

COORDINATES CHOICES IMPLICATIONS IN THE INVERSE DYNAMICS ANALYSIS OF HUMAN GAIT

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The inverse dynamic analysis of human locomotion requires that the motion of the human subject be known before it can be performed. Results required from analysis are the reaction forces at biomechanical joints and the articular moments, representing the lumped effects of the muscle forces at each joint. This work discusses the choice of coordinates upon which the biomechanical equations of motion are established. The position and orientation of a rigid body modeling a biomechanical segment can be described by a set of points and vectors, provided that the distance between the points and the angles between the vectors remain constant throughout the motion. The Cartesian coordinates of these points and vectors are known as natural coordinates. Alternatively, the rigid body can be represented by the position and orientation of a body fixed coordinate frame described by translational and angular coordinates. The coordinates obtained in this form are simply known as Cartesian coordinates. The three dimensional reconstruction process of human motion requires that a set of anatomical points be identified in the human subject. These must be chosen in such a way that the full three-dimensional motion of each biomechanical segment of the full biomechanical model can be reconstructed. Choosing the anatomical points to be the same as the points defining the rigid bodies by natural coordinates suggests that the information of the biomechanical model can help the reconstruction process. Moreover, when this process is completed, no coordinate transformation is required to perform the inverse dynamic analysis. However, in the use of natural coordinates points are shared by different rigid bodies at the joints. Though it is true that by sharing those points the number of coordinates used to model the system is greatly reduced, it is also true that the reaction forces between adjacent body segments are not generally available and can only be calculated during post-processing stages. When Cartesian coordinates are used in the biomechanical model, the relation between the translation and rotation coordinates of each body are described by kinematic constraints which represent the restriction of the relative motion between adjacent segments. The equations of motion of the biomechanical model include these constraints using the Lagrange multiplier technique. These Lagrange multipliers are directly related to the joint reaction forces and consequently are always available during the analysis. The major drawback of this choice of coordinates for inverse dynamic analysis in biomechanics is that the kinematic data required is in terms of position and orientation of the body-fixed coordinate frames. Consequently, a pre-processing stage is required to evaluate the data from the reconstructed spatial positions of the anatomical points. In the sequel of the discussion, numerical techniques to overcome the shortcomings of each formulation are presented.