

# A SINGLE-STEP SMOOTHING-DIFFERENTIATION PROCEDURE USING THE NEWMARK METHOD

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## INTRODUCTION

The estimation of derivatives of acquired displacement data plays a key role in kinematic and inverse dynamic analysis of biomechanical systems. This computation is obtained by double differentiation of displacement signals using a numerical approach. The procedure will largely amplify the high-frequency low-amplitude noise introduced by the motion capture system. The raw data differentiation problem is well known to be ill-posed in the sense that a small error in position data can induce a large error in the approximate derivatives [1].

## METHODS

In this work we propose the use of a numerical smoothing-differentiation scheme based on the Newmark integration method [2], widely applied in structural dynamics, as an alternative to the traditional digital filtering and spline smoothing methods currently used in biomechanics. This method introduces numerical dissipation so as to damp out the spurious high frequency responses, and provides the smoothing and differentiation of the displacement signal in a single step. This single-step integration formula constitutes a special category of finite difference methods profusely used in solving the multi-DOF second-order differential equations that appear in structural dynamics. The state vector of the system at a time  $t_{n+1} = t_n + h$ , where  $h$  is the incremental time step, is deduced from the already-known state vector at time  $t_n$ , through a Taylor expansion of the displacements and velocities. The following are the two basic equations proposed by Newmark [2] for determining displacements and velocities of the structure at time  $t_{n+1}$

$$\begin{aligned}\dot{\mathbf{q}}_{n+1} &= \dot{\mathbf{q}}_n + h[(1 - \gamma)\ddot{\mathbf{q}}_n + \gamma\ddot{\mathbf{q}}_{n+1}] \\ \mathbf{q}_{n+1} &= \mathbf{q}_n + h\dot{\mathbf{q}}_n + h^2 \left[ \left( \frac{1}{2} - \beta \right) \ddot{\mathbf{q}}_n + \beta \ddot{\mathbf{q}}_{n+1} \right]\end{aligned}$$

To determine the  $\gamma$  and  $\beta$  values that give a cutoff at a certain frequency, one must derive the frequency transfer function of the Newmark scheme. Naming  $\mathbf{q}_n = \mathbf{x}_n$ ,  $\dot{\mathbf{q}}_n = \mathbf{y}_n$  and  $\ddot{\mathbf{q}}_n = \mathbf{z}_n$ , the Newmark scheme can be expressed in the form:

$$\sum_{k=0}^L a_k z_{n-k} = \sum_{k=0}^M w_k x_{n-k}$$

Where  $a_k$ ,  $w_k$ ,  $L$  and  $M$  can be readily determined from the expressions above.

The frequency response function of this difference equation is:

$$H(f) = \frac{z(f)}{x(f)} = \frac{\sum_{k=0}^M w_k e^{-ik2\pi f}}{\sum_{k=0}^L a_k e^{-ik2\pi f}}$$

Here  $f$  is the dimensionless frequency  $f = f_c / f_s$ , where  $f_s$  is the sampling frequency and  $f_c$  is the cutoff frequency. A quantitative filtering criterion is to require that the acceleration to displacement gain  $|H(f)|$  be lower than a certain threshold, i.e. 0.1, above the selected cutoff frequency  $f_c$ .

## RESULTS AND DISCUSSION

The applicability of the Newmark method was tested on four kinematic signals with different characteristics. Two are well known signals taken from the literature on biomechanical signal filtering, and the other two were acquired with our own motion capture system.

## CONCLUSIONS

This work shows that the Newmark method produces results that are similar to those of traditional filtering techniques used in biomechanical analysis such as digital Butterworth filter and cross-validated splines, and advanced techniques such as Singular Spectrum Analysis (SSA). Our work uses the numerical dissipation of the Newmark method so as to damp out the high frequency amplification in the differentiation process. This is a key fact in the success of the method when it comes to extracting the latent trend in the signal from the random high-frequency noise inherent to the motion capture system. Moreover, the Newmark method provides the smoothing and differentiation of the displacement signal in a single step.

## REFERENCES

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