TOPOLOGY OPTIMIZATION WITH ALGORITHM BASED ON BACTERIAL CHEMOTAXIS

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ABSTRACT

This paper presents a new topology optimization methodology that combines the FE method for structural analysis with an optimization strategy inspired on bacterial chemotaxis.

The principle of BCBTOA (Bacterial Chemotaxis Based Topology Optimization Algorithm) is very simple. A structure evolves to an optimum configuration by systematically re-distribuiting the material into the desing domain, reforcing the overload zones and removing material where it is not required. Inspired by the model of self organized collective behavior showed by marine bacteria Thiovulum majus [1], the algorithm stablishes rules that drive the structure to an optimum distribution of material.

The design domain is constructed by the FE method and represents the environment in which a colony of bacteria can move. Support conditions and external loads are also applied to this model. As happens in nature, in any place of the environment there are different concentrations of nutrients or noxious substances. Here, these concentrations are represented by the values of the field variables for each element (mean compliance).

An amount of bacteria equal to the desired volume is placed on the design domain. Immersed there, the bacteria develop a chemotactical strategy as a whole considering comunications between them, to increase the chances of survival a maximal number of individuals from the colony. In every iteration bacteria exchanged information regarding the concentration of nutrients at its current location. Based on this information, bacteria located in positions with low concentrations of nutrients move toward more favorable positions. As ESO (Structural Evolutionary Optimization) [2], in this method the design variable is the density trackled directly, so the elements can be turned off or on, depending on the presence or absence of bacteria in them.

The procedure of BCBTOA is:

1. For the giving boundary and load conditions, define the design domain.
2. Perform FE analysis to evaluated the field variables.
3. Located the bacteria in the best positions.
4. Calculate the signal betweem bacteria and exchange information.
5. Remove the bacteria in poorest positions .
6. Locate bacteria in the richest empty positions.
7. Update the density for each element.
8. Return to step 2 until stop criterion be satisfied.

The BCBTOA was implemented in Matlab 7.0 ® making the necessary modifications to the code developed in [3], and has been successfully applied to solved topology optimization problems in a variety of two dimentional structures in a continuum design domain as shown in Figure 1 and Figure 2.
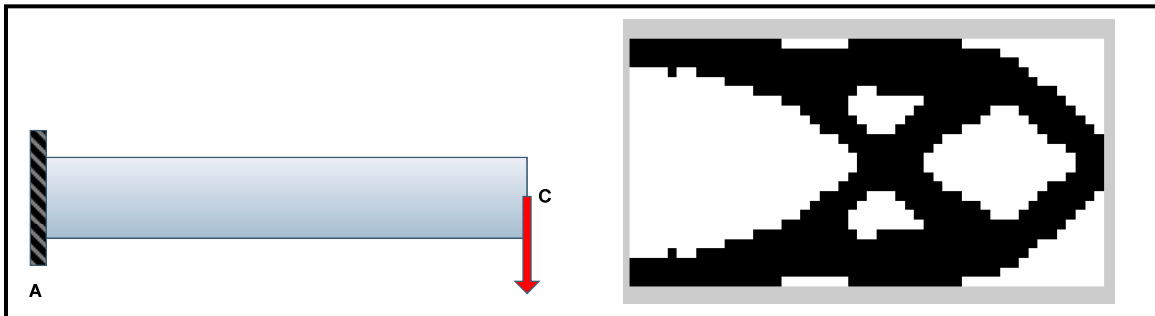

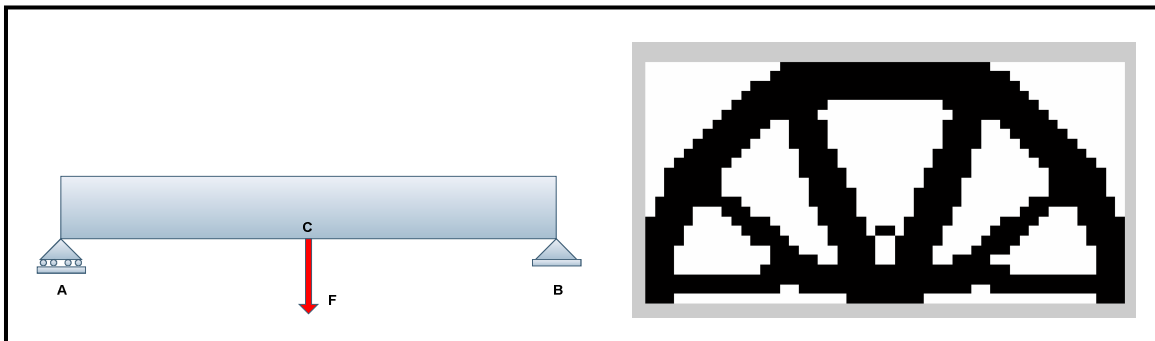Figure 1. Topology optimization of a cantilever beam.

Figure 2. Topology optimization of a Michell type structure.

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