

FLEXIBLE MULTIBODY APPROACH IN APPLICATION TO THE FEEDING MECHANISM IN VERTEBRATE STRUCTURES

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Key Words: *Finite Element Method / Flexible Multibody System Dynamics / Multibody System Dynamics / vertebrate / feeding mechanism.*

The potential of computational mechanics as an analytical technique in biological research has been widely highlighted in recent years facilitating the use of Finite Element Analysis (FEA) or Multibody System Dynamics (MSD) in estimating the performance of vertebrate skeletal and soft tissues [1]. Flexible Multibody System Dynamics (FMSD) is a simulation technique used to study the behaviour of the mechanical systems that exhibit flexibility in its structures.. In this approach, the finite element model of a flexible member is prepared in standard finite element software and subjected to a modal reduction such as Craig-Bampton approach [2]. Then the reduced model can be used in the multibody model.

Coupling of FEA and MSD is explored studying the feeding mechanism in a skull of *Edingerella madagascariensis*, an early amphibian from the Olenekian (Early Triassic) of Madagascar [3]. The digital model of the skull was obtained from a medical CT Siemens® Sensations-16, at 140 kV and 150 mAs giving an output of 512 x 512 pixels per slice. The pixel size and the inter-slice space were 0.586 mm and 0.1 mm, respectively. It has been converted to a CAD model using reverse engineering techniques [4]. The skull was analysed to evaluate the stress state using the Finite Elements Method Package ANSYS® 14.5 for Windows 7 (64-bit system) in a Dell Precision™ Workstation T7600 with 32 GB (4X8GB) and 1600 MHz. The multibody model was created in the MSC Software ADAMS® for Windows XP (64-bit system) and it is based on the input created by modal analysis performed in ANSYS.

Previous considerations of the applicability of this method are tested: Firstly, a static structural analysis is done using FEA and secondly, different solutions of MSD are obtained in function of the number of deformation modes used in the modal analysis. Comparison of the results clearly indicate that the number of deformation modes has an effect on the results accuracy: the higher the number of deformation modes used, the more accurate the results (cases 1B, 2B and 3B of Figure 1). Moreover, the addition of the web of beams in the models is demonstrated as a mandatory procedure because, without them, the accuracy of the results in front of the deformation modes are not assured (cases 1A, 2A and 3A of Figure 1 have more than a 20-50% of error with respect to the static analysis in FEA). The spider web of

beams is built to connect the areas of boundary conditions or forces with the interface point where the force or the boundary condition is applied. This method is recommended because force can be distributed over an area without the creation of mass elements and moments are properly transmitted from the interface point to the structure.

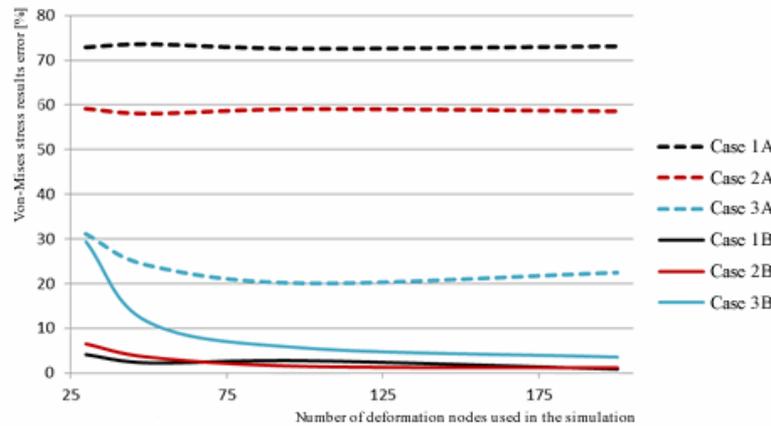


Figure 1 Average error with respect to the number of deformation modes used in the cases studied

Finally, the use of this approach is recommended for the study of feeding mechanisms in vertebrate structures when a dynamic analysis should be tested. It opens a wide range of possible new studies in the field of palaeontology and computational mechanics to improve the knowledge in the area of feeding mechanisms. Especially, that due to high numerical efficiency, the whole chewing process could be studied using FMSD without limiting the research to sole biting. In particular, several advances in the study of the feeding mechanism of the *Edingerella madagascariensis* are discussed according to its biological application using FMSD.

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