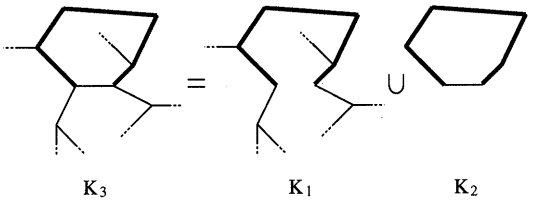



Fig. 4 Elimination of 1-simplex from a loop

In the second half of a string, features are represented by the number of string positions which are never decoded. If all the features in the first half of a string are decoded and $1-\chi(K_0)$ 1-simplexes are eliminated, any structure obtained by the decoding has no loops ($H_1(K)=0$) against the topological constraint of Eq. (2). Thus it is necessary to skip over $N$ string positions in the first half. In the decoding process, the features in the second half of a string are decoded firstly, and $N$ string position numbers are memorized. The first half of a string is decoded subsequently. The number of the first half of a string is $1-\chi(K_0)$ and that of second one is $N$.

The elimination of a 1-simplex from an independent loop can exactly reduce the number of $Z$ in $H_1(K)$ by unity at all times. The proof is as follows. Figure 4 shows complexes $K_1$, $K_2$ and $K_3$ which satisfy $K_3=K_1\cup K_2$, as Fig. 2. Bold lines in Fig. 4 depict $K_1\cap K_2$. When the Mayer-Vietoris theorem is applied to the situation in Fig. 4, the following sequence is obtained.

$$0\longrightarrow \tilde{H}_1(K_1)\oplus Z \xrightarrow{j_*} \tilde{H}_1(K_3)\longrightarrow 0 \tag{36}$$

Hence, the following is obtained.

$$\tilde{H}_1(K_3)\cong\tilde{H}_1(K_1)\oplus Z \tag{37}$$

This equation means that the number of $Z$ in $H_1(K)$ is decreased by unity, when a 1-simplex is eliminated from an independent loop, and proves that the proposed method is valid.

Which loops are independent in a ground structure $K_0$ must be specified before carrying out the GA. Shapes of the loops are not unique, but the optimum structure obtained by the proposed method is always independent of loop shape. Figure 5 shows an example of the case of $N=1$. A complex on the left side in Fig. 5 is a ground structure in this example, having four independent loops. Triangles $a$, $b$, $c$ and $d$ are example of the four loops. A loop $a$ (triangle $a$) consists of three 1-simplexes (sides) whose numbers are 1, 2 and 3. In the same way, loop $b$ consists of 1-simplexes 4, 5 and 6, loop $c$ of 1-simplexes 7, 8 and 9, and loop $d$ of 1-simplexes 10, 11 and 12. A large

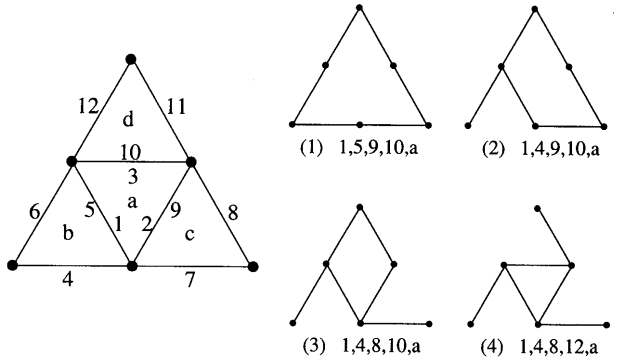



Fig. 5 Examples of strings in GA

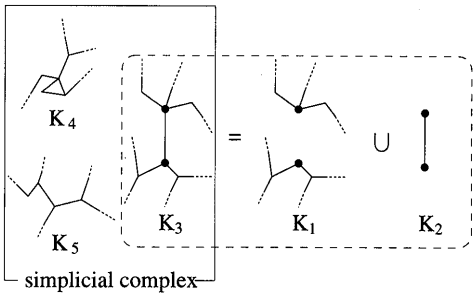



Fig. 6 Connected component $K_3$ and its subcomplexes $K_1$ and $K_2$

triangle of six 1-simplexes 4, 7, 8, 11, 12 and 6 can be taken instead of loop $d$, because independent loops are not unique. 1-simplexes 1 and 5 are identical, because they are common in the loop $a$ and $b$. 1-simplexes 2 and 9, and 1-simplexes 3 and 10, are also identical, respectively. Figures(1)-(4) in Fig. 5 show example of the strings and structures obtained by decoding them. Feature values in each string position are (1, 2, 3), (4, 5, 6), (7, 8, 9), (10, 11, 12) and ($a$, $b$, $c$, $d$). The fifth feature in all strings is the same $a$. The top string position (corresponding to the loop $a$) is to be skipped over in the decoding process. In the case of string (1) in Fig. 5, 1-simplex 5 of the loop $b$, 1-simplex 9 of the loop $c$ and 1-simplex 10 of the loop $d$ are eliminated from the ground structure. The loop $a$ vanishes in the structure (1), though the top position of a string is ignored. And the structure (1) satisfies the topological condition of $N=1$. In cases of the structures (2) and (3), two and one 1-simplexes are removed from the loop $a$, respectively. Whole loop $a$ is left intact only in the structure (4). Therefore, it can be said that skipping over string positions does not mean leaving loops that correspond to the skipped string positions intact throughout the decoding process. This is an advantage of the coding method employed in this study. In actual computation for optimization, the characters $a$, $b$, $c$ and $d$ as features are replaced by combination of numerals, and the number of feature values is reduced, because the large number of feature values often decreases the possibility of obtaining the optimum structure, or increases the number of generations required in the GA to find it.

## 6. Topological Constraint on $H_0(K)$

It is useful from an engineering viewpoint to restrict the number of $Z$ in $H_0(K)$ (the number of connected components) to unity. Only this constraint is discussed in this study. Any number of $Z$ in $H_0(K)$ can be chosen as a constraint by a slight modification in the proposed method, however, as is proved in the following. It is plausible that the following proof implies the generality of the proposed method.

Let a constraint on $H_0(K)$ be

$$H_0(K)\cong Z\oplus Z\oplus\cdots\oplus Z \quad \text{(the number of } Z \text{ is } M), \tag{38}$$

where $M$ is the number of connected components. The number of $Z$ in $H_0(K)$ should be increased by $M-1$ to satisfy the above constraint, because of $H_0(K_0)\cong Z$. This requirement is fulfilled by elimination of $M-1$ 1-simplexes which has no relation with independent loops. Such 1-simplexes correspond to ingredients of $\{n\}$ which are always equal to zero for arbitrary value of $\{h\}$ in Eq.(22). Elimination of 1-simplexes free from 1-cycle (independent loops) makes no change in $H_1(K)$, because $H_1(K)$ of any one-dimensional complex is equal to $Z_1(K)$. Figure 6 illustrates that $K_2$ is an example of 1-simplex free from 1-cycle. $K_3$, $K_4$ and $K_5$ are connected components in a certain complex, and $K_3$ consists of $K_1$ and $K_2$($K_3=K_1\cup K_2$). The number of connected components does not influence the following proof, though it is taken equal to 3 in Fig. 6, for example. The relation of $\tilde{H}_1(K_3)\cong\tilde{H}_1(K_1)$ can be assumed, because elimination of $K_2$ never affects $H_1(K)$. It is assumed, in addition, that the homology groups of complexes in this study need no torsion coefficient. When the Mayer-Vietoris theorem is applied again to the case of Fig. 6, the exact sequence takes the following form.

$$0\longrightarrow\tilde{H}_1(K_1)\xrightarrow{j_*}\tilde{H}_1(K_1)\xrightarrow{\partial_*}Z\xrightarrow{i_*}\tilde{H}_0(K_1)\longrightarrow 0 \tag{39}$$

Exactness of this diagram gives the following formulas,

$$Ker\ j_*=0 \tag{40}$$
$$Im\ j_*=Ker\ \partial_* \tag{41}$$
$$Im\ \partial_*=Ker\ i_* \tag{42}$$
$$Im\ i_*=\tilde{H}_0(K_1) \tag{43}$$

and also the followings are derived from the theorem of homomorphism.

$$\tilde{H}_1(K_1)/Ker\ j_*\cong Im\ j_* \tag{44}$$
$$\tilde{H}_1(K_1)/Ker\ \partial_*\cong Im\ \partial_* \tag{45}$$
$$Z/Ker\ i_*\cong Im\ i_* \tag{46}$$

Therefore, $H_0(K_1)$ results in the following formula.

$$H_0(K_1) \cong \tilde{H}_0(K_1) \oplus Z \cong Z \oplus Z \quad (47)$$

This proof shows that elimination of a 1-simplex free from 1-cycle is equivalent to addition of an additive group $Z$ to $H_0(K)$, because of $H_0(K_3) \cong Z$. Hence, elimination of $M-1$ 1-simplexes free from 1-cycle and $1-\chi(K_0)-N$ 1-simplexes which are component of 1-cycle from a ground structure satisfies both topological constraints of Eqs.(2) and (38). Only $H_0(K) \cong Z$ is used in the subsequent chapter, however, because of its usefulness in the engineering field.

## 7. Numerical Examples of Topology Optimization of Frames

The aforementioned formulation is applied to the minimization of the total strain energy of a frame under the conditions that the frame has one connected component and $N$ loops (Eqs.(1) and (2)), and that the frame weight is kept equal to 7.38 kg in the case of the ground structure (a) in Fig. 1, or 11.1 kg in the case of the ground structure (b). The sum of the uniform load is set equal to 1.36 kPa, and all the members are supposed to be the same in size. The frame material is taken homogeneous, and its mass density, Young's modulus and modulus of rigidity are taken as $7.83 \times 10^3$ kg/m$^3$, 202 GPa and 81.4 GPa, respectively. The cross section of the members is circular, and the diameter is so adjusted that the weight constraint could be satisfied. Two point cross-over is adopted in the GA, and the probability of mutation is assumed to be 2.0%. The population is approximately 30 in the case of the ground structure (a), or 560 for the ground structure (b). Selection of strings is based on only their ranking, and the elite string is preserved in the GA.

The solution obtained by the GA is not guaranteed optimum exactly, in general. Though the word 'optimum' is used for the sake of convenience in this study, each structure obtained in this and in the subsequent chapter is none but the best one among the 30 structures obtained from various initial values of strings.

Figure 7 shows the optimum structures obtained by the GA by use of the ground structure (a) for $N=0, \cdots, 5$, where $N$ and $U$ in Fig. 7 are the number of $Z$ in $H_1(K)$ and the total strain energy of the frame, respectively. $F$ is the number of the optimum structures (to be exact, frames which have the same $U$ as the one in Fig. 7 regardless of the shape) among those structures obtained as the result of 30 runs of the GA. The total strain energy $U$ of the ground structure (a) corresponding to a structure of $N=6$ takes the largest value of 1.89 J. Figure 7 shows that loops are triangular in shape and are placed adjacent to each other. $N$ of a

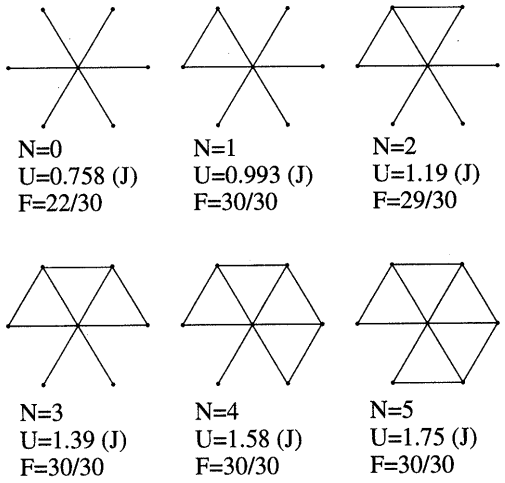



Fig. 7 Optimum structures (ground structure (a))

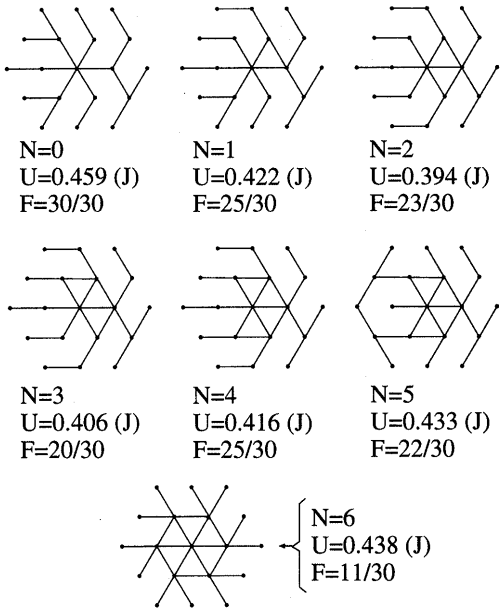



Fig. 8 Optimum structures (ground structure (b))

structure with the smallest $U$ is zero (no loop). The structure of $N=0$ which is called 'a tree' also has the smallest $F$. The reason may be the uniqueness of the structure. For instance, a structure of $N=1$ can be derived from more than six kinds of strings in this case, because any rotation of the structure by 60 degrees never changes the value of $U$.

Figure 8 depicts the optimum structures derived from the ground structure (b) for $N=0, \cdots, 6$. The ground structure (b) has the largest value of $U=0.984$ J as a structure of $N=24$. The difference of the cases shown in Fig. 8 from those in Fig. 7 is as follows.

A structure of $N=5$ has a hexagonal loop.

A structure of $N=2$ (not a tree) has the smallest $U$.

Geometry of these structures is rather complicated.

Most of these structures have smaller $F$ than those in Fig. 7, though the cases in Fig. 8 cannot be simply compared with those in Fig. 7, because of disparity in their geometrical and loading conditions. A structure of $N=6$ has the smallest $F$. The reason is that the number of kinds of strings which make a structure of $N=6$ and $U=0.438$ J is quite smaller than the other structures.

## 8. Application of Proposed Method to Topology Optimization of Panel Structure

In some cases, the proposed method can be applied to topology optimization of panel structures, whereas it is originally devised for skeleton structures such as frames and trusses.

The numerical example is concerned with the minimization of the total strain energy in a square elastic panel fixed on a rigid wall and subjected to the vertical loading of 9.8 kN as shown in Fig. 9. The optimum shape can be found by elimination of unnecessary triangular elements. Weight of the structure is kept equal to 39.2 kg in both cases of the ground structures (c) and (d). The size of all elements is assumed to be the same. The element thickness is so decided that the weight constraint of 39.2 kg is satisfied. The vertices and sides of the triangular elements are regarded as 0-simplexes and 1-simplexes, respectively. Equations (1) and (2) are employed again as topological constraints. Panel structure does not have topology expressed in Eqs. (1) and (2) as two-dimensional complex, however. These topological constraints considered in this chapter mean that the areas enclosed with $N$ loops consisting of 1-simplexes (sides) are cut out from the ground structure, that is, the structure has not more than $N$ holes. Population employed in the GA is approximately 370 when the ground structure (c) is used, or 940 for the ground structure (d). Elimination of triangular elements is substituted by setting their thickness equal to $10^{-6}$ mm, because finite element analysis of structures having elements, whose thickness is zero exactly, turns to be impossible in some cases. Other data in the GA, such as Young's modulus and selection process, are the same with those in the preceding chapter.

Figure 10 shows the optimum structures of $N=1$, $\cdots$, 4 derived from the ground structure (c). A structure of $N=1$ has a hole placed adjacent to the rigid wall. This site close to the wall is supposed to be most effective for decrease in strain energy. It can be said that the structure with the smallest $U$ has not more than three holes under this condition. The ground structure (c) has strain energy of 0.279 J as a structure of $N=0$. Structures of $N=3$ and 4 have smaller

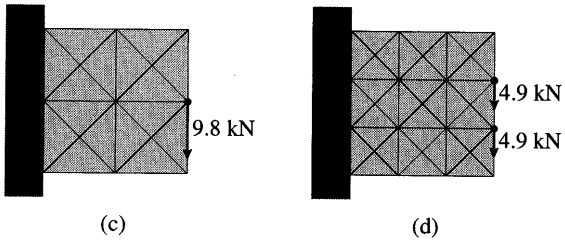



Fig. 9 Ground structures (c) and (d)

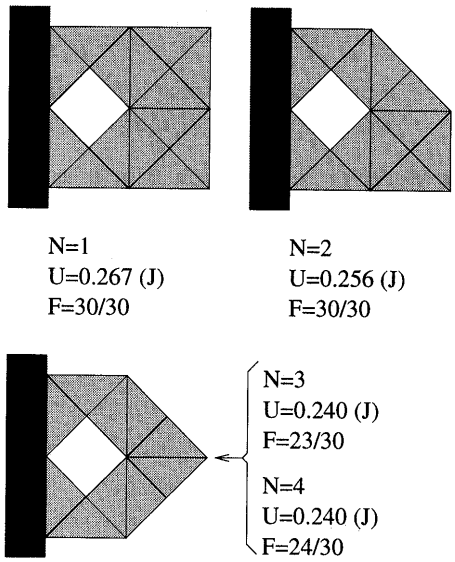



Fig. 10 Optimum structures (ground structure (c))

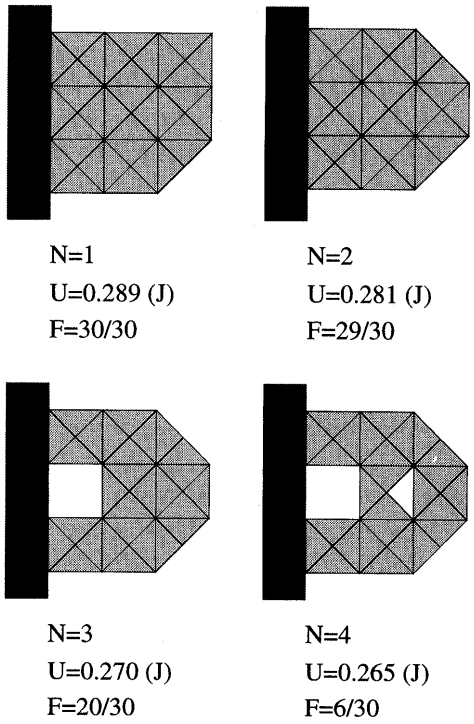
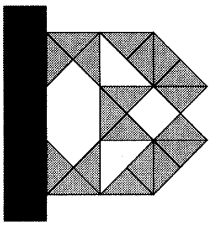



Fig. 11 Optimum structures (ground structure (d))

$F$ than the other two cases of $N=1$ and 2, probably because the strings for the structures of $N=3$ or 4 are much longer than those of $N=1$ or 2.



U=0.242 (J)
F=22/30

Fig. 12 Optimum structure (without topological constraint)

Structures of $N=1, \cdots, 4$ in Fig. 11 are obtained from the ground structure (d). A structure of $N=1$ is made by cutting off a bottom corner from the right side of the ground structure (d). This tendency is obviously different from the situation shown in Fig. 10. The strain energy in the ground structure (d) as a structure of $N=0$ is equal to $U=0.296$ J. $F$ is decreased while $N$ is increased. Length of strings probably causes the decrease of $F$ as well as in Fig. 10. Such structures having more than four holes are expected to have the smallest $U$. Thus, minimization of $U$ without topological constraints is attempted. As the result, a structure corresponding to $N=7$ shown in Fig. 12 is found to exist.

## 9. Concluding Remarks

A formulation is proposed to deal with explicit topological constraints represented by homology groups on one-dimensional complex. The application of homology groups has advantages of explicit and general description of structural topology in expression which makes treatment of topological constraints easy. The validity of this proposed method is verified by the numerical examples in which total strain energy of a frame is minimized under constraints in topology and weight. The numbers of connected components and loops in the frame are limited to unity and $N$, respectively. As the result, it is found that (1) loops are placed next to each other, (2) the number of loops $N$ of a structure which has the minimum total strain energy depends on the arrangement of members in the ground structures. Furthermore, it is shown that the proposed method can also be applied to topological optimization of panel structures represented as two-dimensional complex.

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