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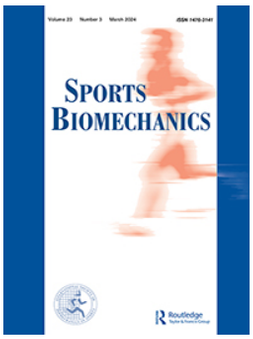

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Predicting elbow load based on individual pelvis and trunk (inter)segmental rotations in fastball pitching

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ABSTRACT

The baseball pitch is a repetitive, full-body throwing motion that exposes the elbow to significant loads, leading to a high incidence of elbow injuries. Elbow injuries in pitching are often attributed to high external valgus torques as these are generally considered to be a good proxy for the load on the Ulnar Collateral Ligament. The aim of the study is to contribute to elbow load monitoring by developing a prediction model based on the pelvis and trunk peak angular velocities and their separation time. Eleven male youth elite baseball pitchers (age 17 ± 2.2 years) threw 25 fastballs at full effort off a mound. Two-level varying-intercept, varying-slope Bayesian models were used to predict external valgus torque based on (inter) segmental rotation in fastball pitching with pitcher's weight and height added to strengthen the individualisation of the prediction. The results revealed the high predictive performance of the models including a set of kinematic parameters trunk peak angular velocity and the separation time between the pelvis and trunk peak angular velocities. Such an approach allows individualised prediction of the external valgus torque for each pitcher, which has a great practical advantage compared to group-based predictions in terms of injury assessment and injury prevention.

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KEYWORDS
External valgus torque; baseball; injury prevention; UCL injuries; kinetic chain

Introduction

The baseball pitch is a full-body throwing motion that, due to its repetitive nature, exposes the elbow to significant loads (Fleisig et al., 1995; Seroyer, Nho, Bach, Bush-Joseph, et al., 2010b). This leads to a high incidence of overused elbow injuries among baseball pitchers at all levels of play (Chen et al., 2001; Erickson et al., 2015; Fleisig & Andrews, 2012). The injury aetiology seen in youth and adult pitchers has been linked to high elbow external valgus torques (Aguinaldo & Chambers, 2009; Chen et al., 2001; Wilson et al., 1983). The external valgus torque imparts a tensile force to the medial elbow structures (Cain et al., 2003; Safran et al., 2005), which in combination with

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repetitive loading results in injuries to the medially located ulnar collateral ligament (UCL). This indicates that external valgus torque can be used as a proxy of elbow load (Anz et al., 2010; Fortenbaugh et al., 2009). Thus, continuous and prospective elbow load monitoring, both in training and in game, plays an essential role in pitchers' performance enhancement whilst minimising the risk of elbow injuries (Vanrenterghem et al., 2017).

To assess the external valgus torque, it is important to understand pitching mechanics. Pitching mechanics can be described by the two well-known biomechanical principles; the summation of speed principle, also known as the kinetic chain, and the principle of optimal coordination of partial momenta (Putnam, 1993). Both principles consider the human body as a linked segment model and explain the biomechanics of pitching in terms of peak angular velocities of body segments and their intersegmental timing. Overhead throwing motion, such as baseball pitching, is more likely to follow the kinetic chain (Putnam, 1993). Regardless of the principle, the high end-point velocities imparted to the ball depend on the contribution of all segments (Leenen et al., 2022).

In the pitching motion, energy is generated in the driving leg and transferred through the stride leg to the pelvis (de Swart et al., 2022). While part of the energy in the pelvis is transferred back to the stride leg to form a stable base around which the pelvis and trunk can rotate (A. Aguinaldo & Nicholson, 2022), most energy is transferred via the trunk up to the throwing arm (Seroyer, Nho, Bach, Bush-joseph, et al., 2010a). In such complex sequential movement, pelvic and trunk kinematics play an essential role in transferring the momentum generated by the lower extremities to the upper extremity. Optimal proximal-to-distal timing between the pelvis and trunk results in the maximised ball velocity at the most distal end (Putnam, 1993; Seroyer, Nho, Bach, Bush-Joseph, et al., 2010b). The timing between the pelvis and trunk peak angular velocities is also referred to as separation time. If this kinematic sequencing or timing is not optimal, energy is dissipated into the upper extremity which results not only in decreased ball velocity (Putnam, 1993; van der Graaff et al., 2018), but also the potentially increased risk of injuries (Urbin et al., 2013).

Manipulation of biomechanical parameters within the kinetic chain may affect the external valgus torque and help in managing the risk of excessive UCL loading. By increasing trunk peak angular velocity, pitchers may throw faster, but with an increased external valgus torque (Cohen et al., 2019). There is likely a threshold above which the exceeded external valgus torque represents a significant injury risk. The efficiency of the kinetic chain may contribute to the reduction of external valgus torque levels at this critical point while still maintaining high levels of ball speed and overall pitching performance (Anz et al., 2010).

We expect that the levels of external valgus torque will differ between pitchers due to variations in anthropometric measures, pitching technique, level of play, and within-individual load variability (Fleisig et al., 1999; Van Trigt et al., 2022). Multilevel modelling is well-suited for the analysis of repeated measurements that are considered to be 'clustered' within individual pitchers (Gomaz et al., 2021). Such measurements are assumed to be independent as the observations within a cluster are more likely to be similar than observations from different clusters. Since regression- and ANOVA-based techniques do not meet this assumption, they are not fully appropriate for dealing with this type of data structure. Multilevel modelling techniques for repeated measurements allow us to analyse

the relationships between data collected at the pitcher- or group-level, and data collected on variables that change with trials at the unit- or individual-level (Cornelius et al., 2007).

The aim of the study is to contribute to monitoring the external valgus torque in baseball pitching by developing a prediction model based on the pelvis and trunk peak angular velocities and their separation time. It is hypothesised that external valgus torque for an individual pitcher can be predicted based on the pelvis and trunk peak angular velocity and separation time between them. In addition, we expect that the model including both pelvis and trunk peak angular velocity and their separation time will have the best predictive performance.

Materials and methods

Participants

Eleven male Dutch national (AAA) youth elite baseball pitchers participated in the study, with a mean age of 17.4 (±2.2) years, mean body mass of 80.6 (±11.7) kg, mean body height of 1.86 (±6.3) m and mean ball speed was 34.0 ± 1.4 m/s (76.6 ± 3.2 mph). Only participants without present musculoskeletal injuries and who did not have musculoskeletal injuries in the last 6 months were included in this study. Participants gave written consent to use the data information for analysis and publication after being fully informed. If participants were under 16 years, their parents or guardians were informed about the study and required to sign an informed consent form. This research was conducted as part of a larger study (Van Trigt et al., 2022) and was performed in accordance with the Declaration of Helsinki and the local ethics committee. The local ethics committee of the Faculty of Behavioral and Movement Sciences (VCWE) approved the study protocol (reference number: VCWE2019–033).

Procedure

Data collection was performed in an indoor movement laboratory at the Royal Netherlands Football Association. The participants wore sneakers, athletic stretch shorts, catching gloves, and no shirts. Forty-three reflective markers were attached with double-sided tape on the bony landmarks. Participants performed their regular warming-up, which contained stretching, drills, and several warming-up pitches. Subsequently, they threw several pitches from the mound to become familiar with the research setup. The participants were instructed to throw 25 fastball pitches at full effort towards a squared strike zone (height 0.64 m; width 0.38 m). The pitching rubber was attached to the top of the mound at 0.55 m above the ground and had a distance of 18.44 m to the home plate. The time between each pitch was not controlled but regulated by the pitcher himself, like in a normal game.

Data acquisition

Full body position data of the pitchers were collected with a VICON eight-camera motion capture system. Data were sampled at 400 Hz (model V5; Vicon Motion

Systems Ltd., Yarnton, UK). The ball speed was measured with a radar gun positioned next to the strike zone (Stalker Radar, Plano, TX, USA).

Data processing

Three-dimensional position data of the fourteen bony landmarks were used in this study (Table 1). The position data were interpolated with a third-order cubic spline polynomial and filtered with a fourth-order Butterworth filter with a cut-off frequency of 12.5 Hz. To calculate the segment angular velocities and the elbow valgus torque an anatomical coordinate system was constructed for the pelvis, trunk, upper arm, forearm, and hand according to the ISB recommendations (Wu et al., 2005).

The segment angular velocities were computed directly from the rotation matrices following the method described in the study of Zatsiorsky (Zatsiorsky, 2002). Subsequently, the Euclidean norm was calculated over all three different axes. The exact moments of peak angular velocities were found analytically by fitting a second-order polynomial function to 11 measured data points. These data points included five samples before and after the samples closest to the maximum angular velocity. The separation time was calculated as the time interval between the pelvis and trunk peak angular velocities (van der Graaff et al., 2018).

Elbow joint torques were calculated based on the top-down method using the Newton-Euler equation of motion, starting in the hand of the throwing arm. The segment centre of mass position and the moments of inertia were estimated according to Zatsiorsky (2002) and de Leva, (1996). The baseball was modelled with a mass of 0.145 kg attached to the hand. The mass linearly reduced by 10% over the last ten samples (0.025 s) before ball release. Ball release was defined as the moment the wrist exceeded the position of the elbow in the forward direction. The elbow joint coordinate system was expressed in the anatomical coordinate system of the forearm, located in the middle between the medial and lateral humeral epicondyle. The time series of external elbow valgus torque was determined for each individual pitch, covering the duration from foot contact to ball release. Subsequently, the peak external valgus torque was derived from this time series data. The time series of the segment angular velocities and external valgus torque were visually checked for errors and mistakes.

Table 1. Bony landmarks used in the study.

Marker number	Bony landmarks
1	Third proximal interphalangeal*
2	Ulnar process styloid
3	Radial process styloid
4	Lateral humeral epicondyle**
5	Medial humeral epicondyle
6	Acromion
7	Xiphoid process
8	Incisura jugularis
9	7th cervical vertebrae
10	8th thoracal vertebrae
11& 12	Left and right anterior superior iliac spine
13 &14	Left and right posterior superior iliac spine

Statistical methods and modelling

For the i-th throw, let y_i, x_{i1}, x_{i2}, x_{i3}, x_{i4} and x_{i5} denote the external valgus torque, pelvis peak angular velocity, trunk peak angular velocity, separation time, weight and height respectively. Set $x_i = (x_{i1}, x_{i2}, x_{i3})$ and $u_i = (x_{i4}, x_{i5})$. We aim to model the relationship between y_i and (x_i, u_i). The simplest type of model for this is the linear model given by

$$y_i|\beta_0, \beta, \sigma^2 \overset{\text{ind}}{\sim} \mathcal{N}\left(\beta_0 + \beta' x_i + \gamma' u_i, \sigma^2\right) \tag{1}$$

where the symbol $\overset{\text{ind}}{\sim}$ denotes 'independently distributed as'.

However, note that the data from repeated measurements such as in this study have the structure in which observations on an individual level (pelvis and trunk peak angular velocities, separation time, external valgus torque) are nested within baseball pitchers on a group level. As such, a simple linear model like Equation (1) will not be able to take into account that throws by the same pitcher tend to be more similar than throws by different pitchers. This phenomenon is illustrated in Figure 1, where we have also included weight and height to see how external valgus torque is affected by these characteristics.

This figure strongly suggests a *two-level linear model, with both varying intercepts and varying slopes*. The need for such a model is most easily seen from the panel with 'Trunk PAV'. If we would fit a single line through the data, this would imply a negative relationship between external valgus torque and trunk peak angular velocity (Trunk PAV), whereas for each individual player, this relationship is positive. This can be seen as an instance of Simpson's paradox, well known in statistics. Specifically, we propose the following model:

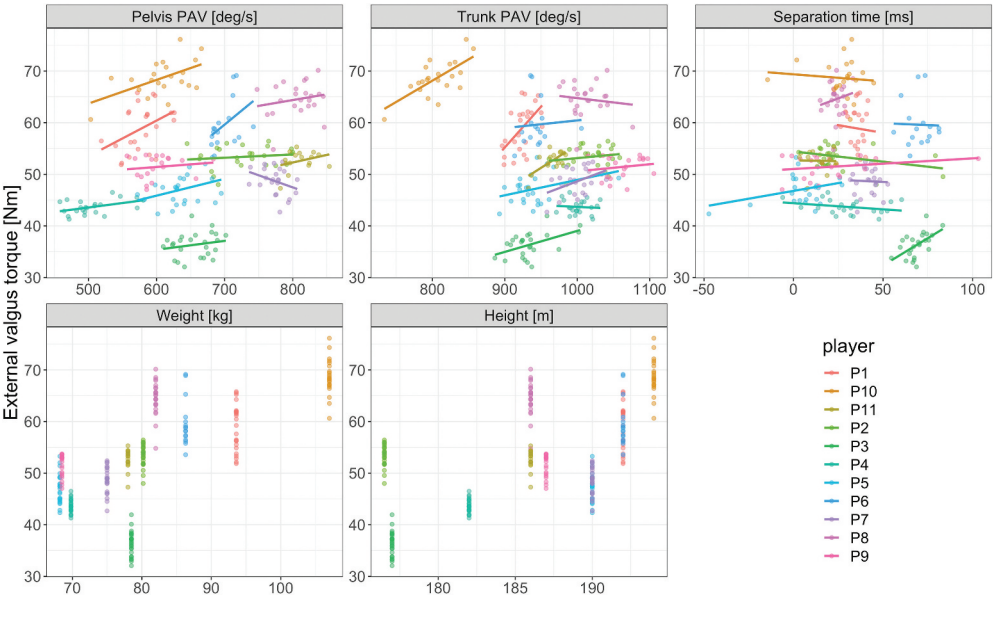

Figure 1. Exploratory data analysis for the relation between external valgus torque and pelvis peak angular velocity (Pelvis PAV), trunk peak angular velocity (Trunk PAV) and Separation time. In each subpanel, the influence of one predictor on external valgus torque is displayed. In the upper three panels, least-squares fits have been superimposed (separately, for each player).

$$y_i|\alpha_1,\ldots,\alpha_J,\beta_1,\ldots,\beta_J,\sigma^2 \overset{\text{ind}}{\sim} \mathcal{N}\left(\mu_i+\gamma' u_i,\sigma^2\right) \tag{2}$$

$$\mu_i = \alpha_{j[i]} + \beta'_{j[i]} x_i$$

We have $J = 11$, the total number of pitchers in the study, and $j[i] = k$ if the i-th throw corresponds to j-th pitcher in the dataset. We follow the Bayesian approach to statistics, where unobserved quantities get assigned a prior distribution, reflecting the (lack of) information we have about their values before collecting the data. We impose $\alpha_1,\ldots,\alpha_J \overset{\text{iid}}{\sim} \mathcal{N}\left(0,\sigma_\alpha^2\right)$, $\beta_1,\ldots,\beta_J \overset{\text{iid}}{\sim} \mathcal{N}_3\left(0,\sigma_\beta^2 I_{3\times 3}\right)$ and $\gamma \sim \mathcal{N}\left(0,\sigma_\gamma I_2\right)$. The symbol $\overset{\text{iid}}{\sim}$ denotes 'independent and identically distributed as'. We took default values from rstanarm (version 2.21.1) (Goodrich et al., 2020), which means $\sigma_\alpha = \sigma_\beta = \sigma_\gamma = 2.5$. Taking mean-zero priors is justified as we standardised (i.e., transformed to zero-mean and unit standard deviation) each of the predictors before fitting the model. Also for σ, σ_α and σ_β we took the default prior mean-one Exponential distribution from rstanarm (Goodrich et al., 2020).

We used leave-one-group-out cross-validation (LOGO-CV) to select the model with the best predictive performance. LOGO-CV is a specific type of k-fold cross-validation that utilises data from each individual pitcher as a test set. The number of folds, therefore, equals the number of pitchers. For every fold, the model is trained on data from J-1 pitchers and tested on the data from the one left-out pitcher. Models were compared according to their expected log-predictive density (*elpd*) as described in the work of Vehtari (Vehtari, Simpson, Gelman, Yao, & Gabry, 2015; Vehtari et al., 2017).

We used posterior predictive distributions to generate data samples whose average is then compared to the real data. We interpret the generated data as the data sample that we might collect tomorrow if the data collection process remains the same as it initially was. Posterior predictive checks were used to test the performance of the model and visually inspect how much generated data samples match the observed ones.

Results

A total of 240 throws by 11 pitchers were included in the analysis. The number of pitches varied from 19 to 25 throws per pitcher. Descriptive statistics of included variables are shown in Table 2.

Expected log-predictive density *(elpd)* was a chosen measure of model fit and it was subsequently used to compare models for model selection. The difference in *elpd* of the fitted two-level varying-intercept, varying-slope Bayesian models is

Table 2. Descriptive statistics for the variables included in the analysis.

Variables	Mean ± Standard Deviation
Pelvis peak angular velocity [deg/s]	669.87 ± 99.06
Trunk peak angular velocity [deg/s]	964.85 ± 68.61
Separation time [ms]	32.70 ± 22.98
Weight [kg]	80.47 ± 11.11
Height [m]	186.26 ± 5.85
External valgus torque [Nm]	52.76 ± 9.59

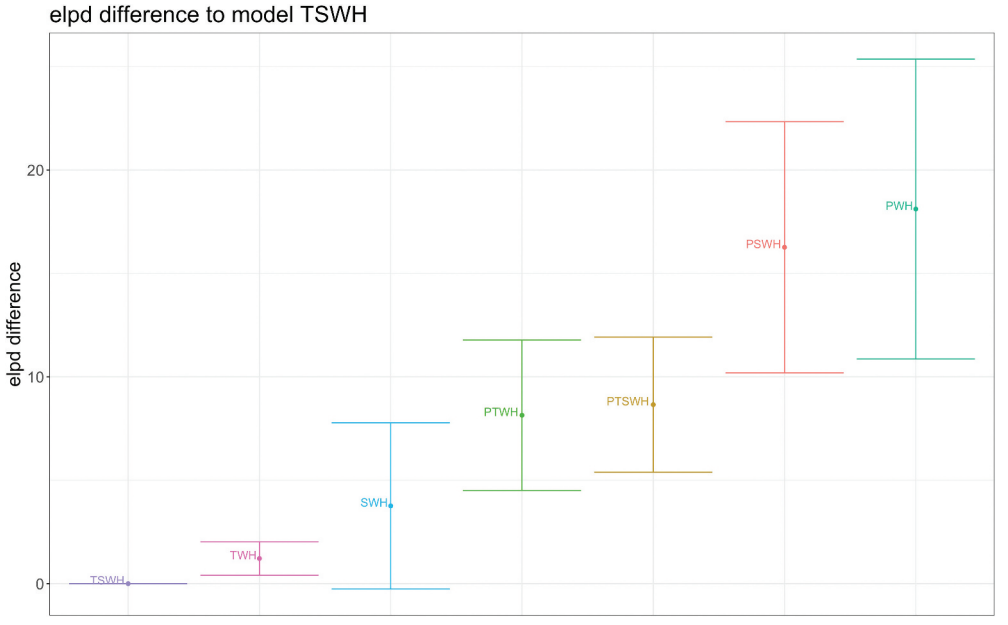

Figure 2. Estimates of absolute elpd difference (dot) using leave-one-group-out cross-validation. Vertical error bar for each model indicates the standard error of the elpd difference estimates. The order on the x-axis follows the ranking starting with the model with best predictive performance on the left. Predictors included in the analysis are pelvis peak angular velocity (P), trunk peak angular velocity (T), separation time (S), pitcher's weight (W) and height (H).

shown in Figure 2. Models include various combinations of observed kinematic predictors (P—pelvis peak angular velocity, T—trunk peak angular velocity, S—separation time) with the addition of pitcher's weight (W) and height (H) to all the models. The ordering of the models in Figure 2 reveals that the model including a set of predictors TSWH showed the best predictive performance, and it is therefore the selected model. Table 3 shows parameter estimates from the selected model TSWH, based on a table generated by shinystan (Gabry, 2018). The small *elpd* differences between the selected model TSWH and the second ranked model TWH indicate almost similar performance in predicting external valgus torque.

The performance of the final model TSWH was tested through a posterior predictive check. In Figure 3 the average of the data samples generated from the posterior predictive distributions is compared to the observed data. If the model is a good fit for the data, then observed and simulated data should be aligned. The posterior predictive check shows that the observed data are more dispersed compared to the average of the generated data samples from the posterior predictive distributions. Bayesian conditional R^2 value is 0.916 (95% CI [0.899, 0.931]), and marginal R^2 value 0.927 (95% CI [0.847, 0.969]), where CI is a confidence interval. The marginal R^2 considers only the variance of the fixed effects, while the conditional R^2 takes both the fixed and random effects into account (Gelman et al., 2019).

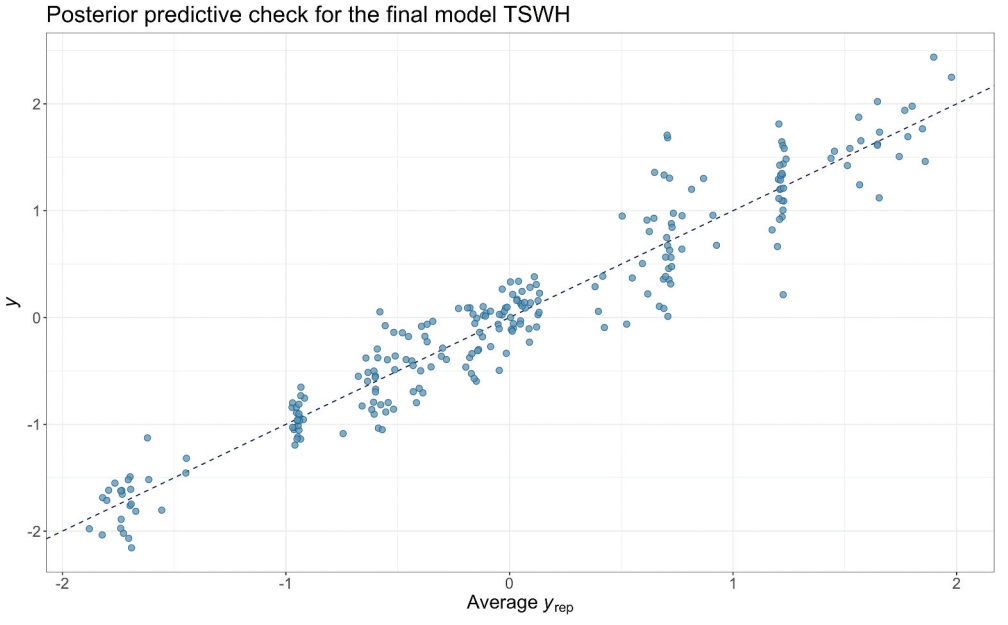

Figure 3. Posterior predictive checks compare the observed outcome variable y to the average of simulated datasets y_rep from the posterior predictive distribution for the selected model TSWH. The model includes a set of predictors of trunk peak angular velocity (T), separation time (S), pitcher's weight (W), and height (H). Bayesian conditional R^2 value is 0.916 (95% CI [0.899, 0.931]), and the marginal R^2 value 0.927 (95% CI [0.847, 0.969]), where CI is a confidence interval. The marginal R^2 considers only the variance of the fixed effects, while the conditional R^2 takes both the fixed and random effects into account (Gelman et al., 2019).

Discussion and implications

Poor pitching mechanics (Davis et al., 2009) and overloading of the pitching arm can negatively affect pitching performance and at the same time put the elbow joint at great risk of injuries (Fleisig et al., 2006; Fortenbaugh et al., 2009). Therefore, estimation of the external valgus torque based on pitching mechanics is an important step towards monitoring the elbow load in the field. This study shows promising results of Bayesian hierarchical models in the prediction of the external valgus torque, used as a proxy of elbow load, based on (inter)segmental rotation in fastball pitching.

The results show that it is possible to predict the elbow external valgus torque based on the pelvis and trunk kinematics and separation time. Although it was hypothesised that the model including all three parameters would have the best performance, according to LOGO-CV the best predictive model is TSWH which includes peak trunk angular velocity, separation time, weight, and height (Bayesian conditional R^2 value is 0.916, marginal R^2 value is 0.927). The reason why the pelvis angular velocity was not included in the final model might be explained by the fact that the trunk angular velocity contains information from the proximal pelvis segment according to the proximal-to-distal sequence. The contribution of the separation time to the prediction of the external valgus torque indicates the importance of optimal timing between the pelvis and trunk segments in the kinetic chain for safe and efficient pitching. However, it is yet unknown what the

'optimal' separation time is. The results in this study showed that certain pitchers exhibited a positive correlation between separation time and external valgus torque, while others demonstrated a negative or no correlation (Figure 1). Oyama et al. (2014) did not find a relationship between the separation time and external valgus torque on group level. This might indicate that the optimal timing is individually depended, with the proviso that the pelvis and trunk are in sequence. The trunk can produce a lot of power due to its segmental mass, although proper timing is needed for optimal contribution to the ball speed (A. Aguinaldo & Escamilla, 2019; Naito et al., 2014). The increase in trunk rotation does not only increase the ball speed, but it increases the external valgus torque as well (Cohen et al., 2019). In line with our results, several studies showed a relationship between trunk kinematics and the external valgus torque (A. L. Aguinaldo & Chambers, 2009; A. Aguinaldo & Escamilla, 2019; Cohen et al., 2019). In addition, we showed that it is possible to predict the external valgus torque for individual pitchers based on their trunk peak angular velocity and the separation time.

Predictions of the external valgus torque based on the trunk peak angular velocity and the separation time are important in relation to elbow injuries. Manipulation of these biomechanical parameters with training increases the ball speed (van der Graaff, 2019) and may decrease the external valgus torque (Cohen et al., 2019). However, a pitcher throwing according to an optimal kinetic chain, with a reduced level of external valgus torque is still at risk of sustaining an injury due to repetitive pitching. Therefore, monitoring the external valgus torque is important for managing the risk of excessive elbow loading. Taking into account that the values of external valgus torque vary among pitchers of different ages, levels of play (Fleisig et al., 1999), and the variability within-individual pitchers (Van Trigt et al., 2022), understanding the elbow loading for each pitcher based on his individual characteristics and pitching mechanics may be the base for the development of an 'early warning system' for safe and efficient pitching.

This paper introduces the application of Bayesian hierarchical models to repeated measurements of pitching kinematic and temporal parameters. Such models account for the within-pitcher similarity and at the same time allow for the gradation of differences between the pitchers in the prediction of the external valgus torque. The small difference in *elpd* between the selected model TSWH and the model TWH ranked second in terms of LOGO-CV refers to their similar predictive performance (Figure 2). In addition, posterior predictive checks reveal similar model fit for the TWH model compared to the TSWH model. From the practical point of view, this means that monitoring external valgus torque is already possible based on the single kinematic variable (trunk peak angular velocity). However, the separation time is related to the efficiency of the kinetic chain and its breakdown may be an indicator of the fatigue (Erickson et al., 2016). Therefore, considering the practical relevance of both parameters for elbow load monitoring over a longer period, we select the predictive model including trunk peak angular velocity and separation time as the final one. The comparison between the Bayesian and frequentist approach to multilevel analysis and fitting the final TSWH model is discussed in the Appendix.

One of the limitations of this study is the inclusion of only fastball pitches. Studies have shown that the elbow load is lower in the change-up or breaking balls (Fleisig et al., 2016); however, the link between the torso kinematics and elbow load has not been investigated yet. Furthermore, the current study had

a very low sample size ($n = 11$) and included repeated measurements from a single data collection event. The low sample size could affect Bayesian mixed models in terms of overfitting and imprecise inferences. However, the selected model performance criteria based on *elpd* can help mitigate these issues. The lack of longitudinal data collection limits the detection of patterns in elbow loading based on pitching mechanics. A larger data sample including a wider range of age groups and levels of play may improve the predictive performance and lower the uncertainty in predicted external valgus torque. Collecting longitudinal data, including reported injuries, would allow us to link the loading on the elbow joint to injury occurrence in individual pitchers. This information can be used as a base for setting a pitcher's injury threshold. If the elbow loading exceeds the estimated threshold, the pitcher will likely have increased injury risk. Such information may help coaches in training subscription and modification of the pitching technique that leads to reducing the external valgus torque and therefore the risk of elbow injury.

The final model proposed in this paper considered the practical relevance of trunk kinematics and separation time between the pelvis and trunk in managing injury risk and shows its potential utilisation for elbow load monitoring on the field. Trunk peak angular velocity and the separation time can be recorded with wearable sensors, like inertial measurement units (Gomaz et al., 2021; Lapinski et al., 2019). Such data recorded with sensors may be used as input for the proposed model and provide actionable insight for injury prevention in baseball pitching.

Conclusion

In this study, a model has been proposed to predict elbow load based on the pelvis and trunk peak angular velocities and separation time between them. Application of Bayesian hierarchical models on data including the trunk peak angular velocity and the separation time between the pelvis and trunk peak angular velocities show promising results for the prediction of the external valgus torque in fastball pitching. Such an approach allows individualised prediction of the external valgus torque for each pitcher, which has a great practical advantage compared to group-based predictions in terms of injury assessment and injury prevention.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Appendix

In the Appendix we compare the outcome of the multilevel linear model fitted within frequentist framework with the outcome of the Bayesian hierarchical model presented in the paper.

We used a frequentist approach to fit the final model (TSWH) including trunk peak angular velocity, separation time, pitcher's weight, and height as predictors. The analysis was performed using the lme4 R package (version 1.1.26). When fitting a multilevel model within the frequentist framework using the lme4 package, parameter estimation is done by performing restricted maximum likelihood (REML) estimation. The extended summary including corresponding p-values from the lmerTest R package is listed in Figure A1.

The residual within-pitcher standard deviation is estimated as 0.28620. The estimated standard deviations of the pitcher intercepts are 0.58907. The estimated standard deviations of the pitcher slope for *Trunk_PAV* and *Separation_Pelvis_Trunk* are 0.37041 and 0.03299 respectively. The fixed regression slopes for *Weight* and *Height* are significant, meaning taller and heavier pitchers have higher external valgus torque. The error term (Variance) for the slope of *Trunk_PAV* is 0.137205 and for the slope of *Separation_Pelvis_Trunk* is 0.001088.

Unlike the frequentist approach, the Bayesian approach accounts for all the uncertainty in the parameter estimates when predicting varying intercepts and slopes. We used rstanarm R package (version 2.21.1) to obtain simulations that summarize uncertainty about coefficients and predictions. Bayesian estimation is performed via Markov Chain Monte Carlo (MCMC) estimation approach whose each step involves random draws from the parameter space.

The summary of the final TSWH model whose parameter estimates are listed in Table 3 is shown in Figure A2.

The estimated standard deviations of the pitcher intercepts are 0.626, which is larger than the ML estimate (0.58907). The estimated standard deviations of the pitcher slopes for *Trunk_PAV*

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Elbow_Adduction_MER ~ 0 + (1 | Participant) + (0 + Trunk_PAV +
    Separation_Pelvis_Trunk | Participant) + Weight + Height
   Data: dT

REML criterion at convergence: 148.5

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.5323 -0.5629  0.0464  0.5520  3.5031

Random effects:
 Groups        Name                    Variance Std.Dev. Corr
 Participant   (Intercept)             0.347006 0.58907
 Participant.1 Trunk_PAV               0.137205 0.37041
               Separation_Pelvis_Trunk 0.001088 0.03299  -1.00
 Residual                              0.081909 0.28620
Number of obs: 240, groups:  Participant, 11

Fixed effects:
       Estimate Std. Error      df t value Pr(>|t|)
Weight   0.8200     0.2114 10.1735   3.879  0.00297 **
Height   0.3935     0.2087  8.6233   1.886  0.09337 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
       Weight
Height -0.408
```

Figure A1. Outcome of the linear mixed-effects TSWH model using R package lme4. TSWH model includes following set of predictors: trunk peak angular velocity, separation time between pelvis and trunk peak angular velocity, pitcher's weight and height.

and *Separation_Pelvis_Trunk* are 0.353 and 0.092, both larger than the ML estimates (0.37041 and 0.03299 respectively).

The difference in estimates between frequentist and Bayesian approaches lies in the difference in estimation approaches. While lme4 uses in this case restricted maximum likelihood (REML) estimation, rstanarm performs full Bayesian inference via MCMC. REML tends to underestimate uncertainties due to relying on point estimates of hyperparameters. On the other hand, the Bayesian approach propagates the uncertainty in the hyperparameters throughout all levels of the model (Goodrich et al., 2020).

The advantage of multilevel models fitted within the Bayesian framework is a specification of prior distributions over the regression coefficients and any unknown covariance matrices. This can help in stabilizing computation as well as in incorporating important information into the analysis that is not included in the data.

One of the limitations of multilevel models fitted with rstanarm compared to lme4 is the computation speed. Fitting models with REML tends to be much faster than fitting a similar model using MCMC.

Table 3. Parameter estimates for the final model TSWH. Predictors are trunk peak angular velocity (Trunk_pav), separation time (separation), pitcher's weight (weight) and height (height). The standard deviation of the errors is called sigma and the variance-covariance matrix of the pitcher-specific deviations from the common parameters is called sigma.

	mean	sd	2.5%	25%	50%	75%	97.5%
Weight	0.8	0.2	0.3	0.6	0.8	0.9	1.2
Height	0.4	0.2	0	0.3	0.4	0.5	0.8
b [(Intercept) Participant: P1]	−0.3	0.3	−0.8	−0.4	−0.3	−0.1	0.3
b [(Intercept) Participant: P10]	0.3	0.5	−0.6	0	0.3	0.6	1.2
b [(Intercept) Participant: P11]	0.2	0.1	−0.1	0.1	0.2	0.2	0.4
b [(Intercept) Participant: P2]	0.6	0.4	−0.1	0.4	0.6	0.9	1.4
b [(Intercept) Participant: P3]	−0.8	0.4	−1.5	−1	−0.8	−0.6	−0.1
b [(Intercept) Participant: P4]	0.1	0.2	−0.4	−0.1	0.1	0.2	0.5
b [(Intercept) Participant: P5]	0.1	0.3	−0.5	−0.1	0.1	0.3	0.8
b [(Intercept) Participant: P6]	0	0.2	−0.5	−0.2	−0.1	0.1	0.4
b [(Intercept) Participant: P7]	−0.4	0.2	−0.9	−0.6	−0.4	−0.3	0
b [(Intercept) Participant: P8]	1.1	0.1	0.9	1.1	1.1	1.2	1.4
b [(Intercept) Participant: P9]	0.5	0.3	−0.1	0.3	0.5	0.7	1.1
b [Trunk_PAV Participant: P1]	0.7	0.3	0.2	0.5	0.7	0.8	1.2
b [Separation Participant: P1]	0	0.1	−0.3	−0.1	0	0	0.2
b [Trunk_PAV Participant: P10]	0.4	0.1	0.1	0.3	0.4	0.5	0.7
b [Separation Participant: P10]	0	0.1	−0.2	−0.1	0	0	0.1
b [Trunk_PAV Participant: P11]	0.3	0.2	−0.1	0.1	0.3	0.5	0.8
b [Separation Participant: P11]	0	0.1	−0.2	−0.1	0	0	0.2
b [Trunk_PAV Participant: P2]	0.1	0.1	−0.2	0	0.1	0.2	0.4
b [Separation Participant: P2]	0	0.1	−0.2	−0.1	0	0	0
b [Trunk_PAV Participant: P3]	0.3	0.1	0	0.2	0.2	0.3	0.5
b [Separation Participant: P3]	0	0.1	−0.2	0	0	0	0.2
b [Trunk_PAV Participant: P4]	0	0.2	−0.4	−0.1	0	0.1	0.4
b [Separation Participant: P4]	0	0.1	−0.1	−0.1	0	0	0.1
b [Trunk_PAV Participant: P5]	0.2	0.1	−0.1	0.1	0.2	0.2	0.4
b [Separation Participant: P5]	0	0.1	−0.1	0	0	0.1	0.2
b [Trunk_PAV Participant: P6]	0.1	0.2	−0.3	−0.1	0.1	0.2	0.5
b [Separation Participant: P6]	0	0.1	−0.2	0	0	0	0.1
b [Trunk_PAV Participant: P7]	0.2	0.2	−0.1	0.1	0.2	0.4	0.6
b [Separation Participant: P7]	0	0.1	−0.2	−0.1	0	0	0.1
b [Trunk_PAV Participant: P8]	0	0.2	−0.3	−0.1	0	0.1	0.3
b [Separation Participant: P8]	0	0.1	−0.1	0	0	0	0.2
b [Trunk_PAV Participant: P9]	0.1	0.1	−0.2	0	0.1	0.2	0.4
b [Separation Participant: P9]	0	0	−0.1	0	0	0	0.1
sigma	0.3	0	0.3	0.3	0.3	0.3	0.3
Sigma [Participant:(Intercept),(Intercept)]	0.4	0.2	0.1	0.3	0.3	0.5	0.9
Sigma[Participant:Trunk_PAV,Trunk_PAV]	0.1	0.1	0	0.1	0.1	0.2	0.3
Sigma [Participant:Separation,Trunk_PAV]	0	0	−0.1	0	0	0	0

```
stan_lmer
 family:       gaussian [identity]
 formula:      Elbow_Adduction_MER ~ 0 + (1 | Participant) + (0 + Trunk_PAV +
           Separation_Pelvis_Trunk | Participant) + Weight + Height
 observations: 240
------
       Median MAD_SD
Weight 0.8    0.2
Height 0.4    0.2

Auxiliary parameter(s):
      Median MAD_SD
sigma 0.3    0.0

Error terms:
 Groups      Name                    Std.Dev. Corr
 Participant (Intercept)             0.626
 Participant Trunk_PAV               0.353
             Separation_Pelvis_Trunk 0.092    -0.20
 Residual                            0.290
Num. levels: Participant 11
```

Figure A2. Outcome of the Bayesian hierarchical TSWH model using R package rstanarm. TSWH model includes following set of predictors: trunk peak angular velocity, separation time between pelvis and trunk peak angular velocity, pitcher's weight and height.