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Chapter 1

Residual Analysis and Influence Diagnostics for Method Comparison

Model validation and model appraisal are vital parts of the modelling process, yet are too often overlooked. Using a small set of simple measures and methods, such as the AIC and R^2 measures, is insufficient to properly assess the usefulness of a fitted model. In classical linear models model diagnostics are now considered a required part of any statistical analysis, and the methods are commonly available in statistical packages and standard textbooks on applied regression. A full and comprehensive analysis that comprises residual analysis and influence analysis for testing model assumptions, should be carried out. However it has been noted by several papers (??) that model diagnostics do not often accompany LME model analyses. Furthermore, a suite of diagnostic procedures designed for method comparison should be adopted.

Chapter 2

Residual Analysis and Influence Diagnostics for Method Comparison

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A comprehensive analysis that comprises residual analysis and influence analysis for testing model assumptions, should be carried out.

Following model specification and estimation, it is of interest to explore the model-data agreement by raising pertinent questions. Pinheiro and Bates provide some insight into how to compute and interpret model diagnostic plots for LME models. Unfortunately this aspect of LME theory is not as expansive as the corresponding body of work for linear models. Their particular observations will be reverted to shortly.

? discusses the state of LME diagnostics tools, providing a useful summary of established measures. Further to the analysis of residuals, ? recommends the examination of the following questions:

Model diagnostics techniques determine whether or not the distributional assumptions are satisfied, and to assess the influence of unusual observations, and have become a required part of any statistical analysis. Well established methods are commonly described and implemented available on standard statistics textbooks, and implemented in software packages. However it has been noted by several papers that model diagnostics do not often accompany LME model analyses. ? discusses the state of LME diagnostics tools, providing a useful summary of established measures.

A full and comprehensive analysis that comprises residual analysis and influence analysis for testing model assumptions, should be carried out. In classical linear models model diagnostics are now considered a required part of any statistical analysis, and the methods are commonly available in statistical packages and standard textbooks on applied regression. However it has been noted by several papers (??) that model diagnostics do not often accompany LME model analyses.

Following model specification and estimation, it is of interest to explore the model-data agreement by raising pertinent questions. Further to the analysis of residuals, ? recommends the examination of the following questions:

? provide some insight into how to compute and interpret model diagnostic plots for LME models. Unfortunately this aspect of LME theory is not as expansive as the corresponding body of work for linear models.

Influential points are of particular interest in the context of method comparison. After fitting an LME model, it is important to carry out model diagnostics to check whether distributional assumptions for the residuals are satisfied and whether the fit the model is sensitive to unusual assumptions. ? remarks that the concept of critiquing the model-data agreement applies in LME models in the same way as in linear fixed-effects models. ? argues that model and data diagnostics are even more important because of the more complex model structure,.

2.1 Residual Analysis

As with classical models, there are two key techniques for LME models: a residual plot and the normal probability plot. The rationale is that, if the model is properly fitted to the model, then the residuals would approximate the random errors that one should expect. If the residuals behave randomly, with no discernible trend, the model has fitted the data well. Conversely, if some sort of non-random trend is evident in the model, then the model can be considered to be poorly fitted.

The underlying assumptions for LME models are similar to those of classical linear models. However, for LME models the matter of residuals are more complex, both from a theoretical point of view and from the practicalities of implementing a comprehensive analysis using statistical software. ? discusses residuals for LME model, providing a useful summary of various techniques. Prominent in literature is the taxonomy of residuals for LME Models, distinguishing between condition residuals, marginal residuals and EBLUPS, including ????.

Statistical software environments, such as the R programming language, provides a suite of tests and graphical procedures for appraising a fitted LME model, with several of these procedures analysing the model residuals. Texts such as ??? describe what can be implemented for LME residual analyses with statistical software, such as R and SAS.

In the context of method comparison, a residual analysis would be carried out just as any other LME model would, testing normality. There is little scope for adding additional insights, other than to say that it is possible to create plots specific to each method. The figures on the next page depict the residual analysis for the *Blood* data, which can be used to indicate which methods disagree with the rest, but these would be

a confirmation of something detected previously.

Analysis of the residuals could determine if the methods of measurement disagree systematically, or whether or not erroneous measurements associated with a subset of the cases are the cause of disagreement. The figure depicts residual plot for the systolic blood pressure example used in ?. Points are labelled by subjects, with cases 67, 68 and 71 being among the prominent cases. Prominent cases warrant further investigation, but an analyst should procede to influence diagnostics beforehand.

LME Residual Analysis

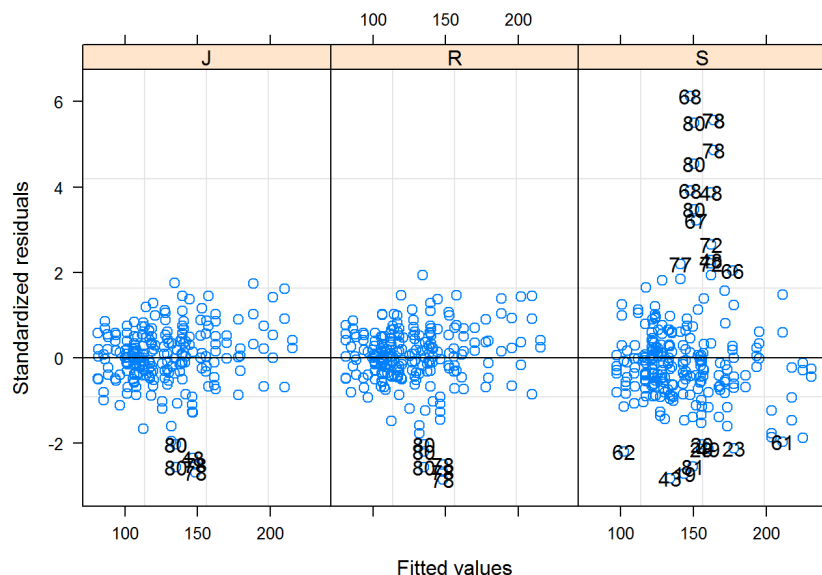


Figure 2.1: LME Residuals by Method (Blood Pressure Data)

Residual analysis is a widely used model validation technique. A residual is simply the difference between an observed value and the corresponding fitted value, as predicted by the model. Residuals are used to examine model assumptions and to detect outliers and potentially influential data point.

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For classical analyses, residual diagnostics are typically implemented as a plot of the observed residuals and the predicted values. A visual inspection for the presence of trends inform the analyst on the validity of distributional assumptions, and to detect outliers and influential observations.

However, for LME models the matter of residual is more complex, both from a theoretical point of view and for implementing a comprehensive analysis using statistical software. As the LME model can be tailored to the needs of the particular research question, the rationale behind the model appraisal must follow accordingly.

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Statistical software environments, such as the R Programming language, provides a suite of tests and graphical procedures for appraising a fitted linear model, with several of these procedures analysing the model residuals. Texts such as ??? describe what can be implemented for LME residual analyses with statistical software, such as R and SAS.

2.1.1 Residual Analysis for MCS

In the context of method comparison, a residual analysis would be carried out just as any other LME model would, testing normality. As such there is little scope for adding additional insights, other than to say that it is possible to create plots specific to each method.

Analysis of the residuals could determine if the methods of measurement disagree systematically, or whether or not erroneous measurements associated with a subset of the cases are the cause of disagreement.

LME Residual Analysis

However, for LME models the matter of residual is more complex, both from a theoretical point of view and from the practical matter of implementing a comprehensive analysis using statistical software. ? discusses residuals for LME model, providing a useful summary of various techniques. Prominent in literature is the taxonomy of residuals for LME models, distinguishing between condition residuals, marginal residuals and EBLUPS, including ?????. The underlying assumptions for LME models are similar to those of classical linear models.

For classical analyses, residual diagnostics are typically implemented as a plot of the observed residuals and the predicted values. A visual inspection for the presence of trends inform the analyst on the validity of distributional assumptions, and to detect outliers and influential observations. Diagnostics plots for the systolic blood pressure are featured in figure 2.2

As the LME model can be tailored to the needs of the particular research question, the rationale behind the model appraisal must follow accordingly. For method comparison studies, one can create plots specific to each method, useful in determining which methods disagree with the rest.

The next figure depicts residual plot for the Systolic Blood Pressure example, panelled by the various measurement methods. It serves to confirm agreement between methods J and R, with lack of agreement between those two methods and method S. However, little insight can be gained as to what actually causes lack of agreement here.

The underlying assumptions for LME models are similar to those of classical linear models. There are two key techniques: a residual plot and the normal probability plot. Using the nlme package it is possible to create plots specific to each method. This is useful in determine which methods disagree with the rest.

Analysis of the residuals would determine if the methods of measurement disagree systematically, or whether or not erroneous measurements associated with a subset of the cases are the cause of disagreement. Erroneous measurements are incorrect measurements that indicate disagreement between methods that would otherwise be in agreement. Once the residuals are computed, they can be used to make an assessment about the model fit. For LME models, we can plot the residuals against the fitted values, to assess the assumption of constant variance.

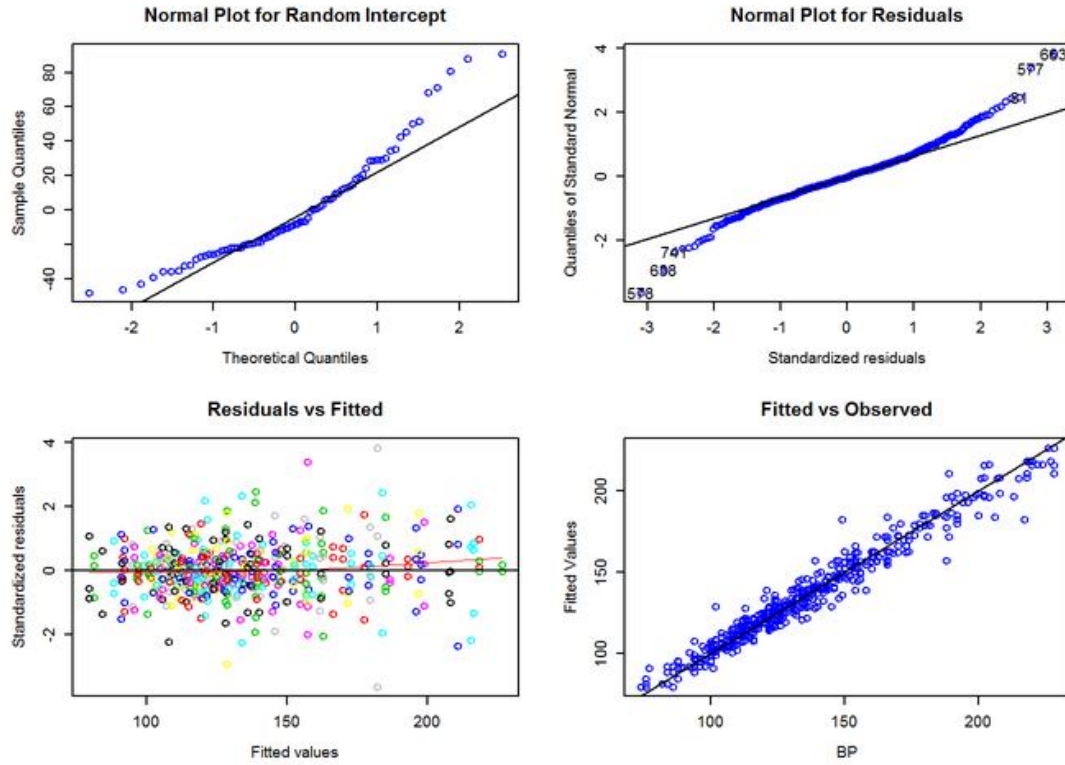


Figure 2.2:

Normal probability plots can be rendered for each level of the random effects. LME models assume that not only the within-cluster residuals are normally distributed, but that each level of the random effects are as well. LME models assume that the residuals of the model are normally distributed. The residuals can be divided according to groups according to the method of measurement. In the following examples, we separately assess normality the *J* method residuals (the first 255 residuals) and *S* method residuals (the remaining 255). Importantly the residuals from the *J* method are normally distributed, but there is non-normality of the residuals according to the *S* method.

Taxonomy of LME Residuals

Standard residual and influence diagnostics for linear models can be extended to linear mixed models. The dependence of fixed-effects solutions on the covariance parameter estimates has important ramifications in perturbation analysis. To gauge the full impact of a set of observations on the analysis, covariance parameters need to be updated, which requires refitting of the model.

? describes three types of residual that describe the variabilities present in LME models

1. marginal residuals, $\hat{\xi}$, which predict marginal errors,

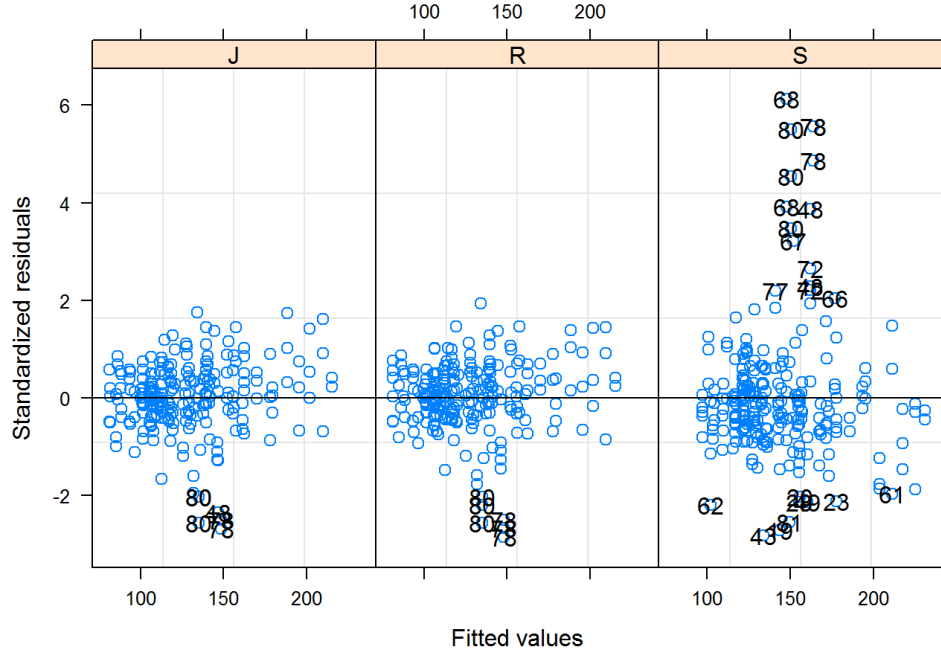


Figure 2.3: LME Residuals by Method (Blood Pressure Data)

2. conditional residuals, $\hat{\epsilon}$, which predict conditional errors,
3. the BLUP, $\mathbf{Z}\hat{\mathbf{b}}$, that predicts random effects.

Each type of residual is useful to evaluate some assumption of the model.

? describes three types of residual that describe the variabilities present in LME models, marginal residuals, $\hat{\xi}$, which predict marginal errors, conditional residuals, $\hat{\epsilon}$, which predict conditional errors, and the BLUP, $\mathbf{Z}\hat{\mathbf{b}}$, that predicts random effects. Each type of residual is useful to evaluate some assumption of the model.

The definitions of both marginal residuals (r_m) and conditional residuals (r_c) follow from the definitions of marginal and conditional means in the LME model $E[Y] = X\beta$ and $E[Y|u] = X\beta + Zu$, respectively.

A marginal residual is the difference between the observed data and the estimated marginal mean. A conditional residual is the difference between the observed data and the predicted value of the observation. In a model without random effects, both sets of residuals coincide.

The conditional (subject-specific) and marginal (population-averaged) formulations in the linear mixed model enable you to consider conditional residuals that use the estimated BLUPs of the random effects, and marginal residuals which are deviations from the overall mean. Residuals using the BLUPs are useful to diagnose whether the random effects components in the model are specified correctly, marginal residuals are useful to diagnose the fixed-effects components.

The raw residuals r_{mi} and r_{ci} are usually not well suited for these purposes.

According to Hilton & Minton (1995), a residual is considered pure for a specific type of error if it depends only on the fixed components and on the error that it is supposed to predict. Residuals that depend on other types of error are known as ‘confounded errors’.

The marginal raw residual is

$$r_{Mar} = y - X\hat{\beta}.$$

Conditional residuals include contributions from both fixed and random effects, whereas marginal residuals include contribution from only fixed effects.

Marginal residuals are good for checking fixed effects.

Conditional residuals include contributions from both fixed and random effects, whereas marginal residuals include contribution from only fixed effects. Marginal residuals should have mean of zero, but may show grouping structure. Also they may not be homoscedastic.

Summary of Paper

Standard residual and influence diagnostics for linear models can be extended to LME models. The dependence of the fixed effects solutions on the covariance parameters has important ramifications on the perturbation analysis. Calculating the studentized residual and influence statistics whereas each software procedure can calculate both conditional and marginal raw residuals, only SAS Proc Mixed is currently the only program that provide studentized residuals Which are preferred for model diagnostics. The conditional raw residuals are not well suited to detecting outliers as are the studentized conditional residuals (?).

LME are flexible tools for the analysis of clustered and repeated measurement data. LME extend the capabilities of standard linear models by allowing unbalanced and missing data, as long as the missing data are MAR. Structured covariance matrices for both the random effects G and the residuals R.

2.2 Influence Diagnostics

Influential points have a large influence on the fit of the model. Influential points are a set of one or more observations whose removal would cause a different conclusion in the analysis, e.g. substantially changes the estimate of the regression coefficients. ? remarks that influence diagnostics play an important role in the interpretation of results, because influential data can negatively influence the statistical model and generalizability of the model. Influence diagnostics are formal techniques that allow the identification observation that heavily influence estimates of parameters.

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Influence can be thought of as consequence of leverage and outlierness. Outliers are the most noteworthy data points in an analysis, and an objective of influence analysis is how influential they are, and the manner in which they are influential. They can point to a model breakdown and lead to development of a better model.

LME model are a useful framework for fitting a wide range of models. However, they are known to be sensitive to outliers. Specifically likelihood based estimation techniques, such as ML and REML, are sensitive

to outliers. ? advises that identification of outliers is necessary before conclusions may be drawn from the fitted model. The leverage of an observation is a further consideration.

2.2.1 Deletion Diagnostics

Deletion diagnostics provide a means of assessing the influence of an observation (or groups of observations) on parameters inferences for a fitted model. For classical linear models, ? greatly expands the study of residuals and influence measures. The key to making deletion diagnostics useable is the development of efficient computational formulas, allowing one to obtain the case deletion diagnostics by making use of basic building blocks, computed only once for the full model. Cook's key observation was the effects of deleting each observation in turn could be calculated with little additional computation. Cook proposed a measure that combines the information of leverage and residual of the observation, now known simply as the Cook's Distance, $D_{(i)}$, which can be calculated without fitting a new regression coefficient each time an observation is deleted. Consequently deletion diagnostics have become an integral part of assessing linear models.

It must be pointed out that the effect on the precision of estimates is separate from the effect on the point estimates. Data points that have a small Cook's distance, for example, can still greatly affect hypothesis tests and confidence intervals, if their influence on the precision of the estimates is large.

? notes the case deletion diagnostics techniques have not been applied to linear mixed effects models and seeks to develop methodologies in that respect. ? developed their global influences for the deletion of single observations in two steps: a one-step estimate for the REML (or ML) estimate of the variance components, and an ordinary case-deletion diagnostic for a weighted regression problem (conditional on the estimated covariance matrix) for fixed effects.

The computation of case deletion diagnostics in the classical model is made simple by the fact that estimates of β and σ^2 , which exclude the i th observation, can be computed without re-fitting the model. Such update formulas are available in the mixed model only if you assume that the covariance parameters are not affected by the removal of the observation in question. This is rarely a reasonable assumption, and undermines the use of many proposed procedures for method comparison.