CARLETON UNIVERSITY

SCHOOL OF
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HONOURS PROJECT

TITLE: Analyzing Pixel Intensity Data Using Linear Regression Model and Linear Mixed Model

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1. Introduction

Over the last decade, the literature on model selection in linear mixed-effect models has been growing exponentially. The problem became more complicated than in linear regression, because the selection on the covariance structure was not simple, due to the computational issues and boundary problems arising from positive semi-definite constraints on covariance matrices. Hence, the Linear Mixed-Effects Model (LMMs) was proposed in the classical paper by Laird and Ware (1982).

The linear mixed-effect models, also known as “multi-level models” or “hierarchical models”, are a type of regression model that contemplates both (1) variation that is explained by the independent variables of interest – fixed effects, and (2) variation that is not explained by the independent variables of interest – random effects. Due to the aspect of this model having a mixture of fixed and random effects, it is classified as a mixed model. In terms of random effects, it gives an error term ϵ to the structure, and this represents the deviation from the predictions due to “random” factors that cannot be controlled experimentally.

The general linear mixed model provides a useful approach for analysing a wide variety of data structures which practising statisticians often encounter. Such data structures which can be problematic, are imbalanced repetitive measured data and longitudinal data. The model is similar in many aspects to ordinary multiple regression, but because it allows correlation between the observations, it requires an additional work to specify models and assess goodness-of-fit.

In linear regression models, the responses are independent, whereas, in linear mixed-effect models, they are typically dependent. This dependence impacts on model selection by reducing the effective sample size, a quantity that affects the theoretical properties of procedures and is used explicitly in some model selection procedures such as the Bayesian Information Criteria (BIC; Schwarz, 1978). The dependence also means that linear mixed-effect models have both regression parameters—which describe the mean structure, and variance parameters – that describe the sources of variability and the dependence structure. These parameters have a different relative importance in the analysis. Thence, this should be reflected in model selection.

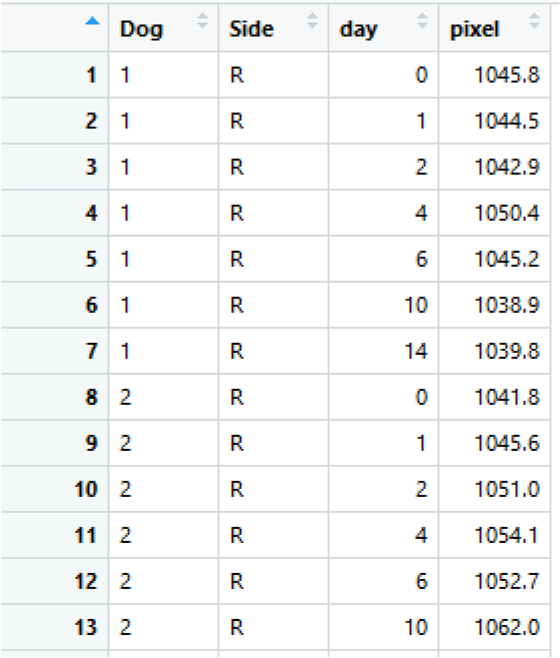
From this research project, an exploratory analysis was performed to discover the basic structure of data based on the X-ray pixel intensity dataset acquired from an experiment. Thus, the linear regression analysis was implemented to find the relations between the response and covariates. Both exploratory analysis and linear regression analysis indicated that there was a two-level nested group effect in the data. Based on this analysis, a linear mixed-effect model was created to fit the data. The construction of this model referenced the information from the linear regression model. Consequently, the linear mixed-effect model built was optimal in terms of trade-off between fitting and robustness.

2. Data Description

The dataset used for this research project is chosen from R 'MEMSS' dataset package, 'Pixel', and it was described in Pinheiro and Bates (2000). The dataset is from an experiment conducted by Deborah Darien, Department of Medical Sciences, School of Veterinary Medicine, University of Wisconsin, Madison. The experimenters injected ten individual dogs with a dye contrast, then recorded the mean X-ray pixel intensities from CT scans of the right and left lymph nodes in the axillary region of each dog on several occasions up to 21 days post injection. The main interest of this experiment was to study the change of the mean pixel intensity over the time

This 'Pixel' data frame has 102 rows and 4 columns of data based on the above information and data frame contains the following columns:

Dog: a factor with levels A to J designating the dog on which the scan was made
Side: a factor with levels L and R designating the side of the dog being scanned
Day: a numeric vector giving the day post injection of the contrast on which the scan was made
Pixel: a numeric vector of pixel intensities



	Dog	Side	day	pixel
1	1	R	0	1045.8
2	1	R	1	1044.5
3	1	R	2	1042.9
4	1	R	4	1050.4
5	1	R	6	1045.2
6	1	R	10	1038.9
7	1	R	14	1039.8
8	2	R	0	1041.8
9	2	R	1	1045.6
10	2	R	2	1051.0
11	2	R	4	1054.1
12	2	R	6	1052.7
13	2	R	10	1062.0

Figure 1: Pixel dataset (98 rows are omitted)

Because a dog is a group factor and the side are a factor nested within the dog, this paper refers the “dog level” to the individual effect of the dog, and the “side level” or “side within dog level” represents the effect of each side of a dog. Also, the “within group” factor refers to the effect of each observation.

Since the data was obtained from an experiment, there were few assumptions to proceed the research:

1. Assume that the experiment is well randomized.
2. Assume that the scans are carried out independent within the side level
3. The pixel observations are numerical values obtained from a continuous variable, and we assume that each observation is obtained from a normal distribution.

3. Models Analysis

From this section, linear regression model and linear mixed effect model will be explained theoretically before the implementation of concepts to the dataset.

3.1 Linear Regression Model

The linear regression model,

$$y_i = \beta_1 x_{1i} + \beta_2 x_{2i} + \cdots + \beta_p x_{pi} + \epsilon_i$$
$$\epsilon_i \sim NID(0, \sigma^2)$$

has one random effect, the random error term, denoted ϵ_i. The parameters of the model are the regression coefficients, $\beta_1, \beta_2, \ldots, \beta_p$, and the error variance, σ^2. In most cases, $x_{1i} = 1$, and so β_1 is a constant or intercept. Therefore, the linear model in matrix form has the following structure;

$$Y = X\beta + \epsilon$$
$$\epsilon \sim N_n(0, \sigma^2 I_n)$$

Where $\boldsymbol{Y} = (y_1, y_2, \ldots, y_n)'$ is the response vector; **X** is the model matrix, with typical row $\boldsymbol{x}_i' = (x_{1i}, x_{2i}, \ldots, x_{pi})$; $\boldsymbol{\beta} = (\beta_1, \beta_2, \ldots \beta_p)'$ is the vector of regression coefficients; $\epsilon = (\epsilon_1, \epsilon_2, \ldots, \epsilon_n)'$ is the vector of random errors; $\boldsymbol{N}_n$ represents the n-variable multivariate-normal distribution; $\mathbf{0}$ is an $n \times 1$ vector of zeroes; and $\mathbf{I}_n$is the order-n identity matrix.

3.2 Linear Mixed-Effect Model

The mixed-effect models include additional random-effect terms and are often appropriate for representing clusters. Therefore, they are claimed to be independent. For instance, when data are collected hierarchically, when observations are taken on related individuals, or when data are gathered over time on the same individuals. For hierarchical data with a single level of grouping, we can formulate the classical LMM at a given level of a grouping factor as follows:

$$\boldsymbol{y_i} = \mathrm{X}_i\beta + Z_i b_i + \epsilon_i$$
$$\boldsymbol{b_i} \sim \mathrm{N_q}(0, \boldsymbol{\psi})$$
$$\boldsymbol{\epsilon_i} \sim N_n(0, \sigma^2 \wedge_i)$$

Where;

$\boldsymbol{y_i}$ is the $n_i \times 1$ response vector for observations in the ith group.

$\mathbf{X}_{\boldsymbol{i}}$ is the $n_i \times p$ model matrix for the fixed effects for observations in group i.

$\boldsymbol{\beta}$ is the $p \times 1$ vector of fixed-effect coefficients.

$\boldsymbol{Z_i}$ is the $n_i \times 1$ model matrix for the random effects for observations in group i.

$\boldsymbol{b_i}$ is the $q \times 1$ vector of random-effect coefficients for group i and independent.

$\boldsymbol{\epsilon_i}$ is the $n_i \times 1$ vector of errors for observations in group i and independent.

$\boldsymbol{\psi}$ is the $q \times q$ covariance matrix for the random effects.

$\boldsymbol{\sigma^2} \wedge_{\boldsymbol{i}}$ is the $n_i \times n_i$ covariance matrix for the errors in group i.

Specifically, where $\boldsymbol{y_i}, \mathbf{X}_{\boldsymbol{i}}, \boldsymbol{\beta}$, and $\boldsymbol{\epsilon_i}$ are the vectos, the design matrix, and the vector of residual errors for group i, respectively, while $\boldsymbol{Z_i}$ and $\boldsymbol{b_i}$ are the matrix of covariates and the corresponding vector of random effects:

$$\boldsymbol{Z_i} = \begin{bmatrix} z_{i1}^{(1)} & z_{i1}^{(2)} & \cdots & z_{i1}^{(q)} \\ z_{i2}^{(1)} & z_{i2}^{(2)} & \cdots & z_{i2}^{(q)} \\ \vdots & \vdots & \ddots & \vdots \\ z_{in_i}^{(1)} & z_{in_i}^{(2)} & \cdots & z_{in_i}^{(q)} \end{bmatrix} = \begin{pmatrix} z_i^{(1)} & z_i^{(2)} & \cdots & z_i^{(q)} \end{pmatrix}, \qquad \boldsymbol{b_i} = \begin{pmatrix} b_{i1} \\ b_{i2} \\ \vdots \\ b_{iq} \end{pmatrix}.$$

3.2.1 Random Effects

The core of mixed models is incorporation of fixed and random effects. A fixed effect is a parameter that does not vary. For example, it can be assumed that there are some true regression lines in the population, β, and estimation of it, $\hat{\beta}$. In contrast, random effects are parameters that are themselves random variables. For instance, assume β as a distributed random normal variate with mean value of μ and standard deviation of σ, or equation form $\beta \sim N(\mu, \sigma)$. This is essentially equivalent to linear regression, where the data are random variables. However, the parameters are fixed effects. Then, the data are random variables and the parameters are random variables at one level but fixed at the highest level.

4. Exploratory Analysis

In order to investigate the change of the pixel over the time, the model should be built with pixel in terms of response and time (day) as covariate factors. Hence, to build the previously described model, following aspects can be used: the type of relationship between pixels and time, the applicability of relationship applied for different dogs or even each side of a dog, and finally, according to the data, the possible assumptions to be made for building a regression model.

4.1 Basic Structure of Data

As mentioned in Section 2, Data Description, the dataset contains 102 observations in total, and the number of observations for each dog is shown in Table 1, where N represents the total number of observations for each dog. Additionally, basic statistics for pixels and time are shown in Table 2.

Table 1: Number of observations for each dog

Dog	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
N	13	13	14	14	9	10	8	8	4	6

Table 2: Basic Statistics for Pixel and Dog

	Min	**1st Qu.**	**Median**	**Mean**	**3rd Qu.**	**Max**
Pixel	1034	1054	1088	1087	1110	1161
Dog	1.000	3.000	5.000	4.902	7.000	10.000

Prior to the further analysis, there are few things to point out from Table 1 and Table 2. First of all, the number of observations for each dog is different. Thus, the distributions of response pixel and covariate time is not seriously skewed. To check if there are any differences among the groups at dog level and side level, the structure of pixel for different dogs and both sides of each dog's lymph nodes should be studied as the data was collected from different dogs, and for each dog, response values of two sides of lymph nodes were always recorded. From this statement, the "groups" represents the groups of most inside level (i.e. side level).

Additionally, box plots are drawn at the dog level and side level. Referring to the left diagram in Figure 2, at dog level, the differences among mean values were obvious and the variation of the spreads among the different dogs is shown. Roughly speaking, dogs with smaller mean pixel intensities have smaller variances. However, dog 10 is an exception, because it has a medium mean value, but the values are widely spread out, which represents the dog 10 as having large range of values. Also, there are two outliers with very small pixel values for dog 4 and one outlier each for dog 2 and dog 3. Referring to the diagram on the right side of Figure 2, at side level which was nested within dog, mean values as well as variances of two sides of each dog's lymph nodes are different especially for dog 6, 7, 8, 9 and 10. At both dog and side levels, dog 10 is sufficient to be call as an exception.

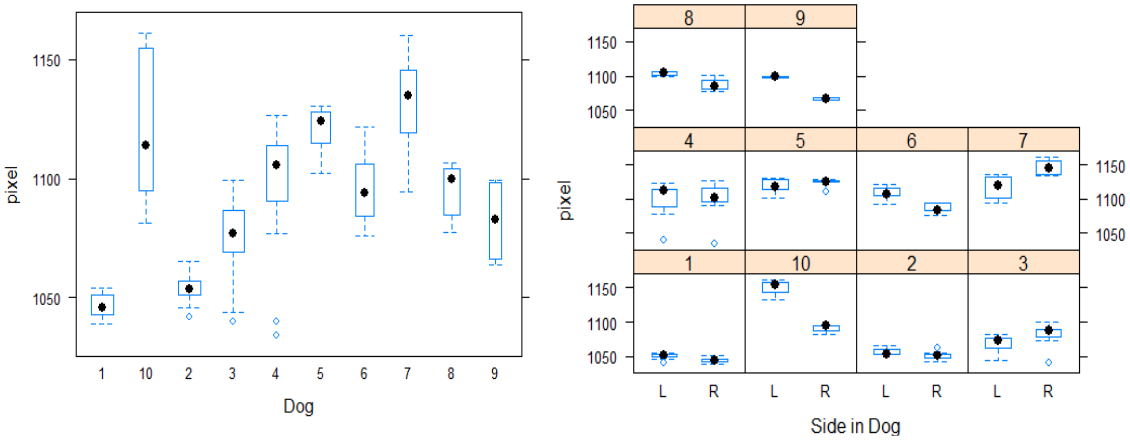


Figure 2: Pixel for each dog (left) and Pixel for each side of every dog (right)

4.2 Relationship Between Response and Time

In section 4.1, the analysis is based on the relationship between Pixel and Dogs. Moreover, from these results, it is ambiguous to state that these differences are caused by group effects or by the non-homogeneity of time for different groups. For instance, different groups observed the pixel at different days to figure out the clear cause of the difference. Thus, the change of response over time was studied.

Table 3: Basic Statistics for Pixel and Day

	Min	1st Qu.	Median	Mean	3rd Qu.	Max
Pixel	1034	1054	1088	1087	1110	1161
Time (day)	0.00	4.00	6.00	7.49	10.00	21.00

To study the change of response over time, the scatter plot of pixel versus time was drawn for the entire data and a smoothed curve was fit using Local Polynomial Regression Fitting (LOESS), shown in Figure 3. This fitted curve showed a quadratic pattern for the relationship between pixel and day and this indicated that for each day, the variability of pixel was high. Due to the fact that different observations were made from different dogs and different sides, the variabilities were present. Hence, the effect of individual group was investigated with days at dog level and side level versus pixel intensity scatter plots (Figure 4). There were few details to point out from Figure 4.

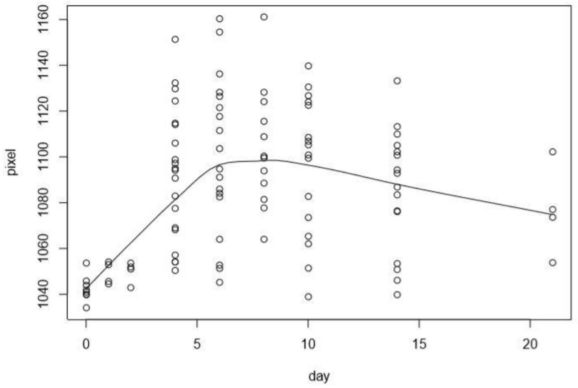


Figure 3: Scatter Plot of pixel vs time of entire data with fitted curve

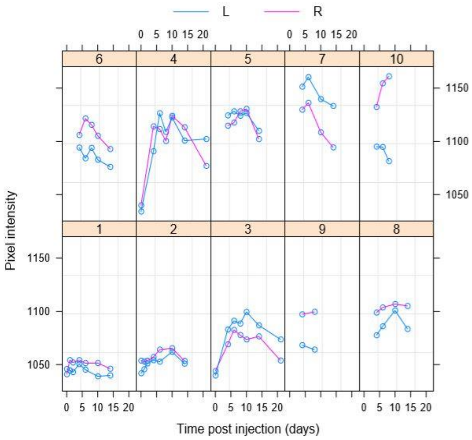


Figure 4: Scatter Plots of pixel vs time at dog level and side level

First, for each group at side level, the relationship between pixel and day (time) were non-linear and for most dogs, they had a shape of quadratic. Especially for dog 4, pixel on both sides of lymph nodes showed greater variability than pixel on both sides of other dogs' lymph nodes. This indicated heteroscedasticity of within group error.

Furthermore, within dog level, curvatures were very similar for both sides of lymph nodes for most dogs, except that there was a constant drift. For all dogs, except 9 and 10, even though they had different left and right lymph node values, the patterns were similar as described above. However, the graphs of dog 9 and dog 10 showed that left and right lymph node values were different, as well as the patterns. Consequently, there were differences between slopes of two sides of lymph nodes, but this may have been caused by the small sample sizes. As shown in Table 1 in section 4.1, dog 9 and dog 10 had only four and six observations respectively.

Ultimately, from the left diagram on Figure 2, obvious contrasts were seen between dogs, sample means and sample variances. Although, the pattern of relationship between pixel and time for most of dogs was quadratic, the shapes varied.

4.3 Summary of Exploratory Analysis

Referring back to Section 4.1 and 4.2, the following preliminary conclusions can be made: the time on pixel density is different for each dog and each side of lymph node. At dog level, there were difference between means, variances and the curvature. At side level, the curvatures were similar but different intercepts. Within groups at side level, there was a possibility of heteroscedasticity, especially for dog 4. Also, the relationship between pixel density and day (time) was nearly quadratic for most dogs.

5. Data Analysis Using Regression Models

From this section, linear regression model and linear mixed effect model was analyzed and compared technically for the corresponding dataset described in the Section 2 and 4.

5.1 Analysis Using Linear Regression

Prior to the usage of linear regression models, recall three assumptions made at the end of Section 2.

1. Assume that the experiment is well randomized.
2. Assume that the scans are carried out independent within the side level
3. The pixel observations are numerical values obtained from a continuous variable, hence assume that each observation is obtained from a normal distribution.

In consideration of the three assumptions above, especially with the last assumption, the linear regression model can be built to study the relationship between pixel and day (time). The linear regression model used in this section is providing very useful guide for building a linear mixed-effect model. Furthermore, the result from this model was used as reference to compare with a mixed model.

5.1.1 Model Building and Variable Selection

Preliminary analysis showed that the relationship between pixel and day(time) is nearly quadratic. Therefore, the term day^2 was used for the model. Additionally, the dog and side both had few effects on the response. Consequently, there were used as covariates. Then, the simple model was defined as:

$$\begin{aligned} Y_i &= \beta_0 + \beta_1 day_i + \beta_2 day_i^2 + \beta_3 Dog_i + \beta_4 Side_i + \epsilon_i \\ &= \overrightarrow{\beta'}\,\overrightarrow{X_i} + \epsilon_i \end{aligned} \tag{1}$$

where $\epsilon_i \overset{i.i.d.}{\sim} N(0,\sigma^2)$, $\overrightarrow{\beta'} = (\beta_0, \cdots, \beta_4)$ and $\overrightarrow{X_i} = (day_i, day_i^2, Dog_i, Side_i)'$. Then, the step-wise selection on this model was performed and concluded with three covariates: day, day^2 and dog. The variable Side was excluded, since it did not pass the significant test with p-value of 0.1 for t-test. Furthermore, the R-squared statistics for the reduced model was 0.7541 where the higher R-squared value represents a better result with 1 being the best. Therefore, this was not a good fit for the model. (Refer to Appendix A for the outputs)

With the previous analysis, for each dogs and sides, the relationship between pixel and time may be different. Consequently, the cross effect terms, such as “day:Dog”, “day:Dog:Side” and etc., was implemented to the model, in order to achieve the desired results. Prior to the selection of hyperparameters, all possible terms including intercept, main effects and interaction between cross effects terms were taken into consideration. Then, the following procedure was used for performing variable selection method:

1. Fit models to each of the variables individually, then choose the qualifying variables that pass the t-test.

2. Then, a model is generated with the selected variables from step 1. From this model, t-test is performed once again for each individual variable, to remove the variables that may not pass the test. At each removal, F-test is used to compare the nested model to see if the removal leads to the worst fit. If it leads to the worst fit, keep the variable, otherwise remove it.
3. Variables removed from step 1 may become significant variables for the presence of others. Thus, those variables are added one at a time to the model from step 2 whether it leads to the better fit. Similar to step 2, F-test is used to compare fits.
4. The last step is to verify the model from step 3, to ensure if this is the best model by checking that no variable should be either removed from or added to the current model using F-test for the best fit.

Note that Appendix B contains the outputs. After going through this selection procedure, the final model is found, and this model is called *lmfit*.

$$lmfit: \text{ pixel} \sim \text{day}^2 + \text{Dog} + \text{day:Dog} + \text{day:Side} + \text{day}^2\text{:Dog} + \text{Dog:Side}$$

The model above was labeled as la2 in the codes and the Residual standard error is 8.63 on 63 degrees of freedom. Also, the R-Squared statistic of this model is 0.9292. Compared with previous simple linear model, R-Squared statistic was 0.3465. This model explained more variability of the data. Also, this provide better fit as p-value of F-test for comparing those two models is $1.520e^{-13}$.

5.1.2 Diagnostic for Linear Regression Model

Seven residual plots were generated to test the corresponding model assumptions: independence, normality, constant variance and linearity. Since there were no patterns shown for the top left plot (Residuals values versus Fitted values), and the second top left plot (Scale-Location), which represents the standardized residual values versus fitted values, indicated that the model was in a reasonably good fit. Thus, it justified the constant variance assumption and indicated that the errors were independent.

However, with these plots, several outliers were identified, such as 24, 27, 28 and 74. Furthermore, the Q-Q plot showed that the normality assumption was suitable, and it also showed outliers, such as 27, 28 and 74. The Residual versus Leverage plot and Half Normal Plot of Leverage plot suggested that there were several influential points, such as 28, 47, 49, 98 and 100. The partial residual plot of main effect of day plot showed a good linear relationship. The Partial Residual Plot of day^2 plot which is the main effect of day^2, is not strictly linear and this may have been occurred by the higher order nature of this variable. Overall, the model fits the data reasonably well.

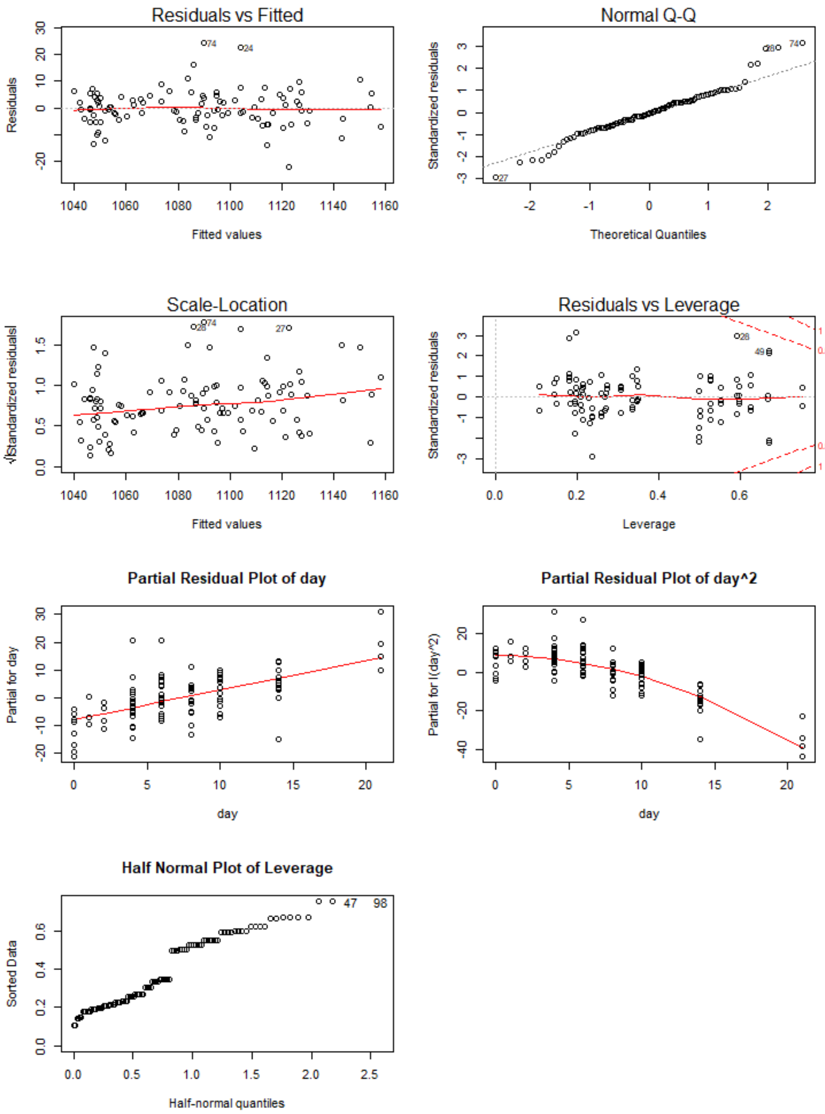


Figure 5: Residual plots for linear regression model: lmfit

5.1.3 Analysis and Interpretation

Clearly, from the model construction, several cross-effect terms were considered significant in the model. At dog level, the cross-effect terms day:Dog and day^2:Dog were present. With the main effect terms of day, day^2 and Dog, was included in the final model. This can be justified as day and day^2 have interactions with Dog level and this agreed with the exploratory analysis with Figure 4 that for each dog, the mean value of pixels is different, and the curvature of the relationships are also different.

At side level, the cross-effect terms day:Side and Dog:Side were present but the main effect of side was not present in the model. This indicated that there was a nested effect of side on the pixel values. Furthermore, the cross-effect term $\text{day}^2\text{: Side}$ was not included in the final model and this implies that no significant difference between the quadratic terms of two sides of lymph nodes for each dog were shown. Moreover, this agreed with the exploratory analysis, Section 4.3, within dog level, the curvature for two sides are nearly parallel with a constant drift, and for dog 9 and 10, there were differences between slopes.

Even though, the linear regression model, ***lmfit***, is an excellent fit, there were some issues to be discussed:

1. There were only 102 observed data, however, there were 50 parameters present in the model due to the complicated group effects. As a consequence, the average magnitude of sample size was 5 for each group at side level, since for each side of a dog, the biggest size was 7 and the smallest size was 2. In some cases, the model was easily fitted to few samples in the group, but it missed the true relationship from the population, such as overfitting.
2. In Section 5.1.2, several outliers and influential points were identified. It is not surprising that all the outliers came from dog 4. According to Figure 1 and 4, and exploratory analysis, pixels on both sides of lymph nodes of dog 4 showed large variability compared to other dogs. Additionally, this may had been occurred by the heteroscedasticity of within group error. Therefore, it cannot be reduced with a constant variance assumption. On the other hand, four of the influential points

originated from dog 9 and 10. Hence, according to Table 2, Dog 9 had only 4 observations and Dog 10 had only 6 observations. Since both sides of lymph nodes were observed individually, the number 4 and 6 represented that dog 9 was observed only twice for each side and dog 10 was observed for 3 times for each side. Considering that the sample sizes of those two dogs were very small, it can be concluded that the inference is actually made toward the few points. Due to the fact that these few points were used to generate the inference, a small estimated variance occurred, hence these points were indeed influential.

Table 4: List of Outliers

	Dog	**Side**	**Day**	**pixel**
24	4	R	6	1126.4
27	4	R	14	1100.7
28	4	R	21	1102.2
74	4	L	4	1114.1

Table 5: List of Influential Points

	Dog	**Side**	**Day**	**pixel**
28	4	R	21	1102.2
47	9	R	4	1068.2
49	10	R	4	1095.0
98	9	L	4	1097.2
100	10	L	4	1132.3

5.2 Analysis Using Linear Mixed-Effect Model

A linear mixed-effect model would be an ideal candidate to build and compare with the linear regression model ***lmfit.*** This is because the linear mixed-effect model would help avoid issues that are listed at the end of Section 5.1 and help incorporate the effects of different groups. The effects of different groups are assumed to be a random sample from a common population with common covariance structure in the linear mixed-effect model, and this covariance structure reflects the variability between groups. Therefore, the effects of groups and its correlations are incorporated whilst the numbers of parameter are visibly reduced.

5.2.1 Choosing Structure for Linear Mixed-Effect Model

For forming the linear mixed-effect model for data, there are two questions that must be considered:

1. Which variables should be considered for having random effects?
2. What is the covariance structure of the random effects at each level?

For the first question, the linear regression model *lmfit* has answered partially. All variables appeared in the *lmfit*'s cross effect terms at dog level and side level could be considered as a random effect. More specifically, intercept, day and day^2 from the dog level, intercept and day from the side level are considered as random effects. Furthermore, this agrees with the exploratory analysis as shown in the previous sections.

To discover the covariance structure, two paired plots can be drawn for the coefficients of the cross-effect terms from *lmfit* at dog level, Figure 6, and at side level Figure 7. With these two plots, it is easy to see if there is any correlation existing for cross-effect terms. Hence, the full variance-covariance structure will be used in the mixed model as it appears that the variables are correlated at each level.

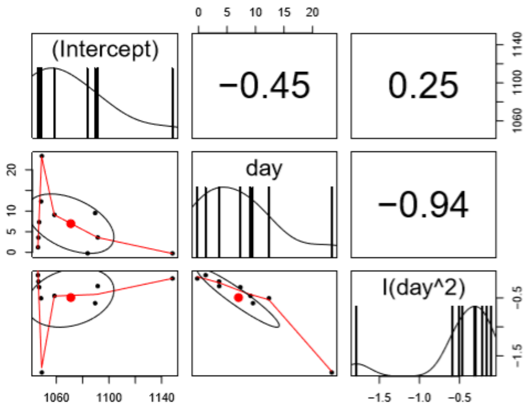


Figure 6: Correlation of coefficients of cross-effect terms at dog level

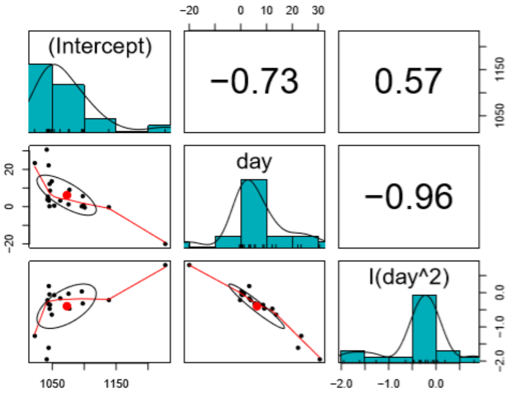


Figure 7: Correlation of coefficients of cross-effect terms at side level

5.2.2 Building Linear Mixed-Effect Model

According to above analysis for the linear mixed-effect model, the model can be built as follow:

$$Y_{ijk} = \beta_0 + \beta_1 day_{ijk} + \beta_2 day_{ijk}^2 + \eta_i Dog_{ijk} + \eta_i day_i \mathbb{1}_{(i\neq1)} + \gamma_{i0} + \gamma_{i1} day_{ijk} + \gamma_{i2} day_{ijk}^2 + \alpha_{ij0} + \alpha_{ij1} day_{ijk} + \epsilon_{ijk}$$

Where $i = 1, \dots, 10$ is the label for dogs, $j = 1{,}2$ is the label for sides, $k = 1, \dots n_{ij}$ is the label for observations for side j of dog I and $\mathbb{1}_{(i\neq 1)}$ is the indicator function which takes value 1 if $i = k$ and 0 otherwise, and $\mathbb{1}_{(i\neq k)} := 1 - \mathbb{1}_{(i=k)}$. In the model, β_i and η_i are fixed effects, and γ_{ij} and α_{ijk} are random effects.

Define,

$$\vec{Y}_{ij} = \left(Y_{ij1}, \cdots, Y_{ij\eta_{ij}}\right)^T$$

$$X_{ij} = \begin{pmatrix} 1 & day_{ij1} & day_{ij1}^2 & \mathbb{1}_{(i=2)} & \mathbb{1}_{(i=3)} & \cdots & \mathbb{1}_{(i=10)} \\ \vdots & \vdots & \vdots & \vdots & \vdots & & \vdots \\ 1 & day_{ij\eta_{ij}} & day_{ij\eta_{ij}}^2 & \mathbb{1}_{(i=2)} & \mathbb{1}_{(i=3)} & \cdots & \mathbb{1}_{(i=10)} \end{pmatrix}$$

And

$$\vec{\beta} = \left(\beta_0, \beta_1, \beta_2, \eta_{2,}, \cdots, \eta_{10}\right)^T$$

Note that “dog” is a categorical variable of 10 levels.
In addition, let

$$Z_{ij} = \begin{pmatrix} 1 & day_{ij1} & day_{ij1}^2 \\ \vdots & \vdots & \vdots \\ 1 & day_{ij\eta_{ij}} & day_{ij\eta_{ij}}^2 \end{pmatrix}$$

$$W_{ij} = \begin{pmatrix} 1 & day_{ij1} \\ \vdots & \vdots \\ 1 & day_{ij\eta_{ij}} \end{pmatrix}$$

$$\vec{\gamma}_i = (\gamma_{i0}, \gamma_{i1}, \gamma_{i2})^T \quad and \quad \vec{\alpha}_{ij} = \left(\alpha_{ij1}, \alpha_{ij2}\right)^T$$

Then the model can be represented as following:

$$\vec{Y}_{ij} = X_{ij}\vec{\beta} + Z_{ij}\vec{\gamma}_i + W_{ij}\vec{\alpha}_{ij} + \vec{\epsilon}_{ij} \quad where \ \vec{\epsilon}_{ij} = \left(\epsilon_{ij1}, \cdots, \epsilon_{ij\eta_{ij}}\right)^T$$

We assume that $\vec{\gamma}_i \overset{i.i.d.}{\sim} N(0, \psi_1)$, $\vec{\alpha}_{ij} \overset{i.i.d.}{\sim} N(0, \psi_2)$ and $\vec{\epsilon}_{ij} \overset{i.i.d.}{\sim} N(0, \sigma^2 I)$, where ψ_1, ψ_2 and σ^2 are unknown parameters. Additionally, assume that $\vec{\gamma}_i$, $\vec{\alpha}_{ij}$, and $\vec{\epsilon}_{ij}$ are independent and this model can be called as *lmefit*. Results of *lmefit* showed that all fixed effects are significant in this model. To compare models, covariance matrices should be modified to diagonal matrices. After that, chi-square test can be used to compare models. According to R, *lmefit* has a p-value as 00.000133 and when this model is compared to the reduced model, it is significantly a better model.

As mentioned in Section 5.1.1, the chi-square test is used instead of the F-test to perform the same variable selection method for this model. The reason behind this is that the chi-square test is intended to test how likely it is that an observed distribution is due to chance. It is also called a “goodness of fit” (All outputs can be found in Appendix B) because of its ability to measure how well the observed distribution of data fits with the distribution that is expected if the variables are independent. According to Appendix B, the model Imefit19 representing the above linear mixed-effect model is the best output as it has the smallest chi-squared value, 0.01491.

5.2.3 Diagnostic for Linear Mixed-Effect Model

For linear mixed-effect model, following two types of model assumptions were examined:

1. Within-group errors are independent and identically normally distributed with mean zero and constant variance, and they are independent of the random effects.
2. The random effects are normally distributed.

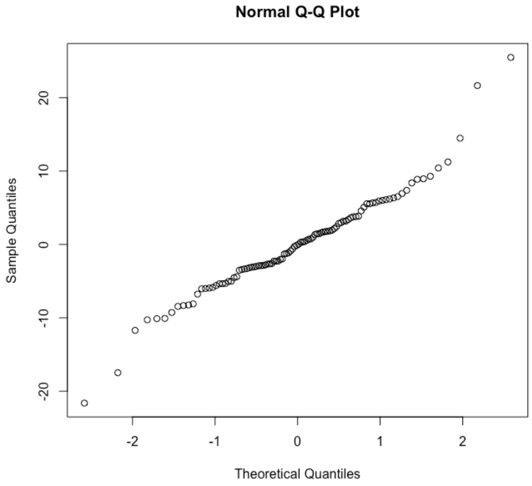


Figure 8: Q-Q plot of residual of lmefit

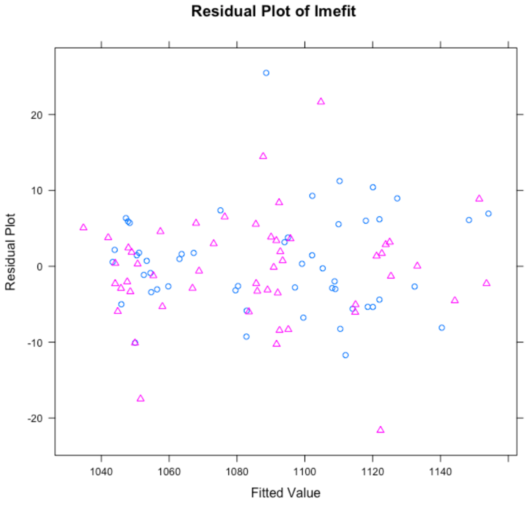


Figure 9: Residual plot of lmefit

For within-group error, the residual Q-Q plot, figure 8, and residual scatter plot, figure 9, are draw. For the Q-Q plot, it shows that the points in a plot are straight therefore, the normality assumption is reasonably satisfied. Additionally, the residual scatter plot has no pattern. A residual plot shows the residuals on the vertical axis and the independent variable on the horizontal axis. If the points in a residual plot are randomly dispersed around the horizontal axis, a linear regression model is appropriate for the data. Since the residual plot has no pattern, the model fits well and the constant variance assumption is satisfied.

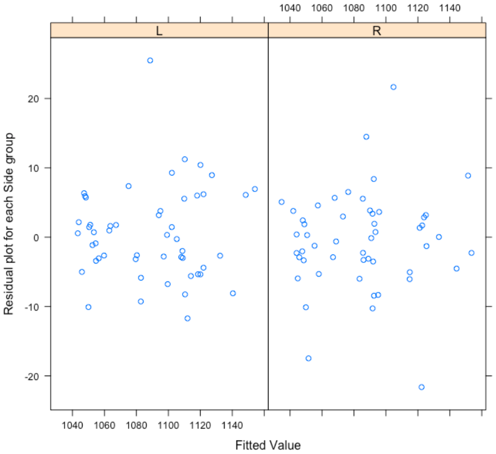


Figure 10: Residual plot of lmefit by side

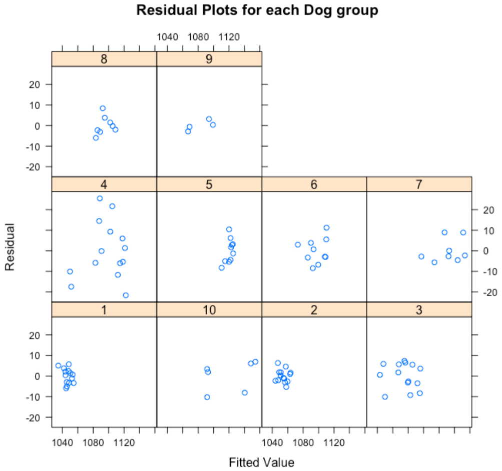


Figure 11: Residual plot of lmefit by group

Figure 10 represents the scatter plots of residual for each side and this indicates that the right-side points of plot are more clustered than the left side. This indicates that the residual of the right side of lymph nodes has a slightly larger variability than the residual of the left side of lymph nodes. However, they are basically identical. Moreover, Figure 11 represents the residual plot of *lmefit* by group and points for plots of dog 3, dog 4, dog 6, dog 7 and dog 10 are spread especially dog 4. This shows that dog 4 has the greatest variability compare to other dogs. However, for other groups, scatter plots show no relationship between within-group error and effects of groups. This justifies assumption of within-group errors are independent of random effects.

For random effects, Q-Q plots of estimated random effects at dog level, Figure 12, and side level, Figure 13, can be draw. As mentioned earlier, points of each plot are shown as straight therefore, the normal assumption for random effects are well satisfied.

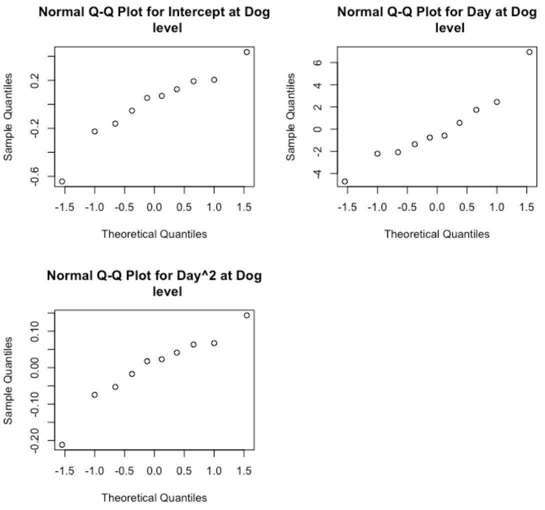


Figure 12: Q-Q plots of random effect at dog level

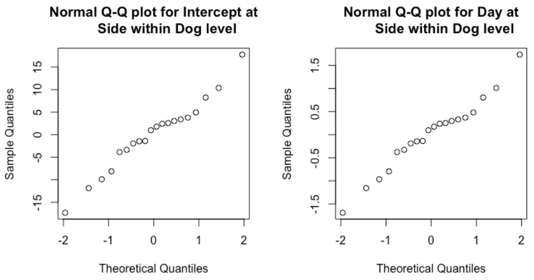


Figure 13: Q-Q plot of random effect at side level

5.3 Analysis, Comparison and Interpretation

From beginning to end of the perfect fit model finding procedure, there are few major points to be reviewed:

1. Why is the mixed model needed even though a linear regression can fit the data quite well?
2. how does the number of parameters effect the test result?
3. Outliers.

To answer the first question, two models, *lmfit* and *lmefit*, should be compared. Recall that, *lmfit* is the normal linear regression model and *lmefit* is the linear mixed-effect model. Table 6 represents some goodness-of-fit statistics of *lmfit* and *lmefit*.

For AIC, two models have analogous values but *lmfit* has slightly smaller value than *lmefit*. This can be concluded as the model *lmfit* is slightly better than *lmefit*. For BIC, *lmefit* has smaller value than *lmfit*. For AIC, the difference between *lmfit* and *lmefit* was only 9.9333 however, for BIC, the difference is 37.3162 which is much bigger than AIC. there are 50 parameters in the model *lmfit* but, there are only 21 parameters in *lmefit*. Since BIC penalizes more on number of parameters than AIC does, *lmefit* has much better value on BIC. Therefore, this can be concluded as the model *lmefit* is a better fit. For log-likelihood values, *lmfit* has lower log likelihood value than *lmefit* because *lmfit* contains more parameters.

Table 6: Statistics for lmfit and lmefit

	Number of parameters	**AIC**	**BIC**	**Log Likelihood**
lmfit	50	759.9864	864.9853	-339.9932 (df = 40)
lmefit	21	769.9197	827.6691	-362.9599 (df = 22)
Difference	29	9.9333	37.3162	22.9667

The analysis described above leads to the second question of the key points and to answer this question, fitted values of two models for different groups at each level should be compared. Figure 14 and 15 represent Fitted Values by Linear regression model and Linear Mixed-Effect Model accordingly. Those two figures look similar but when each fitted curve is compared, the curves fitted by linear mixed-effect model is “flatter” than the curves fitted by linear regression model, especially for the groups with small samples, Dog 5, 6, 7, 8 and 10 for both sides. This indicates that the linear mixed-effect model is less “plagued” by the small sample size problem, i.e. provides more robust estimates of parameters than linear regression. It is because, the normal linear regression model *lmfit* has parameters for day and day^2 for each group at every level. Hence, the sample points used to estimate those parameters in each group are very small. However, for linear mixed-effect model, the group effects share a few sample parameters at each level and this increased the number of observations used to estimate each parameter efficiently.

Additionally, the last key point outliers can be considered as a problem. As shown in Figure 11, dog 4 has some extra variability that is not explained by the model *lmefit* and this was also observed in exploratory analysis section. There are two possible following reasons:

1. The sample size for dog 4 is too small.
2. Dog 4 is from a distribution that has different variance with other groups.

For this case, it is more likely to be caused by the second reason. It is because for dog 4, there are total of 14 observations, 7 for each side, which is the largest sample size in entire dogs, so the first reason doesn’t count. Also, beginning of this research, there were three assumptions in Section 2 and one of those was, we assume that at each level, the random effects come from a same normal distribution. If the second reason is the case, the model *lmefit* cannot capture this variability since it comes from different normal distribution.

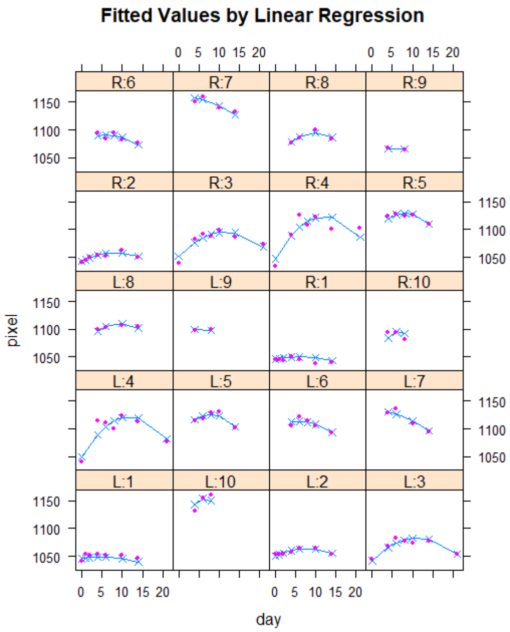


Figure 14: Fitted Values by Normal Linear Regression Model

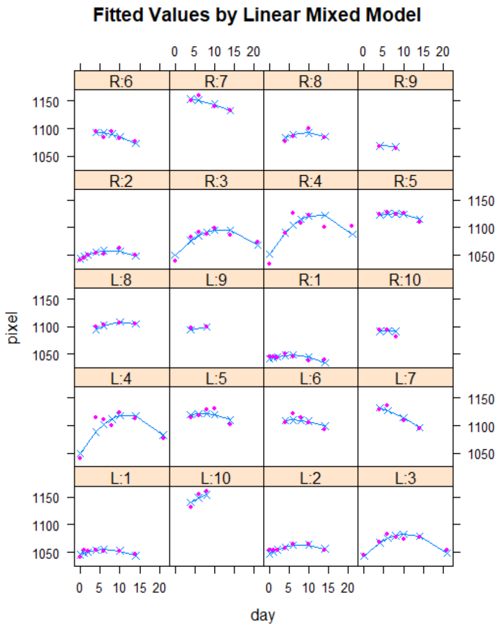


Figure 15: Fitted Values by Linear Mixed-Effect Model

Finally, the last key point, outliers can be considered as a problem. As shown in Figure 11, dog 4 has some extra variability that is not explained by the model *lmefit* and this was also observed in exploratory analysis section. There are two possible following reasons:

1. The sample size for dog 4 is too small.
2. Dog 4 is from a distribution that has different variance with other groups.

For this case, it is more likely to be caused by the second reason. It is because for dog 4, there are total of 14 observations, 7 for each side, which is the largest sample size

in entire dogs, so the first reason doesn't count. Also, beginning of this research, there were three assumptions in Section 2 and one of those was, we assume that at each level, the random effects come from a same normal distribution. If the second reason is the case, the model *lmefit* cannot capture this variability since it comes from different normal distribution.

6. Conclusion and Discussion

For the X-ray pixel intensities data, both models from normal linear regression *lmfit* and linear mixed-effect model *lmefit* were adequate. Comprehensively, both models agreed with the results from the following exploratory analysis: the relationship between pixel density and day was nearly quadratic for most dogs, the group effects on the relationship, at dog level. Moreover, there were differences between means, variance, and curvature and at side level, the curvatures were similar but had different intercepts.

Through out the model construction procedure, the conclusion was leaning towards the linear mixed-effect model for grouped data, because it has capabilities of modeling the differences between groups and the correlation within groups. Thus, at the same time, at each level, shared parameters were used, and this introduced "robustness" to the model. On the other hand, Normal linear regression model was adequate, but to use normal linear regression model, usually more parameters were required, and this could possibly cause "overfitting" issue. Once overfitting happens to the model, it fails to generalize, then malfunctions. Overfitting usually occurs when sample size at each group is too small.

Both exploratory analysis and linear regression analysis was available to provide some useful guidance, especially on the choice of variables for random effects and the covariance structure of random effects at each level.

From the analysis and interpretation of the dataset, dog 4 showed much greater variability than all other dogs, where it can be easily confirmed with Figure 4 and 11. Furthermore, both linear regression model and mixed effect model had few points of dog 4, that were outliers and this can be checked with Figure 2 and Table 4. Additionally, for mixed model, there were few assumptions made and the most important assumption was common covariance structures of the random effects for each dog group. However, it was extremely likely that the effect of dog 4 came from a population that had different variance from other groups. One possible way to deal with this problem was to “push” variability into the within-group error, then create a model that is capable of dealing with heteroscedasticity errors. Nevertheless, neither of these two models incorporated this problem and this can be studied further to improve the models.

7. Appendix

Code

```
# install.packages("rpart")
# install.packages("nlme")
# install.packages("lattice")
# install.packages("faraway")
# install.packages("lme4")
# install.packages("xtable")
# install.packages("Hmisc")
# install.packages("partykit")
# install.packages("robustHD")
# install.packages("sqldf")

# Random Effects Models
rm(list=ls())

## Pixel
require(nlme)
require(lattice)
require(faraway)
require(lme4)
require(xtable)
##require(Hmisc)

data(Pixel)
attach(Pixel)
print(Pixel)
View(Pixel)
class(Pixel)
getGroupsFormula(Pixel)
attach(Pixel)

## Preliminary Analysis
str(Pixel)
summ1 <- summary(pixel)
print(summ1)
summ2 <- summary(Pixel$Dog)
print(summ2)
summ3<- summary(Pixel)
print(summ3)

bwplot(pixel~Dog, xlab='Dog',varwidth=T)
bwplot(pixel~Side|Dog, xlab='Side in Dog')
```

```
## scatter plot
scatter.smooth(day, pixel)

## Pixel~day|Dog/Side
plot(Pixel, display = "Dog", inner = ~Side)

## Linearity and transformation
dogsize <- 1:10
sidesize <- 1:2
meand <- rep(0,length(dogsize))
sdd <- rep(0,length(dogsize))
means <- rep(0, length(sidesize)*length(dogsize))
sds <- rep(0, length(sidesize)*length(dogsize))
for (i in 1:length(dogsize)) {
  meand[i] <- mean(pixel[Dog==dogsize[i]])
  sdd[i] <- sd(pixel[Dog==dogsize[i]])
  means[i] <- mean(pixel[Dog==dogsize[i] & Side=='L'])
  means[length(dogsize)+i] <- mean(pixel[Dog==dogsize[i] & Side=='R'])
  sds[i] <- sd(pixel[Dog==dogsize[i] & Side=='R'])
  sds[length(dogsize)+i] <- sd(pixel[Dog==dogsize[i] & Side=='R'])
}
Lfit <- lm(log(sdd)~log(meand))
summary(Lfit)
plot(log(meand), log(sdd))
abline(Lfit)
Lfit <- lm(log(sds)~log(means))
summary(Lfit)
plot(log(means), log(sds))
abline(Lfit)

## lm fit
lmfit0 <- lm(pixel~day+I(day^2))
lmfit1 <- lm(pixel~day+I(day^2)+Dog)
lmfit2 <- lm(pixel~day+I(day^2)+Dog+day:Dog)
lmfit3 <- lm(pixel~day+I(day^2)+Dog+day:Dog+I(day^2):Dog)
lmfit4 <- lm(pixel~day+I(day^2)+Dog+Side)
summary(lmfit4)
anova(lmfit4)
lmfit5 <- lm(pixel~day+I(day^2)+Dog+Side+day:Dog+day:Side)
lmfitfull0 <-
  lm(pixel~day+I(day^2)+Dog+Side+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side)
lmfitfull1 <-
  lm(pixel~day+I(day^2)+Dog+Side+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side
     +Dog:Side)  ## the Best
lmfitfull2 <-
  lm(pixel~day+I(day^2)+Dog+Side+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side
```

```
    +Dog:Side+day:Dog:Side)
lmfitfull3 <-
  lm(pixel~day+I(day^2)+Dog+Side+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side
    +Dog:Side+day:Dog:Side+I(day^2):Dog:Side)
anova(lmfitfull1, lmfitfull0)
## lmfitfull1 best so far
lmfitfull1a <-
  lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side
    +Dog:Side)
anova(lmfitfull1a, lmfitfull1)  ## 1a better
lmfitfull1a1 <-
  lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side)
anova(lmfitfull1a, lmfitfull1a1)  ## 1a better
lmfitfull1a2 <-
  lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+Dog:Side)
anova(lmfitfull1a, lmfitfull1a2)  ## 1a2 better
lmfitfull1a3 <-
  lm(pixel~day+I(day^2)+Dog+day:Dog+I(day^2):Dog+Dog:Side)
anova(lmfitfull1a, lmfitfull1a3)  ## 1a2 better
anova(lmfitfull1a2, lmfitfull1a3)  ## 1a2 better

lmfitfull1b <-
  lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side
    +Dog:Side)
anova(lmfitfull1a, lmfitfull1b)  ## 1a better
lmfitfull1c <-
  lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side)
anova(lmfitfull1a, lmfitfull1b)  ## 1a better
lmfitfull1d <-
  lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog)
anova(lmfitfull1a, lmfitfull1d)  ## 1a better
lmfitfull1e <-
  lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog)
anova(lmfitfull1a, lmfitfull1d)  ## 1a better

lmFinal <-
  lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+Dog:Side)  ## 1a2
length(coef(lmFinal))
summary(lmFinal)
anova(lmFinal)

graphics.off()
par(mfrow=c(4,2))
plot(lmFinal)
termplot(lmFinal, partial=T, term=1, main='Partial Residual Plot of day',
        col.res='black')
```

```
termplot(lmFinal, partial=T, term=2, main='Partial Residual Plot of day^2',
        col.res='black')
halfnorm(influence(lmFinal)$hat,main='Half Normal Plot of Leverage')
print(RatPupWeight[influence(lmFinal)$hat>0.2,])
print(influence(lmFinal)$hat>0.2)
graphics.off()

## lmList
detach(Pixel)
pixel <- Pixel$pixel
day <- Pixel$day
Dog <- Pixel$Dog
Side <- Pixel$Side
Side_in_Dog<-c(rep(1,7),rep(2,7),rep(3,7),rep(4,7), rep(5,7), rep(6,7),
             rep(7,7),rep(8,7), rep(9,5),rep(10,5), rep(11, 5), rep(12,5),
             rep(13, 4),rep(14,4),rep(15,4),rep(16,4),rep(17,2),
             rep(18,2),rep(19,3),rep(20,3))
tmpdata <- data.frame(pixel, day, Dog, Side, Side_in_Dog)
lmListfit1 <- lmList(pixel~day+I(day^2) | Dog, tmpdata)
lmListfit2 <- lmList(pixel~day+I(day^2) | Side_in_Dog, tmpdata)
plot(lmListfit1)
plot(lmListfit2)

pairs(coef(lmListfit1))
pairs(coef(lmListfit2))

#install.packages("psych")
library(psych)
pairs.panels(coef(lmListfit1),
            method = "pearson", # correlation method
            hist.col = "#00AFBB",
            density = TRUE,  # show density plots
            ellipses = TRUE # show correlation ellipses
)
dev.copy2pdf(file='Pairs graph 1.pdf')

pairs.panels(coef(lmListfit2),
            method = "pearson", # correlation method
            hist.col = "#00AFBB",
            density = TRUE,  # show density plots
            ellipses = TRUE # show correlation ellipses
)
graphics.off()

## lme
require(lme4)
```

```
attach(Pixel)
lmefit1 <- lme(pixel~day+I(day^2), data=Pixel, random=list(Dog=~day+I(day^2),
                                                Side=~day+I(day^2)))
lmefit1 <- lme(pixel~day+I(day^2), data=Pixel, random=list(Dog=~day+I(day^2),
                                                Side=~day+I(day^2)))
lmefit2 <- lme(pixel~day+I(day^2), data=Pixel, random=list(Dog=~day,
                                                Side=~1))

lmefit0 <- lmer(pixel~day+I(day^2)+(1|Dog)+(0+day|Dog), data=Pixel)
lmefit01 <- lmer(pixel~day+I(day^2)+(day|Dog), data=Pixel)
lmefit1 <- lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(day+day^2|Side:Dog),
             data=Pixel)
lmefit2 <- lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(day|Side:Dog),
             data=Pixel)
lmefit3 <- lmer(pixel~day+I(day^2)+(day|Dog)+(day|Side:Dog),
             data=Pixel)
lmefit4 <- lmer(pixel~day+I(day^2)+(day|Dog)+(1|Side:Dog),
             data=Pixel)
lmefit5 <- lmer(pixel~day+I(day^2)+(1|Dog)+(0+day|Dog)+(1|Side:Dog), data=Pixel)
lmefit6 <- lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(1|Side:Dog),
             data=Pixel)
lmefit7 <-
  lmer(pixel~day+I(day^2)+(1|Dog)+(0+day|Dog)+(0+I(day^2)|Dog)+(1|Side:Dog),
      data=Pixel)
lmefit8 <- lmer(pixel~day+I(day^2)+Dog+Side+(day+I(day^2)|Dog)+(1|Side:Dog),
             data=Pixel)
lmefit9 <- lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(1|Side:Dog),
             data=Pixel)
lmefit10 <- lmer(pixel~day+I(day^2)+Side+(day+I(day^2)|Dog)+(1|Side:Dog),
              data=Pixel)
## only lmefit9 beat lmefit6
lmefit19 <- lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day|Side:Dog),
              data=Pixel)
summary(lmefit19)
anova(lmefit19)
lmefit29 <-
  lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day+I(day^2)|Side:Dog),
      data=Pixel)  ## put this one in
anova(lmefit9, lmefit19)
anova(lmefit9, lmefit29)
anova(lmefit19, lmefit29)
## So far 19 is the best one
lmefit39 <-

lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day|Side:Dog)+(0+I(day^2)|Side:D
og), data=Pixel)
```

```
lmefit49 <-
  lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(1|Side:Dog)+(0+day|Side:Dog),
      data=Pixel)  ## put this one in
anova(lmefit19, lmefit49)

## Finally the best one is model lmefit19
lmeFinal <- lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day|Side:Dog),
              data=Pixel)
lmeFinal1 <- lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(day|Side:Dog),
               data=Pixel) ##### worse than lmefitFinal
lmeFinal2 <- lmer(pixel~day+I(day^2)+Dog+(day|Dog)+(1|Side:Dog),
               data=Pixel)
anova(lmeFinal, lmeFinal2)
lmeFinal3 <- lmer(pixel~day+I(day^2)+Dog+(1|Dog)+(0+day|Dog) +
                 (0+I(day^2)|Dog) + (1|Side:Dog) + (0+day|Side:Dog),
               data=Pixel)
anova(lmeFinal, lmeFinal3)
lmeFinal4 <- lmer(pixel~day+I(day^2)+Dog+(1|Dog)+(0+day|Dog) +
                 (1|Side:Dog),
               data=Pixel)
anova(lmeFinal, lmeFinal4)

## lmeFinal is always the best
tvalues <- c(129.91, 3,26, -5.29, 3.32, 0.19, -0.32, 0.57, 5.18, 4.03, 7.85, 1.83, 1.75)
print(pvalues <- (1-pt(abs(tvalues),60))*2)

## Diagnostic
## within-group
xyplot(resid(lmeFinal)~Side|Dog,xlab='Sides in Dog', ylab='Residual')
xyplot(resid(lmeFinal)~Dog, xlab = 'Dog', ylab='Residual')
(1:102)[resid(lmeFinal) > 20]
(1:102)[resid(lmeFinal) < -20]

qqnorm(resid(lmeFinal))
xyplot(resid(lmeFinal)~fitted(lmeFinal), group=Side, pch=c(1,2), xlab='Fitted Value',
ylab='Residual Plot', main='Residual Plot of lmefit')
xyplot(resid(lmeFinal)~fitted(lmeFinal)|Dog, xlab='Fitted Value',
      ylab='Residual', main='Residual Plots for each Dog group')
xyplot(resid(lmeFinal)~fitted(lmeFinal)|Side, xlab='Fitted Value',
      ylab='Residual plot for each Side group')
plot(fitted(lmeFinal)~pixel, xlab='Observed Pixel', ylab='Fitted Pixel')
abline(lm(fitted(lmeFinal)~pixel))
graphics.off()

## Diagnostic for random effects
par(mfrow=c(2,2))
```

```
qqnorm(ranef(lmeFinal)$Dog[,1], main='Normal Q-Q Plot for Intercept at Dog
      level')
qqnorm(ranef(lmeFinal)$Dog[,2], main='Normal Q-Q Plot for Day at Dog
      level')
qqnorm(ranef(lmeFinal)$Dog[,3], main='Normal Q-Q Plot for Day^2 at Dog
      level')

par(mfrow=c(1,2))
qqnorm(ranef(lmeFinal)$`Side:Dog`[,1], main='Normal Q-Q plot for Intercept at
      Side within Dog level')
qqnorm(ranef(lmeFinal)$`Side:Dog`[,2], main='Normal Q-Q plot for Day at
      Side within Dog level')
graphics.off()

## Compare
AIC(lmeFinal)
BIC(lmeFinal)
logLik(lmeFinal)
AIC(lmFinal)
BIC(logLik(lmFinal))
logLik(lmFinal)
print(llratio <- -2*(-362.9599-(-339.9932)))
print(ddf <- 40-22)
print(pchiok <- 1-pchisq(llratio, ddf))

## fitted value plot
par(mfrow=c(1,2))
xyplot(fitted(lmeFinal)+pixel~day|Side:Dog, panel=panel.superpose,
      distribute.type=TRUE, pch=c(4,20), type=c('o','p'), ylab='pixel',
      main='Fitted Values by Linear Mixed Model')
xyplot(fitted(lmFinal)+pixel~day|Side:Dog, panel=panel.superpose,
      distribute.type=TRUE, pch=c(4,20), type=c('o','p'), ylab='pixel',
      main='Fitted Values by Linear Regression')
graphics.off()
```

Appendix A

```
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + Side + day:Dog + day:Side +
I(day^2):Dog +
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + Dog + Side + day:Dog + day:Side +
I(day^2):Dog +
    I(day^2):Side
  Res.Df     RSS Df Sum of Sq      F    Pr(>F)
1     61  4372.8
```

```
2     70 13242.2 -9   -8869.4 13.748 9.441e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> ## lmfitfull1 best so far
> lmfitfull1a <-
+ 
lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side
+       +Dog:Side)
> anova(lmfitfull1a, lmfitfull1)  ## 1a better
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side + 
I(day^2):Dog + 
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + Dog + Side + day:Dog + day:Side + 
I(day^2):Dog + 
    I(day^2):Side + Dog:Side
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1     62 4455.2                           
2     61 4372.8  1    82.427 1.1499 0.2878
> lmfitfull1a1 <-
+ 
lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side)
> anova(lmfitfull1a, lmfitfull1a1)  ## 1a better
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side + 
I(day^2):Dog + 
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side + 
I(day^2):Dog + 
    I(day^2):Side
  Res.Df     RSS Df Sum of Sq      F    Pr(>F)    
1     62  4455.2                                  
2     71 13347.0 -9   -8891.8 13.749 7.845e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> lmfitfull1a2 <-
+   lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+Dog:Side)
> anova(lmfitfull1a, lmfitfull1a2)  ## 1a2 better
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side + 
I(day^2):Dog + 
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side + 
I(day^2):Dog + 
    Dog:Side
  Res.Df    RSS Df Sum of Sq      F  Pr(>F)  
1     62 4455.2                              
2     63 4692.1 -1   -236.88 3.2965 0.07426 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> lmfitfull1a3 <-
+   lm(pixel~day+I(day^2)+Dog+day:Dog+I(day^2):Dog+Dog:Side)
> anova(lmfitfull1a, lmfitfull1a3)  ## 1a2 better
Analysis of Variance Table
```

```
Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side +
I(day^2):Dog +
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + Dog + day:Dog + I(day^2):Dog +
Dog:Side
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1     62 4455.2
2     63 4617.6 -1   -162.43 2.2605 0.1378
> anova(lmfitfull1a2, lmfitfull1a3)  ## 1a2 better
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side +
I(day^2):Dog +
    Dog:Side
Model 2: pixel ~ day + I(day^2) + Dog + day:Dog + I(day^2):Dog +
Dog:Side
  Res.Df    RSS Df Sum of Sq F Pr(>F)
1     63 4692.1
2     63 4617.6  0    74.446
> lmfitfull1b <-
+   lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side
+      +Dog:Side)
> anova(lmfitfull1a, lmfitfull1b)  ## 1a better
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side +
I(day^2):Dog +
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + day:Dog + day:Side + I(day^2):Dog +
    I(day^2):Side + Dog:Side
  Res.Df    RSS Df Sum of Sq      F   Pr(>F)
1     62 4455.2
2     70 6654.9 -8   -2199.7 3.8265 0.001039 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> lmfitfull1c <-
+   lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog+I(day^2):Side)
> anova(lmfitfull1a, lmfitfull1b)  ## 1a better
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side +
I(day^2):Dog +
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + day:Dog + day:Side + I(day^2):Dog +
    I(day^2):Side + Dog:Side
  Res.Df    RSS Df Sum of Sq      F   Pr(>F)
1     62 4455.2
2     70 6654.9 -8   -2199.7 3.8265 0.001039 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> lmfitfull1d <-
+   lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog)
> anova(lmfitfull1a, lmfitfull1d)  ## 1a better
Analysis of Variance Table
```

```
Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side +
I(day^2):Dog +
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + day:Dog + day:Side + I(day^2):Dog
  Res.Df     RSS  Df Sum of Sq      F    Pr(>F)
1     62  4455.2
2     80 17507.5 -18    -13052 10.091 2.409e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> lmfitfull1e <-
+   lm(pixel~day+I(day^2)+day:Dog+day:Side+I(day^2):Dog)
> anova(lmfitfull1a, lmfitfull1d)  ## 1a better
Analysis of Variance Table

Model 1: pixel ~ day + I(day^2) + Dog + day:Dog + day:Side +
I(day^2):Dog +
    I(day^2):Side + Dog:Side
Model 2: pixel ~ day + I(day^2) + day:Dog + day:Side + I(day^2):Dog
  Res.Df     RSS  Df Sum of Sq      F    Pr(>F)
1     62  4455.2
2     80 17507.5 -18    -13052 10.091 2.409e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> lmFinal <-
+   lm(pixel~day+I(day^2)+Dog+day:Dog+day:Side+I(day^2):Dog+Dog:Side)
## 1a2
> length(coef(lmFinal))
[1] 40
> summary(lmFinal)

Call:
lm(formula = pixel ~ day + I(day^2) + Dog + day:Dog + day:Side +
    I(day^2):Dog + Dog:Side)

Residuals:
    Min      1Q  Median      3Q     Max
-22.028  -4.121  -0.369   3.699  24.287

Coefficients: (1 not defined because of singularities)
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    1045.94343    4.45298 234.886  < 2e-16 ***
day               1.07784    1.80718   0.596 0.553032
I(day^2)         -0.10783    0.12585  -0.857 0.394793
Dog10            33.22150   63.97076   0.519 0.605355
Dog2              4.06366    6.76442   0.601 0.550168
Dog3             -3.91261    7.54531  -0.519 0.605892
Dog4              3.20157    7.54531   0.424 0.672783
Dog5             42.59467   19.83029   2.148 0.035570 *
Dog6             57.61432   19.83029   2.905 0.005055 **
Dog7             88.94735   21.64211   4.110 0.000116 ***
Dog8             22.02461   21.64211   1.018 0.312725
Dog9             51.22918   14.80626   3.460 0.000975 ***
day:Dog10        22.13078   22.59678   0.979 0.331139
day:Dog2          2.35105    2.54480   0.924 0.359082
day:Dog3          6.09947    2.14900   2.838 0.006096 **
day:Dog4         11.11590    2.14900   5.173 2.55e-06 ***
day:Dog5          8.30475    4.97841   1.668 0.100249
```

```
day:Dog6          2.38877    4.97841   0.480 0.633013    
day:Dog7         -1.46827    5.65921  -0.259 0.796135    
day:Dog8          7.87183    5.65921   1.391 0.169125    
day:Dog9         -0.16272    2.22278  -0.073 0.941874    
day:SideR         0.28276    0.33405   0.846 0.400509    
I(day^2):Dog10   -1.67967    1.87269  -0.897 0.373172    
I(day^2):Dog2    -0.11035    0.17798  -0.620 0.537491    
I(day^2):Dog3    -0.20821    0.13627  -1.528 0.131526    
I(day^2):Dog4    -0.39887    0.13627  -2.927 0.004754 ** 
I(day^2):Dog5    -0.48333    0.28152  -1.717 0.090914 .  
I(day^2):Dog6    -0.18922    0.28152  -0.672 0.503945    
I(day^2):Dog7    -0.05765    0.31952  -0.180 0.857395    
I(day^2):Dog8    -0.35757    0.31952  -1.119 0.267351    
I(day^2):Dog9          NA         NA      NA       NA    
Dog10:SideR     -60.62987    7.32590  -8.276 1.17e-11 ***
Dog2:SideR       -7.48028    4.93932  -1.514 0.134917    
Dog3:SideR        9.64091    5.50619   1.751 0.084827 .  
Dog4:SideR       -1.77338    5.50619  -0.322 0.748466    
Dog5:SideR        1.64485    6.13716   0.268 0.789564    
Dog6:SideR      -24.37515    6.13716  -3.972 0.000186 ***
Dog7:SideR       26.54657    6.73061   3.944 0.000204 ***
Dog8:SideR      -19.05343    6.73061  -2.831 0.006223 ** 
Dog9:SideR      -33.94654    8.85971  -3.832 0.000296 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 8.63 on 63 degrees of freedom
Multiple R-squared:  0.9558,   Adjusted R-squared:  0.9292 
F-statistic: 35.88 on 38 and 63 DF,  p-value: < 2.2e-16

> anova(lmFinal)
Analysis of Variance Table

Response: pixel
             Df Sum Sq Mean Sq  F value    Pr(>F)    
day           1   4562  4561.9  61.2517 7.181e-11 ***
I(day^2)      1  20617 20617.0 276.8224 < 2.2e-16 ***
Dog           9  57294  6366.0  85.4753 < 2.2e-16 ***
day:Dog       9   7469   829.9  11.1433 3.488e-10 ***
day:Side      1     80    80.0   1.0736   0.30409    
I(day^2):Dog  8   1169   146.1   1.9617   0.06612 .  
Dog:Side      9  10351  1150.2  15.4431 6.271e-13 ***
Residuals    63   4692    74.5                      
---
Signif
. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Appendix B

```
> summary(lmefit1)
Linear mixed model fit by REML ['lmerMod']
Formula: pixel ~ day + I(day^2) + (day + I(day^2) | Dog) + (day + day^2 
|       Side:Dog)
   Data: Pixel
```

```
REML criterion at convergence: 810.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.6865 -0.4857  0.0239  0.4637  3.1629

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 Side:Dog (Intercept) 108.69536 10.4257
          day           0.60441  0.7774  1.00
 Dog      (Intercept) 829.16140 28.7952
          day           9.80357  3.1311  -0.25
          I(day^2)      0.01406  0.1186  -0.31 -0.84
 Residual              63.37445  7.9608
Number of obs: 102, groups:  Side:Dog, 20; Dog, 10

Fixed effects:
             Estimate Std. Error t value
(Intercept) 1073.8458     9.8984 108.487
day            5.7130     1.2410   4.604
I(day^2)      -0.3335     0.0537  -6.210

Correlation of Fixed Effects:
         (Intr) day
day      -0.315
I(day^2) -0.035 -0.861
convergence code: 1
> anova(lmefit1)
Analysis of Variance Table
         Df  Sum Sq Mean Sq F value
day       1  134.22  134.22  2.1179
I(day^2)  1 2443.67 2443.67 38.5593
>
> summary(lmefit1)
Linear mixed model fit by REML ['lmerMod']
Formula: pixel ~ day + I(day^2) + (day + I(day^2) | Dog) + (day + day^2
|       Side:Dog)
   Data: Pixel

REML criterion at convergence: 810.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.6865 -0.4857  0.0239  0.4637  3.1629

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 Side:Dog (Intercept) 108.69536 10.4257
          day           0.60441  0.7774  1.00
 Dog      (Intercept) 829.16140 28.7952
          day           9.80357  3.1311  -0.25
          I(day^2)      0.01406  0.1186  -0.31 -0.84
 Residual              63.37445  7.9608
Number of obs: 102, groups:  Side:Dog, 20; Dog, 10

Fixed effects:
```

```
             Estimate Std. Error t value
(Intercept) 1073.8458     9.8984 108.487
day            5.7130     1.2410   4.604
I(day^2)      -0.3335     0.0537  -6.210

Correlation of Fixed Effects:
         (Intr) day
day      -0.315
I(day^2) -0.035 -0.861
convergence code: 1
> anova(lmefit1)
Analysis of Variance Table
         Df  Sum Sq Mean Sq F value
day       1  134.22  134.22  2.1179
I(day^2)  1 2443.67 2443.67 38.5593
>
> lmefit2 <- lme(pixel~day+I(day^2), data=Pixel, random=list(Dog=~day,
+                                                            Side=~1))
>
> summary(lmefit2)
Linear mixed-effects model fit by REML
 Data: Pixel
       AIC      BIC    logLik
  841.2102 861.9712 -412.6051

Random effects:
 Formula: ~day | Dog
 Structure: General positive-definite, Log-Cholesky parametrization
            StdDev   Corr
(Intercept) 28.36990 (Intr)
day          1.84375 -0.555

 Formula: ~1 | Side %in% Dog
        (Intercept) Residual
StdDev:    16.82431 8.989606

Fixed effects: pixel ~ day + I(day^2)
                Value Std.Error DF   t-value p-value
(Intercept) 1073.3391 10.171686 80 105.52225       0
day            6.1296  0.879321 80   6.97083       0
I(day^2)      -0.3674  0.033945 80 -10.82179       0
 Correlation:
         (Intr) day
day      -0.517
I(day^2)  0.186 -0.668

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-2.8290572 -0.4491811  0.0255493  0.5572163  2.7519651

Number of Observations: 102
Number of Groups:
          Dog Side %in% Dog
           10            20
> anova(lmefit2)
            numDF denDF   F-value p-value
(Intercept)     1    80 16771.715  <.0001
```

```
day              1    80     0.116  0.7345
I(day^2)         1    80   117.111  <.0001
> lmefit0 <- lmer(pixel~day+I(day^2)+(1|Dog)+(0+day|Dog), data=Pixel)
> lmefit01 <- lmer(pixel~day+I(day^2)+(day|Dog), data=Pixel)
> lmefit1 <-
lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(day+day^2|Side:Dog),
+                  data=Pixel)
> lmefit2 <- lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(day|Side:Dog),
+                  data=Pixel)

> lmefit3 <- lmer(pixel~day+I(day^2)+(day|Dog)+(day|Side:Dog),
+                  data=Pixel)
> lmefit4 <- lmer(pixel~day+I(day^2)+(day|Dog)+(1|Side:Dog),
+                  data=Pixel)  ## !!!!!!!!!
> lmefit5 <- lmer(pixel~day+I(day^2)+(1|Dog)+(0+day|Dog)+(1|Side:Dog),
data=Pixel)
> lmefit6 <- lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(1|Side:Dog),
+                  data=Pixel)  ## !!!!!!!!!
> summary(lmefit6)
Linear mixed model fit by REML ['lmerMod']
Formula: pixel ~ day + I(day^2) + (day + I(day^2) | Dog) + (1 |
Side:Dog)
   Data: Pixel

REML criterion at convergence: 813.3

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.43538 -0.47622  0.03253  0.43589  2.97456

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 Side:Dog (Intercept) 259.38092 16.1053
 Dog      (Intercept) 779.62551 27.9218
          day          10.42998  3.2295  -0.26
          I(day^2)      0.01329  0.1153  -0.28 -0.86
 Residual              67.70714  8.2284
Number of obs: 102, groups:  Side:Dog, 20; Dog, 10

Fixed effects:
              Estimate Std. Error t value
(Intercept) 1074.52882   10.02075 107.230
day            5.49232    1.23552   4.445
I(day^2)      -0.31904    0.05041  -6.328

Correlation of Fixed Effects:
         (Intr) day
day      -0.344
I(day^2) -0.021 -0.873
convergence code: 1
> anova(lmefit6)
Analysis of Variance Table
         Df  Sum Sq Mean Sq F value
day       1  330.55  330.55   4.882
I(day^2)  1 2711.56 2711.56  40.048
>
> lmefit7 <-
```

```
+
lmer(pixel~day+I(day^2)+(1|Dog)+(0+day|Dog)+(0+I(day^2)|Dog)+(1|Side:Do
g),
+         data=Pixel)  ## !!!!!!!!!!
> summary(lmefit7)
Linear mixed model fit by REML ['lmerMod']
Formula: pixel ~ day + I(day^2) + (1 | Dog) + (0 + day | Dog) + (0 +
I(day^2) |
    Dog) + (1 | Side:Dog)
   Data: Pixel

REML criterion at convergence: 826.7

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.63975 -0.45962  0.02743  0.55890  2.73078

Random effects:
 Groups   Name        Variance  Std.Dev.
 Side.Dog (Intercept) 2.846e+02 16.87041
 Dog      I(day^2)    2.276e-03  0.04771
 Dog.1    day         3.746e+00  1.93545
 Dog.2    (Intercept) 7.042e+02 26.53650
 Residual             7.716e+01  8.78385
Number of obs: 102, groups:  Side:Dog, 20; Dog, 10

Fixed effects:
              Estimate Std. Error t value
(Intercept) 1072.40903    9.68675 110.709
day            6.31417    0.93656   6.742
I(day^2)      -0.37512    0.04198  -8.937

Correlation of Fixed Effects:
         (Intr) day
day      -0.210
I(day^2)  0.193 -0.638
> anova(lmefit7)
Analysis of Variance Table
         Df Sum Sq Mean Sq F value
day       1  140.5   140.5  1.8211
I(day^2)  1 6162.0  6162.0 79.8644
>
>
> lmefit8 <-
lmer(pixel~day+I(day^2)+Dog+Side+(day+I(day^2)|Dog)+(1|Side:Dog),
+                  data=Pixel)
> lmefit9 <-
lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(1|Side:Dog),
+                  data=Pixel)  ## !!!!!!!!!
> summary(lmefit9)
Linear mixed model fit by REML ['lmerMod']
Formula: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (1 |
Side:Dog)
   Data: Pixel

REML criterion at convergence: 729.8
```

```
Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.3868 -0.5134  0.0696  0.4737  2.9572

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 Side:Dog (Intercept) 287.39707 16.9528
 Dog      (Intercept)  77.40022  8.7977
          day          14.43036  3.7987   0.18
          I(day^2)      0.01294  0.1137  -0.05 -0.99
 Residual              70.25703  8.3819
Number of obs: 102, groups:  Side:Dog, 20; Dog, 10

Fixed effects:
              Estimate Std. Error t value
(Intercept) 1043.94237   14.93062  69.920
day            4.42683    1.40205   3.157
I(day^2)      -0.25833    0.04994  -5.173
Dog10         56.16444   24.99952   2.247
Dog2           1.79265   21.06698   0.085
Dog3          -4.54461   20.99398  -0.216
Dog4           5.13051   20.99398   0.244
Dog5          70.69182   22.68475   3.116
Dog6          55.22997   22.68475   2.435
Dog7         108.16314   22.71789   4.761
Dog8          24.65224   22.71789   1.085
Dog9          29.62569   25.07613   1.181

Correlation of Fixed Effects:
         (Intr) day    I(d^2) Dog10  Dog2   Dog3   Dog4   Dog5   Dog6
Dog7   Dog8
day       0.016
I(day^2)  0.006 -0.945
Dog10    -0.598 -0.110  0.095
Dog2     -0.705  0.000  0.000  0.421
Dog3     -0.700 -0.054  0.095  0.425  0.502
Dog4     -0.700 -0.054  0.095  0.425  0.502  0.525
Dog5     -0.653 -0.066  0.078  0.397  0.464  0.476  0.476
Dog6     -0.653 -0.066  0.078  0.397  0.464  0.476  0.476  0.438
Dog7     -0.652 -0.063  0.075  0.397  0.464  0.475  0.475  0.437  0.437
Dog8     -0.652 -0.063  0.075  0.397  0.464  0.475  0.475  0.437  0.437
0.436
Dog9     -0.596 -0.109  0.094  0.367  0.420  0.424  0.424  0.396  0.396
0.395  0.395
convergence code: 0
unable to evaluate scaled gradient
Model failed to converge: degenerate  Hessian with 1 negative
eigenvalues

> anova(lmefit9)
Analysis of Variance Table
         Df Sum Sq Mean Sq F value
day       1 1758.0 1757.96 25.0218
I(day^2)  1 2253.1 2253.09 32.0692
Dog       9 3275.6  363.96  5.1804
>
>
```

```
> lmefit10 <-
lmer(pixel~day+I(day^2)+Side+(day+I(day^2)|Dog)+(1|Side:Dog),
+                    data=Pixel)
> ## only lmefit9 beat lmefit6
> lmefit19 <-
lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day|Side:Dog),
+                    data=Pixel)
> summary(lmefit19)
Linear mixed model fit by REML ['lmerMod']
Formula: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day |
Side:Dog)
   Data: Pixel

REML criterion at convergence: 725.9

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.6844 -0.4211 -0.0060  0.4649  3.1645

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 Side:Dog (Intercept) 106.9086 10.3397
          day           1.0187  1.0093  1.00
 Dog      (Intercept)  92.7085  9.6285
          day          13.5799  3.6851   0.38
          I(day^2)      0.0126  0.1122  -0.38 -1.00
 Residual              64.8810  8.0549
Number of obs: 102, groups:  Side:Dog, 20; Dog, 10

Fixed effects:
              Estimate Std. Error t value
(Intercept) 1045.53113   11.30284  92.502
day            4.51704    1.38676   3.257
I(day^2)      -0.26435    0.05001  -5.286
Dog10         53.76256   21.84830   2.461
Dog2           0.52257   15.76778   0.033
Dog3          -8.37906   15.83115  -0.529
Dog4          -3.35252   15.83115  -0.212
Dog5          69.47243   18.33215   3.790
Dog6          55.32561   18.33215   3.018
Dog7         110.67758   18.35956   6.028
Dog8          20.98427   18.35956   1.143
Dog9          29.30346   21.92173   1.337

Correlation of Fixed Effects:
         (Intr) day    I(d^2) Dog10  Dog2   Dog3   Dog4   Dog5   Dog6
Dog7   Dog8
day       0.114
I(day^2) -0.065 -0.938
Dog10    -0.523 -0.137  0.116
Dog2     -0.698  0.000  0.000  0.361
Dog3     -0.684 -0.066  0.114  0.363  0.498
Dog4     -0.684 -0.066  0.114  0.363  0.498  0.523
Dog5     -0.602 -0.092  0.111  0.320  0.430  0.445  0.445
Dog6     -0.602 -0.092  0.111  0.320  0.430  0.445  0.445  0.384
Dog7     -0.601 -0.089  0.107  0.320  0.429  0.444  0.444  0.382  0.382
```

```
Dog8     -0.601 -0.089  0.107  0.320  0.429  0.444  0.444  0.382  0.382
0.381
Dog9     -0.522 -0.136  0.114  0.280  0.360  0.361  0.361  0.319  0.319
0.318  0.318
convergence code: 0
> anova(lmefit19)
Analysis of Variance Table
         Df Sum Sq Mean Sq F value
day       1 1299.9 1299.87 20.0348
I(day^2)  1 2583.5 2583.46 39.8185
Dog       9 4955.0  550.56  8.4857
> lmefit29 <-
+
lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day+I(day^2)|Side:Dog),
+         data=Pixel)  ## put this one in
> anova(lmefit9, lmefit19)
refitting model(s) with ML (instead of REML)
Data: Pixel
Models:
lmefit9: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (1 |
lmefit9:     Side:Dog)
lmefit19: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
|
lmefit19:     Side:Dog)
         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
lmefit9  20 830.33 882.83 -395.16   790.33
lmefit19 22 825.85 883.60 -390.92   781.85 8.4821      2    0.01439 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> anova(lmefit9, lmefit29)
refitting model(s) with ML (instead of REML)
Data: Pixel
Models:
lmefit9: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (1 |
lmefit9:     Side:Dog)
lmefit29: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
+
lmefit29:     I(day^2) | Side:Dog)
         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
lmefit9  20 830.33 882.83 -395.16   790.33
lmefit29 25 826.81 892.44 -388.41   776.81 13.517      5    0.01899 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> anova(lmefit19, lmefit29)
refitting model(s) with ML (instead of REML)
Data: Pixel
Models:
lmefit19: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
|
lmefit19:     Side:Dog)
lmefit29: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
+
lmefit29:     I(day^2) | Side:Dog)
         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
lmefit19 22 825.85 883.60 -390.92   781.85
lmefit29 25 826.81 892.44 -388.41   776.81 5.0346      3     0.1693
> ## So far 19 is the best one
```

```
> lmefit39 <-
+
lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day|Side:Dog)+(0+I(day^
2)|Side:Dog), data=Pixel)
> lmefit49 <-
+
lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(1|Side:Dog)+(0+day|Side
:Dog),
+        data=Pixel)  ## put this one in
> anova(lmefit19, lmefit49)
refitting model(s) with ML (instead of REML)
Data: Pixel
Models:
lmefit49: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (1 |
lmefit49:     Side:Dog) + (0 + day | Side:Dog)
lmefit19: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
|
lmefit19:     Side:Dog)
         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
lmefit49 21 824.45 879.57 -391.22   782.45
lmefit19 22 825.85 883.60 -390.92   781.85 0.5998      1     0.4387
>
> ## Finally the best one is model lmefit19
> ## 12+30 = 42 parameters so 102-42=60 d.f for t-test
> ## use (1-pt(,60))*2
> lmeFinal <-
lmer(pixel~day+I(day^2)+Dog+(day+I(day^2)|Dog)+(day|Side:Dog),
+                  data=Pixel)
> lmeFinal1 <-
lmer(pixel~day+I(day^2)+(day+I(day^2)|Dog)+(day|Side:Dog),
+                   data=Pixel) ##### worse than lmefitFinal
> lmeFinal2 <- lmer(pixel~day+I(day^2)+Dog+(day|Dog)+(1|Side:Dog),
+                   data=Pixel)
> anova(lmeFinal, lmeFinal2)
refitting model(s) with ML (instead of REML)
Data: Pixel
Models:
lmeFinal2: pixel ~ day + I(day^2) + Dog + (day | Dog) + (1 | Side:Dog)
lmeFinal: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
|
lmeFinal:     Side:Dog)
          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
lmeFinal2 17 832.85 877.48 -399.43   798.85
lmeFinal  22 825.85 883.60 -390.92   781.85 17.006      5   0.004488 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> lmeFinal3 <- lmer(pixel~day+I(day^2)+Dog+(1|Dog)+(0+day|Dog) +
+                     (0+I(day^2)|Dog) + (1|Side:Dog) +
(0+day|Side:Dog),
+                   data=Pixel)
> anova(lmeFinal, lmeFinal3)
refitting model(s) with ML (instead of REML)
Data: Pixel
Models:
lmeFinal3: pixel ~ day + I(day^2) + Dog + (1 | Dog) + (0 + day | Dog) +
lmeFinal3:     (0 + I(day^2) | Dog) + (1 | Side:Dog) + (0 + day |
Side:Dog)
```

```
lmeFinal: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
|
lmeFinal:     Side:Dog)
          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
lmeFinal3 18 825.17 872.42 -394.58   789.17
lmeFinal  22 825.85 883.60 -390.92   781.85 7.3209      4     0.1199
> lmeFinal4 <- lmer(pixel~day+I(day^2)+Dog+(1|Dog)+(0+day|Dog) +
+                      (1|Side:Dog),
+                    data=Pixel)
> anova(lmeFinal, lmeFinal4)
refitting model(s) with ML (instead of REML)
Data: Pixel
Models:
lmeFinal4: pixel ~ day + I(day^2) + Dog + (1 | Dog) + (0 + day | Dog) +
lmeFinal4:     (1 | Side:Dog)
lmeFinal: pixel ~ day + I(day^2) + Dog + (day + I(day^2) | Dog) + (day
|
lmeFinal:     Side:Dog)
          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
lmeFinal4 16 833.94 875.94 -400.97   801.94
lmeFinal  22 825.85 883.60 -390.92   781.85 20.093      6   0.002666 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

05 ‘.’ 0.1 ‘ ’ 1

8. References

Andrew Gelman and Jennifer Hill. (2007). *Data Analysis Using Regression and Multilevel/Hierarchical Models.* New York: Cambridge University Press.

Andrzej Gatecki and Tomasz Burzykowski. (2013). *Linear Mixed-Effects Models Using R.* Springer.

Bates, Jose C. Pinheiro and Douglas M. Bates. (2002). *Mixed Effects Models in S and S-Plus.* Springer.

Cai, S. (n.d.). Analyzing Pixel Intensity Data Using Linear Mixed Model.