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KINEMATIC AND FORCE TRAJECTORY ANALYSIS USING VECTOR FIELD STATISTICS

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INTRODUCTION

Multi-dimensional kinematic and force trajectories can be described as vector processes $\boldsymbol{q}(t)$, where the components of $\boldsymbol{q}$ represent orthogonal joint rotations, force components, etc., and where time is commonly normalizable as: $0 \leq t \leq 100\%$ [1]. In the literature studies often aim to broadly examine changes in $\boldsymbol{q}(t)$ (e.g. the effects of running speed on stance-phase ground reaction forces), and often analyze the components of $\boldsymbol{q}(t)$ separately, and often at single instants in time.

One may alternatively regard $\boldsymbol{q}(t)$ as a bounded, continuous vector field, within which temporal smoothness arises naturally from biological tissue viscoelasticity. From this perspective $\boldsymbol{q}(t)$ is ideally suited to analysis using vector field statistics [2,3], for which the smooth, bounded continuum is the fundamental unit of observation.

The purpose of this study was to compare the results of separate-component and single-instant analyses with those of vector field analyses. We were particularly interested in discovering what features of $\boldsymbol{q}(t)$ could produce discrepancies between traditional and vector field results.

METHODS

Simple Simulation: A two-group two-component vector dataset (representing the maximum planar forces of patients vs. controls, for example) was constructed to demonstrate scalar vs. vector analyses (Fig.1). Results of (scalar) t tests on the individual components were compared with the results of a (vector) Hotelling's T^2 test; the latter reduces to the former for one-component vectors (i.e. scalars).

Dataset A: From a publicly available ten-subject dataset [4] three-dimensional stance-phase knee kinematics during side-shuffle and v-cut maneuvers were analyzed (Fig.2a). Two scalars were extracted: (i) maximum extension and (ii) knee ad-abduction, and differences between the side-shuffle and v-cut were assessed, as above, using univariate t tests. Vector field statistics were conducted by first computing the value of the Hotelling's T^2 statistic at each instant in time, next estimating vector field smoothness from the residuals using the average field gradient [5], and then determining the T^2 threshold above which only α=5% of the time nodes would be expected to reach from purely random (Gaussian) field variations of identical smoothness [3]; the threshold is depicted as a dotted line in Figs.2b and 3b. The statistical significance of supra-threshold temporal clusters was assessed using random field theory [2,3].

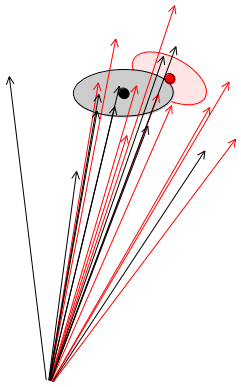

Figure 1: Simulated vector dataset. Dots:means. Covariance clouds: two principal axes standard deviations.

Dataset B: From a second publicly available dataset [6] the computed force trajectories from ten knee muscles of 16 Controls and 27 PatelloFemoral Pain (PFP) patients were analyzed (Fig.3a). Inter-group differences were assessed, as above, using both t tests (here on maximal forces) and a vector-field Hotelling's T2 test.

RESULTS AND DISCUSSION

Single-component analysis of the simulated dataset (Fig.1) yielded (t=1.926, p=0.070) and (t=0.808, p=0.430) for the horizontal and vertical components, respectively, and thus failed to reach both uncorrected (p<0.05) and Bonferroni-corrected (p<0.0253) thresholds. Vector analysis yielded T^2=4.810, p=0.042. Another *ad hoc* simulation could easily be constructed that shows the opposite: one of the single-component t tests reaches significance while the corresponding T^2 does not. It is thus clear that scalar analyses can misrepresent true vector behavior because they fail to consider inter-component covariance.

Dataset A (Fig.2a) yielded significant differences between side-shuffle and v-cut maneuvers for both maximal knee flexion (t=3.093, p=0.018) and abduction at 0% stance (t=3.948, p=0.006). Nevertheless, vector field analysis failed to reach significance (Fig.2b). This demonstrates *regional*

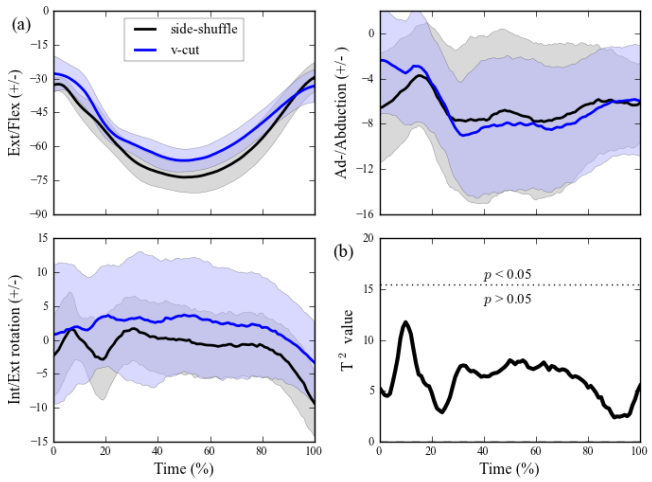

Figure 2: Dataset A. (a) Mean trajectories and st.dev. clouds. (b) Vector field analysis (Hotelling's T^2 trajectory).

focus bias: selecting only a small number of instants and/or only those that appear to differ..

Dataset B (Fig.3a) revealed that maximum medial gastrocnemius force was greater in PFP vs. Controls (t=2.617, p=0.013), but like the nine other muscles (t<1.91, p>0.063) failed to reach the Bonferroni threshold (p<0.0051 across ten muscles). In contrast vector field analysis found significance across essentially the entire trajectory (Fig.3b) (p<0.001). This discrepancy is explained by the large degree of correlation amongst the muscles (e.g. Semimem, Biceps – Fig.3a). That is, a failure to consider covariation amongst the muscles has led to an underestimation of the muscular differences between the groups.

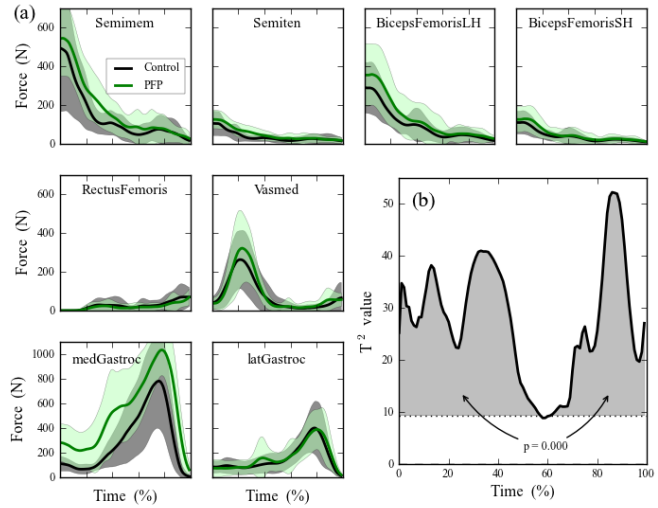

Figure 3: Dataset B. (presented as Fig.2).

CONCLUSIONS

Various sources of bias were discovered in the single-component and/or single-instant (i.e. scalar) analysis of vector trajectories. It was presently inferred that:

1. Separate-component analysis can bias results because it ignores covariance amongst the vector components, and:
2. Single-instant analysis can bias results because it reduces the trajectory to overly simplified scalars in a manner that is logically inconsistent with the original hypothesis.

These observations pertain to studies of time-normalizable vector trajectories in which specific *a priori* hypotheses are made regarding neither specific vector components nor specific time instants. In other words, single-component and/or single-instant analyses should be limited to cases of specific *a priori* hypotheses. We conclude that scalar extraction can introduce non-trivial, even catastrophic statistical basis during non-directed hypothesis testing of kinematic and force trajectories

ACKNOWLEDGEMENTS

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