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Modelling finger force produced from different tasks using linear mixed models with `lme` R function

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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. The variable in 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 effects models. Different random effects structures and complex variance-covariance matrices of the error are considered. We highlight how to use the `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, 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 variable data independence is not valid. The linear mixed model (Laird and Ware, 1982) then provides then 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 modeling.

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 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 (Insightful Corporation (1992)) for fitting mixed models to data. Among them are the `nlme` (Pinheiro et al., 2014) and more recently the `lme4` (Bates et al., 2013) libraries. The `lmer` function in the `lme4` library provides an improvement over the `lme` function in the `nlme` library, 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 (Bates et al., 2013). First, `lme` offers a much broader class of covariance structures for the random effects. Secondly, concerning the variance-covariance structures for the residuals, the `lme` function takes into account spatial or temporal autocorrelation, heteroscedasticity or covariate-dependent variability in the `weights` argument, while `lmer` only allows fixed prior weights for the observations. Because `lmer` has been implemented more recently and because its primary objective is to propose a tool much faster and with sufficient flexibility for most applications, `lmer` presents these limitations compared to `lme` to date. Note also that the summary of a linear mixed model fit by `lme` provides estimates of the fixed-effects parameters, standard errors for these parameters, t-ratios and p-values, contrary to `lmer` that produces no p-values. This `lmer` limitation is related to the F statistic which, in an unbalanced data context, do not exactly follow an F distribution (Onyango (2009), Pinheiro and Bates (2000)). Some websites (Bates et al. (2013); Wikidot (2013)) provide comparisons between `nlme`, `lme4` and others packages and softwares. All analyses in the present paper have thus been performed using the `lme` function in the `nlme` library, described in detail in Pinheiro and Bates (2000) and 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 ANOVA with repetitions and its limits. Mixed model specification is presented in Section 4, with details on the modeling 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 experimental 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
...
46   7.550049    ExtP3      M     1     1
47   6.848145    ExtP3      M     1     2
48   6.945801    ExtP3      M     1     3
49   4.431152    ExtP3      M     2     4
50   4.528809    ExtP3      M     2     5
51   4.699707    ExtP3      M     2     6
...
181 22.454834   FlexP3      I     1    46
182 25.079346   FlexP3      I     1    47
183 22.003174   FlexP3      I     1    48
184 29.632568   FlexP3      I     2    49
185 34.143066   FlexP3      I     2    50
186 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 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 with repetitions and its limitations*

In Quaine et al. (2012), the data were treated with a two-factor ANOVA even though it is not convenient in this context since the subject effect and the dependence between simultaneous finger measurements were omitted. In other words, the study was done as if measurements had been done finger by finger, and with 45 different subjects. Here, we begin our study with a two-factor ANOVA with repetitions, taking into account the fact that measurements are repeated on the same subjects. Following R conventions, our model is thus:

$$F_{lfik} = \mu + \alpha_l + \beta_f + \gamma_{lf} + \delta_i + \varepsilon_{lfik} \qquad (1)$$

where

- F_{lfik} is the k^{th} trial $k \in \{1,\dots,3\}$ of individual $i \in \{1,\dots,15\}$, in location $l \in \{ExtP3, FlexP3, ExtP1\}$ and finger $f \in \{I, M, R, L\}$
- μ is the population measurement of index in location ExtP3
- α_l is the overall difference between measurements in location ExtP3 and location l for index ($\alpha_{ExtP3} = 0$)
- β_f is the overall difference between measurements of index and finger f in location ExtP3 ($\beta_I = 0$)
- γ_{lf} is the interaction term of location l and finger f ($\gamma_{ExtP3,f} = \gamma_{l,I} = 0$)
- δ_i is the effect of individual i with respect to individual 1, considered as a fixed effect ($\delta_1 = 0$)
- ε_{lfik} is the residual error, supposed to be normally distributed, centred, with

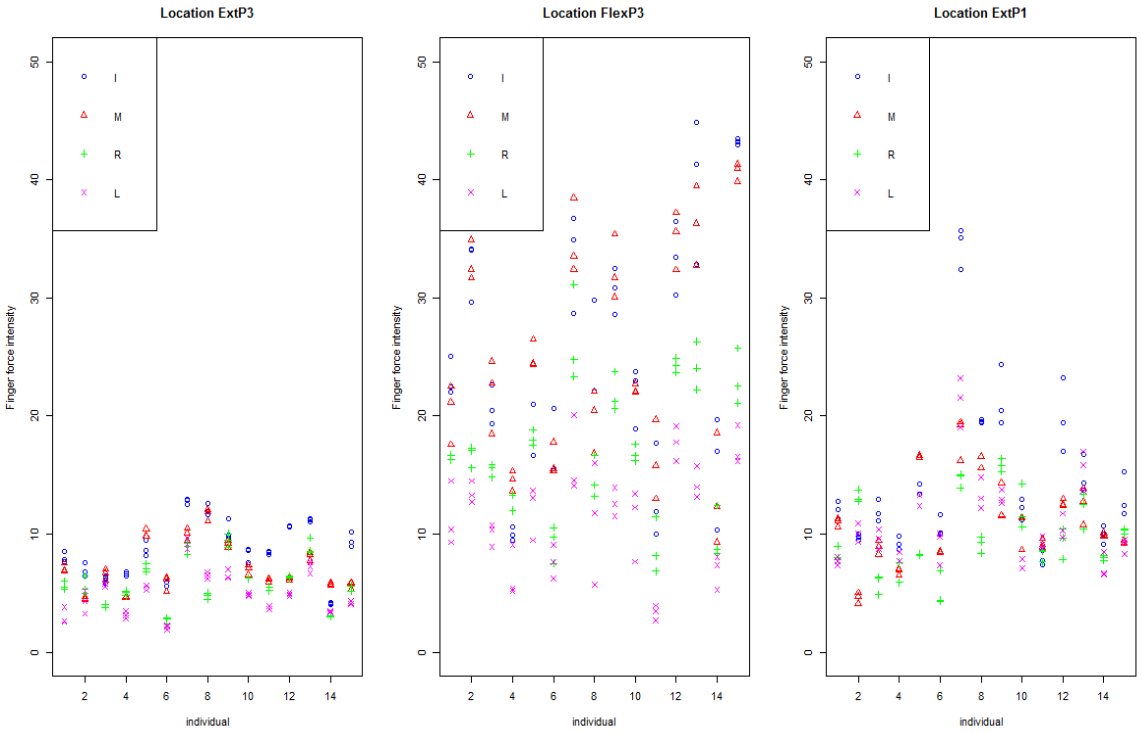

Figure 1: Finger force intensity by location (left ExtP3, centre FlexP3, right ExtP1), by subject (on the x axis) and finger (blue circle for index, red triangle for middle, green plus for ring and magenta times for little).

variance σ^2. Moreover, all residual errors are supposed to be independent.

Note that this model implies the estimation of 14 individual fixed effects. 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 well been taken into account.
- Residuals still remain quite 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_{lfik} as the force measured on finger f of individual i at trial k in location l with $l = ExtP3, FlexP3, ExtP1$, $f = I, M, R, L$, $i = 1, \ldots, 15$ and $k = 1, 2, 3$. The linear mixed model M_0 for the response F_{lfik} is defined as

$$F_{lfik} = \mu + \alpha_l + \beta_f + \gamma_{l,f} + \xi_i + \varepsilon_{lfik} \qquad (2)$$

with $\alpha_{ExtP3} = 0, \beta_I = 0, \gamma_{ExtP3,f} = \gamma_{l,I} = 0$. In this model, μ is the mean for location ExtP3 and finger index, α_l is the fixed effect of location l with respect to location ExtP3, β_f is the fixed effect of finger f with respect to finger index and $\gamma_{l,f}$ is the interaction between location l and finger f. The random effect ξ_i in (2) is the individual random effect and is supposed to be a centred gaussian random variable with variance τ_1^2. The main difference between the ANOVA with repeated measurements (eq. 1) and the model M_0 (eq. 2) lies in the definition of the individual effects:

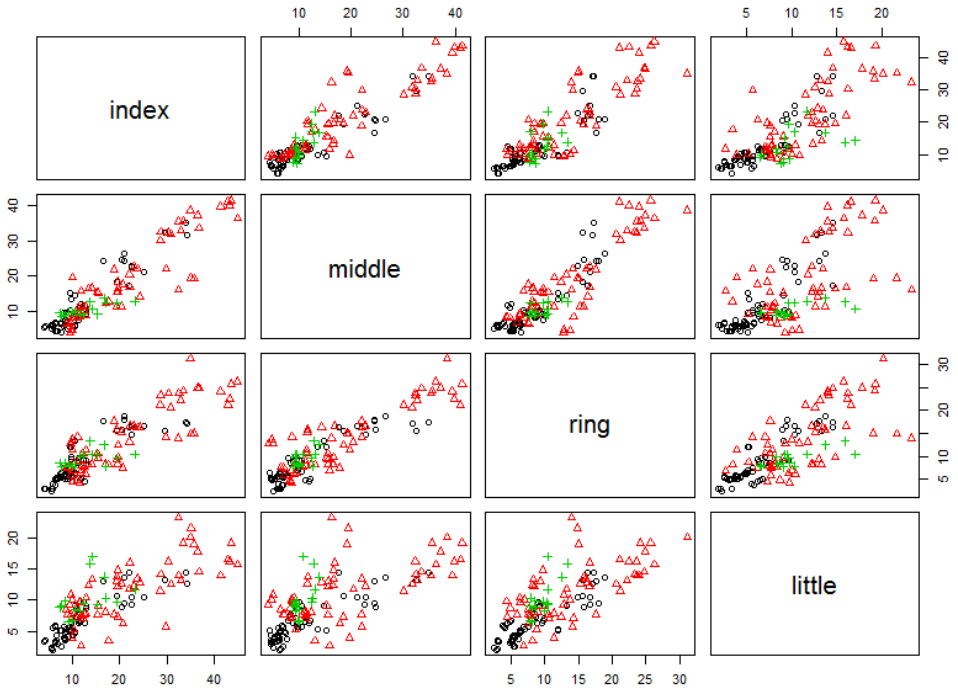

Figure 2: Pairwise scatter plots of force intensity measures for each pair of fingers (circle ExtP3, triangle FlexP3, plus ExtP1). Empirical correlations are 0.921 between index and middle, 0.876 between index and ring, 0.801 between index and little, 0.898 between middle and ring, 0.704 between middle and little, 0.764 between ring and little.

- In the first one, the individual effects are fixed (non-random) and we need to estimate 14 mean coefficients $\delta_i, i = 2, \ldots, 15$.
- In the latter one, the individual are random, centred at 0 and we only need to estimate the variance of this random variable τ_1^2.

The linear mixed model (2) can be rewritten as

$$\begin{bmatrix} F_{lIik} \\ F_{lMik} \\ F_{lRik} \\ F_{lLik} \end{bmatrix} = \mu \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} + \alpha_l \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} + \begin{bmatrix} \beta_I \\ \beta_M \\ \beta_R \\ \beta_L \end{bmatrix} + \begin{bmatrix} \gamma_{lI} \\ \gamma_{lM} \\ \gamma_{lR} \\ \gamma_L \end{bmatrix} + \xi_i \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} + \begin{bmatrix} \varepsilon_{lIik} \\ \varepsilon_{lMik} \\ \varepsilon_{lRik} \\ \varepsilon_{lLik} \end{bmatrix} \quad (3)$$

with $\xi_i \sim \mathcal{N}(0, \tau_1^2)$ and $\varepsilon_{lik} = \begin{bmatrix} \varepsilon_{lIik} \\ \varepsilon_{lMik} \\ \varepsilon_{lRik} \\ \varepsilon_{lLik} \end{bmatrix} \sim \mathcal{N}(0, \sigma^2 I)$ with I the identity matrix. All random effects are assumed independent from each other and independent from the error term. Note that the assumption $Var(\varepsilon_{lik}) = \sigma^2 I$ 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 `lme` function of the `nlme` package to fit models. We use the maximum likelihood estimation criterion by specifying `method="ML"` and we compare several nested models using the `anova` function which performs likelihood ratio tests and displays AIC and BIC values. Note that, here, since all considered models have the same fixed-effects structure, they could be fitted using the REML (Restricted Maximum Likelihood) method and still be compared using likelihood ratio tests. However, whatever the estimation method (ML or REML), be aware that the p-values of the likelihood ratio test may be conservative while testing the random effects structure (Pinheiro and Bates (2000)). Model M_0 is fitted using the R code displayed in Code 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

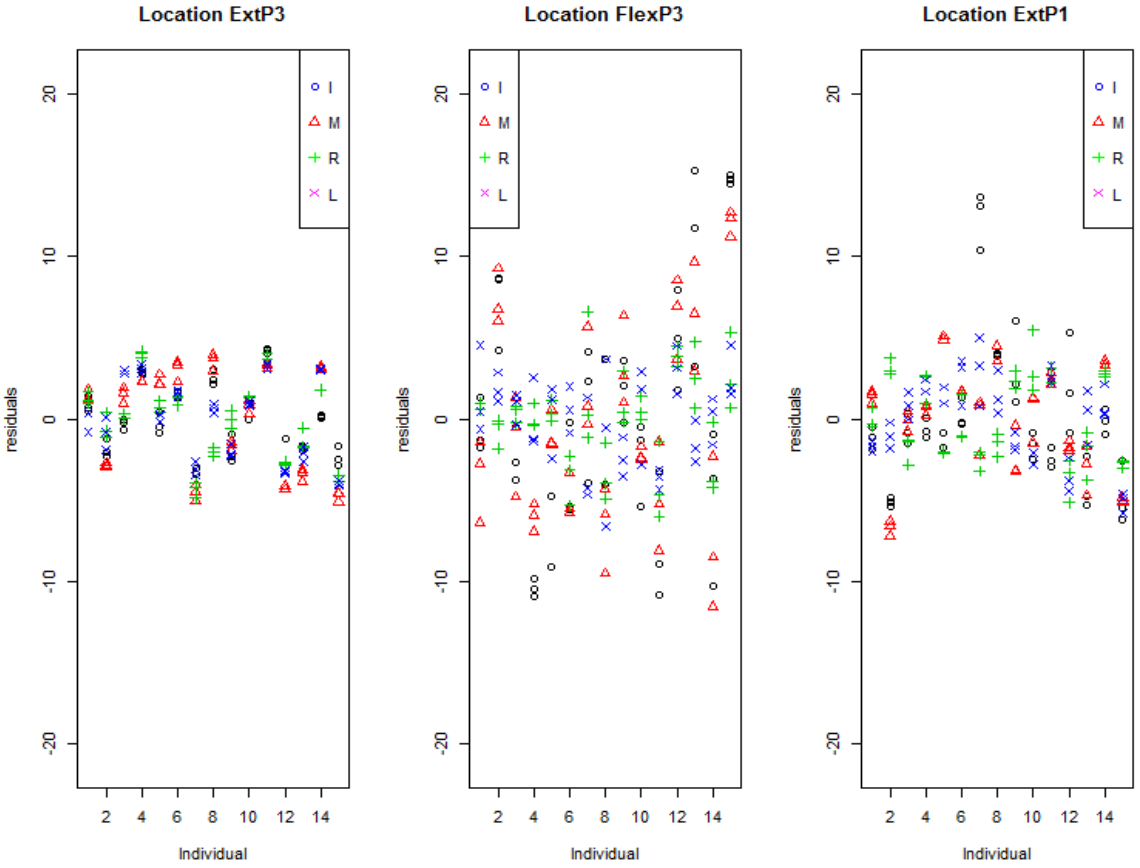

Figure 3: ANOVA with repeated measurements residuals by location (left ExtP3, centre FlexP3, right ExtP1), by subject (on the x axis) and finger (blue circle for index, red triangle for middle, green plus for ring and magenta times for little).

one finger to another.

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

$$\begin{bmatrix} F_{lIik} \\ F_{lMik} \\ F_{lRik} \\ F_{lLik} \end{bmatrix} = \mu \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} + \alpha_l \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} + \begin{bmatrix} \beta_I \\ \beta_M \\ \beta_R \\ \beta_L \end{bmatrix} + \begin{bmatrix} \gamma_{lI} \\ \gamma_{lM} \\ \gamma_{lR} \\ \gamma_L \end{bmatrix} + \xi_i \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} + \xi_{il} \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} + \begin{bmatrix} \xi_{iI} \\ \xi_{iM} \\ \xi_{iR} \\ \xi_{iL} \end{bmatrix} + \begin{bmatrix} \xi_{ilI} \\ \xi_{ilM} \\ \xi_{ilR} \\ \xi_{ilL} \end{bmatrix} + \begin{bmatrix} \varepsilon_{lIik} \\ \varepsilon_{lMik} \\ \varepsilon_{lRik} \\ \varepsilon_{lLik} \end{bmatrix} \quad (4)$$

with $\xi_i \sim \mathcal{N}(0, \tau_1^2)$, $\xi_{il} \sim \mathcal{N}(0, \tau_2^2)$, $\xi_{if} \sim \mathcal{N}(0, \tau_3^2)$, $\xi_{ilf} \sim \mathcal{N}(0, \tau_4^2)$ and

$$\varepsilon_{lik} = \begin{bmatrix} \varepsilon_{lIik} \\ \varepsilon_{lMik} \\ \varepsilon_{lRik} \\ \varepsilon_{lLik} \end{bmatrix} \sim \mathcal{N}(0, \sigma^2 I).$$

We fit model M_1 using the R code displayed in Code 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 ξ_{il} i.e $\xi_{il} \sim \mathcal{N}(0, \tau_l^2)$. This model is fitted in R using the code displayed in Code 3. To compare these models, we first use the ANOVA function as displayed in Code 4. The AIC and BIC values and the p-value of the like-

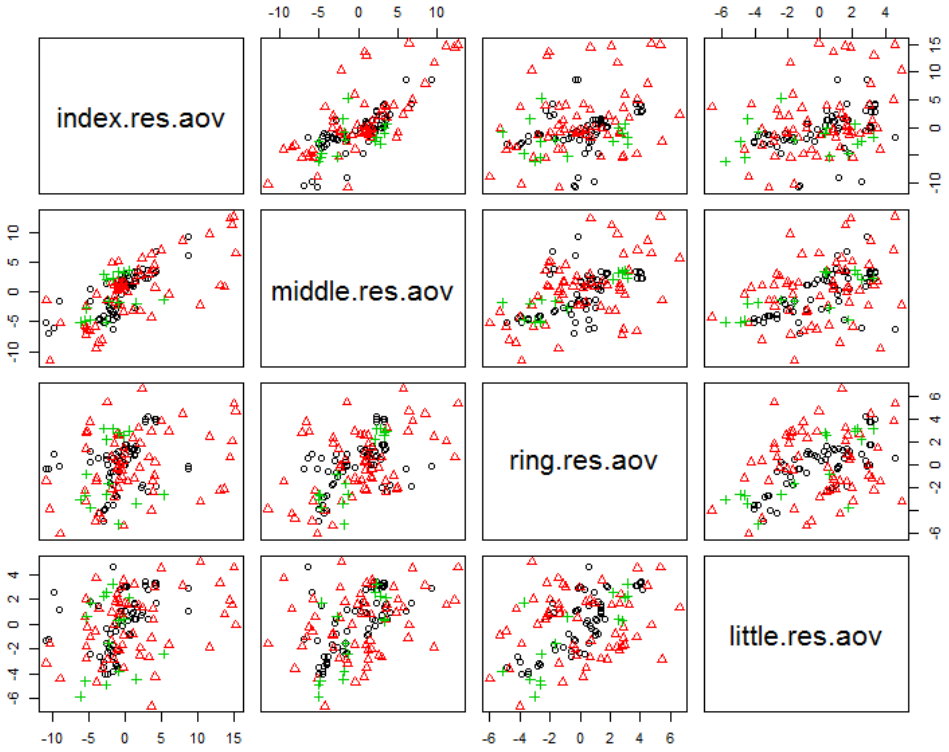

Figure 4: Pairwise scatter plots of the ANOVA with repeated measurements residuals for each pair of fingers (circle ExtP3, triangle FlexP3, plus ExtP1). Empirical correlations are 0.717 between index and middle, 0.297 between index and ring, 0.330 between index and little, 0.510 between middle and ring, 0.446 between middle and little, 0.440 between ring and little.

lihood 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 M_2, but allowing different variances by location for the within-group errors. Moreover, by plotting the pairwise scatter plots of model M_2 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 M_2 by assuming $\varepsilon_{lik} = \begin{bmatrix} \varepsilon_{lIik} \\ \varepsilon_{lMik} \\ \varepsilon_{lRik} \\ \varepsilon_{lLik} \end{bmatrix} \sim \mathcal{N}(0, \sigma^2 \Lambda_l)$. Note that the within-group errors ε_{lik} are assumed to be independent for different l , for different i and different k and independent of the random effects. The 4×4 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 ε_{lik}. This decomposition of Λ_l into a variance structure component and a correlation structure component is convenient both

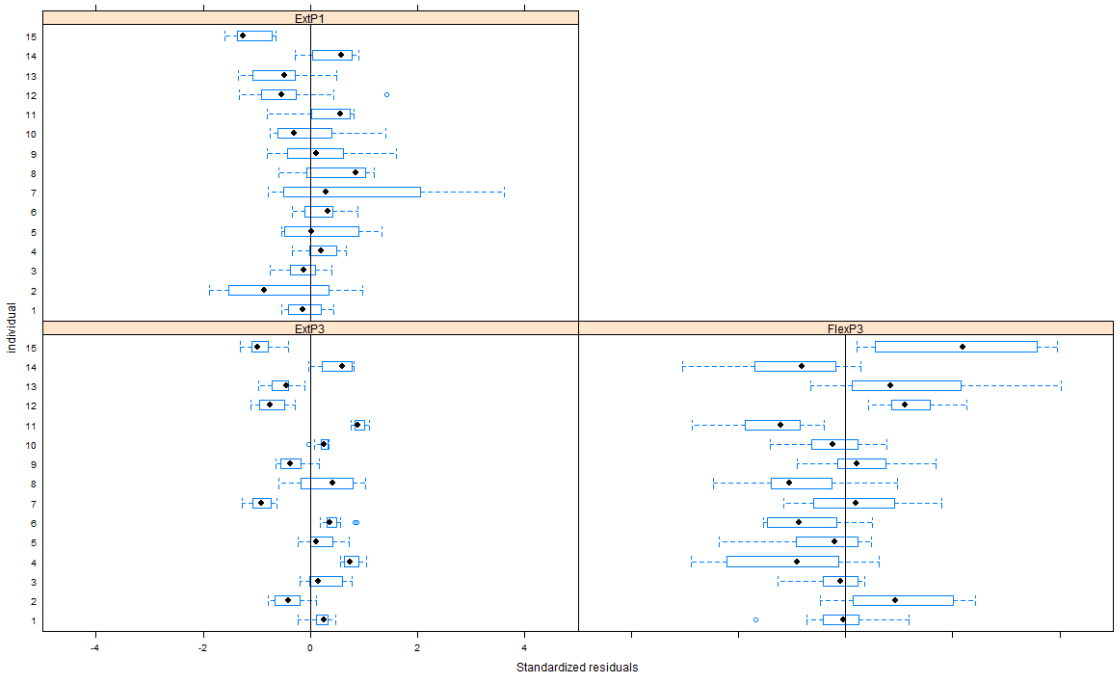

Figure 5: Individual boxplots of the standardized residuals by location for model M_0.

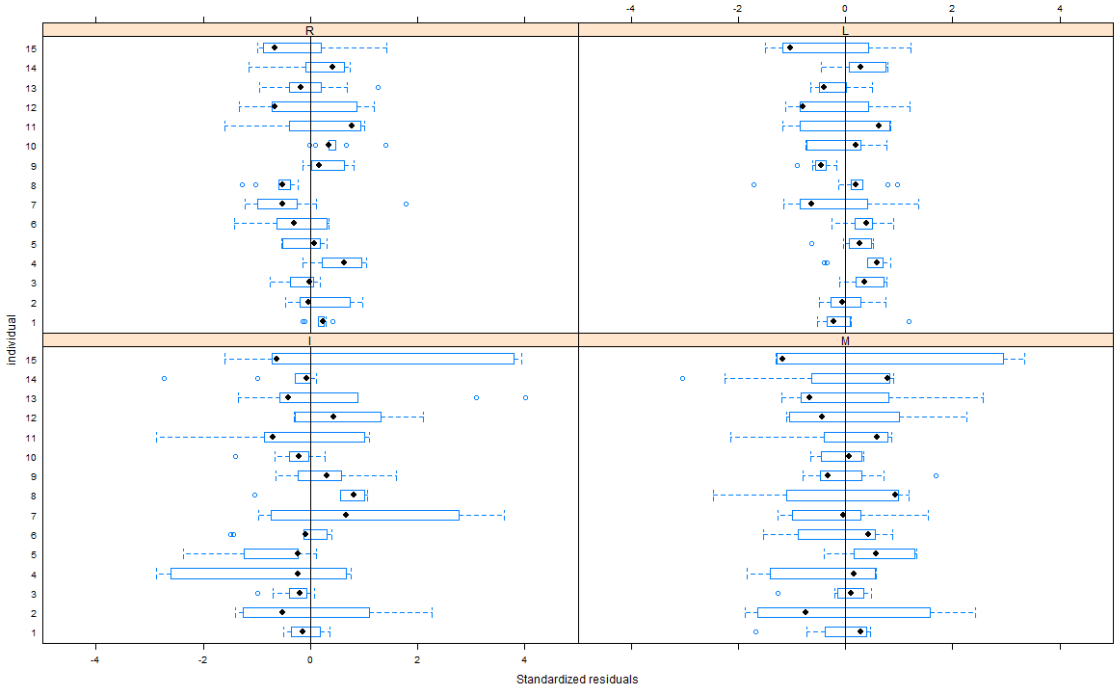

Figure 6: Individual boxplots of the standardized residuals by finger for model M_0.

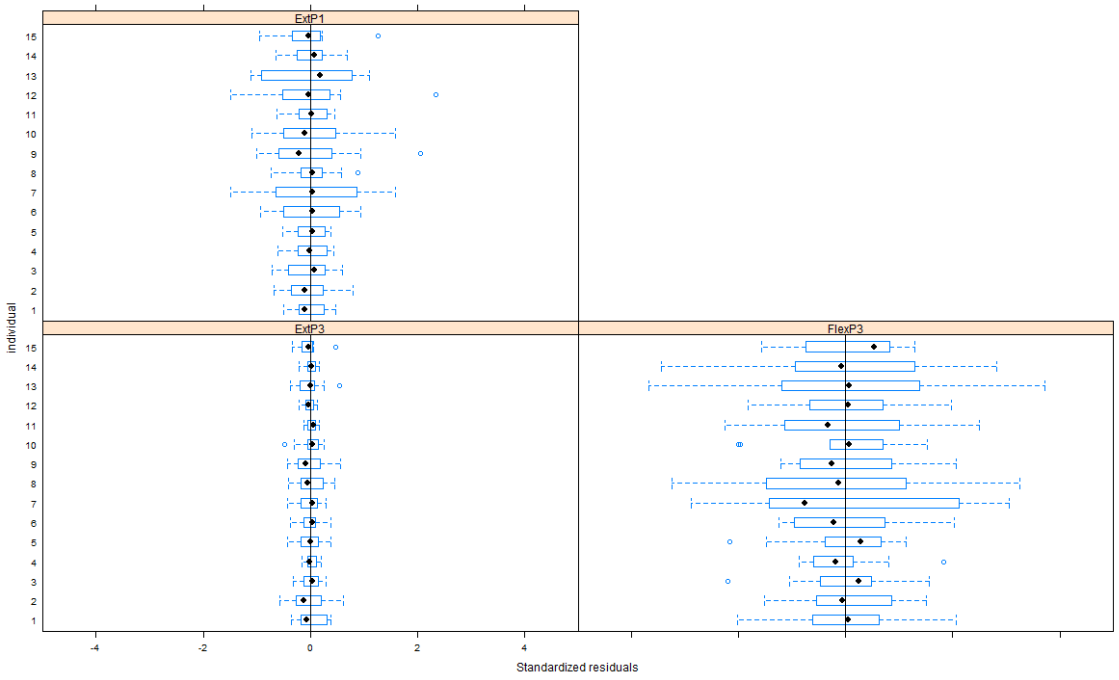

Figure 7: Individual boxplots of the standardized residuals by location for model M_1.

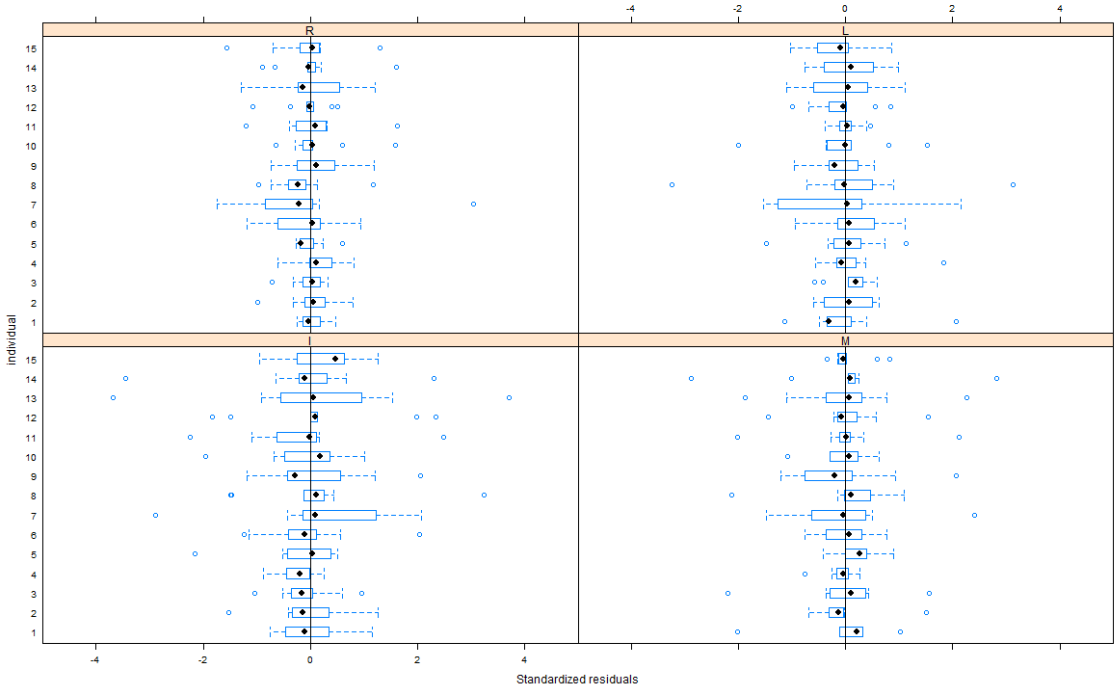

Figure 8: Individual boxplots of the standardized residuals by finger for model M_1.

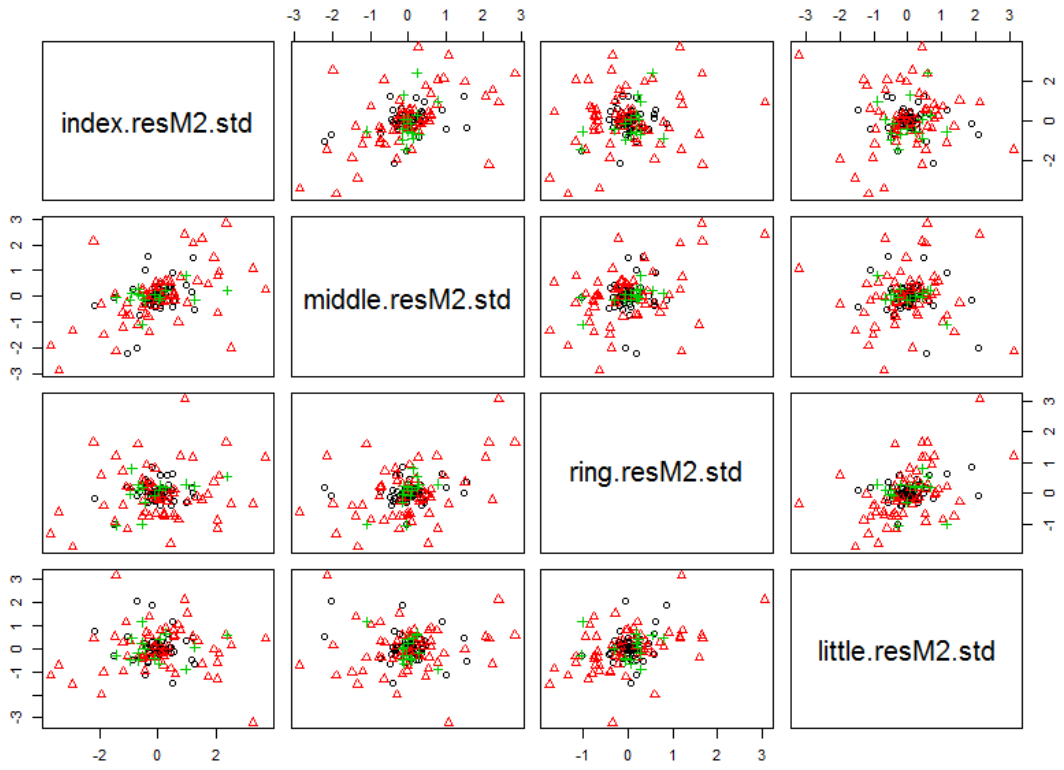

Figure 9: Pairwise scatter plots of model M_2 residuals for each pair of fingers (circle ExtP3, triangle FlexP3, plus ExtP1). Empirical correlations are 0.482 between index and middle, 0.187 between index and ring, 0.005 between index and little, 0.370 between middle and ring, -0.026 between middle and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

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 M_2, noted model $M_{2.1}$, assuming a different variance from one location to another

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

Note that, in this model, the correlation matrix C_l, equal to the identity matrix, assumes no correlation between fingers. To fit model $M_{2.1}$, we use the `weights` argument of the `lme` function (see Code 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 $M_{2.1}$ to model M_2 using the `anova` function (Code 6). The p-value of

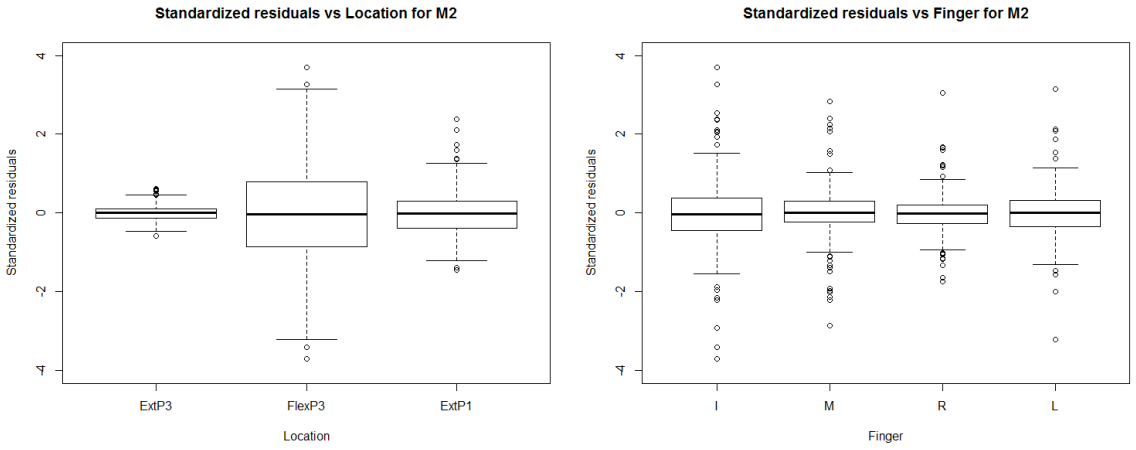

Figure 10: Boxplots of the standardized residuals by location and by finger for model M_2.

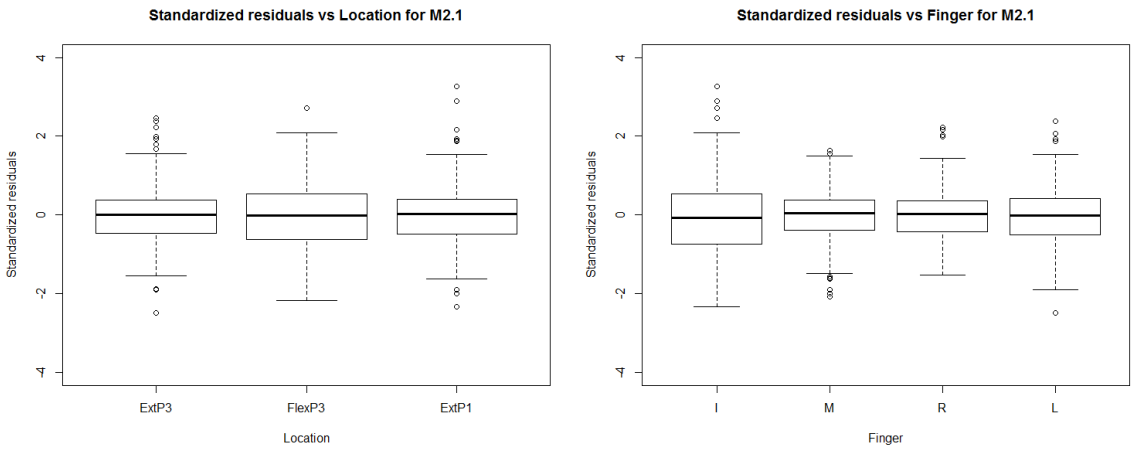

Figure 11: Boxplots of the standardized residuals by location and by finger for model $M_{2.1}$.

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 M_2 and $M_{2.1}$ respectively. Note that, because of different variances by location in model $M_{2.1}$, the standardized residuals, displayed in Figure 11, are calculated as the differences between the data F_{lfik} and the fitted values $\hat{F}_{lfik}$ divided by the estimated standard deviation $\hat{\sigma}_l$.

Figure 11 shows that, in comparison to model M_2, 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 $M_{2.2}$ by assuming a different residual variance for the index in each location (denoted σ^2_{lI} for the index and σ^2_{lo} for the other fingers):

$$V_l = \begin{bmatrix} \sigma_{lI} & 0 & 0 & 0 \\ 0 & \sigma_{lo} & 0 & 0 \\ 0 & 0 & \sigma_{lo} & 0 \\ 0 & 0 & 0 & \sigma_{lo} \end{bmatrix}, C_l = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$

The `R` code for model $M_{2.2}$ is displayed in Code 7. 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 Code 8. 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 (see `R` code in Code 9).

Code 10 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 $\hat{C}_l$. However, we can observe in Code 11 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 Code 12. 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:

$$C_l = \begin{bmatrix} 1 & \sigma_{MIl} & \sigma_{RIl} & \sigma_{LIl} \\ \sigma_{MIl} & 1 & \sigma_{RMl} & \sigma_{LMl} \\ \sigma_{RIl} & \sigma_{RMl} & 1 & \sigma_{LRl} \\ \sigma_{LIl} & \sigma_{LMl} & \sigma_{LRl} & 1 \end{bmatrix}.$$

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 $M_{2.3}$ by REML which is often preferred to ML estimation because it produces unbiased and non-negative 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

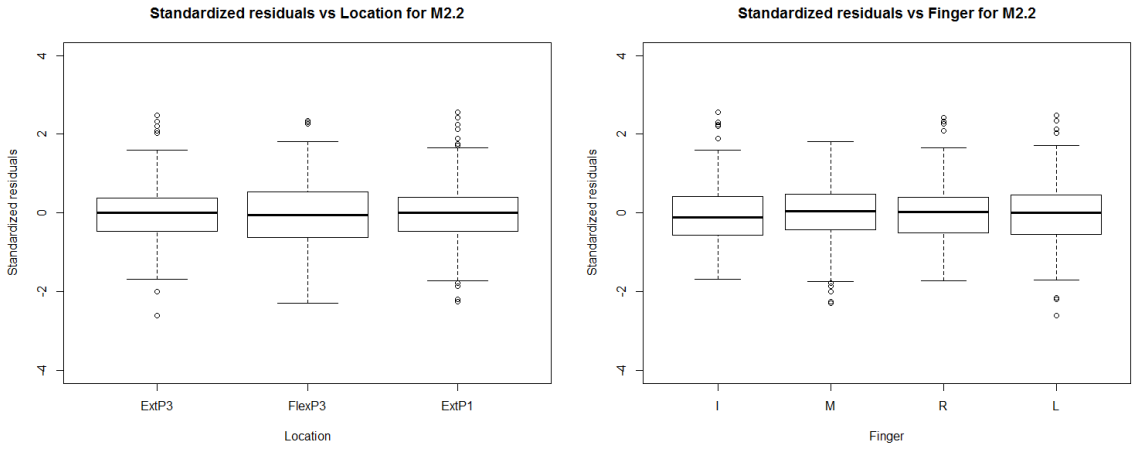

Figure 12: Boxplots of the standardized residuals by location and by finger for model $M_{2.2}$.

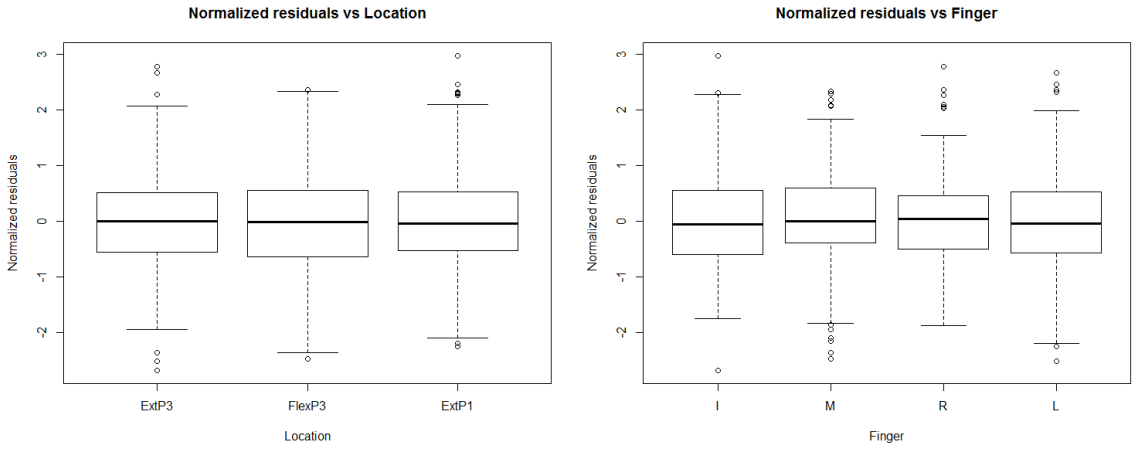

Figure 13: Boxplots of the normalized residuals by location and by finger for model $M_{2.3}$.

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 Code 13, we summarize the REML estimates of the standard deviation components in Table 1. Estimated standard deviations ($\hat{\tau}_1, \hat{\tau}_l, \hat{\tau}_2, \hat{\tau}_4$) 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 1, 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 $\hat{\tau}_l$ 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 Code 13 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 2 the estimated mean level of each finger in each location.

Table 2: Estimated mean levels of the location-finger crossing groups.

Location/finger	Index	Middle	Ring	Little
ExtP3	8.64	7.25	5.90	4.97
FlexP3	25.28	25.47	17.24	11.47
ExtP 1	14.73	11.16	9.83	10.94

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 Code 14. Extract of results are displayed in Codes 15 and 16. We only interpret the lines of the first 8 (resp. 9) groups corresponding to the number of tested contrasts in Code 15 (resp. Table 16). Code 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 Code 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 Code 13). 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 one hand and ring and little fingers on the other hand seem to vary in the same way.

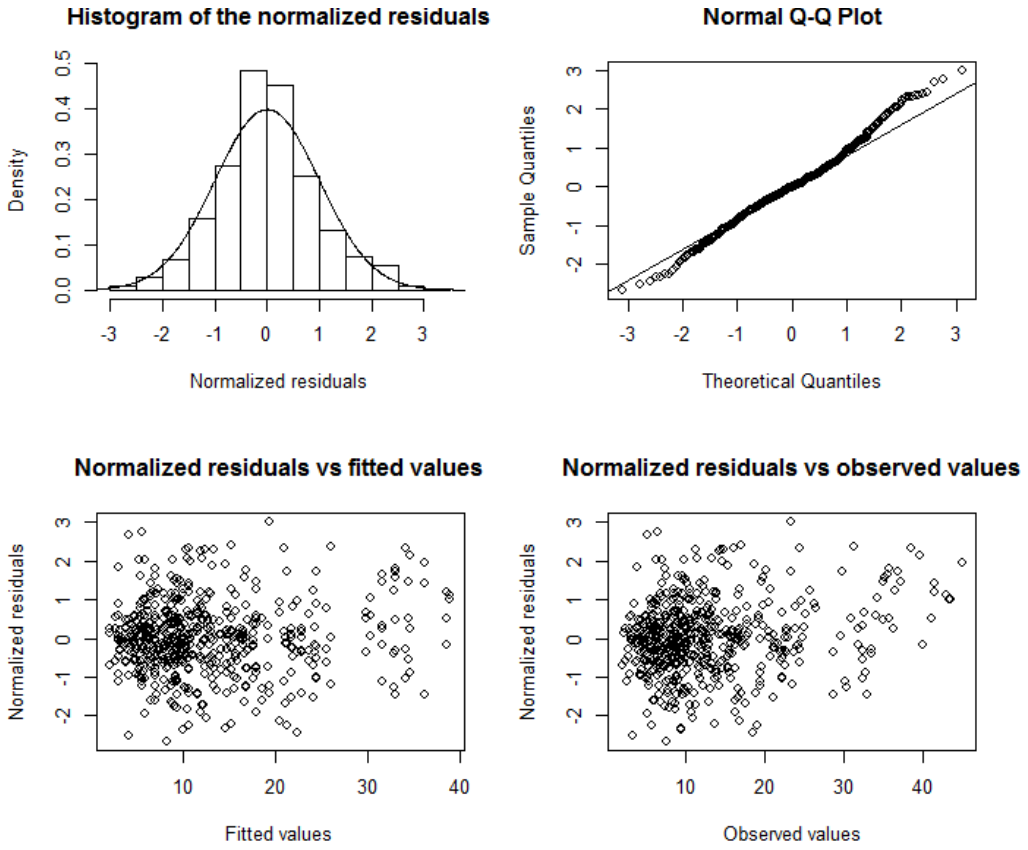

Figure 14: Diagnostic plots for model $M_{2.3}$.

6. Conclusion

In this paper, we have proposed a methodology to handle 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

Table 1: REML estimates of the standard deviation components for the final model

		Standard deviation of the random effects				Residual standard deviation
Location	Finger	$\hat{\tau}_1$	$\hat{\tau}_l$	$\hat{\tau}_3$	$\hat{\tau}_4$	$\hat{\sigma}_{lf}$
ExtP3	I	2.02	3.98×10^{-4}	0.50	2.13	0.47
	M,R,L	2.02	3.98×10^{-4}	0.50	2.13	0.39
FlexP3	I	2.02	5.46	0.50	2.13	3.61
	M,R,L	2.02	5.46	0.50	2.13	2.29
ExtP1	I	2.02	1.92	0.50	2.13	1.49
	M,R,L	2.02	1.92	0.50	2.13	0.99

tool is demonstrated.

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Codes

Code 1: R code for fitting model M_0 and plotting the residuals

```
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")
```

Code 2: R code for fitting model M_1 and plotting the residuals

```
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")
```

Code 3: R code for fitting model M_2

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

Code 4: R code for comparing models M_0 M_1 and M_2

```
> anova(fitM0,fitM1,fitM2)
      Model df      AIC      BIC    logLik   Test  L.Ratio p-value
fitM0     1 14 3062.614 3122.696 -1517.307
fitM1     2 17 2559.554 2632.511 -1262.777 1 vs 2 509.0603  <.0001
fitM2     3 19 2536.623 2618.163 -1249.312 2 vs 3  26.9310  <.0001
```

Code 5: R code for fitting model $M_{2.1}$

```
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))
```

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

```
> 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
```

Code 7: R code for fitting model $M_{2.2}$

```
Index<-(finger=="I")
Index[Index==TRUE]<-"I"
Index[Index==FALSE]<-"other"
```

```
fitM2.2 <- 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*Index),
               method="ML",control=lmeControl(msMaxIter=1000))
```

Code 8: Correlation between finger residuals from model $M_{2.2}$

```
                  index.resM2.2.std middle.resM2.2.std ring.resM2.2.std little.resM2.2.std
index.resM2.2.std        1.000000000         0.44993429       0.05285808
0.002880021
middle.resM2.2.std       0.449934291         1.00000000       0.19787515
-0.054273560
ring.resM2.2.std         0.052858083         0.19787515       1.00000000
0.330040375
little.resM2.2.std       0.002880021        -0.05427356       0.33004037
1.000000000
```

Code 9: R code for fitting model $M_{2.3}$

```
fitM2.3 <- 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*Index),
               correlation=corSymm(form=~1|individual/trial),
               method="ML", control=lmeControl(msMaxIter=1000))
```

Code 10: R code for comparing models $M_{2.2}$ and $M_{2.3}$

```
> 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
```

Code 11: Correlation between finger residuals from model $M_{2.3}$

```
                   index.resM2.3.norm middle.resM2.3.norm ring.resM2.3.norm little.resM2.3.norm
index.resM2.3.norm        1.0000000000           0.4349577        0.07690754
-0.0009446519
middle.resM2.3.norm       0.4349576964           1.0000000        0.18661419
-0.1000402521
ring.resM2.3.norm         0.0769075435           0.1866142        1.00000000
0.3160102365
little.resM2.3.norm      -0.0009446519          -0.1000403        0.31601024
1.0000000000
```

Code 12: Correlation between finger residuals from model $M_{2.3}$

```
[1] "ExtP3"
             index.ExtP3 middle.ExtP3 ring.ExtP3 little.ExtP3
index.ExtP3   1.00000000   0.29703108 0.01567086   0.11589476
middle.ExtP3  0.29703108   1.00000000 0.12379029   0.04456328
ring.ExtP3    0.01567086   0.12379029 1.00000000   0.44970726
little.ExtP3  0.11589476   0.04456328 0.44970726   1.00000000

[1] "FlexP3"
              index.FlexP3 middle.FlexP3 ring.FlexP3 little.FlexP3
index.FlexP3    1.00000000     0.5020148  0.08159964    -0.1710437
middle.FlexP3   0.50201479     1.0000000  0.32596412    -0.1405854
ring.FlexP3     0.08159964     0.3259641  1.00000000     0.4255994
little.FlexP3  -0.17104373    -0.1405854  0.42559940     1.0000000
```

```
[1] "ExtP1"
             index.ExtP1 middle.ExtP1 ring.ExtP1 little.ExtP1
index.ExtP1    1.0000000    0.4922102  0.1277424    0.0731796
middle.ExtP1   0.4922102    1.0000000  0.1167627   -0.1922833
ring.ExtP1     0.1277424    0.1167627  1.0000000    0.1220772
little.ExtP1   0.0731796   -0.1922833  0.1220772    1.0000000
```

Code 13: 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:fingerM, locationFlexP3:fingerM, locationExtP1:fingerM,
          locationExtP3:fingerR, locationFlexP3:fingerR, locationExtP1:fingerR,
          locationExtP3:fingerL, locationFlexP3:fingerL, locationExtP1:fingerL
 Formula: ~location:finger - 1 | individual
 Structure: Multiple of an Identity
        locationExtP3:fingerI locationFlexP3:fingerI locationExtP1:fingerI
StdDev:              2.131903              2.131903              2.131903
        locationExtP3:fingerM locationFlexP3:fingerM locationExtP1:fingerM
StdDev:              2.131903              2.131903              2.131903
        locationExtP3:fingerR locationFlexP3:fingerR locationExtP1:fingerR
StdDev:              2.131903              2.131903              2.131903
        locationExtP3:fingerL locationFlexP3:fingerL locationExtP1:fingerL
StdDev:              2.131903              2.131903              2.131903
        Residual
StdDev: 0.467283

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:
     ExtP3*I  ExtP3*other     FlexP3*I FlexP3*other      ExtP1*I  ExtP1*other
```

```
   1.0000000    0.8353108    7.7366386    4.8954079    3.1937128    2.1329918
Fixed effects: F ~ finger * location
                            Value Std.Error  DF   t-value p-value
(Intercept)              8.644884 0.7714543 514 11.205958  0.0000
fingerM                 -1.393365 0.8019731 514 -1.737421  0.0829
fingerR                 -2.742242 0.8040684 514 -3.410458  0.0007
fingerL                 -3.677165 0.8044585 514 -4.570981  0.0000
locationFlexP3          16.632080 1.7004357 514  9.781070  0.0000
locationExtP1            6.084934 0.9522260 514  6.390220  0.0000
fingerM:locationFlexP3   1.585422 1.2000256 514  1.321157  0.1870
fingerR:locationFlexP3  -5.294868 1.2633332 514 -4.191188  0.0000
fingerL:locationFlexP3 -10.126682 1.2747899 514 -7.943804  0.0000
fingerM:locationExtP1   -2.174479 1.1202164 514 -1.941124  0.0528
fingerR:locationExtP1   -2.153727 1.1338847 514 -1.899424  0.0581
fingerL:locationExtP1   -0.107558 1.1364151 514 -0.094646  0.9246
```

Code 14: R code for contrast analysis

```
group <- gl(12,45,540,labels=c("ExtP3:I","ExtP3:M","ExtP3:R","ExtP3:L",
                               "FlexP3:I","FlexP3:M","FlexP3:R","FlexP3:L",
                               "ExtP1:I","ExtP1:M","ExtP1:R","ExtP1:L"))

library(MASS)
M.location<-cbind(
  c(1,0,0,0,-1,0,0,0,0,0,0,0), # ExtP3/FlexP3,I
  c(0,1,0,0,0,-1,0,0,0,0,0,0), # ExtP3/FlexP3,M
  c(0,0,1,0,0,0,-1,0,0,0,0,0), # ExtP3/FlexP3,R
  c(0,0,0,1,0,0,0,-1,0,0,0,0), # ExtP3/FlexP3,L
  c(1,0,0,0,0,0,0,0,-1,0,0,0), # ExtP3/ExtP1,I
  c(0,1,0,0,0,0,0,0,0,-1,0,0), # ExtP3/ExtP1,M
  c(0,0,1,0,0,0,0,0,0,0,-1,0), # 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),
                                            pdDiag(~location-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(0,0,0,0,0,0,0,0,1,-1,0,0), # 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(0,0,0,0,0,0,0,0,0,1,-1,0), # 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(0,0,0,0,0,0,0,0,0,0,1,-1) # R/L, ExtP1
)
contrasts(group)<-t(ginv(M.finger))
fitM2.3.REML.finger <- lme(F ~ group,
                           random=list(individual=
                           pdBlocked(list(pdIdent(~1),
                                          pdDiag(~location-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)
```

Code 15: Extract of the R output for contrat analysis for comparing each finger force intensity between locations (group1

```
Fixed effects: F ~ group
                 Value Std.Error  DF    t-value p-value
(Intercept)  12.741371 0.7462516 514  17.073827  0.0000
group1      -16.632080 1.7004340 514  -9.781079  0.0000
group2      -18.217502 1.6479859 514 -11.054404  0.0000
group3      -11.337212 1.6479859 514  -6.879435  0.0000
group4       -6.505398 1.6479859 514  -3.947484  0.0001
group5       -6.084934 0.9522274 514  -6.390211  0.0000
group6       -3.910455 0.9369387 514  -4.173651  0.0000
group7       -3.931207 0.9369387 514  -4.195799  0.0000
group8       -5.977376 0.9369387 514  -6.379688  0.0000
group9        2.927701 0.6237270 514   4.693882  0.0000
group10      -9.304134 0.6694338 514 -13.898513  0.0000
group11      -0.337429 0.6151191 514  -0.548558  0.5835
```

Code 16: Extract of the R output for contrat analysis for comparing nearby finger force intensities for each location (group1

```
Fixed effects: F ~ group
                Value Std.Error  DF   t-value p-value
(Intercept) 12.741371 0.7462530 514 17.073797  0.0000
group1       1.393365 0.8019732 514  1.737421  0.0829
group2      -0.192057 0.9288755 514 -0.206763  0.8363
group3       3.567844 0.8231851 514  4.334194  0.0000
group4       1.348877 0.8026559 514  1.680517  0.0935
group5       8.229167 0.9060900 514  9.082063  0.0000
group6       1.328125 0.8206804 514  1.618322  0.1062
group7       0.934923 0.8020522 514  1.165663  0.2443
group8       5.766737 0.8875402 514  6.497438  0.0000
group9      -1.111247 0.8168230 514 -1.360450  0.1743
group10      2.733225 1.1135839 514  2.454440  0.0144
group11     18.614637 2.3509517 514  7.917916  0.0000
```