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Vector field statistical analysis of kinematic and force trajectories

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ABSTRACT

When investigating the dynamics of three-dimensional multi-body biomechanical systems it is often difficult to derive spatiotemporally directed predictions regarding experimentally induced effects. A paradigm of 'non-directed' hypothesis testing has emerged in the literature as a result. Non-directed analyses typically consist of *ad hoc* scalar extraction, an approach which substantially simplifies the original, highly multivariate datasets (many time points, many vector components). This paper describes a commensurately multivariate method as an alternative to scalar extraction. The method, called 'statistical parametric mapping' (SPM), uses random field theory to objectively identify field regions which co-vary significantly with the experimental design. We compared SPM to scalar extraction by re-analyzing three publicly available datasets: 3D knee kinematics, a ten-muscle force system, and 3D ground reaction forces. Scalar extraction was found to bias the analyses of all three datasets by failing to consider sufficient portions of the dataset, and/or by failing to consider covariance amongst vector components. SPM overcame both problems by conducting hypothesis testing at the (massively multivariate) vector trajectory level, with random field corrections simultaneously accounting for temporal correlation and vector covariance. While SPM has been widely demonstrated to be effective for analyzing 3D scalar fields, the current results are the first to demonstrate its effectiveness for 1D vector field analysis. It was concluded that SPM offers a generalized, statistically comprehensive solution to scalar extraction's over-simplification of vector trajectories, thereby making it useful for objectively guiding analyses of complex biomechanical systems.

1. Introduction

Measurements of motion and the forces underlying that motion are fundamental to biomechanical experimentation. These measurements are often manifested as one-dimensional (1D) scalar trajectories $y_i(q)$, where i represents a particular physical body, joint, axis or direction, and where q represents 1D time or space. Experiments typically involve repeated measurements of $y_i(q)$ followed by registration (i.e. homologously optimal temporal or spatial normalization) to a domain of 0%–100% (Sadeghi et al., 2003). This paper pertains to analysis of registered data $y_i(q)$.

Given that many potential sources of bias exist in $y_i(q)$ analysis (Rayner, 1985; James and Bates, 1997; Mullineaux et al., 2001; Knudson, 2009), a non-trivial challenge is to employ statistical methods that are consistent with one's null hypothesis. Consider first 'directed' null hypotheses: those which claim response equivalence in particular vector components i, and in particular points q or windows $[q_0, q_1]$:

Example 'directed' null hypothesis: Controls and Patients exhibit identical maximum knee flexion during walking between 20% and 30% stance.

To test this hypothesis only maximum knee flexion should be assessed, and only in the specified time window. Testing other time windows, joints, or joint axes in a *post hoc* sense would constitute bias. This is because increasing the number of statistical tests increases our risk of incorrectly rejecting the null hypothesis (see Supplementary Material – Appendix A). In other words, it is biased to expand the scope of one's null hypothesis after seeing the data. We refer to this type of bias as '*post hoc* regional focus bias'.

Next consider 'non-directed' null hypotheses: those which broadly claim kinematic or dynamic response equivalence:

Example 'non-directed' null hypothesis: Controls and Patients exhibit identical hip and knee kinematics during stance phase.

To address this hypothesis both hip and knee joint rotations should be assessed, about all three orthogonal spatial axes, and from 0% to 100% stance (i.e. the entire dataset $y_i(q)$). It would be biased to assess only maximum hip flexion, for example, in a *post hoc* sense but for the opposite reason: it is biased to reduce the scope of one's null hypothesis after seeing the data.

Non-directed hypotheses expose a second potential source of bias: covariance among the I vector components. Scalar analyses ignore covariance and are therefore coordinate-system dependent (see Supplementary Material – Appendix B). This is important because a particular coordinate system — even one defined anatomically and local to a moving segment — may not reflect underlying mechanical function (Kutch and Valero-Cuevas, 2011).

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Joint rotations, for example, may not be independent because muscle lines of action are generally not parallel to externally defined axes (Jensen and Davy, 1975). Joint moments may also not be independent because endpoint force control, for example, requires coordinated joint moment covariance (Wang et al., 2000). Under a non-directed hypothesis this covariance must be analyzed because separate analysis of the I components is equivalent to an assumption of independence, an assumption which may not be justified (see Supplementary Material – Appendix B). We refer to this source of bias as ‘inter-component covariance bias’.

Both *post hoc* regional focus bias and inter-component covariance bias have been acknowledged previously (Rayner, 1985; James and Bates, 1997; Mullineaux et al., 2001; Knudson, 2009). However, to our knowledge no study has proposed a comprehensive solution.

The purpose of this paper is to show that a method called Statistical Parametric Mapping (SPM) (Friston et al., 2007) greatly mitigates both bias sources. The method begins by regarding the data $y_i(q)$ as a vector field $\boldsymbol{y}(q)$, a multi-component vector $\boldsymbol{y}$ whose values change in time or space q (Fig. 1). When regarding the data in this manner, it is possible to use random field theory (RFT) (Adler and Taylor, 2007) to calculate the probability that observed vector field changes resulted from chance vector field fluctuations.

We use SPM and RFT to conduct formalized hypothesis testing on three separate, publicly available biomechanical vector field datasets. We then contrast these results with the traditional scalar extraction approach. Based on statistical disagreement between the two methods we infer that, by definition, at least one of the methods is biased. We finally use mathematical arguments (Supplementary Material) and logical interpretations of the original data to conclude that scalar extraction constitutes a biased approach to non-directed hypothesis testing, and that SPM overcomes these biases.

2. Methods

2.1. Datasets

We reanalyzed three publicly available datasets (Table 1):

- Dataset A (Neptune et al., 1999) (http://isbweb.org/data/rrn/): stance-phase lower extremity dynamics in ten subjects performing ballistic side-shuffle and v-cut tasks (Fig. 2). Present focus was on within-subject mean three dimensional knee rotations for the eight subjects whose data were labeled unambiguously in the public dataset.

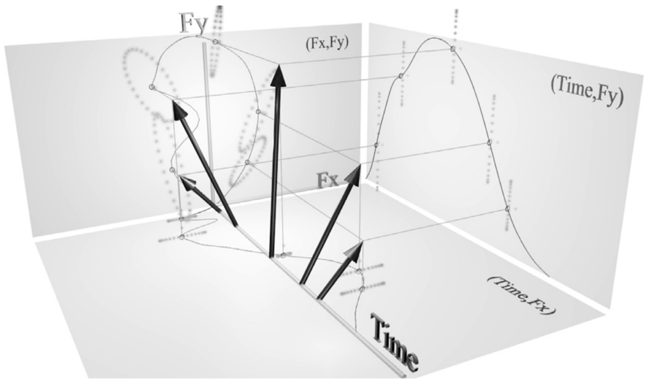

Fig. 1. Vector field schematic: a two-component vector varying in time. Depicted are mean ground reaction force (GRF) vectors $\boldsymbol{F} = [Fx,\ Fy]^\top$ from one subject during running (Dorn et al., 2012), where $+x$ and $+y$ represent the anterior and vertical directions, respectively. These vectors, when projected on the (*Time*, *Fx*) and (*Time*, *Fy*) planes, produce common GRF plots (see Fig. 4a, b); here vertical dotted lines depict standard deviation ‘clouds’. When $\boldsymbol{F}$ is projected on the (*Fx*, *Fy*) plane these standard deviations are revealed to arise from covariance ellipses, where ellipse orientation indicates the direction of maximum covariance between *Fx* and *Fy* (see Supplementary Material – Appendix B).

Table 1
Dataset and scalar extraction overview. I, J, Q and N are the numbers of vector components, responses, time points, and extracted scalars, respectively. For vector field analyses, *post hoc* scalar field analyses, and extracted scalar analyses we conducted one, I and N tests, respectively. Šidák thresholds of $p=0.0253$, $p=0.0170$ and $p=0.0051$ maintained a family-wise error rate of $\alpha=0.05$ across 2, 3, and 10 tests, respectively (see Eq. (1)).

	I	J	Q	N	Extracted scalars
Dataset A	3	8	101	2	(1) Max. flexion (at ~50% stance) (2) Ad-abduction at 0% stance
Dataset B	10	43	100	10	Max. force for each muscle ($J_1=16$, $J_2=27$)
Dataset C	3	8	100	3	(1) Max. propulsion force (GRF_x, ~75% stance) (3) Max. vertical force (GRF_y, ~30–50% stance) (3) Max. lateral force (GRF_z, ~15% stance)

- Dataset B (Besier et al., 2009) (https://simtk.org/home/muscleforces): stance-phase knee-muscle forces during walking and running in 16 Controls and 27 Patello-Femoral Pain (PFP) patients, as estimated from EMG-driven forward-dynamics simulations. Present focus was on walking and absolute forces (newtons) (Fig. 3).
- Dataset C (Dorn et al., 2012) (https://simtk.org/home/runningspeeds): one subject's full-body kinematics and ground reaction forces (GRF) during running at four different speeds: 3.56, 5.20, 7.00, and 9.49 ms^{-1}. Present focus was on three-dimensional left-foot GRF (Fig. 4), for which a total of eight responses were available. We linearly interpolated the GRF data across stance phase to $Q=100$ time points.

These three datasets were chosen, first, to represent a range of biomechanical data modalities: kinematics, modeled (internal) muscle forces, and external forces. Second, they were chosen to demonstrate how vector field analysis applies to a range of statistical tests: (A) paired t tests, (B) two-sample t tests, and (C) linear regression.

2.2. Traditional scalar extraction analysis

Two, ten, and three scalars were respectively extracted from the three datasets (Table 1). These particular scalars were chosen either because they appeared to be most affected by the experiment (Datasets A and C), or because they were physiologically relevant (Dataset B: maximum force). As indicated above, Dataset A's task effects were assessed using paired t tests, Dataset B's group effects were assessed using two-sample (independent) t tests, and Dataset C's speed effects were assessed using linear regression.

Since we conducted one test for each scalar, we performed $N=2$, $N=10$ and $N=3$ tests on Datasets A, B and C, respectively, where N is the number of extracted scalars. To retain a family-wise Type I error rate of $\alpha=0.05$ we adopted Šidák thresholds of $p=0.0253$, $p=0.0051$, and $p=0.0170$ respectively, where the Šidák threshold is

$$p_{\text{critical}} = 1-(1-\alpha)^{1/N} \tag{1}$$

These scalar analyses superficially appear to be legitimate analysis options. However, through comparison with the equivalent vector field analyses (Section 2.3), we will show how and why scalar extraction is biased for non-directed null hypothesis testing.

2.3. Statistical parametric mapping (SPM)

SPM analyses (Friston et al., 2007) were conducted using vector field analogs to the aforementioned univariate tests (Section 2.2). Before detailing SPM procedures, we note that they are conceptually identical to univariate procedures: conducting a one-sample t test on ten scalar values, for example, is nearly identical to conducting a one-sample t test on ten vector fields. The only differences are that SPM: (i) considers vector covariance when computing the test statistic, (ii) considers field smoothness and size when computing the critical test statistic threshold, and (iii) considers random field behavior when computing p values (see Appendix A and B – Supplementary Material).

Ultimately each SPM test results in a test statistic field (e.g. the t statistic as a function of time), and RFT is used to assess the significance of this statistical field. Sections 2.3.1–2.3.3 below detail test statistic field computations for the current datasets, Section 2.3.4 describes RFT computations of critical test statistic values