Techniques of modelling and simulation are discussed as they relate to bioengineering systems. The advantages and disadvantages of different analytical engineering methods utilized to gather information concerning the behavior of complex physiological and neuromuscular control mechanisms are explained. An Inners Criterion is developed to determine if the roots of a model lie within a certain "biologically realistic region" $\Gamma_b$, in the complex plane which contains the roots of linearized models for a large variety of neuromuscular systems. Several algorithmic methods based on the Jury Inners Test are described which specify whether the model roots lie within the desired region, thereby providing an indication as to the validity of the proposed model. This technique can help to eliminate tedious simulation on an unrealistic model with roots lying far outside this region. An exemplary model for control of vergence eye movements is presented and shown to satisfy the $\Gamma_b$ criterion; several counter-examples are also discussed. The Inners approach can be adapted to other classes of bioengineering systems by specifying the region based on models that are contained in the class of interest.

1. Bioengineering Modelling Process. This paper is directed toward elucidating a number of important features in modelling in bioengineering, putting forward a new physiological criterion for a class of bioengineering models which indicates when such models may be inaccurate or unrealistic, illustrating this criteria by means of a brief review of models of several kinds of physiological neuromuscular systems, and finally by working through the algorithm for a particular example.

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Modelling allows the researcher to create an approximation to the physical system based on its known structural and functional characteristics. In many cases, experimenting with an accurate model is less destructive, less time consuming, less difficult, and more useful than testing the actual system. Furthermore, in building the model, one is required to define the salient components of the original system and their inter-relationships and to neglect features which are not functionally significant since the model is by definition simpler than the system from which it was created. Frequently experimentation with the model yields interesting characteristics which may be immediately apparent in the original system when one examines it anew in light of modelling results. An example of such a sequence of events was presented by Stark and Cornsweet (1958) in their examination of the pupil. They used a pupil model to predict its natural oscillation and subsequently verified the result in the human pupil.

There are many techniques of modelling, and they are created utilizing varied analytical methods. System models are collections of functional blocks in which an input–output relationship is specified for each block as well as the interconnections between blocks. Transfer functions are typical input–output relationships for these blocks; this method does not attempt to explain the topology within a single entity. Circuit models attempt to define the interaction between single elements within a block, e.g., this technique would specify the inter-relationship between all elements whose overall behavior would yield a transfer function. Frequently it is impossible to define a model in this detail due to insufficient experimental evidence, so system models are more appealing and less demanding. Transient and frequency analysis are the two main ways in which information is gathered in order to create a systems model.

Most bioengineering models are constructed by first extracting essential system features from physiological and anatomical information. Unfortunately, many behavioral aspects of biological organisms are only partially known and not well defined; this problem causes the model to suffer in accuracy. Furthermore, the complexity of such systems with time delays and multiple paths of interaction which operate both in series and in parallel often yields a model which is difficult to analyze. Modelling is useful where an overall transfer function is not easily derived; however, the transfer functions of subcomponents can still be utilized, and a computer simulation often well represents the interactions of these subsystems. The resultant model may become unstable or contain unrealistic characteristics due to unknown interactions of the subcomponents.

Extensive simulations of unstable or biologically unrealistic models of neuromuscular systems may be avoided if a criterion can be developed to test the reasonableness of a proposed model. It is desirable, therefore, to develop a