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HAL Id: hal-00998910
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Submitted on 3 Jun 2014

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Modelling finger force produced from different tasks using linear mixed models with \texttt{lme} R function

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May 27, 2014

Abstract

The biomechanical data considered in this paper are obtained from a study carried out to understand the coordination patterns of finger forces produced from different tasks. This data cannot be considered independent because of within-individual repeated measurements, and because of simultaneous finger measurements. To fit these data, we propose a methodology focused on linear mixed models. Different random effects structures and complex variance-covariance matrices of the error are considered. We highlight how to use the \texttt{lme} R function to deal with such a modelling. The paper is accessible to an audience experienced with linear models. Some familiarity with the R software is also helpful.

Keywords: Linear mixed model, Repeated measures, Heteroscedasticity, Correlation, \texttt{lme} R function, Biomechanics.
1. Introduction

In experimental sciences (agronomy, biology, experimental psychology, ...), analysis of variance (ANOVA) is often used to explain one continuous response with respect to different experimental conditions, assuming homoscedastic errors. In studies where individuals contribute more than one observation, such as longitudinal or repeated-measures studies, classical ANOVA is no longer convenient since the assumption of data independence is not valid. The linear mixed model (Laird and Ware, 1982) then provides a better framework to take correlation between these observations into account. By introducing random effects, mixed models allow to take into account the variability of the response among the different individuals and the possible within-individual correlation. Published case studies using a mixed model approach (Baayen et al., 2008; Onyango, 2009) often assume a classical homoscedastic error term, i.e. normally distributed with mean zero and constant variance. In this paper, we consider a case study in which this assumption is relaxed by allowing heteroscedastic and correlated within-group errors. This work highlights, in an educational way, the different steps of such a modelling.

The data considered in this paper have been obtained from a biomechanical study described in detail in Quaine et al. (2012). Experiments have been carried out to better understand the coordination patterns of finger forces produced from different tasks corresponding to different experimental conditions. One of the objectives is to compare each finger force intensity between the various tasks and, for each task, to compare nearby fingers force intensity. Subjects are required to press ledges maximally with four fingers simultaneously in different experimental conditions. Experiments have been repeated three times per experimental condition. In Quaine et al. (2012), data have been analyzed first using a two-factor ANOVA model by considering the force measurement as response and fingers and experimental conditions as factors to be tested. Nevertheless, as pointed out by the authors, in this particular context, the ANOVA model is not convenient since it does not take into account nor the dependency between the fingers due to simultaneous measurements, nor the within-subject dependency due to repeated measurements.

There are several facilities in R (R Development Core Team (2008)) and S-PLUS (S-P (1992)) for fitting mixed models to data. Among them are the nlm4 (Pinheiro et al., 2014) and lmer4 (Bates et al., 2013) libraries. All analyses in the present paper have been performed using the lmer function in the nlme library, described in detail in Pinheiro and Bates (2000). The lmer function in the lmer4 library has been developed more recently. This function provides an improvement over the lme function, in particular by implementing crossed random effects in a way that is both easier for the user and much faster. However, this function does not offer the same flexibility as the lme function for composing complex variance-covariance structures. In this paper, all analyses have been performed with the 64-bit R version 3.1.0 (2014-04-10). The paper is organized as follows. Section 2 presents the data set. Section 3 exposes a preliminary study including the basic ANOVA and its limits. Mixed model specification is presented in Section 4, with details on the modelling steps. We present and discuss the results in Section 5 and we end with conclusions in Section 6.

2. The data

The data considered in this paper have been first described in Quaine et al. (2012). Biomechanical researchers propose experiments where subjects are submitted to various tasks with the four long fingers (without the thumb). In this study, 15 subjects were required to press ledges maximally with the four fingers simultaneously in flexion and extension. First in extension, two force locations at the first (ExtP1) and at the third (ExtP3) phalanx were tested and then in flexion, only the third phalanx location (FlexP3) was tested. From now on, we call location the three experimen-
tal conditions, ExtP3, FlexP3, ExtP1. After 20 trials at low and intermediate intensity, subjects are asked to press maximally three times per location, with a one-minute rest to avoid muscular fatigue. Experiments in the three different locations were separated by five minute rests.

The data set thus includes 540 measures of finger force intensity (F), subject number (individual from 1 to 15), location (with values ExtP3, FlexP3, and ExtP1), finger (with values I for index, M for middle, R for ring, and L for little). For coding purpose, a reiteration variable (trial from 1 to 135) has been added with different numbers from one subject to another and from one location to another. In other words, only 4 simultaneous measures of the four fingers of one reiteration of a given individual in a given location share the same value of the reiteration variable. The `head` command in R helps to observe the data structure:

```
> head(Data.new,200)

   F location finger indiv trial
1  8.551025      ExtP3    I     1     1
2  7.836914      ExtP3    I     1     2
3  7.653809      ExtP3    I     1     3
4  7.598877      ExtP3    I     2     4
5  6.805420      ExtP3    I     2     5
6  6.506348      ExtP3    I     2     6
... 7.560049      ExtP3    M     1     1
46 7.848145      ExtP3    M     1     2
47 6.948501      ExtP3    M     1     3
48 4.431152      ExtP3    M     2     4
49 4.528809      ExtP3    M     2     5
50 4.699707      ExtP3    M     2     6
... 22.454834     FlexP3    I     1     46
181 25.079346     FlexP3    I     1     47
182 22.003174     FlexP3    I     1     48
183 29.632686     FlexP3    I     2     49
184 34.143066     FlexP3    I     2     50
185 34.051514     FlexP3    I     2     51
...```

3. Preliminary study

3.1. Exploratory data analysis

The raw data set is shown in Figure 1. One can see that the intensities are clearly higher in FlexP3 location than in ExtP1 location and in ExtP3 location, in position but also in scattering. Index measures (blue circles) are nearly always higher than middle measures (red triangles), themselves higher than ring measures (green plus), themselves higher than little measures (magenta times), except in the ExtP1 location where this order appears less often. Differences between subjects are also to be observed. For instance, individual 4 always has low measures whatever the location, whereas individual 7 always has high measures. One can also see that index and middle measures on the one hand, and ring and little measures on the other hand, are close. This is confirmed by the correlation between fingers illustrated in Figure 2.

This exploratory data analysis suggests that intensity measures are different from a location to another, from a finger to another, but also that a subject effect has to be taken into account. Moreover, simultaneous finger measurements imposed by the experimental design cannot be considered as independent.

3.2. Two-factor ANOVA and its limits

As already done in Quaine et al. (2012), and even though it is not convenient in this context since we omit the subject effect and the dependence between simultaneous finger measurements, we begin our study with a two-factor ANOVA, namely the location and the finger effects. In other words, the study is done as if measurements had been done finger by finger, and with 45 different subjects. Following R conventions, our model is thus:

\[ F_{li} = \mu + \alpha_i + \beta_f + \gamma_{lf} + \epsilon_{li} \] (1)

where

- \( F_{li} \) is the measurement of individual \( i \in \{1, \ldots, 45\} \), in location \( l \in \{\text{ExtP3, FlexP3, ExtP1}\} \) and finger \( f \in \{I, M, R, L\} \)
- \( \mu \) is the population measurement of index in location ExtP3
- \( \alpha_i \) is the overall difference between measurements in location ExtP3 and location \( l \) for index \( (\alpha_{\text{ExtP3}} = 0) \)
- \( \beta_f \) is the overall difference between measurements of index and finger \( f \) in location ExtP3 \( (\beta_f = 0) \)
- \( \gamma_{lf} \) is the interaction term of location \( l \) and finger \( f \) \( (\gamma_{\text{ExtP3},L} = \gamma_{I,L} = 0) \)
- \( \epsilon_{li} \) is the residual error, supposed to be normally distributed, centred, with variance \( \sigma^2 \).
Moreover, all residual errors are supposed to be independent.

Residuals of the model appear in Figure 3. They suffer from several defects:

- They are clearly not identically scattered from one location to another, whereas ANOVA model imposes equal variances in all groups.
- Some subjects have either all positive or all negative residuals, which suggests a subject effect that has not yet been taken into account.
- Residuals still remain very correlated from a finger to another, as it can be seen in Figure 4.

To deal with these defects, in Section 4, we focus on linear mixed-effects models to fit the data set.

4. Model specification using a linear mixed-effects model

4.1. Modelling the random effect structure

Let denote \( F_{fik} \) the force measured on finger \( f \) of individual \( i \) at trial \( k \) in location \( l \) with \( l = \text{ExtP3, FlexP3, ExtP1, f = 1, M, R, L, i = 1, \ldots, 15} \) and \( k = 1, 2, 3 \). The linear mixed model \( M_0 \) for the response \( F_{fik} \) is defined as

\[
F_{fik} = \mu + a_i + \beta_f + \gamma_{l,f} + \xi_i + \epsilon_{fik}
\]

with \( a_{\text{ExtP3}} = 0, \beta_1 = 0, \gamma_{\text{ExtP3}, f} = \gamma_{l,L} = 0 \). In this model, \( \mu \) is the mean for location ExtP3 and finger index, \( a_i \) is the fixed effect of location \( l \) with respect to location ExtP3, \( \beta_f \) is the fixed effect of finger \( f \) with respect to finger index, \( \gamma_{l,f} \) is the interaction between location \( l \) and finger \( f \). The random effect \( \xi_i \) in (2) is the individual random effect. The linear mixed model (2) can be rewritten as

\[
\begin{bmatrix}
F_{lIk} \\
F_{Mik} \\
F_{Rik} \\
F_{Lik}
\end{bmatrix} =
\begin{bmatrix}
\mu \\
1 \\
1 \\
1
\end{bmatrix} +
\begin{bmatrix}
a_i \\
1 \\
1 \\
1
\end{bmatrix} +
\begin{bmatrix}
\beta_f \\
\beta_M \\
\beta_R \\
\beta_L
\end{bmatrix} +
\begin{bmatrix}
\gamma_{lL} \\
\gamma_{LM} \\
\gamma_{LR} \\
\gamma_{LL}
\end{bmatrix} +
\begin{bmatrix}
\xi_i \\
\xi_{II} \\
\xi_{IM} \\
\xi_{IL}
\end{bmatrix} +
\begin{bmatrix}
\epsilon_{fik}
\end{bmatrix}
\]

with \( \xi_i \sim N(0, \tau_i^2) \) and \( \epsilon_{fik} \) are independent from each other.

\[
\text{Var}(\epsilon_{fik}) = \sigma^2 I
\]

can be relaxed as shown in section 4.2 in order to model unequal variances and specific within-group correlation structures. In the sequel, we use the \texttt{nlme} function of the \texttt{nlme} package to fit models. We use the maximum likelihood estimation criterion by specifying method=“ML” in order to compare several models using the \texttt{anova} function.

Model \( M_0 \) is fitted using the R code displayed in Table 1. Figures 5 and 6 show that for each location and for each finger, the boxplots of the standardized residuals by individual for model \( M_0 \) are not centred at zero. This clearly suggests that there are different individual effects from one location to another and from one finger to another.

To solve this problem, we introduce a location within individual random effect \( \xi_{il} \), a finger within individual random effect \( \xi_{if} \) and an interaction random effect between location and finger \( \xi_{ilf} \) leading to model \( M_1 \):

\[
\begin{bmatrix}
F_{lIk} \\
F_{Mik} \\
F_{Rik} \\
F_{Lik}
\end{bmatrix} =
\begin{bmatrix}
\mu \\
1 \\
1 \\
1
\end{bmatrix} +
\begin{bmatrix}
a_i \\
1 \\
1 \\
1
\end{bmatrix} +
\begin{bmatrix}
\beta_f \\
\beta_M \\
\beta_R \\
\beta_L
\end{bmatrix} +
\begin{bmatrix}
\gamma_{lI} \\
\gamma_{IM} \\
\gamma_{IR} \\
\gamma_{IL}
\end{bmatrix} +
\begin{bmatrix}
\xi_{il} \\
\xi_{II} \\
\xi_{IM} \\
\xi_{IL}
\end{bmatrix} +
\begin{bmatrix}
\xi_{if} \\
\xi_{IF} \\
\xi_{IR} \\
\xi_{IL}
\end{bmatrix} +
\begin{bmatrix}
\xi_{ilf} \\
\xi_{IL} \\
\xi_{IR} \\
\xi_{IL}
\end{bmatrix} +
\begin{bmatrix}
\epsilon_{fik}
\end{bmatrix}
\]

with \( \xi_i \sim N(0, \tau_i^2) \), \( \xi_{il} \sim N(0, \tau_{il}^2) \), \( \xi_{if} \sim N(0, \tau_{if}^2) \), \( \xi_{ilf} \sim N(0, \tau_{ilf}^2) \), and \( \epsilon_{fik} \sim N(0, \sigma^2 I) \).

We fit model \( M_1 \) using the R code displayed in Table 2. For each location and for each finger, the boxplots of the standardized residuals (Figures 7 and 8) by individual for model \( M_1 \) are now centred at zero. However, Figure 7 also indicates that the residual variability is different from a location to another. To take this variability into account, we define a new model \( M_2 \) assuming a different variance per location for \( \xi_{il} \) i.e \( \xi_{il} \sim N(0, \tau_{il}^2) \). This model is fitted in R using the code displayed in Table 3. To compare these models, we first use the ANOVA function as displayed in Table 4. The AIC and BIC values and the \( p \)-value of the likelihood ratio statistic show that model \( M_2 \) gives a better fit. However, note that this model does not improve the residual graphs: there
still remains different residual variability from one location to another.
To deal with this problem, a more general model will be considered in Subsection 4.2.1 keeping the random effects structure defined in model M2, but allowing different variances by location for the within-group errors. Moreover, by plotting the pairwise scatter plots of model M2 residuals by each pair of fingers in Figure 9, we note that introducing random effect terms in the model did reduce correlations between fingers. Therefore, in Subsection 4.2.2, we will consider different correlation structures for the within-group errors.

4.2. Modelling the residual variance-covariance structure
The linear mixed model defined in Section 4.1 allows flexibility in the specification of the random effects structure, but restricts the within-group errors to be independent, identically distributed with mean zero and constant variance. As observed previously, we need to relax this assumption by allowing heteroscedastic and correlated within-group errors. Thus, we extend model M2 by assuming

$$\varepsilon_{l|ik} = \begin{bmatrix} \varepsilon_{l|ik} \\ \varepsilon_{M|ik} \\ \varepsilon_{R|ik} \\ \varepsilon_{L|ik} \end{bmatrix} \sim \mathcal{N}(0, \sigma^2 \Lambda_l).$$

Note that the within-group errors $\varepsilon_{l|ik}$ are assumed to be independent for different $l$, for different $i$ and different $k$ and independent of the random effects. The $4 \times 4$ matrices $\Lambda_l, l = ExtP3, FlexP3, ExtP1$ can be decomposed into a product of simpler matrices $\Lambda_l = V_l C_l V_l$, where $V_l$ is a diagonal matrix containing the standard deviation of each finger in location $l$ and $C_l$ is a positive-definite matrix with all diagonal elements equal to 1 describing the correlation of the random vector $\varepsilon_{l|ik}$. This decomposition of $\Lambda_l$ into a variance structure component and a correlation structure component is convenient both theoretically and computationally. It allows us to model separately the two structures and to combine them into a flexible family of models. More detail on variance-covariance structures can be found in Pinheiro and Bates (2000).

The *nlme* library provides a set of classes of variance functions, the *varFunc* classes, which are used to specify within-group variance structures. The *nlme* library also provides a set of classes of correlation structures, the *corStruct* classes, which are used to model dependence among the within-group errors in the context of linear mixed effects models (Pinheiro and Bates (2000)).

4.2.1 Modelling the variance matrix $V_l$ for each location
In this subsection, several variance structures $V_l$ are tested to model residuals. As already pointed out in Section 4.1, the variance of residuals clearly differs from one location to another. We therefore consider a first model derived from model M2, noted model $M_{2\perp}$, assuming a different variance from one location to another

$$V_l = \begin{bmatrix} \sigma_l^2 & 0 & 0 & 0 \\ 0 & \sigma_l^2 & 0 & 0 \\ 0 & 0 & \sigma_l^2 & 0 \\ 0 & 0 & 0 & \sigma_l^2 \end{bmatrix}, C_l = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$  

Note that, in this model, the correlation matrix $C_l$, equal to the identity matrix, assumes no correlation between fingers. To fit model $M_{2\perp}$, we use the *weights* argument of the *lme* function (see Table 5). The option *control=lmeControl(msMaxIter=1000)* makes it possible to increase the maximum number of iterations of the algorithm to achieve convergence. We compare model $M_{2\perp}$ to model M2 using the *anova* function (Table 6). The p-value of the likelihood ratio statistic shows that the former best fits the data. Figures 10 and 11 display boxplots of the standardized residuals by location and by finger from models M2 and $M_{2\perp}$ respectively. Note that, because of different variances by location in model $M_{2\perp}$, the standardized residuals, displayed in Figure 11, are calculated as the differences between the data $T_{l|ik}$ and the fitted values $\hat{T}_{l|ik}$ divided by the estimated standard deviation $\hat{\sigma}_l$.

Figure 11 shows that, in comparison to model M2, the standardized residuals are now similarly scattered from one location to another. It means that we successfully captured the location variability of the data. However, the index finger variability appears to be different from that of the other fingers. Thus, we introduce model $M_{2\perp}$ by assuming a different residual variance for the index in each location (denoted $\sigma^2_{l|I}$ for the index and $\sigma^2_{l|o}$ for the other fingers):

$$V_l = \begin{bmatrix} \sigma_{l|I}^2 & 0 & 0 & 0 \\ 0 & \sigma_{l|I}^2 & 0 & 0 \\ 0 & 0 & \sigma_{l|I}^2 & 0 \\ 0 & 0 & 0 & \sigma_{l|o}^2 \end{bmatrix}, C_l = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$  

Figure 12 shows that finger variabilities are now similar. Finally, the empirical correlations of the standardized residuals between fingers in model
$M_{2.2}$ are given in Table 7. They are lower than in the previous models but they remain non negligible between index and middle (0.450) and between ring and little (0.330).

### 4.2.2 Modelling the correlation matrix $C_l$

Here, we retain the $V_l$ matrix defined in model $M_{2.2}$ and we propose different correlation matrix structures to model finger dependence.

In a first step, we define model $M_{2.3}$ using the following correlation matrix:

$$C_l = \begin{bmatrix} 1 & \sigma_{MI} & \sigma_{RI} & \sigma_{LI} \\ \sigma_{MI} & 1 & \sigma_{RM} & \sigma_{LM} \\ \sigma_{RI} & \sigma_{RM} & 1 & \sigma_{LR} \\ \sigma_{LI} & \sigma_{LM} & \sigma_{LR} & 1 \end{bmatrix}.$$  

To do that, we use the `correlation` argument of the `lme` function.

Table 8 displays AIC and BIC criteria for models $M_{2.2}$ and $M_{2.3}$. Using these criteria to compare both models, we prefer model $M_{2.3}$ taking into account the correlation residuals between fingers since it has the lowest AIC and BIC. Our choice is confirmed by Figure 13, which displays the boxplots of the normalized residuals by location and by finger for Model $M_{2.3}$. Note that the normalized residuals are calculated by multiplying the standardized residuals by the inverse square-root factor of the estimated error correlation matrix $C_l$. However, we can observe in Table 9 that the correlations between fingers are not really improved with respect to model $M_{2.2}$. Nevertheless, we keep model $M_{2.3}$ as our final model because it gives us an interpretable estimated correlation matrix.

To explore further this correlation issue, we also compute residual correlations between fingers, location by location in Table 10. It appears that there is a different correlation matrix by location. An improvement of the final model would thus be to introduce $C_l$ defined as:

$$C_l = \begin{bmatrix} 1 & \sigma_{MII} & \sigma_{RII} & \sigma_{LII} \\ \sigma_{MII} & 1 & \sigma_{RMI} & \sigma_{LMII} \\ \sigma_{RII} & \sigma_{RMI} & 1 & \sigma_{LRII} \\ \sigma_{LII} & \sigma_{LMII} & \sigma_{LRII} & 1 \end{bmatrix}.$$  

Unfortunately, to the best of our knowledge, the `correlation` option of the `lme` function does not allow such a modelling.

### 5. Results

For exploration of parameter estimates, we again fit model $M_{2.3}$ with the REML (restricted maximum likelihood) method. REML is often preferred to ML estimation because it produces unbiased variance parameter estimates (Patterson and Thompson, 1971).

#### 5.1. Residuals analysis of the final model

To confirm the validation of model $M_{2.3}$, we use the classical plots (Figure 14) for diagnostics purposes: normalized residuals histogram, normal QQ-plot, normalized residuals versus fitted values plot, normalized residuals versus observed values plot. The histogram of the residuals and the normal QQ-plot suggest that the residuals fit the normal distribution reasonably well, except for the extreme tails. The residuals versus fitted values plot and the residuals versus observed values plot do not highlight any residual structure.

#### 5.2. Results analysis

From the `lme` output in Table 11, we summarize the REML estimates of the standard deviation components in Table 12. Estimated standard deviations ($\hat{\tau}_1, \hat{\tau}_2, \hat{\tau}_4$) of the random effects are directly obtained from the output in the `Random effects` part. Moreover, the estimated within-group standard deviations, $\hat{\sigma}_{lf}$, in the last column of Table 12, are obtained by multiplying the residual term 0.47 by the parameter estimates of the `Variance function` part.

Most variance components have a greater standard deviation than the residual one, hence justifying their inclusion as random effects in the model. The high estimates of the standard deviation components $\hat{\tau}_1$ and $\hat{\tau}_4$ indicate that the individuals and the interaction between finger and location clearly contribute to the variability of the data. Concerning the location within individual random effect, an important variability is observed for locations FlexP3 and ExtP1 with $\hat{\tau}_1$ equal to 5.46 and 1.92 respectively. Concerning the finger within individual random effect, some variability is also observed, but is lower than the previous ones. Finally, it means that variability of the force measures highly depends on the individual and on the experimental conditions, in particular in flexion at third phalanx location and in extension at first phalanx location.
The lme output in Table 11 also provides estimates of the fixed parameters. The intercept (8.64) is interpreted as the average force intensity measure for the index finger in the ExtP3 location. This group of measures is considered as the baseline group and all other groups are compared to this one. For instance, we can see a significant decrease (−2.74) of the force intensity measure for the ring finger in the ExtP3 location compared to the force intensity measure for the index finger in the same location. The average force intensity measure for the former is thus \( 8.64 - 2.74 = 5.90 \). In the same way, we calculate and display in Table 13 the estimated mean level of each finger in each location.

In order to provide answers to study objectives, we introduce two contrast analyses. Once the location-finger crossing groups variable (named group) is created, we use the constrasts function of the library MASS (Venables and Ripley, 2002), as presented in Table 14. Extract of results are displayed in Tables 15 and 16. We only interpret the lines of the first 8 (resp. 9) groups corresponding to the number of tested contrasts in Table 15 (resp. Table 16). Table 15 shows that, for one given finger, force intensities of each considered pair of locations are significantly different at 5%. On the contrary, one can see in Table 16 that the two-by-two finger comparisons show some significant differences:

- In the extension movement, the only significant difference between nearby fingers average force intensities is between the index and the middle on the first phalanx (p-value<1e − 06).
- In the flexion movement, we notice a significantly higher average force intensity for the middle than for the ring (p-value<1e − 16), and a significantly higher average force intensity for the ring than for the little (p-value<1e − 11).

The estimation of the correlation matrix between measures of the four fingers is also provided in the Correlation section part of the lme output (see Table 11). High positive correlations are observed between the measures of index and middle fingers (0.50), ring and little fingers (0.36) and, to a lesser degree, middle and ring fingers (0.22). It means that, in extension and flexion movements, index and middle fingers on the one hand, ring and little fingers on the other hand, seem to vary in the same way.

6. Conclusion

In this paper, we have proposed a methodology to handle with biomechanical data. The main features of these data lie in the repetition of the force intensity measures by individual and the simultaneity of the measures of the four fingers obtained from different tasks. Observations have been fitted using a linear mixed model with a complex random effects structure and a non-diagonal residual variance-covariance matrix using the lme R function from the nlme package. Although some limitations in the implementation of a more complex model have been pointed out, this methodology has been shown to provide the behavior of the force among fingers during different experimental conditions. The force intensity is different for flexion and extension. In extension, we have found contrasting intensity levels of the index and the middle fingers on the first phalanx. In flexion, we have observed different intensity levels concerning the middle and the ring fingers, as well as concerning the ring and little fingers. Moreover, we have highlighted various sources of variability for the force intensities, as the individual, the finger and the experimental conditions.

The analysis of the residual correlations in Section 4.2.2 fails at giving independent normalized residuals, suggesting that a more complex correlation matrix should be introduced. Unfortunately, as far as we know, although the nlme library provides a large set of classes of correlation structures (the corStruct classes), it does not allow such a modelling. To deal with this issue, an extension to our work would be to develop a new corStruct class, integrating a more complex correlation matrix. Thus, the difficulty of dealing with complex data involving the use of linear mixed effects models is clearly illustrated, and the need for further evidence on the implications of this tool is demonstrated.

Acknowledgements

The authors would like to thank Franck Quaine and Florent Paclet for providing access to the data. Collecting the data was financially supported by a PHRC grant (Rhône Alpes). The data analysis has been partially supported by the LabEx PERSYVAL-Lab (ANR-11-LABX-0025-01). The authors thank the PEPS program of the Communauté d’Universités et d’Etablissements Université de Grenoble and CNRS for financial support.
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# Tables

**Table 1**: R code for fitting model $M_0$ and plotting the residuals

```r
fitM0 <- lme(F ~ finger*location, random="1|individual, method="ML")
summary(fitM0)
resM0.std <- residuals(fitM0,type="pearson")
plot(fitM0,individual~resM0.std|location,abline=0,xlim=c(-5,5),xlab="Standardized residuals")
plot(fitM0,individual~resM0.std|finger,abline=0,xlim=c(-5,5), xlab="Standardized residuals")
```

**Table 2**: R code for fitting model $M_1$ and plotting the residuals

```r
fitM1 <- lme(F ~ finger*location,
             random=list(individual=pdBlocked(list(pdIdent(~1),
                                                  pdIdent(~location-1),
                                                  pdIdent(~finger-1),
                                                  pdIdent(~location:finger-1)))),
             method="ML")
resM1.std <- residuals(fitM1,type="pearson")
plot(fitM1,individual~resM1.std|location,abline=0,xlim=c(-5,5),
     xlab="Standardized residuals")
plot(fitM1,individual~resM1.std|finger,abline=0,xlim=c(-5,5),
     xlab="Standardized residuals")
```

**Table 3**: R code for fitting model $M_2$

```r
fitM2 <- lme(F ~ finger*location,
             random=list(individual=pdBlocked(list(pdIdent(~1),
                                                  pdDiag(~location-1),
                                                  pdIdent(~finger-1),
                                                  pdIdent(~location:finger-1)))),
             method="ML")
```

**Table 4**: R code for comparing models $M_0$, $M_1$ and $M_2$

```r
> anova(fitM0,fitM1,fitM2)

<table>
<thead>
<tr>
<th>Model</th>
<th>df</th>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
<th>Test L.Ratio</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>fitM0</td>
<td>14</td>
<td>3062.614</td>
<td>3122.696</td>
<td>-1517.307</td>
<td></td>
<td></td>
</tr>
<tr>
<td>fitM1</td>
<td>17</td>
<td>2559.554</td>
<td>2632.511</td>
<td>-1262.777</td>
<td>1 vs 2</td>
<td>509.0603</td>
</tr>
<tr>
<td>fitM2</td>
<td>19</td>
<td>2536.623</td>
<td>2618.163</td>
<td>-1249.312</td>
<td>2 vs 3</td>
<td>26.9310</td>
</tr>
</tbody>
</table>
```
Table 5: R code for fitting model $M_{2.1}$

```r
fitM2.1 <- lme(F ~ finger*location,
               random=list(individual=pdBlocked(list(pdIdent(~1),
                                                  pdDiag("location-1"),
                                                  pdIdent("finger-1"),
                                                  pdIdent("location:finger-1")))))
weights=varIdent(form="1|location),
method="ML",control=lmeControl(msMaxIter=1000))
```

Table 6: R code for comparing models $M_2$ and $M_{2.1}$.

```r
> anova(fitM2,fitM2.1)
          Model df  AIC   BIC logLik Test L.Ratio p-value
fitM2     1  19 2536.623 2618.163 -1249.312
fitM2.1   2  21 2209.450 2299.573 -1083.725 1 vs 2  331.1733  <.0001
```

Table 7: Correlation between finger residuals from model $M_{2.2}$

<table>
<thead>
<tr>
<th></th>
<th>index.resM2.2.std</th>
<th>middle.resM2.2.std</th>
<th>ring.resM2.2.std</th>
<th>little.resM2.2.std</th>
</tr>
</thead>
<tbody>
<tr>
<td>index.resM2.2.std</td>
<td>1.0000000000</td>
<td>0.44993429</td>
<td>0.05285808</td>
<td>0.002880021</td>
</tr>
<tr>
<td>middle.resM2.2.std</td>
<td>0.449934291</td>
<td>1.000000000</td>
<td>0.19787515</td>
<td>-0.054273560</td>
</tr>
<tr>
<td>ring.resM2.2.std</td>
<td>0.052858083</td>
<td>0.19787515</td>
<td>1.000000000</td>
<td>0.330040375</td>
</tr>
<tr>
<td>little.resM2.2.std</td>
<td>0.002880021</td>
<td>-0.05427356</td>
<td>0.33004037</td>
<td>1.000000000</td>
</tr>
</tbody>
</table>

Table 8: R code for comparing models $M_{2.2}$ and $M_{2.3}$.

```r
> anova(fitM2.2, fitM2.3)
          Model df  AIC   BIC logLik Test L.Ratio p-value
fitM2.2   1  24 2196.181 2299.178 -1074.090
fitM2.3   2  30 2163.984 2292.731 -1051.992 1 vs 2 44.19657  <.0001
```

Table 9: Correlation between finger residuals from model $M_{2.3}$

<table>
<thead>
<tr>
<th></th>
<th>index.resM2.3.norm</th>
<th>middle.resM2.3.norm</th>
<th>ring.resM2.3.norm</th>
<th>little.resM2.3.norm</th>
</tr>
</thead>
<tbody>
<tr>
<td>index.resM2.3.norm</td>
<td>1.0000000000</td>
<td>0.4349577</td>
<td>0.07690754</td>
<td>-0.0009446519</td>
</tr>
<tr>
<td>middle.resM2.3.norm</td>
<td>0.4349576964</td>
<td>1.000000000</td>
<td>0.18661419</td>
<td>-0.1000402521</td>
</tr>
<tr>
<td>ring.resM2.3.norm</td>
<td>0.0769075435</td>
<td>0.1866142</td>
<td>1.000000000</td>
<td>0.3160102365</td>
</tr>
<tr>
<td>little.resM2.3.norm</td>
<td>-0.0009446519</td>
<td>-0.1000403</td>
<td>0.31601024</td>
<td>1.000000000</td>
</tr>
</tbody>
</table>
### Table 10: Correlation between finger residuals from model $M_{23}$

<table>
<thead>
<tr>
<th></th>
<th>index.ExtP3</th>
<th>middle.ExtP3</th>
<th>ring.ExtP3</th>
<th>little.ExtP3</th>
</tr>
</thead>
<tbody>
<tr>
<td>index.ExtP3</td>
<td>1.00000000</td>
<td>0.29703108</td>
<td>0.01567086</td>
<td>0.11589476</td>
</tr>
<tr>
<td>middle.ExtP3</td>
<td>0.29703108</td>
<td>1.00000000</td>
<td>0.12379029</td>
<td>0.04456328</td>
</tr>
<tr>
<td>ring.ExtP3</td>
<td>0.01567086</td>
<td>0.12379029</td>
<td>1.00000000</td>
<td>0.44970726</td>
</tr>
<tr>
<td>little.ExtP3</td>
<td>0.11589476</td>
<td>0.04456328</td>
<td>0.44970726</td>
<td>1.00000000</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>index.FlexP3</th>
<th>middle.FlexP3</th>
<th>ring.FlexP3</th>
<th>little.FlexP3</th>
</tr>
</thead>
<tbody>
<tr>
<td>index.FlexP3</td>
<td>1.00000000</td>
<td>0.5020148</td>
<td>0.08159964</td>
<td>-0.1710437</td>
</tr>
<tr>
<td>middle.FlexP3</td>
<td>0.5020148</td>
<td>1.00000000</td>
<td>0.32596412</td>
<td>-0.1405854</td>
</tr>
<tr>
<td>ring.FlexP3</td>
<td>0.08159964</td>
<td>0.32596412</td>
<td>1.00000000</td>
<td>0.4255994</td>
</tr>
<tr>
<td>little.FlexP3</td>
<td>-0.1710437</td>
<td>-0.1405854</td>
<td>0.42559940</td>
<td>1.00000000</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>index.ExtP1</th>
<th>middle.ExtP1</th>
<th>ring.ExtP1</th>
<th>little.ExtP1</th>
</tr>
</thead>
<tbody>
<tr>
<td>index.ExtP1</td>
<td>1.00000000</td>
<td>0.4922102</td>
<td>0.1277424</td>
<td>0.0731796</td>
</tr>
<tr>
<td>middle.ExtP1</td>
<td>0.4922102</td>
<td>1.00000000</td>
<td>0.1167627</td>
<td>-0.1922833</td>
</tr>
<tr>
<td>ring.ExtP1</td>
<td>0.1277424</td>
<td>0.1167627</td>
<td>1.00000000</td>
<td>0.1220772</td>
</tr>
<tr>
<td>little.ExtP1</td>
<td>0.0731796</td>
<td>-0.1922833</td>
<td>0.1220772</td>
<td>1.00000000</td>
</tr>
</tbody>
</table>
Table 11: Extract from the lme output for the final model

Linear mixed-effects model fit by REML
Data: NULL
   AIC  BIC logLik
2148.537 2276.61 -1044.268

Random effects:
  Composite Structure: Blocked

  Block 1: (Intercept)
  Formula: ~1 | individual
           (Intercept)
  StdDev: 2.015483

  Block 2: locationExtP3, locationFlexP3, locationExtP1
  Formula: ~location - 1 | individual
  Structure: Diagonal
      locationExtP3 locationFlexP3 locationExtP1
  StdDev: 0.0003979309 5.463777 1.922453

  Block 3: fingerI, fingerM, fingerR, fingerL
  Formula: ~finger - 1 | individual
  Structure: Multiple of an Identity
      fingerI  fingerM  fingerR  fingerL
  StdDev: 0.4971519 0.4971519 0.4971519 0.4971519

  Block 4: locationExtP3:fingerI, locationFlexP3:fingerI, locationExtP1:fingerI, locationExtP3:fingerI
  Formula: ~location:finger - 1 | individual
  Structure: Multiple of an Identity
      locationExtP3:fingerI locationFlexP3:fingerI locationExtP1:fingerI
  StdDev: 2.131903 2.131903 2.131903

Correlation Structure: General
  Formula: ~1 | individual/trial
  Parameter estimate(s):
  Correlation:
    1  2  3
  2  0.498
  3  0.082 0.217
  4  0.005 -0.039 0.360
Variance function:
Structure: Different standard deviations per stratum
Formula: ~1 | location * Index
Parameter estimates:

<table>
<thead>
<tr>
<th></th>
<th>ExtP3*I</th>
<th>ExtP3*other</th>
<th>FlexP3*I</th>
<th>FlexP3*other</th>
<th>ExtP1*I</th>
<th>ExtP1*other</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1.000000</td>
<td>0.8353108</td>
<td>7.7366386</td>
<td>4.8954079</td>
<td>3.1937128</td>
<td>2.1329918</td>
</tr>
</tbody>
</table>

Fixed effects: F ~ finger * location

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>ExtP3</td>
<td>2.02</td>
<td>0.835</td>
<td>3.98 × 10^-4</td>
<td>0.50</td>
</tr>
<tr>
<td>FlexP3</td>
<td>8.64</td>
<td>0.771</td>
<td>11.205</td>
<td>514</td>
</tr>
<tr>
<td>ExtP1</td>
<td>2.02</td>
<td>0.804</td>
<td>-1.737</td>
<td>514</td>
</tr>
<tr>
<td>FlexP1</td>
<td>-2.742</td>
<td>0.804</td>
<td>-3.410</td>
<td>514</td>
</tr>
<tr>
<td>location</td>
<td>-3.677</td>
<td>0.804</td>
<td>-4.570</td>
<td>514</td>
</tr>
</tbody>
</table>

Table 12: REML estimates of the standard deviation components for the final model

<table>
<thead>
<tr>
<th>Location / finger</th>
<th>Index</th>
<th>Middle</th>
<th>Ring</th>
<th>Little</th>
</tr>
</thead>
<tbody>
<tr>
<td>ExtP3</td>
<td>8.64</td>
<td>7.25</td>
<td>5.90</td>
<td>4.97</td>
</tr>
<tr>
<td>FlexP3</td>
<td>25.28</td>
<td>25.47</td>
<td>25.47</td>
<td>11.47</td>
</tr>
<tr>
<td>ExtP1</td>
<td>14.73</td>
<td>11.16</td>
<td>9.83</td>
<td>10.94</td>
</tr>
</tbody>
</table>

Table 13: Estimated mean levels of the location-finger crossing groups.
Table 14: R code for contrast analysis.

```r

library(MASS)
M.location <- cbind(
  c(1,0,0,0,-1,0,0,0,0,0,0,0), # ExtP3/FlexP3,I
  c(1,0,0,0,-1,0,0,0,0,0,0,0), # ExtP3/FlexP3,M
  c(0,1,0,0,0,-1,0,0,0,0,0,0), # ExtP3/FlexP3,R
  c(0,0,1,0,0,0,-1,0,0,0,0,0), # ExtP3/FlexP3,L
  c(1,0,0,0,0,0,0,0,-1,0,0,0), # ExtP3/ExtP1,I
  c(1,0,0,0,0,0,0,0,-1,0,0,0), # ExtP3/ExtP1,M
  c(0,0,1,0,0,0,0,0,0,-1,0,0,0), # ExtP3/ExtP1,R
  c(0,0,0,1,0,0,0,0,0,0,0,-1) # ExtP3/ExtP1,L
)
contrasts(group)<-t(ginv(M.location))
fitM2.3.REML.location <- lme(F ~ group, random=list(individual=pdBlocked(list(pdIdent(~1), pdIdent(~finger-1)),
  pdIdent(~location:finger-1)))),
  weights=varIdent(form="1|location*Index),
correlation=corSymm(form="1|individual/trial),
  method="REML", control=lmeControl(msMaxIter=1000))
summary(fitM2.3.REML.location)

M.finger<-cbind(
  c(1,-1,0,0,0,0,0,0,0,0,0,0), # I/M, ExtP3
  c(0,0,0,0,1,-1,0,0,0,0,0,0), # I/M, FlexP3
  c(0,0,0,0,0,0,0,1,-1,0,0,0), # I/M, ExtP1
  c(0,1,-1,0,0,0,0,0,0,0,0,0), # M/R, ExtP3
  c(0,0,0,0,0,1,-1,0,0,0,0,0), # M/R, FlexP3
  c(0,0,0,0,0,0,0,0,0,0,1,-1), # M/R, ExtP1
  c(0,0,1,-1,0,0,0,0,0,0,0,0), # R/L, ExtP3
  c(0,0,0,0,0,0,1,-1,0,0,0,0), # R/L, FlexP3
  c(0,0,0,0,0,0,0,0,0,0,0,1,-1) # R/L, ExtP1
)
contrasts(group)<-t(ginv(M.finger))
fitM2.3.REML.finger <- lme(F ~ group,
  random=list(individual=pdBlocked(list(pdIdent(~1),
  pdIdent(~finger-1)),
  pdIdent(~location:finger-1)))),
  weights=varIdent(form="1|location*Index),
correlation=corSymm(form="1|individual/trial),
  method="REML", control=lmeControl(msMaxIter=1000))
summary(fitM2.3.REML.finger)
```
**Table 15:** Extract of the R output for contrast analysis for comparing each finger force intensity between locations (group1=ExtP3/FlexP3 I, group2=ExtP3/FlexP3 M, group3=ExtP3/FlexP3 R, group4=ExtP3/FlexP3 L, group5=ExtP3/ExtP1 I, group6=ExtP3/ExtP1 M, group7=ExtP3/ExtP1 R, group8=ExtP3/ExtP1 L)

<table>
<thead>
<tr>
<th></th>
<th>Fixed effects: F ~ group</th>
</tr>
</thead>
<tbody>
<tr>
<td>Value</td>
<td>Std. Error</td>
</tr>
<tr>
<td>(Intercept)</td>
<td>12.741371</td>
</tr>
<tr>
<td>group1</td>
<td>-16.632080</td>
</tr>
<tr>
<td>group2</td>
<td>-18.217502</td>
</tr>
<tr>
<td>group3</td>
<td>-11.337212</td>
</tr>
<tr>
<td>group4</td>
<td>-6.505398</td>
</tr>
<tr>
<td>group5</td>
<td>-6.084934</td>
</tr>
<tr>
<td>group6</td>
<td>-3.910455</td>
</tr>
<tr>
<td>group7</td>
<td>-3.931207</td>
</tr>
<tr>
<td>group8</td>
<td>-5.977376</td>
</tr>
<tr>
<td>group9</td>
<td>2.927701</td>
</tr>
<tr>
<td>group10</td>
<td>-9.304134</td>
</tr>
<tr>
<td>group11</td>
<td>-0.337429</td>
</tr>
</tbody>
</table>

**Table 16:** Extract of the R output for contrast analysis for comparing nearby finger force intensities for each location (group1=I/M, ExtP3, group2=I/M, FlexP3, group3=I/M, ExtP1, group4=M/R, ExtP3, group5=M/R, FlexP3, group6=M/R, ExtP1, group7=R/L, ExtP3, group8=R/L, FlexP3, group9=R/L, ExtP1)

<table>
<thead>
<tr>
<th></th>
<th>Fixed effects: F ~ group</th>
</tr>
</thead>
<tbody>
<tr>
<td>Value</td>
<td>Std. Error</td>
</tr>
<tr>
<td>(Intercept)</td>
<td>12.741371</td>
</tr>
<tr>
<td>group1</td>
<td>1.393365</td>
</tr>
<tr>
<td>group2</td>
<td>-0.192057</td>
</tr>
<tr>
<td>group3</td>
<td>3.567844</td>
</tr>
<tr>
<td>group4</td>
<td>1.348877</td>
</tr>
<tr>
<td>group5</td>
<td>8.229167</td>
</tr>
<tr>
<td>group6</td>
<td>1.328125</td>
</tr>
<tr>
<td>group7</td>
<td>0.934923</td>
</tr>
<tr>
<td>group8</td>
<td>5.766737</td>
</tr>
<tr>
<td>group9</td>
<td>-1.111247</td>
</tr>
<tr>
<td>group10</td>
<td>2.733225</td>
</tr>
<tr>
<td>group11</td>
<td>18.614637</td>
</tr>
</tbody>
</table>
Figures

**Figure 1:** Finger force intensity by location (left ExtP3, centre FlexP3, right ExtP1), by subject (on the x axis) and finger (blue circle for index, red triangle for middle, green plus for ring and magenta times for little).
Figure 2: Pairwise scatter plots of force intensity measures for each pair of fingers (circle ExtP3, triangle FlexP3, plus ExtP1). Empirical correlations are 0.921 between index and middle, 0.876 between index and ring, 0.801 between index and little, 0.898 between middle and ring, 0.704 between middle and little, 0.764 between ring and little.
Figure 3: ANOVA residuals by location (left ExtP3, centre FlexP3, right ExtP1), by subject (on the x axis) and finger (blue circle for index, red triangle for middle, green plus for ring and magenta times for little).
Figure 4: Pairwise scatter plots of the ANOVA residuals for each pair of fingers (circle ExtP3, triangle FlexP3, plus ExtP1). Empirical correlations are 0.863 between index and middle, 0.742 between index and ring, 0.787 between index and little, 0.753 between middle and ring, 0.732 between middle and little, 0.741 between ring and little.
Figure 5: Individual boxplots of the standardized residuals by location for model $M_0$.

Figure 6: Individual boxplots of the standardized residuals by finger for model $M_0$. 
Figure 7: Individual boxplots of the standardized residuals by location for model $M_1$.

Figure 8: Individual boxplots of the standardized residuals by finger for model $M_1$. 

Figure 9: Pairwise scatter plots of model $M_2$ residuals for each pair of fingers (circle ExtP3, triangle FlexP3, plus ExtP1). Empirical correlations are 0.482 between index and middle, 0.187 between index and ring, 0.005 between index and little, 0.370 between middle and ring, $-0.026$ between middle and little, 0.405 between ring and little.

Figure 10: Boxplots of the standardized residuals by location and by finger for model $M_2$. 
Figure 11: Boxplots of the standardized residuals by location and by finger for model $M_{2.1}$. 

Figure 12: Boxplots of the standardized residuals by location and by finger for model $M_{2.2}$. 
Figure 13: Boxplots of the normalized residuals by location and by finger for model $M_{2,3}$. 
Figure 14: Diagnostic plots for model $M_{23}$. 